dask Documentation

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Getting Started

Dask is a flexible library for parallel computing in Python.

Dask is composed of two parts:

1. **Dynamic task scheduling** optimized for computation. This is similar to *Airflow, Luigi, Celery, or Make*, but optimized for interactive computational workloads.
2. **"Big Data" collections** like parallel arrays, dataframes, and lists that extend common interfaces like *NumPy, Pandas, or Python iterators* to larger-than-memory or distributed environments. These parallel collections run on top of dynamic task schedulers.

Dask emphasizes the following virtues:

- **Familiar**: Provides parallelized NumPy array and Pandas DataFrame objects
- **Flexible**: Provides a task scheduling interface for more custom workloads and integration with other projects.
- **Native**: Enables distributed computing in pure Python with access to the PyData stack.
- **Fast**: Operates with low overhead, low latency, and minimal serialization necessary for fast numerical algorithms
- **Scales up**: Runs resiliently on clusters with 1000s of cores
- **Scales down**: Trivial to set up and run on a laptop in a single process
- **Responsive**: Designed with interactive computing in mind, it provides rapid feedback and diagnostics to aid humans

See the dask.distributed documentation (separate website) for more technical information on Dask's distributed scheduler.

CHAPTER 1

Familiar user interface

Dask DataFrame mimics Pandas - *documentation*

```
import pandas as pd
df = pd.read_csv('2015-01-01.csv')
df.groupby(df.user_id).value.mean()
```

```
import dask.dataframe as dd
df = dd.read_csv('2015-*-*.csv')
df.groupby(df.user_id).value.mean().compute()
```

Dask Array mimics NumPy - *documentation*

```
import numpy as np
f = h5py.File('myfile.hdf5')
x = np.array(f['/small-data'])

x - x.mean(axis=1)
```

```
import dask.array as da
f = h5py.File('myfile.hdf5')
x = da.from_array(f['/big-data'],
                  chunks=(1000, 1000))
x - x.mean(axis=1).compute()
```

Dask Bag mimics iterators, Toolz, and PySpark - *documentation*

```
import dask.bag as db
b = db.read_text('2015-*-*.json.gz').map(json.loads)
b.pluck('name').frequencies().topk(10, lambda pair: pair[1]).compute()
```

Dask Delayed mimics for loops and wraps custom code - *documentation*

```
from dask import delayed
L = []
for fn in filenames:                  # Use for loops to build up computation
    data = delayed(load)(fn)          # Delay execution of function
    L.append(delayed(process)(data))  # Build connections between variables

result = delayed(summarize)(L)
result.compute()
```

The **concurrent.futures** interface provides general submission of custom tasks: - *documentation*

```
from dask.distributed import Client
client = Client('scheduler:port')

futures = []
for fn in filenames:
    future = client.submit(load, fn)
    futures.append(future)

summary = client.submit(summarize, futures)
summary.result()
```

CHAPTER 2

Scales from laptops to clusters

Dask is convenient on a laptop. It *installs* trivially with `conda` or `pip` and extends the size of convenient datasets from “fits in memory” to “fits on disk”.

Dask can scale to a cluster of 100s of machines. It is resilient, elastic, data local, and low latency. For more information, see the documentation about the distributed scheduler.

This ease of transition between single-machine to moderate cluster enables users to both start simple and grow when necessary.

CHAPTER 3

Complex Algorithms

Dask represents parallel computations with *task graphs*. These directed acyclic graphs may have arbitrary structure, which enables both developers and users the freedom to build sophisticated algorithms and to handle messy situations not easily managed by the `map/filter/groupby` paradigm common in most data engineering frameworks.

We originally needed this complexity to build complex algorithms for n-dimensional arrays but have found it to be equally valuable when dealing with messy situations in everyday problems.

3.1 Install Dask

You can install dask with `conda`, with `pip`, or by installing from source.

3.1.1 Conda

Dask is installed by default in Anaconda. You can update Dask using the conda command:

```
conda install dask
```

This installs Dask and **all** common dependencies, including Pandas and NumPy. Dask packages are maintained both on the default channel and on conda-forge. Optionally, you can obtain a minimal Dask installation using the following command:

```
conda install dask-core
```

This will install a minimal set of dependencies required to run Dask similar to (but not exactly the same as) `pip install dask` below.

3.1.2 Pip

You can install everything required for most common uses of Dask (arrays, dataframes, . . .) This installs both Dask and dependencies like NumPy, Pandas, and so on that are necessary for different workloads. This is often the right choice for Dask users:

```
pip install "dask[complete]"    # Install everything
```

You can also install only the Dask library. Modules like `dask.array`, `dask.dataframe`, `dask.delayed`, or `dask.distributed` won't work until you also install NumPy, Pandas, Toolz, or Tornado, respectively. This is common for downstream library maintainers:

```
pip install dask                # Install only core parts of dask
```

We also maintain other dependency sets for different subsets of functionality:

```
pip install "dask[array]"       # Install requirements for dask array
pip install "dask[bag]"         # Install requirements for dask bag
pip install "dask[dataframe]"   # Install requirements for dask dataframe
pip install "dask[delayed]"     # Install requirements for dask delayed
pip install "dask[distributed]" # Install requirements for distributed dask
```

We have these options so that users of the lightweight core Dask scheduler aren't required to download the more exotic dependencies of the collections (Numpy, Pandas, Tornado, etc.).

3.1.3 Install from Source

To install Dask from source, clone the repository from github:

```
git clone https://github.com/dask/dask.git
cd dask
pip install .
```

You can also install all dependencies as well:

```
pip install ".[complete]"
```

You can view the list of all dependencies within the `extras_require` field of `setup.py`.

Or do a developer install by using the `-e` flag:

```
pip install -e .
```

3.1.4 Anaconda

Dask is included by default in the Anaconda distribution.

3.1.5 Optional dependencies

Specific functionality in Dask may require additional optional dependencies. For example, reading from Amazon S3 requires `s3fs`. These optional dependencies and their minimum supported versions are listed below.

Dependency	Version	Description
bokeh	>=1.0.0	Visualizing dask diagnostics
cloudpickle	>=0.2.1	Pickling support for Python objects
cityhash		Faster hashing of arrays
distributed	>=2.0	Distributed computing in Python
fastparquet		Storing and reading data from parquet files
fsspec	>=0.5.1	Used for local, cluster and remote data IO
gcsfs		File-system interface to Google Cloud Storage
murmurhash		Faster hashing of arrays
numpy	>=1.13.0	Required for dask.array
pandas	>=0.21.0	Required for dask.dataframe
partd	>=0.3.10	Concurrent appendable key-value storage
psutil		Enables a more accurate CPU count
pyarrow	>=0.9.0	Python library for Apache Arrow
s3fs		Reading from Amazon S3
sqlalchemy		Writing and reading from SQL databases
toolz	>=0.7.3	Utility functions for iterators, functions, and dictionaries
xxhash		Faster hashing of arrays

3.1.6 Test

Test Dask with `py.test`:

```
cd dask
py.test dask
```

Please be aware that installing Dask naively may not install all requirements by default. Please read the `pip` section above which discusses requirements. You may choose to install the `dask[complete]` version which includes all dependencies for all collections. Alternatively, you may choose to test only certain submodules depending on the libraries within your environment. For example, to test only Dask core and Dask array we would run tests as follows:

```
py.test dask/tests dask/array/tests
```

3.2 Setup

This page describes various ways to set up Dask on different hardware, either locally on your own machine or on a distributed cluster. If you are just getting started, then this page is unnecessary. Dask does not require any setup if you only want to use it on a single computer.

Dask has two families of task schedulers:

1. **Single machine scheduler**: This scheduler provides basic features on a local process or thread pool. This scheduler was made first and is the default. It is simple and cheap to use. It can only be used on a single machine and does not scale.
2. **Distributed scheduler**: This scheduler is more sophisticated. It offers more features, but also requires a bit more effort to set up. It can run locally or distributed across a cluster.

If you import Dask, set up a computation, and then call `compute`, then you will use the single-machine scheduler by default. To use the `dask.distributed` scheduler you must set up a `Client`

```
import dask.dataframe as dd
df = dd.read_csv(...)
df.x.sum().compute()  # This uses the single-machine scheduler by default
```

```
from dask.distributed import Client
client = Client(...)  # Connect to distributed cluster and override default
df.x.sum().compute()  # This now runs on the distributed system
```

Note that the newer `dask.distributed` scheduler is often preferable, even on single workstations. It contains many diagnostics and features not found in the older single-machine scheduler. The following pages explain in more detail how to set up Dask on a variety of local and distributed hardware.

- **Single Machine:**
  - *Default Scheduler*: The no-setup default. Uses local threads or processes for larger-than-memory processing
  - *dask.distributed*: The sophistication of the newer system on a single machine. This provides more advanced features while still requiring almost no setup.
- **Distributed computing:**
  - *Manual Setup*: The command line interface to set up `dask-scheduler` and `dask-worker` processes. Useful for IT or anyone building a deployment solution.
  - *SSH*: Use SSH to set up Dask across an un-managed cluster.
  - *High Performance Computers*: How to run Dask on traditional HPC environments using tools like MPI, or job schedulers like SLURM, SGE, TORQUE, LSF, and so on.
  - *Kubernetes*: Deploy Dask with the popular Kubernetes resource manager using either Helm or a native deployment.
  - YARN / Hadoop: Deploy Dask on YARN clusters, such as are found in traditional Hadoop installations.
  - *Python API (advanced)*: Create `Scheduler` and `Worker` objects from Python as part of a distributed Tornado TCP application. This page is useful for those building custom frameworks.
  - *Docker* containers are available and may be useful in some of the solutions above.
  - *Cloud* for current recommendations on how to deploy Dask and Jupyter on common cloud providers like Amazon, Google, or Microsoft Azure.

3.2.1 Single-Machine Scheduler

The default Dask scheduler provides parallelism on a single machine by using either threads or processes. It is the default choice used by Dask because it requires no setup. You don't need to make any choices or set anything up to use this scheduler. However, you do have a choice between threads and processes:

1. **Threads**: Use multiple threads in the same process. This option is good for numeric code that releases the GIL (like NumPy, Pandas, Scikit-Learn, Numba, . . .) because data is free to share. This is the default scheduler for `dask.array`, `dask.dataframe`, and `dask.delayed`
2. **Processes**: Send data to separate processes for processing. This option is good when operating on pure Python objects like strings or JSON-like dictionary data that holds onto the GIL, but not very good when operating on numeric data like Pandas DataFrames or NumPy arrays. Using processes avoids GIL issues, but can also result in a lot of inter-process communication, which can be slow. This is the default scheduler for `dask.bag`, and it is sometimes useful with `dask.dataframe`

Note that the `dask.distributed` scheduler is often a better choice when working with GIL-bound code. See *dask.distributed on a single machine*

3. **Single-threaded**: Execute computations in a single thread. This option provides no parallelism, but is useful when debugging or profiling. Turning your parallel execution into a sequential one can be a convenient option in many situations where you want to better understand what is going on

Selecting Threads, Processes, or Single Threaded

You can select between these options by specifying one of the following three values to the `scheduler=` keyword:

- `"threads"`: Uses a ThreadPool in the local process
- `"processes"`: Uses a ProcessPool to spread work between processes
- `"single-threaded"`: Uses a for-loop in the current thread

You can specify these options in any of the following ways:

- When calling `.compute()`

```
x.compute(scheduler='threads')
```

- With a context manager

```
with dask.config.set(scheduler='threads'):
    x.compute()
    y.compute()
```

- As a global setting

```
dask.config.set(scheduler='threads')
```

Use the Distributed Scheduler

Dask's newer distributed scheduler also works well on a single machine and offers more features and diagnostics. See *this page* for more information.

3.2.2 Single Machine: dask.distributed

The `dask.distributed` scheduler works well on a single machine. It is sometimes preferred over the default scheduler for the following reasons:

1. It provides access to asynchronous API, notably *Futures*
2. It provides a diagnostic dashboard that can provide valuable insight on performance and progress
3. It handles data locality with more sophistication, and so can be more efficient than the multiprocessing scheduler on workloads that require multiple processes

You can create a `dask.distributed` scheduler by importing and creating a `Client` with no arguments. This overrides whatever default was previously set.

```
from dask.distributed import Client
client = Client()
```

You can navigate to http://localhost:8787/status to see the diagnostic dashboard if you have Bokeh installed.

Client

You can trivially set up a local cluster on your machine by instantiating a Dask Client with no arguments

```
from dask.distributed import Client
client = Client()
```

This sets up a scheduler in your local process and several processes running single-threaded Workers.

If you want to run workers in your same process, you can pass the `processes=False` keyword argument.

```
client = Client(processes=False)
```

This is sometimes preferable if you want to avoid inter-worker communication and your computations release the GIL. This is common when primarily using NumPy or Dask Array.

LocalCluster

The `Client()` call described above is shorthand for creating a LocalCluster and then passing that to your client.

```
from dask.distributed import Client, LocalCluster
cluster = LocalCluster()
client = Client(cluster)
```

This is equivalent, but somewhat more explicit. You may want to look at the keyword arguments available on `LocalCluster` to understand the options available to you on handling the mixture of threads and processes, like specifying explicit ports, and so on.

class `distributed.deploy.local.`**LocalCluster**(*n_workers=None, threads_per_worker=None, processes=True, loop=None, start=None, host=None, ip=None, scheduler_port=0, silence_logs=30, dashboard_address=':8787', worker_dashboard_address=None, diagnostics_port=None, services=None, worker_services=None, service_kwargs=None, asynchronous=False, security=None, protocol=None, blocked_handlers=None, interface=None, worker_class=None, **worker_kwargs*)

Create local Scheduler and Workers

This creates a "cluster" of a scheduler and workers running on the local machine.

Parameters

n_workers: int Number of workers to start

processes: bool Whether to use processes (True) or threads (False). Defaults to True

threads_per_worker: int Number of threads per each worker

scheduler_port: int Port of the scheduler. 8786 by default, use 0 to choose a random port

silence_logs: logging level Level of logs to print out to stdout. `logging.WARN` by default. Use a falsey value like False or None for no change.

host: string Host address on which the scheduler will listen, defaults to only localhost

ip: string Deprecated. See `host` above.

dashboard_address: str Address on which to listen for the Bokeh diagnostics server like 'localhost:8787' or '0.0.0.0:8787'. Defaults to ':8787'. Set to `None` to disable the dashboard. Use ':0' for a random port.

diagnostics_port: int Deprecated. See dashboard_address.

asynchronous: bool (False by default) Set to True if using this cluster within async/await functions or within Tornado gen.coroutines. This should remain False for normal use.

worker_kwargs: dict Extra worker arguments, will be passed to the Worker constructor.

blocked_handlers: List[str] A list of strings specifying a blacklist of handlers to disallow on the Scheduler, like `['feed', 'run_function']`

service_kwargs: Dict[str, Dict] Extra keywords to hand to the running services

security [Security]

protocol: str (optional) Protocol to use like `tcp://`, `tls://`, `inproc://` This defaults to sensible choice given other keyword arguments like `processes` and `security`

interface: str (optional) Network interface to use. Defaults to lo/localhost

worker_class: Worker Worker class used to instantiate workers from.

Examples

```
>>> cluster = LocalCluster()  # Create a local cluster with as many workers as␣
↪cores  # doctest: +SKIP
>>> cluster  # doctest: +SKIP
LocalCluster("127.0.0.1:8786", workers=8, threads=8)
```

```
>>> c = Client(cluster)  # connect to local cluster  # doctest: +SKIP
```

Scale the cluster to three workers

```
>>> cluster.scale(3)  # doctest: +SKIP
```

Pass extra keyword arguments to Bokeh

```
>>> LocalCluster(service_kwargs={'dashboard': {'prefix': '/foo'}})  # doctest:␣
↪+SKIP
```

3.2.3 Command Line

This is the most fundamental way to deploy Dask on multiple machines. In production environments, this process is often automated by some other resource manager. Hence, it is rare that people need to follow these instructions explicitly. Instead, these instructions are useful for IT professionals who may want to set up automated services to deploy Dask within their institution.

A `dask.distributed` network consists of one `dask-scheduler` process and several `dask-worker` processes that connect to that scheduler. These are normal Python processes that can be executed from the command line. We launch the `dask-scheduler` executable in one process and the `dask-worker` executable in several processes, possibly on different machines.

To accomplish this, launch `dask-scheduler` on one node:

```
$ dask-scheduler
Scheduler at:   tcp://192.0.0.100:8786
```

Then, launch `dask-worker` on the rest of the nodes, providing the address to the node that hosts `dask-scheduler`:

```
$ dask-worker tcp://192.0.0.100:8786
Start worker at:  tcp://192.0.0.1:12345
Registered to:    tcp://192.0.0.100:8786

$ dask-worker tcp://192.0.0.100:8786
Start worker at:  tcp://192.0.0.2:40483
Registered to:    tcp://192.0.0.100:8786

$ dask-worker tcp://192.0.0.100:8786
Start worker at:  tcp://192.0.0.3:27372
Registered to:    tcp://192.0.0.100:8786
```

The workers connect to the scheduler, which then sets up a long-running network connection back to the worker. The workers will learn the location of other workers from the scheduler.

Handling Ports

The scheduler and workers both need to accept TCP connections on an open port. By default, the scheduler binds to port `8786` and the worker binds to a random open port. If you are behind a firewall then you may have to open particular ports or tell Dask to listen on particular ports with the `--port` and `--worker-port` keywords.:

```
dask-scheduler --port 8000
dask-worker --dashboard-address 8000 --nanny-port 8001
```

Nanny Processes

Dask workers are run within a nanny process that monitors the worker process and restarts it if necessary.

Diagnostic Web Servers

Additionally, Dask schedulers and workers host interactive diagnostic web servers using Bokeh. These are optional, but generally useful to users. The diagnostic server on the scheduler is particularly valuable, and is served on port `8787` by default (configurable with the `--dashboard-address` keyword).

For more information about relevant ports, please take a look at the available *command line options*.

Automated Tools

There are various mechanisms to deploy these executables on a cluster, ranging from manually SSH-ing into all of the machines to more automated systems like SGE/SLURM/Torque or Yarn/Mesos. Additionally, cluster SSH tools exist to send the same commands to many machines. We recommend searching online for “cluster ssh” or “cssh”.

CLI Options

Note: The command line documentation here may differ depending on your installed version. We recommend referring to the output of `dask-scheduler --help` and `dask-worker --help`.

dask-scheduler

```
dask-scheduler [OPTIONS] [PRELOAD_ARGV]...
```

Options

--host `<host>`
URI, IP or hostname of this server

--port `<port>`
Serving port

--interface `<interface>`
Preferred network interface like 'eth0' or 'ib0'

--protocol `<protocol>`
Protocol like tcp, tls, or ucx

--tls-ca-file `<tls_ca_file>`
CA cert(s) file for TLS (in PEM format)

--tls-cert `<tls_cert>`
certificate file for TLS (in PEM format)

--tls-key `<tls_key>`
private key file for TLS (in PEM format)

--bokeh-port `<bokeh_port>`
Deprecated. See –dashboard-address

--dashboard-address `<dashboard_address>`
Address on which to listen for diagnostics dashboard [default: :8787]

--dashboard, --no-dashboard
Launch the Dashboard [default: –dashboard]

--bokeh, --no-bokeh
Deprecated. See –dashboard/–no-dashboard.

--show, --no-show
Show web UI [default: –show]

--dashboard-prefix `<dashboard_prefix>`
Prefix for the dashboard app

--use-xheaders `<use_xheaders>`
User xheaders in dashboard app for ssl termination in header [default: False]

--pid-file `<pid_file>`
File to write the process PID

--scheduler-file `<scheduler_file>`
File to write connection information. This may be a good way to share connection information if your cluster is on a shared network file system.

--local-directory <local_directory>
Directory to place scheduler files

--preload <preload>
Module that should be loaded by the scheduler process like "foo.bar" or "/path/to/foo.py".

--idle-timeout <idle_timeout>
Time of inactivity after which to kill the scheduler

--version
Show the version and exit.

Arguments

PRELOAD_ARGV
Optional argument(s)

dask-worker

```
dask-worker [OPTIONS] [SCHEDULER] [PRELOAD_ARGV]...
```

Options

--tls-ca-file <tls_ca_file>
CA cert(s) file for TLS (in PEM format)

--tls-cert <tls_cert>
certificate file for TLS (in PEM format)

--tls-key <tls_key>
private key file for TLS (in PEM format)

--worker-port <worker_port>
Serving computation port, defaults to random

--nanny-port <nanny_port>
Serving nanny port, defaults to random

--bokeh-port <bokeh_port>
Deprecated. See –dashboard-address

--dashboard-address <dashboard_address>
Address on which to listen for diagnostics dashboard

--dashboard, --no-dashboard
Launch the Dashboard [default: –dashboard]

--bokeh, --no-bokeh
Deprecated. See –dashboard/–no-dashboard.

--listen-address <listen_address>
The address to which the worker binds. Example: tcp://0.0.0.0:9000

--contact-address <contact_address>
The address the worker advertises to the scheduler for communication with it and other workers. Example: tcp://127.0.0.1:9000

--host `<host>`
Serving host. Should be an ip address that is visible to the scheduler and other workers. See –listen-address and –contact-address if you need different listen and contact addresses. See –interface.

--interface `<interface>`
Network interface like 'eth0' or 'ib0'

--protocol `<protocol>`
Protocol like tcp, tls, or ucx

--nthreads `<nthreads>`
Number of threads per process.

--nprocs `<nprocs>`
Number of worker processes to launch. [default: 1]

--name `<name>`
A unique name for this worker like 'worker-1'. If used with –nprocs then the process number will be appended like name-0, name-1, name-2, …

--memory-limit `<memory_limit>`
Bytes of memory per process that the worker can use. This can be an integer (bytes), float (fraction of total system memory), string (like 5GB or 5000M), 'auto', or zero for no memory management [default: auto]

--reconnect, --no-reconnect
Reconnect to scheduler if disconnected [default: –reconnect]

--nanny, --no-nanny
Start workers in nanny process for management [default: –nanny]

--pid-file `<pid_file>`
File to write the process PID

--local-directory `<local_directory>`
Directory to place worker files

--resources `<resources>`
Resources for task constraints like "GPU=2 MEM=10e9". Resources are applied separately to each worker process (only relevant when starting multiple worker processes with '–nprocs').

--scheduler-file `<scheduler_file>`
Filename to JSON encoded scheduler information. Use with dask-scheduler –scheduler-file

--death-timeout `<death_timeout>`
Seconds to wait for a scheduler before closing

--dashboard-prefix `<dashboard_prefix>`
Prefix for the dashboard

--lifetime `<lifetime>`
If provided, shut down the worker after this duration.

--lifetime-stagger `<lifetime_stagger>`
Random amount by which to stagger lifetime values [default: 0 seconds]

--lifetime-restart, --no-lifetime-restart
Whether or not to restart the worker after the lifetime lapses. This assumes that you are using the –lifetime and –nanny keywords [default: False]

--preload `<preload>`
Module that should be loaded by each worker process like "foo.bar" or "/path/to/foo.py"

--version
Show the version and exit.

Arguments

SCHEDULER
Optional argument

PRELOAD_ARGV
Optional argument(s)

3.2.4 SSH

It is easy to set up Dask on informally managed networks of machines using SSH. This can be done manually using SSH and the Dask *command line interface*, or automatically using either the `SSHCluster` Python command or the `dask-ssh` command line tool. This document describes both of these options.

Python Interface

`distributed.deploy.ssh.`**`SSHCluster`**(*hosts: List[str] = None*, *connect_options: dict = {}*, *worker_options: dict = {}*, *scheduler_options: dict = {}*, *worker_module: str = 'distributed.cli.dask_worker'*, ***kwargs*)

Deploy a Dask cluster using SSH

The SSHCluster function deploys a Dask Scheduler and Workers for you on a set of machine addresses that you provide. The first address will be used for the scheduler while the rest will be used for the workers (feel free to repeat the first hostname if you want to have the scheudler and worker co-habitate one machine.)

You may configure the scheduler and workers by passing `scheduler_options` and `worker_options` dictionary keywords. See the `dask.distributed.Scheduler` and `dask.distributed.Worker` classes for details on the available options, but the defaults should work in most situations.

You may configure your use of SSH itself using the `connect_options` keyword, which passes values to the `asyncssh.connect` function. For more information on these see the documentation for the `asyncssh` library https://asyncssh.readthedocs.io .

Parameters

hosts: List[str] List of hostnames or addresses on which to launch our cluster The first will be used for the scheduler and the rest for workers

connect_options: Keywords to pass through to asyncssh.connect known_hosts: List[str] or None

The list of keys which will be used to validate the server host key presented during the SSH handshake. If this is not specified, the keys will be looked up in the file .ssh/known_hosts. If this is explicitly set to None, server host key validation will be disabled.

worker_options: Keywords to pass on to dask-worker

scheduler_options: Keywords to pass on to dask-scheduler

worker_module: Python module to call to start the worker

See also:

dask.distributed.Scheduler, dask.distributed.Worker, asyncssh.connect

Examples

```
>>> from dask.distributed import Client, SSHCluster
>>> cluster = SSHCluster(
...     ["localhost", "localhost", "localhost", "localhost"],
...     connect_options={"known_hosts": None},
...     worker_options={"nthreads": 2},
...     scheduler_options={"port": 0, "dashboard_address": ":8797"}
... )
>>> client = Client(cluster)
```

An example using a different worker module, in particular the `dask-cuda-worker` command from the `dask-cuda` project.

```
>>> from dask.distributed import Client, SSHCluster
>>> cluster = SSHCluster(
...     ["localhost", "hostwithgpus", "anothergpuhost"],
...     connect_options={"known_hosts": None},
...     scheduler_options={"port": 0, "dashboard_address": ":8797"},
...     worker_module='dask_cuda.dask_cuda_worker')
>>> client = Client(cluster)
```

Command Line

The convenience script `dask-ssh` opens several SSH connections to your target computers and initializes the network accordingly. You can give it a list of hostnames or IP addresses:

```
$ dask-ssh 192.168.0.1 192.168.0.2 192.168.0.3 192.168.0.4
```

Or you can use normal UNIX grouping:

```
$ dask-ssh 192.168.0.{1,2,3,4}
```

Or you can specify a hostfile that includes a list of hosts:

```
$ cat hostfile.txt
192.168.0.1
192.168.0.2
192.168.0.3
192.168.0.4

$ dask-ssh --hostfile hostfile.txt
```

The `dask-ssh` utility depends on the `paramiko`:

```
pip install paramiko
```

Note: The command line documentation here may differ depending on your installed version. We recommend referring to the output of `dask-ssh --help`.

dask-ssh

Launch a distributed cluster over SSH. A 'dask-scheduler' process will run on the first host specified in [HOSTNAMES] or in the hostfile (unless –scheduler is specified explicitly). One or more 'dask-worker' processes will be run each host in [HOSTNAMES] or in the hostfile. Use command line flags to adjust how many dask-worker process are run on each host (–nprocs) and how many cpus are used by each dask-worker process (–nthreads).

```
dask-ssh [OPTIONS] [HOSTNAMES]...
```

Options

--scheduler <scheduler>
Specify scheduler node. Defaults to first address.

--scheduler-port <scheduler_port>
Specify scheduler port number. [default: 8786]

--nthreads <nthreads>
Number of threads per worker process. Defaults to number of cores divided by the number of processes per host.

--nprocs <nprocs>
Number of worker processes per host. [default: 1]

--hostfile <hostfile>
Textfile with hostnames/IP addresses

--ssh-username <ssh_username>
Username to use when establishing SSH connections.

--ssh-port <ssh_port>
Port to use for SSH connections. [default: 22]

--ssh-private-key <ssh_private_key>
Private key file to use for SSH connections.

--nohost
Do not pass the hostname to the worker.

--log-directory <log_directory>
Directory to use on all cluster nodes for the output of dask-scheduler and dask-worker commands.

--remote-python <remote_python>
Path to Python on remote nodes.

--memory-limit <memory_limit>
Bytes of memory that the worker can use. This can be an integer (bytes), float (fraction of total system memory), string (like 5GB or 5000M), 'auto', or zero for no memory management [default: auto]

--worker-port <worker_port>
Serving computation port, defaults to random

--nanny-port <nanny_port>
Serving nanny port, defaults to random

--remote-dask-worker <remote_dask_worker>
Worker to run. [default: distributed.cli.dask_worker]

--version
Show the version and exit.

Arguments

HOSTNAMES
Optional argument(s)

3.2.5 High Performance Computers

Relevant Machines

This page includes instructions and guidelines when deploying Dask on high performance supercomputers commonly found in scientific and industry research labs. These systems commonly have the following attributes:

1. Some mechanism to launch MPI applications or use job schedulers like SLURM, SGE, TORQUE, LSF, DRMAA, PBS, or others
2. A shared network file system visible to all machines in the cluster
3. A high performance network interconnect, such as Infiniband
4. Little or no node-local storage

Where to start

Most of this page documents various ways and best practices to use Dask on an HPC cluster. This is technical and aimed both at users with some experience deploying Dask and also system administrators.

The preferred and simplest way to run Dask on HPC systems today both for new, experienced users or administrator is to use dask-jobqueue.

However, dask-jobqueue is slightly oriented toward interactive analysis usage, and it might be better to use tools like dask-mpi in some routine batch production workloads.

Dask-jobqueue and Dask-drmaa

The following projects provide easy high-level access to Dask using resource managers that are commonly deployed on HPC systems:

1. dask-jobqueue for use with PBS, SLURM, LSF, SGE and other resource managers
2. dask-drmaa for use with any DRMAA compliant resource manager

They provide interfaces that look like the following:

```python
from dask_jobqueue import PBSCluster

cluster = PBSCluster(cores=36,
                     memory="100GB",
                     project='P48500028',
                     queue='premium',
                     interface='ib0',
                     walltime='02:00:00')

cluster.scale(100)  # Start 100 workers in 100 jobs that match the description above

from dask.distributed import Client
client = Client(cluster)    # Connect to that cluster
```

Dask-jobqueue provides a lot of possibilities like adaptive dynamic scaling of workers, we recommend reading the dask-jobqueue documentation first to get a basic system running and then returning to this documentation for fine-tuning if necessary.

Using MPI

Note: This section may not be necessary if you use a tool like dask-jobqueue.

You can launch a Dask network using `mpirun` or `mpiexec` and the `dask-mpi` command line executable.

```
mpirun --np 4 dask-mpi --scheduler-file /home/$USER/scheduler.json
```

```
from dask.distributed import Client
client = Client(scheduler_file='/path/to/scheduler.json')
```

This depends on the mpi4py library. It only uses MPI to start the Dask cluster and not for inter-node communication. MPI implementations differ: the use of `mpirun --np 4` is specific to the `mpich` or `open-mpi` MPI implementation installed through conda and linked to mpi4py.

```
conda install mpi4py
```

It is not necessary to use exactly this implementation, but you may want to verify that your `mpi4py` Python library is linked against the proper `mpirun/mpiexec` executable and that the flags used (like `--np 4`) are correct for your system. The system administrator of your cluster should be very familiar with these concerns and able to help.

In some setups, MPI processes are not allowed to fork other processes. In this case, we recommend using `--no-nanny` option in order to prevent dask from using an additional nanny process to manage workers.

Run `dask-mpi --help` to see more options for the `dask-mpi` command.

Using a Shared Network File System and a Job Scheduler

Note: This section is not necessary if you use a tool like dask-jobqueue.

Some clusters benefit from a shared File System (NFS, GPFS, Lustre or alike), and can use this to communicate the scheduler location to the workers:

```
dask-scheduler --scheduler-file /path/to/scheduler.json  # writes address to file

dask-worker --scheduler-file /path/to/scheduler.json  # reads file for address
dask-worker --scheduler-file /path/to/scheduler.json  # reads file for address
```

```
>>> client = Client(scheduler_file='/path/to/scheduler.json')
```

This can be particularly useful when deploying `dask-scheduler` and `dask-worker` processes using a job scheduler like SGE/SLURM/Torque/etc. Here is an example using SGE's `qsub` command:

```
# Start a dask-scheduler somewhere and write the connection information to a file
qsub -b y /path/to/dask-scheduler --scheduler-file /home/$USER/scheduler.json

# Start 100 dask-worker processes in an array job pointing to the same file
qsub -b y -t 1-100 /path/to/dask-worker --scheduler-file /home/$USER/scheduler.json
```

Note, the `--scheduler-file` option is *only* valuable if your scheduler and workers share a network file system.

High Performance Network

Many HPC systems have both standard Ethernet networks as well as high-performance networks capable of increased bandwidth. You can instruct Dask to use the high-performance network interface by using the `--interface` keyword with the `dask-worker`, `dask-scheduler`, or `dask-mpi` commands or the `interface=` keyword with the dask-jobqueue `Cluster` objects:

```
mpirun --np 4 dask-mpi --scheduler-file /home/$USER/scheduler.json --interface ib0
```

In the code example above, we have assumed that your cluster has an Infiniband network interface called `ib0`. You can check this by asking your system administrator or by inspecting the output of `ifconfig`

```
$ ifconfig
lo          Link encap:Local Loopback                       # Localhost
                        inet addr:127.0.0.1  Mask:255.0.0.0
                        inet6 addr: ::1/128 Scope:Host
eth0        Link encap:Ethernet  HWaddr XX:XX:XX:XX:XX:XX   # Ethernet
                        inet addr:192.168.0.101
                        ...
ib0         Link encap:Infiniband                           # Fast InfiniBand
                        inet addr:172.42.0.101
```

https://stackoverflow.com/questions/43881157/how-do-i-use-an-infiniband-network-with-dask

Local Storage

Users often exceed memory limits available to a specific Dask deployment. In normal operation, Dask spills excess data to disk, often to the default temporary directory.

However, in HPC systems this default temporary directory may point to an network file system (NFS) mount which can cause problems as Dask tries to read and write many small files. *Beware, reading and writing many tiny files from many distributed processes is a good way to shut down a national supercomputer.*

If available, it's good practice to point Dask workers to local storage, or hard drives that are physically on each node. Your IT administrators will be able to point you to these locations. You can do this with the `--local-directory` or `local_directory=` keyword in the `dask-worker` command:

```
dask-mpi ... --local-directory /path/to/local/storage
```

or any of the other Dask Setup utilities, or by specifying the following *configuration value*:

```
temporary-directory: /path/to/local/storage
```

However, not all HPC systems have local storage. If this is the case then you may want to turn off Dask's ability to spill to disk altogether. See this page for more information on Dask's memory policies. Consider changing the following values in your `~/.config/dask/distributed.yaml` file to disable spilling data to disk:

```
distributed:
  worker:
    memory:
      target: false  # don't spill to disk
      spill: false  # don't spill to disk
      pause: 0.80  # pause execution at 80% memory use
      terminate: 0.95  # restart the worker at 95% use
```

This stops Dask workers from spilling to disk, and instead relies entirely on mechanisms to stop them from processing when they reach memory limits.

As a reminder, you can set the memory limit for a worker using the `--memory-limit` keyword:

```
dask-mpi ... --memory-limit 10GB
```

Launch Many Small Jobs

Note: This section is not necessary if you use a tool like dask-jobqueue.

HPC job schedulers are optimized for large monolithic jobs with many nodes that all need to run as a group at the same time. Dask jobs can be quite a bit more flexible: workers can come and go without strongly affecting the job. If we split our job into many smaller jobs, we can often get through the job scheduling queue much more quickly than a typical job. This is particularly valuable when we want to get started right away and interact with a Jupyter notebook session rather than waiting for hours for a suitable allocation block to become free.

So, to get a large cluster quickly, we recommend allocating a dask-scheduler process on one node with a modest wall time (the intended time of your session) and then allocating many small single-node dask-worker jobs with shorter wall times (perhaps 30 minutes) that can easily squeeze into extra space in the job scheduler. As you need more computation, you can add more of these single-node jobs or let them expire.

Use Dask to co-launch a Jupyter server

Dask can help you by launching other services alongside it. For example, you can run a Jupyter notebook server on the machine running the `dask-scheduler` process with the following commands

```
from dask.distributed import Client
client = Client(scheduler_file='scheduler.json')

import socket
host = client.run_on_scheduler(socket.gethostname)

def start_jlab(dask_scheduler):
    import subprocess
    proc = subprocess.Popen(['/path/to/jupyter', 'lab', '--ip', host, '--no-browser'])
    dask_scheduler.jlab_proc = proc

client.run_on_scheduler(start_jlab)
```

3.2.6 Kubernetes

Kubernetes and Helm

It is easy to launch a Dask cluster and a Jupyter notebook server on cloud resources using Kubernetes and Helm.

This is particularly useful when you want to deploy a fresh Python environment on Cloud services like Amazon Web Services, Google Compute Engine, or Microsoft Azure.

If you already have Python environments running in a pre-existing Kubernetes cluster, then you may prefer the *Kubernetes native* documentation, which is a bit lighter weight.

Launch Kubernetes Cluster

This document assumes that you have a Kubernetes cluster and Helm installed.

If this is not the case, then you might consider setting up a Kubernetes cluster on one of the common cloud providers like Google, Amazon, or Microsoft. We recommend the first part of the documentation in the guide Zero to JupyterHub that focuses on Kubernetes and Helm (you do not need to follow all of these instructions). Also, JupyterHub is not necessary to deploy Dask:

- Creating a Kubernetes Cluster
- Setting up Helm

Alternatively, you may want to experiment with Kubernetes locally using Minikube.

Helm Install Dask

Dask maintains a Helm chart repository containing various charts for the Dask community https://helm.dask.org/ . You will need to add this to your known channels and update your local charts:

```
helm repo add dask https://helm.dask.org/
helm repo update
```

Now, you can launch Dask on your Kubernetes cluster using the Dask Helm chart:

```
helm install dask/dask
```

This deploys a `dask-scheduler`, several `dask-worker` processes, and also an optional Jupyter server.

Verify Deployment

This might take a minute to deploy. You can check its status with `kubectl`:

```
kubectl get pods
kubectl get services

$ kubectl get pods
NAME                                  READY     STATUS              RESTARTS    AGE
bald-eel-jupyter-924045334-twtxd      0/1       ContainerCreating   0            1m
bald-eel-scheduler-3074430035-cn1dt   1/1       Running             0            1m
bald-eel-worker-3032746726-202jt      1/1       Running             0            1m
bald-eel-worker-3032746726-b8nqq      1/1       Running             0            1m
bald-eel-worker-3032746726-d0chx      0/1       ContainerCreating   0            1m

$ kubectl get services
NAME                 TYPE           CLUSTER-IP      EXTERNAL-IP      PORT(S)          ␣
↪              AGE
bald-eel-jupyter     LoadBalancer   10.11.247.201   35.226.183.149   80:30173/TCP     ␣
↪               2m
bald-eel-scheduler   LoadBalancer   10.11.245.241   35.202.201.129   8786:31166/TCP,
↪80:31626/TCP   2m
kubernetes           ClusterIP      10.11.240.1     <none>           443/TCP
48m
```

You can use the addresses under `EXTERNAL-IP` to connect to your now-running Jupyter and Dask systems.

Notice the name `bald-eel`. This is the name that Helm has given to your particular deployment of Dask. You could, for example, have multiple Dask-and-Jupyter clusters running at once, and each would be given a different name. Note that you will need to use this name to refer to your deployment in the future. Additionally, you can list all active helm deployments with:

```
helm list

NAME            REVISION        UPDATED                         STATUS      CHART     ␣
↪       NAMESPACE
bald-eel        1               Wed Dec  6 11:19:54 2017        DEPLOYED    dask-0.1.
↪0       default
```

Connect to Dask and Jupyter

When we ran `kubectl get services`, we saw some externally visible IPs:

```
mrocklin@pangeo-181919:~$ kubectl get services
NAME                   TYPE           CLUSTER-IP      EXTERNAL-IP      PORT(S)          ␣
↪              AGE
bald-eel-jupyter       LoadBalancer   10.11.247.201   35.226.183.149   80:30173/TCP     ␣
↪              2m
bald-eel-scheduler     LoadBalancer   10.11.245.241   35.202.201.129   8786:31166/TCP,
↪80:31626/TCP   2m
kubernetes             ClusterIP      10.11.240.1     <none>          443/TCP          ␣
↪              48m
```

We can navigate to these services from any web browser. Here, one is the Dask diagnostic dashboard, and the other is the Jupyter server. You can log into the Jupyter notebook server with the password, `dask`.

You can create a notebook and create a Dask client from there. The `DASK_SCHEDULER_ADDRESS` environment variable has been populated with the address of the Dask scheduler. This is available in Python in the `config` dictionary.

```
>>> from dask.distributed import Client, config
>>> config['scheduler-address']
'bald-eel-scheduler:8786'
```

Although you don't need to use this address, the Dask client will find this variable automatically.

```
from dask.distributed import Client, config
client = Client()
```

Configure Environment

By default, the Helm deployment launches three workers using two cores each and a standard conda environment. We can customize this environment by creating a small yaml file that implements a subset of the values in the dask helm chart values.yaml file.

For example, we can increase the number of workers, and include extra conda and pip packages to install on the both the workers and Jupyter server (these two environments should be matched).

```
# config.yaml

worker:
```

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```
  replicas: 8
  resources:
    limits:
      cpu: 2
      memory: 7.5G
    requests:
      cpu: 2
      memory: 7.5G
  env:
    - name: EXTRA_CONDA_PACKAGES
      value: numba xarray -c conda-forge
    - name: EXTRA_PIP_PACKAGES
      value: s3fs dask-ml --upgrade

# We want to keep the same packages on the worker and jupyter environments
jupyter:
  enabled: true
  env:
    - name: EXTRA_CONDA_PACKAGES
      value: numba xarray matplotlib -c conda-forge
    - name: EXTRA_PIP_PACKAGES
      value: s3fs dask-ml --upgrade
```

This config file overrides the configuration for the number and size of workers and the conda and pip packages installed on the worker and Jupyter containers. In general, we will want to make sure that these two software environments match.

Update your deployment to use this configuration file. Note that *you will not use helm install* for this stage: that would create a *new* deployment on the same Kubernetes cluster. Instead, you will upgrade your existing deployment by using the current name:

```
helm upgrade bald-eel dask/dask -f config.yaml
```

This will update those containers that need to be updated. It may take a minute or so.

As a reminder, you can list the names of deployments you have using `helm list`

Check status and logs

For standard issues, you should be able to see the worker status and logs using the Dask dashboard (in particular, you can see the worker links from the `info/` page). However, if your workers aren't starting, you can check the status of pods and their logs with the following commands:

```
kubectl get pods
kubectl logs <PODNAME>
```

```
mrocklin@pangeo-181919:~$ kubectl get pods
NAME                                  READY     STATUS    RESTARTS   AGE
bald-eel-jupyter-3805078281-n1qk2     1/1       Running   0          18m
bald-eel-scheduler-3074430035-cn1dt   1/1       Running   0          58m
bald-eel-worker-1931881914-1q09p      1/1       Running   0          18m
bald-eel-worker-1931881914-856mm      1/1       Running   0          18m
bald-eel-worker-1931881914-9lgzb      1/1       Running   0          18m
bald-eel-worker-1931881914-bdn2c      1/1       Running   0          16m
bald-eel-worker-1931881914-jq70m      1/1       Running   0          17m
```

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```
bald-eel-worker-1931881914-qsgj7      1/1       Running   0          18m
bald-eel-worker-1931881914-s2phd      1/1       Running   0          17m
bald-eel-worker-1931881914-srmmg      1/1       Running   0          17m

mrocklin@pangeo-181919:~$ kubectl logs bald-eel-worker-1931881914-856mm
EXTRA_CONDA_PACKAGES environment variable found.  Installing.
Fetching package metadata ...........
Solving package specifications: .
Package plan for installation in environment /opt/conda/envs/dask:
The following NEW packages will be INSTALLED:
    fasteners: 0.14.1-py36_2 conda-forge
    monotonic: 1.3-py36_0    conda-forge
    zarr:      2.1.4-py36_0  conda-forge
Proceed ([y]/n)?
monotonic-1.3- 100% |###############################| Time: 0:00:00  11.16 MB/s
fasteners-0.14 100% |###############################| Time: 0:00:00 576.56 kB/s
...
```

Delete a Helm deployment

You can always delete a helm deployment using its name:

```
helm delete bald-eel --purge
```

Note that this does not destroy any clusters that you may have allocated on a Cloud service (you will need to delete those explicitly).

Avoid the Jupyter Server

Sometimes you do not need to run a Jupyter server alongside your Dask cluster.

```
jupyter:
  enabled: false
```

Kubernetes Native

See external documentation on Dask-Kubernetes for more information.

Kubernetes is a popular system for deploying distributed applications on clusters, particularly in the cloud. You can use Kubernetes to launch Dask workers in the following two ways:

1. **Helm**: You can launch a Dask scheduler, several workers, and an optional Jupyter Notebook server on a Kubernetes easily using Helm

   ```
   helm repo add dask https://helm.dask.org/    # add the Dask Helm chart repository
   helm repo update                             # get latest Helm charts
   helm install dask/dask                     # deploy standard Dask chart
   ```

   This is a good choice if you want to do the following:

   1. Run a managed Dask cluster for a long period of time
   2. Also deploy a Jupyter server from which to run code

3. Share the same Dask cluster between many automated services
4. Try out Dask for the first time on a cloud-based system like Amazon, Google, or Microsoft Azure (see also our *Cloud documentation*)

Note: For more information, see *Dask and Helm documentation*.

2. **Native**: You can quickly deploy Dask workers on Kubernetes from within a Python script or interactive session using Dask-Kubernetes

```
from dask_kubernetes import KubeCluster
cluster = KubeCluster.from_yaml('worker-template.yaml')
cluster.scale(20)  # add 20 workers
cluster.adapt()    # or create and destroy workers dynamically based on workload

from dask.distributed import Client
client = Client(cluster)
```

This is a good choice if you want to do the following:

1. Dynamically create a personal and ephemeral deployment for interactive use
2. Allow many individuals the ability to launch their own custom dask deployments, rather than depend on a centralized system
3. Quickly adapt Dask cluster size to the current workload

Note: For more information, see Dask-Kubernetes documentation.

You may also want to see the documentation on using *Dask with Docker containers* to help you manage your software environments on Kubernetes.

3.2.7 Python API (advanced)

In some rare cases, experts may want to create `Scheduler`, `Worker`, and `Nanny` objects explicitly in Python. This is often necessary when making tools to automatically deploy Dask in custom settings.

It is more common to create a *Local cluster with Client() on a single machine* or use the *Command Line Interface (CLI)*. New readers are recommended to start there.

If you do want to start Scheduler and Worker objects yourself you should be a little familiar with `async`/`await` style Python syntax. These objects are awaitable and are commonly used within `async with` context managers. Here are a few examples to show a few ways to start and finish things.

Full Example

`Scheduler`([loop, delete_interval, . . .])	Dynamic distributed task scheduler
`Worker`([scheduler_ip, scheduler_port, . . .])	Worker node in a Dask distributed cluster
`Client`([address, loop, timeout, . . .])	Connect to and submit computation to a Dask cluster

We first start with a comprehensive example of setting up a Scheduler, two Workers, and one Client in the same event loop, running a simple computation, and then cleaning everything up.

```python
import asyncio
from dask.distributed import Scheduler, Worker, Client

async def f():
    async with Scheduler() as s:
        async with Worker(s.address) as w1, Worker(s.address) as w2:
            async with Client(s.address, asynchronous=True) as client:
                future = client.submit(lambda x: x + 1, 10)
                result = await future
                print(result)

asyncio.get_event_loop().run_until_complete(f())
```

Now we look at simpler examples that build up to this case.

Scheduler

`Scheduler`([loop, delete_interval, . . .])	Dynamic distributed task scheduler

We create scheduler by creating a `Scheduler()` object, and then `await` that object to wait for it to start up. We can then wait on the `.finished` method to wait until it closes. In the meantime the scheduler will be active managing the cluster..

```python
import asyncio
from dask.distributed import Scheduler, Worker

async def f():
    s = Scheduler()        # scheduler created, but not yet running
    s = await s            # the scheduler is running
    await s.finished()     # wait until the scheduler closes

asyncio.get_event_loop().run_until_complete(f())
```

This program will run forever, or until some external process connects to the scheduler and tells it to stop. If you want to close things yourself you can close any `Scheduler`, `Worker`, `Nanny`, or `Client` class by awaiting the `.close` method:

```python
await s.close()
```

Worker

`Worker`([scheduler_ip, scheduler_port, . . .])	Worker node in a Dask distributed cluster

The worker follows the same API. The only difference is that the worker needs to know the address of the scheduler.

```python
import asyncio
from dask.distributed import Scheduler, Worker

async def f(scheduler_address):
    w = await Worker(scheduler_address)
    await w.finished()
```

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```
asyncio.get_event_loop().run_until_complete(f("tcp://127.0.0.1:8786"))
```

Start many in one event loop

Scheduler([loop, delete_interval, . . .])	Dynamic distributed task scheduler
Worker([scheduler_ip, scheduler_port, . . .])	Worker node in a Dask distributed cluster

We can run as many of these objects as we like in the same event loop.

```
import asyncio
from dask.distributed import Scheduler, Worker

async def f():
    s = await Scheduler()
    w = await Worker(s.address)
    await w.finished()
    await s.finished()

asyncio.get_event_loop().run_until_complete(f())
```

Use Context Managers

We can also use `async with` context managers to make sure that we clean up properly. Here is the same example as from above:

```
import asyncio
from dask.distributed import Scheduler, Worker

async def f():
    async with Scheduler() as s:
        async with Worker(s.address) as w:
            await w.finished()
            await s.finished()

asyncio.get_event_loop().run_until_complete(f())
```

Alternatively, in the example below we also include a `Client`, run a small computation, and then allow things to clean up after that computation..

```
import asyncio
from dask.distributed import Scheduler, Worker, Client

async def f():
    async with Scheduler() as s:
        async with Worker(s.address) as w1, Worker(s.address) as w2:
            async with Client(s.address, asynchronous=True) as client:
                future = client.submit(lambda x: x + 1, 10)
                result = await future
                print(result)

asyncio.get_event_loop().run_until_complete(f())
```

This is equivalent to creating and `awaiting` each server, and then calling `.close` on each as we leave the context. In this example we don't wait on `s.finished()`, so this will terminate relatively quickly. You could have called `await s.finished()` though if you wanted this to run forever.

Nanny

`Nanny`([scheduler_ip, scheduler_port, . . .])	A process to manage worker processes

Alternatively, we can replace `Worker` with `Nanny` if we want your workers to be managed in a separate process. The `Nanny` constructor follows the same API. This allows workers to restart themselves in case of failure. Also, it provides some additional monitoring, and is useful when coordinating many workers that should live in different processes in order to avoid the GIL.

```
# w = await Worker(s.address)
w = await Nanny(s.address)
```

API

These classes have a variety of keyword arguments that you can use to control their behavior. See the API documentation below for more information.

Scheduler

class distributed.**Scheduler**(*loop=None, delete_interval='500ms', synchronize_worker_interval='60s', services=None, service_kwargs=None, allowed_failures=None, extensions=None, validate=False, scheduler_file=None, security=None, worker_ttl=None, idle_timeout=None, interface=None, host=None, port=0, protocol=None, dashboard_address=None, preload=None, preload_argv=(), **kwargs*)

Dynamic distributed task scheduler

The scheduler tracks the current state of workers, data, and computations. The scheduler listens for events and responds by controlling workers appropriately. It continuously tries to use the workers to execute an ever growing dask graph.

All events are handled quickly, in linear time with respect to their input (which is often of constant size) and generally within a millisecond. To accomplish this the scheduler tracks a lot of state. Every operation maintains the consistency of this state.

The scheduler communicates with the outside world through Comm objects. It maintains a consistent and valid view of the world even when listening to several clients at once.

A Scheduler is typically started either with the `dask-scheduler` executable:

```
$ dask-scheduler
Scheduler started at 127.0.0.1:8786
```

Or within a LocalCluster a Client starts up without connection information:

```
>>> c = Client()
>>> c.cluster.scheduler
Scheduler(...)
```

Users typically do not interact with the scheduler directly but rather with the client object `Client`.

State

The scheduler contains the following state variables. Each variable is listed along with what it stores and a brief description.

- **tasks: `{task key: TaskState}`** Tasks currently known to the scheduler
- **unrunnable: `{TaskState}`** Tasks in the "no-worker" state
- **workers: `{worker key: WorkerState}`** Workers currently connected to the scheduler
- **idle: `{WorkerState}`:** Set of workers that are not fully utilized
- **saturated: `{WorkerState}`:** Set of workers that are not over-utilized
- **host_info: `{hostname: dict}`:** Information about each worker host
- **clients: `{client key: ClientState}`** Clients currently connected to the scheduler
- **services: `{str: port}`:** Other services running on this scheduler, like Bokeh
- **loop: `IOLoop`:** The running Tornado IOLoop
- **client_comms: `{client key: Comm}`** For each client, a Comm object used to receive task requests and report task status updates.
- **stream_comms: `{worker key: Comm}`** For each worker, a Comm object from which we both accept stimuli and report results
- **task_duration: `{key-prefix: time}`** Time we expect certain functions to take, e.g. `{'sum': 0.25}`

`adaptive_target`(*comm=None*, *target_duration='5s'*)
Desired number of workers based on the current workload

This looks at the current running tasks and memory use, and returns a number of desired workers. This is often used by adaptive scheduling.

Parameters

target_duration: str A desired duration of time for computations to take. This affects how rapidly the scheduler will ask to scale.

See also:

`distributed.deploy.Adaptive`

`add_client`(*comm*, *client=None*)
Add client to network

We listen to all future messages from this Comm.

`add_keys`(*comm=None*, *worker=None*, *keys=()*)
Learn that a worker has certain keys

This should not be used in practice and is mostly here for legacy reasons. However, it is sent by workers from time to time.

`add_plugin`(*plugin=None*, *idempotent=False*, ***kwargs*)
Add external plugin to scheduler

See https://distributed.readthedocs.io/en/latest/plugins.html

add_worker(*comm=None*, *address=None*, *keys=()*, *nthreads=None*, *name=None*, *resolve_address=True*, *nbytes=None*, *types=None*, *now=None*, *resources=None*, *host_info=None*, *memory_limit=None*, *metrics=None*, *pid=0*, *services=None*, *local_directory=None*, *nanny=None*, *extra=None*)
Add a new worker to the cluster

broadcast(*comm=None*, *msg=None*, *workers=None*, *hosts=None*, *nanny=False*, *serializers=None*)
Broadcast message to workers, return all results

cancel_key(*key*, *client*, *retries=5*, *force=False*)
Cancel a particular key and all dependents

check_idle_saturated(*ws*, *occ=None*)
Update the status of the idle and saturated state

The scheduler keeps track of workers that are ..

- Saturated: have enough work to stay busy
- Idle: do not have enough work to stay busy

They are considered saturated if they both have enough tasks to occupy all of their threads, and if the expected runtime of those tasks is large enough.

This is useful for load balancing and adaptivity.

client_heartbeat(*client=None*)
Handle heartbeats from Client

client_releases_keys(*keys=None*, *client=None*)
Remove keys from client desired list

close(*comm=None*, *fast=False*, *close_workers=False*)
Send cleanup signal to all coroutines then wait until finished

See also:

`Scheduler.cleanup`

close_worker(*stream=None*, *worker=None*, *safe=None*)
Remove a worker from the cluster

This both removes the worker from our local state and also sends a signal to the worker to shut down. This works regardless of whether or not the worker has a nanny process restarting it

coerce_address(*addr*, *resolve=True*)
Coerce possible input addresses to canonical form. *resolve* can be disabled for testing with fake hostnames.

Handles strings, tuples, or aliases.

coerce_hostname(*host*)
Coerce the hostname of a worker.

decide_worker(*ts*)
Decide on a worker for task *ts*. Return a WorkerState.

feed(*comm*, *function=None*, *setup=None*, *teardown=None*, *interval='1s'*, ***kwargs*)
Provides a data Comm to external requester

Caution: this runs arbitrary Python code on the scheduler. This should eventually be phased out. It is mostly used by diagnostics.

gather(*comm=None*, *keys=None*, *serializers=None*)
Collect data in from workers

get_comm_cost(*ts*, *ws*)
Get the estimated communication cost (in s.) to compute the task on the given worker.

get_task_duration(*ts*, *default=0.5*)
Get the estimated computation cost of the given task (not including any communication cost).

get_worker_service_addr(*worker*, *service_name*, *protocol=False*)
Get the (host, port) address of the named service on the *worker*. Returns None if the service doesn't exist.

Parameters

worker [address]

service_name [str] Common services include 'bokeh' and 'nanny'

protocol [boolean] Whether or not to include a full address with protocol (True) or just a (host, port) pair

handle_long_running(*key=None*, *worker=None*, *compute_duration=None*)
A task has seceded from the thread pool

We stop the task from being stolen in the future, and change task duration accounting as if the task has stopped.

handle_worker(*comm=None*, *worker=None*)
Listen to responses from a single worker

This is the main loop for scheduler-worker interaction

See also:

`Scheduler.handle_client` Equivalent coroutine for clients

identity(*comm=None*)
Basic information about ourselves and our cluster

proxy(*comm=None*, *msg=None*, *worker=None*, *serializers=None*)
Proxy a communication through the scheduler to some other worker

rebalance(*comm=None*, *keys=None*, *workers=None*)
Rebalance keys so that each worker stores roughly equal bytes

Policy

This orders the workers by what fraction of bytes of the existing keys they have. It walks down this list from most-to-least. At each worker it sends the largest results it can find and sends them to the least occupied worker until either the sender or the recipient are at the average expected load.

reevaluate_occupancy(*worker_index=0*)
Periodically reassess task duration time

The expected duration of a task can change over time. Unfortunately we don't have a good constant-time way to propagate the effects of these changes out to the summaries that they affect, like the total expected runtime of each of the workers, or what tasks are stealable.

In this coroutine we walk through all of the workers and re-align their estimates with the current state of tasks. We do this periodically rather than at every transition, and we only do it if the scheduler process isn't under load (using psutil.Process.cpu_percent()). This lets us avoid this fringe optimization when we have better things to think about.

register_worker_plugin(*comm*, *plugin*, *name=None*)
Registers a setup function, and call it on every worker

remove_client (*client=None*)
Remove client from network

remove_plugin (*plugin*)
Remove external plugin from scheduler

remove_worker (*comm=None*, *address=None*, *safe=False*, *close=True*)
Remove worker from cluster

We do this when a worker reports that it plans to leave or when it appears to be unresponsive. This may send its tasks back to a released state.

replicate (*comm=None*, *keys=None*, *n=None*, *workers=None*, *branching_factor=2*, *delete=True*)
Replicate data throughout cluster

This performs a tree copy of the data throughout the network individually on each piece of data.

Parameters

keys: Iterable list of keys to replicate

n: int Number of replications we expect to see within the cluster

branching_factor: int, optional The number of workers that can copy data in each generation. The larger the branching factor, the more data we copy in a single step, but the more a given worker risks being swamped by data requests.

See also:

`Scheduler.rebalance`

report (*msg*, *ts=None*, *client=None*)
Publish updates to all listening Queues and Comms

If the message contains a key then we only send the message to those comms that care about the key.

reschedule (*key=None*, *worker=None*)
Reschedule a task

Things may have shifted and this task may now be better suited to run elsewhere

restart (*client=None*, *timeout=3*)
Restart all workers. Reset local state.

retire_workers (*comm=None*, *workers=None*, *remove=True*, *close_workers=False*, *names=None*, ***kwargs*)
Gracefully retire workers from cluster

Parameters

workers: list (optional) List of worker addresses to retire. If not provided we call `workers_to_close` which finds a good set

workers_names: list (optional) List of worker names to retire.

remove: bool (defaults to True) Whether or not to remove the worker metadata immediately or else wait for the worker to contact us

close_workers: bool (defaults to False) Whether or not to actually close the worker explicitly from here. Otherwise we expect some external job scheduler to finish off the worker.

****kwargs: dict** Extra options to pass to workers_to_close to determine which workers we should drop

Returns

Dictionary mapping worker ID/address to dictionary of information about

that worker for each retired worker.

See also:

Scheduler.workers_to_close

run_function(*stream*, *function*, *args=()*, *kwargs={}*, *wait=True*)
Run a function within this process

See also:

Client.run_on_scheduler

scatter(*comm=None*, *data=None*, *workers=None*, *client=None*, *broadcast=False*, *timeout=2*)
Send data out to workers

See also:

Scheduler.broadcast

send_task_to_worker(*worker*, *key*)
Send a single computational task to a worker

start()
Clear out old state and restart all running coroutines

start_ipython(*comm=None*)
Start an IPython kernel

Returns Jupyter connection info dictionary.

stimulus_cancel(*comm*, *keys=None*, *client=None*, *force=False*)
Stop execution on a list of keys

stimulus_missing_data(*cause=None*, *key=None*, *worker=None*, *ensure=True*, ***kwargs*)
Mark that certain keys have gone missing. Recover.

stimulus_task_erred(*key=None*, *worker=None*, *exception=None*, *traceback=None*, ***kwargs*)
Mark that a task has erred on a particular worker

stimulus_task_finished(*key=None*, *worker=None*, ***kwargs*)
Mark that a task has finished execution on a particular worker

story(**keys*)
Get all transitions that touch one of the input keys

transition(*key*, *finish*, **args*, ***kwargs*)
Transition a key from its current state to the finish state

Returns

Dictionary of recommendations for future transitions

See also:

Scheduler.transitions transitive version of this function

Examples

```
>>> self.transition('x', 'waiting')
{'x': 'processing'}
```

transition_story(**keys*)
Get all transitions that touch one of the input keys

transitions (*recommendations*)
Process transitions until none are left

This includes feedback from previous transitions and continues until we reach a steady state

update_data (*comm=None*, *who_has=None*, *nbytes=None*, *client=None*, *serializers=None*)
Learn that new data has entered the network from an external source

See also:

`Scheduler.mark_key_in_memory`

update_graph (*client=None*, *tasks=None*, *keys=None*, *dependencies=None*, *restrictions=None*, *priority=None*, *loose_restrictions=None*, *resources=None*, *submitting_task=None*, *retries=None*, *user_priority=0*, *actors=None*, *fifo_timeout=0*)
Add new computations to the internal dask graph

This happens whenever the Client calls submit, map, get, or compute.

valid_workers (*ts*)
Return set of currently valid workers for key

If all workers are valid then this returns `True`. This checks tracks the following state:

- worker_restrictions
- host_restrictions
- resource_restrictions

worker_objective (*ts*, *ws*)
Objective function to determine which worker should get the task

Minimize expected start time. If a tie then break with data storage.

worker_send (*worker*, *msg*)
Send message to worker

This also handles connection failures by adding a callback to remove the worker on the next cycle.

workers_list (*workers*)
List of qualifying workers

Takes a list of worker addresses or hostnames. Returns a list of all worker addresses that match

workers_to_close (*comm=None*, *memory_ratio=None*, *n=None*, *key=None*, *minimum=None*, *target=None*, *attribute='address'*)
Find workers that we can close with low cost

This returns a list of workers that are good candidates to retire. These workers are not running anything and are storing relatively little data relative to their peers. If all workers are idle then we still maintain enough workers to have enough RAM to store our data, with a comfortable buffer.

This is for use with systems like `distributed.deploy.adaptive`.

Parameters

memory_factor: Number Amount of extra space we want to have for our stored data. Defaults two 2, or that we want to have twice as much memory as we currently have data.

n: int Number of workers to close

minimum: int Minimum number of workers to keep around

key: Callable(WorkerState) An optional callable mapping a WorkerState object to a group affiliation. Groups will be closed together. This is useful when closing workers must be done collectively, such as by hostname.

target: int Target number of workers to have after we close

attribute [str] The attribute of the WorkerState object to return, like "address" or "name". Defaults to "address".

Returns

to_close: list of worker addresses that are OK to close

See also:

`Scheduler.retire_workers`

Examples

```
>>> scheduler.workers_to_close()
['tcp://192.168.0.1:1234', 'tcp://192.168.0.2:1234']
```

Group workers by hostname prior to closing

```
>>> scheduler.workers_to_close(key=lambda ws: ws.host)
['tcp://192.168.0.1:1234', 'tcp://192.168.0.1:4567']
```

Remove two workers

```
>>> scheduler.workers_to_close(n=2)
```

Keep enough workers to have twice as much memory as we we need.

```
>>> scheduler.workers_to_close(memory_ratio=2)
```

Worker

class `distributed.`**`Worker`**(*scheduler_ip=None*, *scheduler_port=None*, *scheduler_file=None*, *ncores=None*, *nthreads=None*, *loop=None*, *local_dir=None*, *local_directory=None*, *services=None*, *service_ports=None*, *service_kwargs=None*, *name=None*, *reconnect=True*, *memory_limit='auto'*, *executor=None*, *resources=None*, *silence_logs=None*, *death_timeout=None*, *preload=None*, *preload_argv=None*, *security=None*, *contact_address=None*, *memory_monitor_interval='200ms'*, *extensions=None*, *metrics={}*, *startup_information={}*, *data=None*, *interface=None*, *host=None*, *port=None*, *protocol=None*, *dashboard_address=None*, *nanny=None*, *plugins=()*, *low_level_profiler=False*, *validate=False*, *profile_cycle_interval=None*, *lifetime=None*, *lifetime_stagger=None*, *lifetime_restart=None*, ***kwargs*)

Worker node in a Dask distributed cluster

Workers perform two functions:

1. **Serve data** from a local dictionary
2. **Perform computation** on that data and on data from peers

Workers keep the scheduler informed of their data and use that scheduler to gather data from other workers when necessary to perform a computation.

You can start a worker with the `dask-worker` command line application:

```
$ dask-worker scheduler-ip:port
```

Use the `--help` flag to see more options:

```
$ dask-worker --help
```

The rest of this docstring is about the internal state the the worker uses to manage and track internal computations.

State

Informational State

These attributes don't change significantly during execution.

- **nthreads: `int`:** Number of nthreads used by this worker process
- **executor: `concurrent.futures.ThreadPoolExecutor`:** Executor used to perform computation
- **local_directory: `path`:** Path on local machine to store temporary files
- **scheduler: `rpc`:** Location of scheduler. See `.ip/.port` attributes.
- **name: `string`:** Alias
- **services: `{str: Server}`:** Auxiliary web servers running on this worker
- **service_ports:** `{str: port}`:
- **total_out_connections: `int`** The maximum number of concurrent outgoing requests for data
- **total_in_connections: `int`** The maximum number of concurrent incoming requests for data
- **total_comm_nbytes**: `int`
- **batched_stream: `BatchedSend`** A batched stream along which we communicate to the scheduler
- **log: `[(message)]`** A structured and queryable log. See `Worker.story`

Volatile State

This attributes track the progress of tasks that this worker is trying to complete. In the descriptions below a `key` is the name of a task that we want to compute and `dep` is the name of a piece of dependent data that we want to collect from others.

- **data: `{key: object}`:** Prefer using the **host** attribute instead of this, unless memory_limit and at least one of memory_target_fraction or memory_spill_fraction values are defined, in that case, this attribute is a zict.Buffer, from which information on LRU cache can be queried.
- **data.memory: `{key: object}`:** Dictionary mapping keys to actual values stored in memory. Only available if condition for **data** being a zict.Buffer is met.
- **data.disk: `{key: object}`:** Dictionary mapping keys to actual values stored on disk. Only available if condition for **data** being a zict.Buffer is met.
- **task_state: `{key: string}`:** The state of all tasks that the scheduler has asked us to compute. Valid states include waiting, constrained, executing, memory, erred
- **tasks: `{key: dict}`** The function, args, kwargs of a task. We run this when appropriate
- **dependencies: `{key: {deps}}`** The data needed by this key to run
- **dependents: `{dep: {keys}}`** The keys that use this dependency
- **data_needed: deque(keys)** The keys whose data we still lack, arranged in a deque

- **waiting_for_data: `{kep: {deps}}`** A dynamic verion of dependencies. All dependencies that we still don't have for a particular key.
- **ready: [keys]** Keys that are ready to run. Stored in a LIFO stack
- **constrained: [keys]** Keys for which we have the data to run, but are waiting on abstract resources like GPUs. Stored in a FIFO deque
- **executing: {keys}** Keys that are currently executing
- **executed_count: int** A number of tasks that this worker has run in its lifetime
- **long_running: {keys}** A set of keys of tasks that are running and have started their own long-running clients.
- **dep_state: `{dep: string}`:** The state of all dependencies required by our tasks Valid states include waiting, flight, and memory
- **who_has: `{dep: {worker}}`** Workers that we believe have this data
- **has_what: `{worker: {deps}}`** The data that we care about that we think a worker has
- **pending_data_per_worker: `{worker: [dep]}`** The data on each worker that we still want, prioritized as a deque
- **in_flight_tasks: `{task: worker}`** All dependencies that are coming to us in current peer-to-peer connections and the workers from which they are coming.
- **in_flight_workers: `{worker: {task}}`** The workers from which we are currently gathering data and the dependencies we expect from those connections
- **comm_bytes: `int`** The total number of bytes in flight
- **suspicious_deps: `{dep: int}`** The number of times a dependency has not been where we expected it
- **nbytes: `{key: int}`** The size of a particular piece of data
- **types: `{key: type}`** The type of a particular piece of data
- **threads: `{key: int}`** The ID of the thread on which the task ran
- **active_threads: `{int: key}`** The keys currently running on active threads
- **exceptions: `{key: exception}`** The exception caused by running a task if it erred
- **tracebacks: `{key: traceback}`** The exception caused by running a task if it erred
- **startstops: `{key: [(str, float, float)]}`** Log of transfer, load, and compute times for a task
- **priorities: `{key: tuple}`** The priority of a key given by the scheduler. Determines run order.
- **durations: `{key: float}`** Expected duration of a task
- **resource_restrictions: `{key: {str: number}}`** Abstract resources required to run a task

Parameters

scheduler_ip: str

scheduler_port: int

ip: str, optional

data: MutableMapping, type, None The object to use for storage, builds a disk-backed LRU dict by default

nthreads: int, optional

loop: tornado.ioloop.IOLoop

local_directory: str, optional Directory where we place local resources

name: str, optional

memory_limit: int, float, string Number of bytes of memory that this worker should use. Set to zero for no limit. Set to 'auto' to calculate as system.MEMORY_LIMIT * min(1, nthreads / total_cores) Use strings or numbers like 5GB or 5e9

memory_target_fraction: float Fraction of memory to try to stay beneath

memory_spill_fraction: float Fraction of memory at which we start spilling to disk

memory_pause_fraction: float Fraction of memory at which we stop running new tasks

executor: concurrent.futures.Executor

resources: dict Resources that this worker has like `{'GPU': 2}`

nanny: str Address on which to contact nanny, if it exists

lifetime: str Amount of time like "1 hour" after which we gracefully shut down the worker. This defaults to None, meaning no explicit shutdown time.

lifetime_stagger: str Amount of time like "5 minutes" to stagger the lifetime value The actual lifetime will be selected uniformly at random between lifetime +/- lifetime_stagger

lifetime_restart: bool Whether or not to restart a worker after it has reached its lifetime Default False

See also:

`distributed.scheduler.Scheduler`, `distributed.nanny.Nanny`

Examples

Use the command line to start a worker:

```
$ dask-scheduler
Start scheduler at 127.0.0.1:8786

$ dask-worker 127.0.0.1:8786
Start worker at:               127.0.0.1:1234
Registered with scheduler at:  127.0.0.1:8786
```

`close_gracefully`()
Gracefully shut down a worker

This first informs the scheduler that we're shutting down, and asks it to move our data elsewhere. Afterwards, we close as normal

`executor_submit`(*key*, *function*, *args=()*, *kwargs=None*, *executor=None*)
Safely run function in thread pool executor

We've run into issues running concurrent.future futures within tornado. Apparently it's advantageous to use timeouts and periodic callbacks to ensure things run smoothly. This can get tricky, so we pull it off into an separate method.

`get_current_task`()
Get the key of the task we are currently running

This only makes sense to run within a task

See also:

get_worker

Examples

```
>>> from dask.distributed import get_worker
>>> def f():
...     return get_worker().get_current_task()
```

```
>>> future = client.submit(f)  # doctest: +SKIP
>>> future.result()  # doctest: +SKIP
'f-1234'
```

local_dir
For API compatibility with Nanny

memory_monitor()
Track this process's memory usage and act accordingly

If we rise above 70% memory use, start dumping data to disk.

If we rise above 80% memory use, stop execution of new tasks

start_ipython(*comm*)
Start an IPython kernel

Returns Jupyter connection info dictionary.

trigger_profile()
Get a frame from all actively computing threads

Merge these frames into existing profile counts

worker_address
For API compatibility with Nanny

Nanny

class distributed.**Nanny**(*scheduler_ip=None, scheduler_port=None, scheduler_file=None, worker_port=0, nthreads=None, ncores=None, loop=None, local_dir=None, local_directory='dask-worker-space', services=None, name=None, memory_limit='auto', reconnect=True, validate=False, quiet=False, resources=None, silence_logs=None, death_timeout=None, preload=None, preload_argv=None, security=None, contact_address=None, listen_address=None, worker_class=None, env=None, interface=None, host=None, port=None, protocol=None, config=None, **worker_kwargs*)
A process to manage worker processes

The nanny spins up Worker processes, watches then, and kills or restarts them as necessary. It is necessary if you want to use the `Client.restart` method, or to restart the worker automatically if it gets to the terminate fractiom of its memory limit.

The parameters for the Nanny are mostly the same as those for the Worker.

See also:

Worker

close(*comm=None*, *timeout=5*, *report=None*)
Close the worker process, stop all comms.

close_gracefully(*comm=None*)
A signal that we shouldn't try to restart workers if they go away

This is used as part of the cluster shutdown process.

instantiate(*comm=None*)
Start a local worker process

Blocks until the process is up and the scheduler is properly informed

kill(*comm=None*, *timeout=2*)
Kill the local worker process

Blocks until both the process is down and the scheduler is properly informed

local_dir
For API compatibility with Nanny

memory_monitor()
Track worker's memory. Restart if it goes above terminate fraction

start()
Start nanny, start local process, start watching

3.2.8 Cloud Deployments

There are a variety of ways to deploy Dask on cloud providers. Cloud providers provide managed services, like Kubernetes, Yarn, or custom APIs with which Dask can connect easily. You may want to consider the following options:

1. A managed Kubernetes service and Dask's *Kubernetes and Helm integraation*.
2. A managed Yarn service, like Amazon EMR or Google Cloud DataProc and Dask-Yarn.

   Specific documentation for the popular Amazon EMR service can be found here
3. Vendor specific services, like Amazon ECS, and Dask Cloud Provider

Data Access

You may want to install additional libraries in your Jupyter and worker images to access the object stores of each cloud:

- s3fs for Amazon's S3
- gcsfs for Google's GCS
- adlfs for Microsoft's ADL

Historical Libraries

Dask previously maintained libraries for deploying Dask on Amazon's EC2 and Google GKE. Due to sporadic interest, and churn both within the Dask library and EC2 itself, these were not well maintained. They have since been deprecated in favor of the *Kubernetes and Helm* solution.

3.2.9 Adaptive Deployments

Motivation

Most Dask deployments are static with a single scheduler and a fixed number of workers. This results in predictable behavior, but is wasteful of resources in two situations:

1. The user may not be using the cluster, or perhaps they are busy interpreting a recent result or plot, and so the workers sit idly, taking up valuable shared resources from other potential users
2. The user may be very active, and is limited by their original allocation.

Particularly efficient users may learn to manually add and remove workers during their session, but this is rare. Instead, we would like the size of a Dask cluster to match the computational needs at any given time. This is the goal of the *adaptive deployments* discussed in this document. These are particularly helpful for interactive workloads, which are characterized by long periods of inactivity interrupted with short bursts of heavy activity. Adaptive deployments can result in both faster analyses that give users much more power, but with much less pressure on computational resources.

Adaptive

To make setting up adaptive deployments easy, some Dask deployment solutions offer an `.adapt()` method. Here is an example with dask_kubernetes.KubeCluster.

```python
from dask_kubernetes import KubeCluster

cluster = KubeCluster()
cluster.adapt(minimum=0, maximum=100)  # scale between 0 and 100 workers
```

For more keyword options, see the Adaptive class below:

`Adaptive`([cluster, interval, minimum, . . .])	Adaptively allocate workers based on scheduler load.

Dependence on a Resource Manager

The Dask scheduler does not know how to launch workers on its own. Instead, it relies on an external resource scheduler like Kubernetes above, or Yarn, SGE, SLURM, Mesos, or some other in-house system (see *setup documentation* for options). In order to use adaptive deployments, you must provide some mechanism for the scheduler to launch new workers. Typically, this is done by using one of the solutions listed in the *setup documentation*, or by subclassing from the Cluster superclass and implementing that API.

`Cluster`(asynchronous)	Superclass for cluster objects

Scaling Heuristics

The Dask scheduler tracks a variety of information that is useful to correctly allocate the number of workers:

1. The historical runtime of every function and task that it has seen, and all of the functions that it is currently able to run for users
2. The amount of memory used and available on each worker
3. Which workers are idle or saturated for various reasons, like the presence of specialized hardware

From these, it is able to determine a target number of workers by dividing the cumulative expected runtime of all pending tasks by the `target_duration` parameter (defaults to five seconds). This number of workers serves as a baseline request for the resource manager. This number can be altered for a variety of reasons:

1. If the cluster needs more memory, then it will choose either the target number of workers or twice the current number of workers (whichever is larger)
2. If the target is outside of the range of the minimum and maximum values, then it is clipped to fit within that range

Additionally, when scaling down, Dask preferentially chooses those workers that are idle and have the least data in memory. It moves that data to other machines before retiring the worker. To avoid rapid cycling of the cluster up and down in size, we only retire a worker after a few cycles have gone by where it has consistently been a good idea to retire it (controlled by the `wait_count` and `interval` parameters).

API

class `distributed.deploy.`**`Adaptive`**(*cluster=None*, *interval='1s'*, *minimum=0*, *maximum=inf*, *wait_count=3*, *target_duration='5s'*, *worker_key=None*, ***kwargs*)

Adaptively allocate workers based on scheduler load. A superclass.

Contains logic to dynamically resize a Dask cluster based on current use. This class needs to be paired with a system that can create and destroy Dask workers using a cluster resource manager. Typically it is built into already existing solutions, rather than used directly by users. It is most commonly used from the `.adapt(...)` method of various Dask cluster classes.

Parameters

cluster: object Must have scale and scale_down methods/coroutines

interval [timedelta or str, default "1000 ms"] Milliseconds between checks

wait_count: int, default 3 Number of consecutive times that a worker should be suggested for removal before we remove it.

target_duration: timedelta or str, default "5s" Amount of time we want a computation to take. This affects how aggressively we scale up.

worker_key: Callable[WorkerState] Function to group workers together when scaling down See Scheduler.workers_to_close for more information

minimum: int Minimum number of workers to keep around

maximum: int Maximum number of workers to keep around

****kwargs:** Extra parameters to pass to Scheduler.workers_to_close

Notes

Subclasses can override `Adaptive.should_scale_up()` and `Adaptive.workers_to_close()` to control when the cluster should be resized. The default implementation checks if there are too many tasks per worker or too little memory available (see `Adaptive.needs_cpu()` and `Adaptive.needs_memory()`).

Examples

This is commonly used from existing Dask classes, like KubeCluster

```
>>> from dask_kubernetes import KubeCluster
>>> cluster = KubeCluster()
>>> cluster.adapt(minimum=10, maximum=100)
```

Alternatively you can use it from your own Cluster class by subclassing from Dask's Cluster superclass

```
>>> from distributed.deploy import Cluster
>>> class MyCluster(Cluster):
...     def scale_up(self, n):
...         """ Bring worker count up to n """
...     def scale_down(self, workers):
...        """ Remove worker addresses from cluster """
```

```
>>> cluster = MyCluster()
>>> cluster.adapt(minimum=10, maximum=100)
```

class `distributed.deploy.`**`Cluster`**(*asynchronous*)

Superclass for cluster objects

This class contains common functionality for Dask Cluster manager classes.

To implement this class, you must provide

1. A `scheduler_comm` attribute, which is a connection to the scheduler following the `distributed.core.rpc` API.
2. Implement `scale`, which takes an integer and scales the cluster to that many workers, or else set `_supports_scaling` to False

For that, should should get the following:

1. A standard `__repr__`
2. A live IPython widget
3. Adaptive scaling
4. Integration with dask-labextension
5. A `scheduler_info` attribute which contains an up-to-date copy of `Scheduler.identity()`, which is used for much of the above
6. Methods to gather logs

3.2.10 Docker Images

Example docker images are maintained at https://github.com/dask/dask-docker and https://hub.docker.com/r/daskdev/ .

Each image installs the full Dask conda package (including the distributed scheduler), Numpy, and Pandas on top of a Miniconda installation on top of a Debian image.

These images are large, around 1GB.

- `daskdev/dask`: This a normal debian + miniconda image with the full Dask conda package (including the distributed scheduler), Numpy, and Pandas. This image is about 1GB in size.
- `daskdev/dask-notebook`: This is based on the Jupyter base-notebook image and so it is suitable for use both normally as a Jupyter server, and also as part of a JupyterHub deployment. It also includes a matching Dask software environment described above. This image is about 2GB in size.

Example

Here is a simple example on the local host network

```
docker run -it --network host daskdev/dask dask-scheduler  # start scheduler

docker run -it --network host daskdev/dask dask-worker localhost:8786 # start worker
docker run -it --network host daskdev/dask dask-worker localhost:8786 # start worker
docker run -it --network host daskdev/dask dask-worker localhost:8786 # start worker

docker run -it --network host daskdev/dask-notebook  # start Jupyter server
```

Extensibility

Users can mildly customize the software environment by populating the environment variables `EXTRA_APT_PACKAGES`, `EXTRA_CONDA_PACKAGES`, and `EXTRA_PIP_PACKAGES`. If these environment variables are set in the container, they will trigger calls to the following respectively:

```
apt-get install $EXTRA_APT_PACKAGES
conda install $EXTRA_CONDA_PACKAGES
pip install $EXTRA_PIP_PACKAGES
```

For example, the following `conda` installs the `joblib` package into the Dask worker software environment:

```
docker run -it -e EXTRA_CONDA_PACKAGES="joblib" daskdev/dask dask-worker␣
↪localhost:8786
```

Note that using these can significantly delay the container from starting, especially when using `apt`, or `conda` (`pip` is relatively fast).

Remember that it is important for software versions to match between Dask workers and Dask clients. As a result, it is often useful to include the same extra packages in both Jupyter and Worker images.

Source

Docker files are maintained at https://github.com/dask/dask-docker. This repository also includes a docker-compose configuration.

3.2.11 Custom Initialization

Often we want to run custom code when we start up or tear down a scheduler or worker. We might do this manually with functions like `Client.run` or `Client.run_on_scheduler`, but this is error prone and difficult to automate.

To resolve this, Dask includes a few mechanisms to run arbitrary code around the lifecycle of a Scheduler or Worker.

Preload Scripts

Both `dask-scheduler` and `dask-worker` support a `--preload` option that allows custom initialization of each scheduler/worker respectively. A module or Python file passed as a `--preload` value is guaranteed to be imported before establishing any connection. A `dask_setup(service)` function is called if found, with a `Scheduler` or `Worker` instance as the argument. As the service stops, `dask_teardown(service)` is called if present.

To support additional configuration, a single `--preload` module may register additional command-line arguments by exposing `dask_setup` as a Click command. This command will be used to parse additional arguments provided to `dask-worker` or `dask-scheduler` and will be called before service initialization.

As an example, consider the following file that creates a scheduler plugin and registers it with the scheduler

```
# scheduler-setup.py
import click

from distributed.diagnostics.plugin import SchedulerPlugin

class MyPlugin(SchedulerPlugin):
    def __init__(self, print_count):
      self.print_count = print_count
      SchedulerPlugin.__init__(self)

    def add_worker(self, scheduler=None, worker=None, **kwargs):
        print("Added a new worker at:", worker)
        if self.print_count and scheduler is not None:
            print("Total workers:", len(scheduler.workers))

@click.command()
@click.option("--print-count/--no-print-count", default=False)
def dask_setup(scheduler, print_count):
    plugin = MyPlugin(print_count)
    scheduler.add_plugin(plugin)
```

We can then run this preload script by referring to its filename (or module name if it is on the path) when we start the scheduler:

```
dask-scheduler --preload scheduler-setup.py --print-count
```

Worker Lifecycle Plugins

You can also create a class with setup and teardown methods, and register that class with the scheduler to give to every worker.

`Client.register_worker_plugin`([plugin, name])	Registers a lifecycle worker plugin for all current and future workers.

`Client.register_worker_plugin`(*plugin=None*, *name=None*)
Registers a lifecycle worker plugin for all current and future workers.

This registers a new object to handle setup, task state transitions and teardown for workers in this cluster. The plugin will instantiate itself on all currently connected workers. It will also be run on any worker that connects in the future.

The plugin may include methods `setup`, `teardown`, and `transition`. See the `dask.distributed.WorkerPlugin` class or the examples below for the interface and docstrings. It must be serializable with the pickle or cloudpickle modules.

If the plugin has a `name` attribute, or if the `name=` keyword is used then that will control idempotency. A a plugin with that name has already registered then any future plugins will not run.

For alternatives to plugins, you may also wish to look into preload scripts.

Parameters

plugin: WorkerPlugin The plugin object to pass to the workers

name: str, optional A name for the plugin. Registering a plugin with the same name will have no effect.

See also:

`distributed.WorkerPlugin`

Examples

```
>>> class MyPlugin(WorkerPlugin):
...     def __init__(self, *args, **kwargs):
...         pass  # the constructor is up to you
...     def setup(self, worker: dask.distributed.Worker):
...         pass
...     def teardown(self, worker: dask.distributed.Worker):
...         pass
...     def transition(self, key: str, start: str, finish: str, **kwargs):
...         pass
```

```
>>> plugin = MyPlugin(1, 2, 3)
>>> client.register_worker_plugin(plugin)
```

You can get access to the plugin with the `get_worker` function

```
>>> client.register_worker_plugin(other_plugin, name='my-plugin')
>>> def f():
...    worker = get_worker()
...    plugin = worker.plugins['my-plugin']
...    return plugin.my_state
```

```
>>> future = client.run(f)
```

3.3 Community

Dask is used and developed by individuals at a variety of institutions. It sits within the broader Python numeric ecosystem commonly referred to as PyData or SciPy.

3.3.1 Discussion

Conversation happens in the following places:

1. **Usage questions** are directed to Stack Overflow with the #dask tag. Dask developers monitor this tag and get e-mails whenever a question is asked
2. **Bug reports and feature requests** are managed on the GitHub issue tracker
3. **Chat** occurs on at gitter.im/dask/dask for general conversation and gitter.im/dask/dev for developer conversation. Note that because gitter chat is not searchable by future users we discourage usage questions and bug reports on gitter and instead ask people to use Stack Overflow or GitHub.

4. **Monthly developer meeting** happens the first Thursday of the month at 11:00 US Central Time in this video meeting. Subscribe to this Google Calendar invite to be notified of changes to the meeting schedule. Meeting notes are available at https://docs.google.com/document/d/1UqNAP87a56ERH_xkQsS5Q_0PKYybd5Lj2WANy_hRzI0/edit

3.3.2 Asking for help

We welcome usage questions and bug reports from all users, even those who are new to using the project. There are a few things you can do to improve the likelihood of quickly getting a good answer.

1. **Ask questions in the right place**: We strongly prefer the use of Stack Overflow or GitHub issues over Gitter chat. GitHub and Stack Overflow are more easily searchable by future users, and therefore is more efficient for everyone's time. Gitter chat is strictly reserved for developer and community discussion.

   If you have a general question about how something should work or want best practices then use Stack Overflow. If you think you have found a bug then use GitHub

2. **Ask only in one place**: Please restrict yourself to posting your question in only one place (likely Stack Overflow or GitHub) and don't post in both

3. **Create a minimal example**: It is ideal to create minimal, complete, verifiable examples. This significantly reduces the time that answerers spend understanding your situation, resulting in higher quality answers more quickly.

   See also this blogpost about crafting minimal bug reports. These have a much higher likelihood of being answered

3.3.3 Paid support

In addition to the previous options, paid support is available from

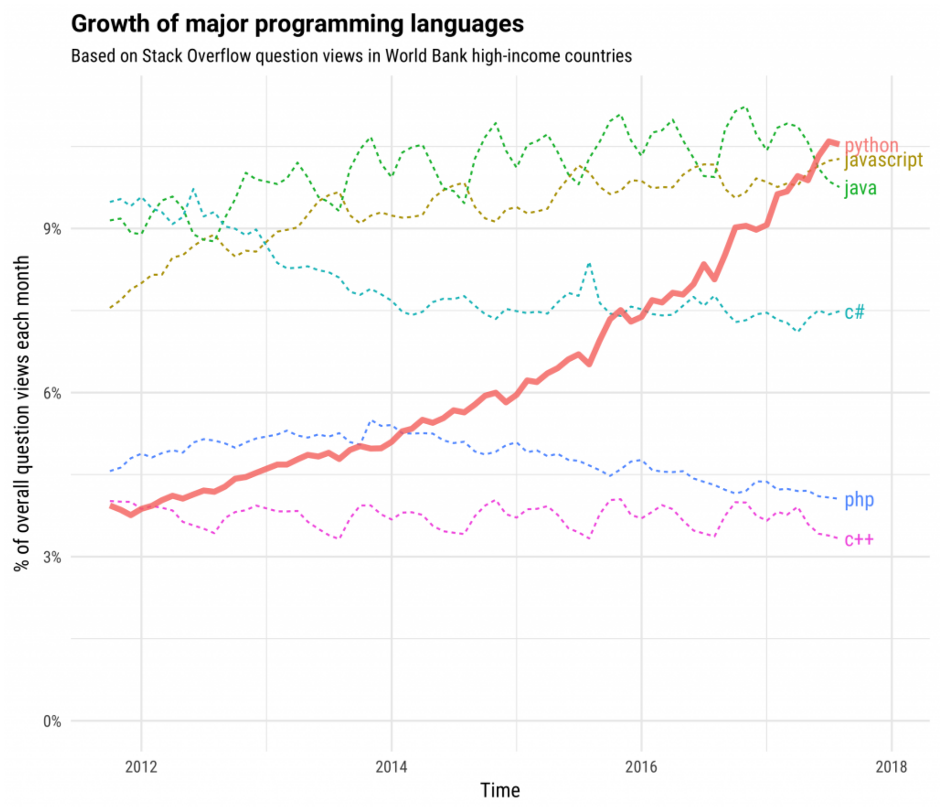
- Anaconda: https://www.anaconda.com/support
- Quansight: https://www.quansight.com/open-source-support

3.4 Why Dask?

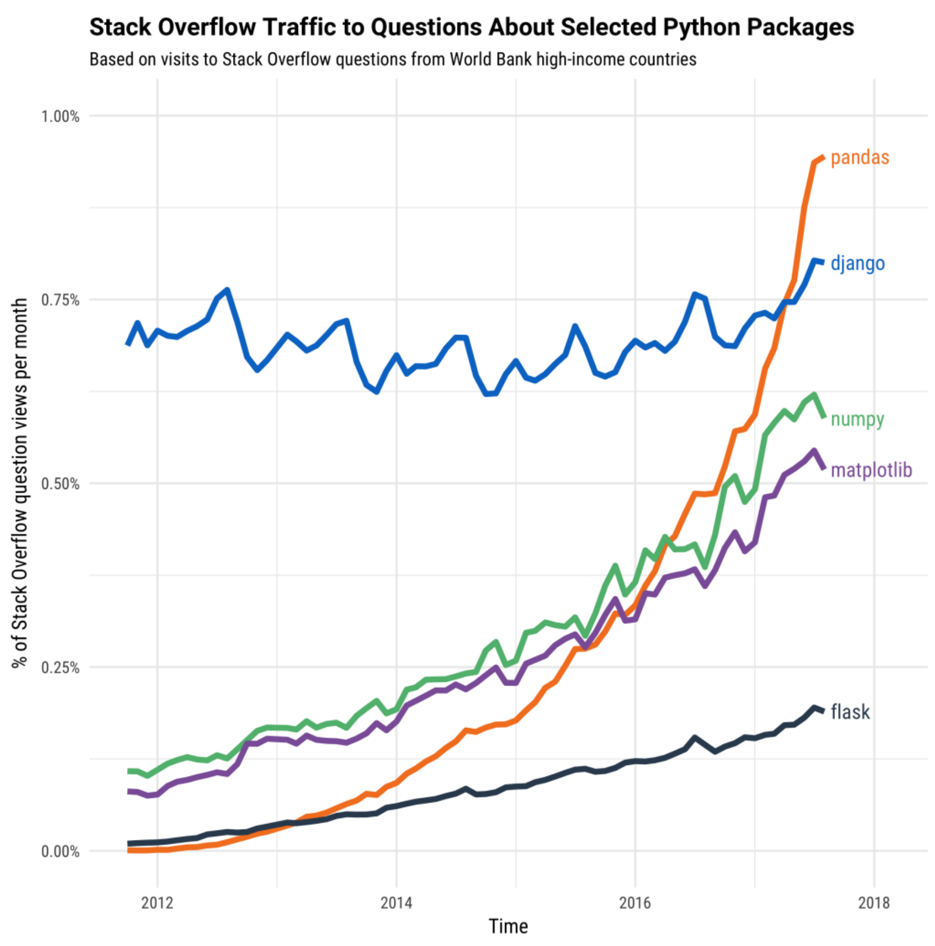
This document gives high-level motivation on why people choose to adopt Dask.

3.4.1 Python's role in Data Science

Python has grown to become the dominant language both in data analytics and general programming:



This is fueled both by computational libraries like Numpy, Pandas, and Scikit-Learn and by a wealth of libraries for visualization, interactive notebooks, collaboration, and so forth.



However, these packages were not designed to scale beyond a single machine. Dask was developed to scale these packages and the surrounding ecosystem. It works with the existing Python ecosystem to scale it to multi-core machines and distributed clusters.

Image credit to Stack Overflow blogposts #1 *and* #2.

3.4.2 Dask has a Familiar API

Analysts often use tools like Pandas, Scikit-Learn, Numpy, and the rest of the Python ecosystem to analyze data on their personal computer. They like these tools because they are efficient, intuitive, and widely trusted. However, when they choose to apply their analyses to larger datasets, they find that these tools were not designed to scale beyond a single machine. And so, the analyst rewrites their computation using a more scalable tool, often in another language altogether. This rewrite process slows down discovery and causes frustration.

Dask provides ways to scale Pandas, Scikit-Learn, and Numpy workflows more natively, with minimal rewriting. It integrates well with these tools so that it copies most of their API and uses their data structures internally. Moreover, Dask is co-developed with these libraries to ensure that they evolve consistently, minimizing friction when transitioning from a local laptop, to a multi-core workstation, and then to a distributed cluster. Analysts familiar with Pandas/Scikit-Learn/Numpy will be immediately familiar with their Dask equivalents, and have much of their intuition carry over to a scalable context.

3.4.3 Dask Scales out to Clusters

As datasets and computations scale faster than CPUs and RAM, we need to find ways to scale our computations across multiple machines. This introduces many new concerns:

- How to have computers talk to each other over the network?
- How and when to move data between machines?
- How to recover from machine failures?
- How to deploy on an in-house cluster?
- How to deploy on the cloud?
- How to deploy on an HPC super-computer?
- How to provide an API to this system that users find intuitive?
- . . .

While it is possible to build these systems in-house (and indeed, many exist), many organizations increasingly depend on solutions developed within the open source community. These tend to be more robust, secure, and fully featured without being tended by in-house staff.

Dask solves the problems above. It figures out how to break up large computations and route parts of them efficiently onto distributed hardware. Dask is routinely run on thousand-machine clusters to process hundreds of terabytes of data efficiently within secure environments.

Dask has utilities and documentation on how to deploy in-house, on the cloud, or on HPC super-computers. It supports encryption and authentication using TLS/SSL certificates. It is resilient and can handle the failure of worker nodes gracefully and is elastic, and so can take advantage of new nodes added on-the-fly. Dask includes several user APIs that are used and smoothed over by thousands of researchers across the globe working in different domains.

3.4.4 Dask Scales Down to Single Computers

But a massive cluster is not always the right choice

Today's laptops and workstations are surprisingly powerful and, if used correctly, can handle datasets and computations for which we previously depended on clusters. A modern laptop has a multi-core CPU, 32GB of RAM, and flash-based hard drives that can stream through data several times faster than HDDs or SSDs of even a year or two ago.

As a result, Dask can empower analysts to manipulate 100GB+ datasets on their laptop or 1TB+ datasets on a workstation without bothering with the cluster at all. This can be preferable for the following reasons:

1. They can use their local software environment, rather than being constrained by what is available on the cluster or having to manage Docker images.
2. They can more easily work while in transit, at a coffee shop, or at home away from the corporate network
3. Debugging errors and analyzing performance is simpler and more pleasant on a single machine
4. Their iteration cycles can be faster
5. Their computations may be more efficient because all of the data is local and doesn't need to flow through the network or between separate processes

Dask can enable efficient parallel computations on single machines by leveraging their multi-core CPUs and streaming data efficiently from disk. It *can* run on a distributed cluster, but it doesn't *have* to. Dask allows you to swap out the cluster for single-machine schedulers which are surprisingly lightweight, require no setup, and can run entirely within the same process as the user's session.

To avoid excess memory use, Dask is good at finding ways to evaluate computations in a low-memory footprint when possible by pulling in chunks of data from disk, doing the necessary processing, and throwing away intermediate values as quickly as possible. This lets analysts perform computations on moderately large datasets (100GB+) even on relatively low-power laptops. This requires no configuration and no setup, meaning that adding Dask to a single-machine computation adds very little cognitive overhead.

Dask is installed by default with Anaconda and so is already deployed on most data science machines.

3.4.5 Dask Integrates Natively with Python Code

Python includes computational libraries like Numpy, Pandas, and Scikit-Learn, and many others for data access, plotting, statistics, image and signal processing, and more. These libraries work together seamlessly to produce a cohesive *ecosystem* of packages that co-evolve to meet the needs of analysts in most domains today.

This ecosystem is tied together by common standards and protocols to which everyone adheres, which allows these packages to benefit each other in surprising and delightful ways.

Dask evolved from within this ecosystem. It abides by these standards and protocols and actively engages in community efforts to push forward new ones. This enables the rest of the ecosystem to benefit from parallel and distributed computing with minimal coordination. Dask does not seek to disrupt or displace the existing ecosystem, but rather to complement and benefit it from within.

As a result, Dask development is pushed forward by developer communities from Pandas, Numpy, Scikit-Learn, Scikit-Image, Jupyter, and others. This engagement from the broader community growth helps users to trust the project and helps to ensure that the Python ecosystem will continue to evolve in a smooth and sustainable manner.

3.4.6 Dask Supports Complex Applications

Some parallel computations are simple and just apply the same routine onto many inputs without any kind of coordination. These are simple to parallelize with any system.

Somewhat more complex computations can be expressed with the map-shuffle-reduce pattern popularized by Hadoop and Spark. This is often sufficient to do most data cleaning tasks, database-style queries, and some lightweight machine learning algorithms.

However, more complex parallel computations exist which do not fit into these paradigms, and so are difficult to perform with traditional big-data technologies. These include more advanced algorithms for statistics or machine learning, time series or local operations, or bespoke parallelism often found within the systems of large enterprises.

Many companies and institutions today have problems which are clearly parallelizable, but not clearly transformable into a big DataFrame computation. Today these companies tend to solve their problems either by writing custom code with low-level systems like MPI, ZeroMQ, or sockets and complex queuing systems, or by shoving their problem into a standard big-data technology like MapReduce or Spark, and hoping for the best.

Dask helps to resolve these situations by exposing low-level APIs to its internal task scheduler which is capable of executing very advanced computations. This gives engineers within the institution the ability to build their own parallel computing system using the same engine that powers Dask's arrays, DataFrames, and machine learning algorithms, but now with the institution's own custom logic. This allows engineers to keep complex business logic in-house while still relying on Dask to handle network communication, load balancing, resilience, diagnostics, etc..

3.4.7 Dask Delivers Responsive Feedback

Because everything happens remotely, interactive parallel computing can be frustrating for users. They don't have a good sense of how computations are progressing, what might be going wrong, or what parts of their code should they focus on for performance. The added distance between a user and their computation can drastically affect how quickly they are able to identify and resolve bugs and performance problems, which can drastically increase their time to solution.

Dask keeps users informed and content with a suite of helpful diagnostic and investigative tools including the following:

1. A *real-time and responsive dashboard* that shows current progress, communication costs, memory use, and more, updated every 100ms
2. A statistical profiler installed on every worker that polls each thread every 10ms to determine which lines in your code are taking up the most time across your entire computation
3. An embedded IPython kernel in every worker and the scheduler, allowing users to directly investigate the state of their computation with a pop-up terminal
4. The ability to reraise errors locally, so that they can use the traditional debugging tools to which they are accustomed, even when the error happens remotely

3.4.8 Links and More Information

From here you may want to read about some of our more common introductory content:

- *User Interfaces*
- *Scheduling*
- *Comparison to Spark*
- Slides

3.5 Institutional FAQ

Question: *Is appropriate for adoption within a larger institutional context?*

Answer: *Yes.* Dask is used within the world's largest banks, national labs, retailers, technology companies, and government agencies. It is used in highly secure environments. It is used in conservative institutions as well as fast moving ones.

This page contains Frequently Asked Questions and concerns from institutions when they first investigate Dask.

3.5.1 For Management

Briefly, what problem does Dask solve for us?

Dask is a general purpose parallel programming solution. As such it is used in *many* different ways.

However, the most common problem that Dask solves is connecting Python analysts to distributed hardware, particularly for data science and machine learning workloads. The institutions for whom Dask has the greatest impact are those who have a large body of Python users who are accustomed to libraries like NumPy, Pandas, Jupyter, Scikit-Learn and others, but want to scale those workloads across a cluster. Often they also have distributed computing resources that are going underused.

Dask removes both technological and cultural barriers to connect Python users to computing resources in a way that is native to both the users and IT.

"*Help me scale my notebook onto the cluster*" is a common pain point for institutions today, and it is a common entry point for Dask usage.

Is Dask mature? Why should we trust it?

Yes. While Dask itself is relatively new (it began in 2015) it is built by the NumPy, Pandas, Jupyter, Scikit-Learn developer community, which is well trusted. Dask is a relatively thin wrapper on top of these libraries and, as a result, the project can be relatively small and simple. It doesn't reinvent a whole new system.

Additionally, this tight integration with the broader technology stack gives substantial benefits long term. For example:

- Because Pandas maintainers also maintain Dask, when Pandas issues a new releases Dask issues a release at the same time to ensure continuity and compatibility.
- Because Scikit-Learn maintainers maintain and use Dask when they train on large clusters, you can be assured that Dask-ML focuses on pragmatic and important solutions like XGBoost integration, and hyper-parameter selection, and that the integration between the two feels natural for novice and expert users alike.
- Because Jupyter maintainers also maintain Dask, powerful Jupyter technologies like JupyterHub and JupyterLab are designed with Dask's needs in mind, and new features are pushed quickly to provide a first class and modern user experience.

Additionally, Dask is maintained both by a broad community of maintainers, as well as substantial institutional support (several full-time employees each) by both Anaconda, the company behind the leading data science distribution, and NVIDIA, the leading hardware manufacturer of GPUs. Despite large corporate support, Dask remains a community governed project, and is fiscally sponsored by NumFOCUS, the same 501c3 that fiscally sponsors NumPy, Pandas, Jupyter, and many others.

Who else uses Dask?

Dask is used by individual researchers in practically every field today. It has millions of downloads per month, and is integrated into many PyData software packages today.

On an *institutional* level Dask is used by analytics and research groups in a similarly broad set of domains across both energetic startups as well as large conservative household names. A web search shows articles by Capital One, Barclays, Walmart, NASA, Los Alamos National Laboratories, and hundreds of other similar institutions.

How does Dask compare with Apache Spark?

This question has longer and more technical coverage here

Dask and Apache Spark are similar in that they both . . .

- Promise easy parallelism for data science Python users
- Provide Dataframe and ML APIs for ETL, data science, and machine learning
- Scale out to similar scales, around 1-1000 machines

Dask differs from Apache Spark in a few ways:

- Dask is more Python native, Spark is Scala/JVM native with Python bindings.

  Python users may find Dask more comfortable, but Dask is only useful for Python users, while Spark can also be used from JVM languages.

- Dask is one component in the broader Python ecosystem alongside libraries like Numpy, Pandas, and Scikit-Learn, while Spark is an all-in-one system that re-invents much of the Python world in a single package.

  This means that it's often easier to compose Dask with new problem domains, but also that you need to install multiple things (like Dask and Pandas or Dask and Numpy) rather than just having everything in an all-in-one solution.

- Apache Spark focuses strongly on traditional business intelligence workloads, like ETL, SQL queries, and then some lightweight machine learning, while Dask is more general purpose.

  This means that Dask is much more flexible and can handle other problem domains like multi-dimensional arrays, GIS, advanced machine learning, and custom systems, but that it is less focused and less tuned on typical SQL style computations.

  If you mostly want to focus on SQL queries then Spark is probably a better bet. If you want to support a wide variety of custom workloads then Dask might be more natural.

3.5.2 For IT

How would I set up Dask on institutional hardware?

You already have cluster resources. Dask can run on them today without significant change.

Most institutional clusters today have a resource manager. This is typically managed by IT, with some mild permissions given to users to launch jobs. Dask works with all major resource managers today, including those on Hadoop, HPC, Kubernetes, and Cloud clusters.

1. **Hadoop/Spark**: If you have a Hadoop/Spark cluster, such as one purchased through Cloudera/Hortonworks/MapR then you will likely want to deploy Dask with YARN, the resource manager that deploys services like Hadoop, Spark, Hive, and others.

   To help with this, you'll likely want to use Dask-Yarn.

2. **HPC**: If you have an HPC machine that runs resource managers like SGE, SLLURM, PBS, LSF, Torque, Condor, or other job batch queuing systems, then users can launch Dask on these systems today using either:

   - Dask Jobqueue , which uses typical

     `qsub`, `sbatch`, `bsub` or other submission tools in interactive settings.

   - Dask MPI which uses MPI for deployment in

     batch settings

   For more information see *High Performance Computers*

3. **Kubernetes/Cloud**: Newer clusters may employ Kubernetes for deployment. This is particularly commonly used today on major cloud providers, all of which provide hosted Kubernetes as a service. People today use Dask on Kubernetes using either of the following:

   - **Helm**: an easy way to stand up a long-running Dask cluster and

     Jupyter notebook

   - **Dask-Kubernetes**: for native Kubernetes integration for fast moving

     or ephemeral deployments.

   For more information see *Kubernetes*

Is Dask secure?

Dask is deployed today within highly secure institutions, including major financial, healthcare, and government agencies.

That being said it's worth noting that, by it's very nature, Dask enables the execution of arbitrary user code on a large set of machines. Care should be taken to isolate, authenticate, and govern access to these machines. Fortunately, your institution likely already does this and uses standard technologies like SSL/TLS, Kerberos, and other systems with which Dask can integrate.

Do I need to purchase a new cluster?

No. It is easy to run Dask today on most clusters. If you have a pre-existing HPC or Spark/Hadoop cluster then that will be fine to start running Dask.

You can start using Dask without any capital expenditure.

How do I manage users?

Dask doesn't manage users, you likely have existing systems that do this well. In a large institutional setting we assume that you already have a resource manager like Yarn (Hadoop), Kubernetes, or PBS/SLURM/SGE/LSF/..., each of which have excellent user management capabilities, which are likely preferred by your IT department anyway.

Dask is designed to operate with user-level permissions, which means that your data science users should be able to ask those systems mentioned above for resources, and have their processes tracked accordingly.

However, there are institutions where analyst-level users aren't given direct access to the cluster. This is particularly common in Cloudera/Hortonworks Hadoop/Spark deployments. In these cases some level of explicit indirection may be required. For this, we recommend the Dask Gateway project, which uses IT-level permissions to properly route authenticated users into secure resources.

How do I manage software environments?

This depends on your cluster resource manager:

- Most HPC users use their network file system
- Hadoop/Spark/Yarn users package their environment into a tarball and ship it around with HDFS (Dask-Yarn integrates with Conda Pack for this capability)
- Kubernetes or Cloud users use Docker images

In each case Dask integrates with existing processes and technologies that are well understood and familiar to the institution.

How does Dask communicate data between machines?

Dask usually communicates over TCP, using msgpack for small administrative messages, and its own protocol for efficiently passing around large data. The scheduler and each worker host their own TCP server, making Dask a distributed peer-to-peer network that uses point-to-point communication. We do not use Spark-style shuffle systems. We do not use MPI-style collectives. Everything is direct point-to-point.

For high performance networks you can use either TCP-over-Infiniband for about 1 GB/s bandwidth, or UCX (experimental) for full speed communication.

Are deployments long running, or ephemeral?

We see both, but ephemeral deployments are more common.

Most Dask use today is about enabling data science or data engineering users to scale their interactive workloads across the cluster. These are typically either interactive sessions with Jupyter, or batch scripts that run at a pre-defined time. In both cases, the user asks the resource manager for a bunch of machines, does some work, and then gives up those machines.

Some institutions also use Dask in an always-on fashion, either handling real-time traffic in a scalable way, or responding to a broad set of interactive users with large datasets that it keeps resident in memory.

3.5.3 For Technical Leads

Will Dask "just work" on our existing code?

No, you will need to make modifications, but these modifications are usually small.

The vast majority of lines of business logic within your institution will not have to change, assuming that they are in Python and use tooling like Numpy, Pandas and Scikit-Learn.

How well does Dask scale? What are Dask's limitations?

The largest Dask deployments that we see today are on around 1000 multi-core machines, perhaps 20,000 cores in total, but these are rare. Most institutional-level problems (1-100 TB) are well solved by deployments of 10-50 nodes.

Technically, the back-of-the-envelope number to keep in mind is that each task (an individual Python function call) in Dask has an overhead of around *200 microseconds*. So if these tasks take 1 second each, then Dask can saturate around 5000 cores before scheduling overhead dominates costs. As workloads reach this limit they are encouraged to use larger chunk sizes to compensate. The *vast majority* of institutional users though do not reach this limit. For more information you may want to peruse our *best practices*

Is Dask resilient? What happens when a machine goes down?

Yes, Dask is resilient to the failure of worker nodes. It knows how it came to any result, and can replay the necessary work on other machines if one goes down.

If Dask's centralized scheduler goes down then you would need to resubmit the computation. This is a fairly standard level of resiliency today, shared with other tooling like Apache Spark, Flink, and others.

The resource managers that host Dask, like Yarn or Kubernetes, typically provide long-term 24/7 resilience for always-on operation.

Is the API exactly the same as NumPy/Pandas/Scikit-Learn?

No, but it's very close. That being said your data scientists will still have to learn some things.

What we find is that the Numpy/Pandas/Scikit-Learn APIs aren't the challenge when institutions adopt Dask. When API inconsistencies do exist, even modestly skilled programmers are able to understand why and work around them without much pain.

Instead, the challenge is building intuition around parallel performance. We've all built up a mental model for what is fast and slow on a single machine. This model changes when we factor in network communication and parallel algorithms, and the performance that we get for familiar operations can be surprising.

Our main solution to build this intuition, other than accumulated experience, is Dask's *Diagnostic Dashboard*. The dashboard delivers a ton of visual feedback to users as they are running their computation to help them understand what is going on. This both helps them to identify and resolve immediate bottlenecks, and also builds up that parallel performance intuition surprisingly quickly.

How much performance tuning does Dask require?

Some other systems are notoriously hard to tune for optimal performance. What is Dask's story here? How many knobs are there that we need to be aware of?

Like the rest of the Python software tools, Dask puts a lot of effort into having sane defaults. Dask workers automatically detect available memory and cores, and choose sensible defaults that are decent in most situations. Dask algorithms similarly provide decent choices by default, and informative warnings when tricky situations arise, so that, in common cases, things should be fine.

The most common knobs to tune include the following:

- The thread/process mixture to deal with GIL-holding computations (which are rare in Numpy/Pandas/Scikit-Learn workflows)
- Partition size, like if should you have 100 MB chunks or 1 GB chunks

That being said, almost no institution's needs are met entirely by the common case, and given the variety of problems that people throw at Dask, exceptional problems are commonplace. In these cases we recommend watching the dashboard during execution to see what is going on. It can commonly inform you what's going wrong, so that you can make changes to your system.

What Data formats does Dask support?

Because Dask builds on NumPy and Pandas, it supports most formats that they support, which is most formats. That being said, not all formats are well suited for parallel access. In general people using the following formats are usually pretty happy:

- **Tabular:** Parquet, ORC, CSV, Line Delimited JSON, Avro, text
- **Arrays:** HDF5, NetCDF, Zarr, GRIB

More generally, if you have a Python function that turns a chunk of your stored data into a Pandas dataframe or Numpy array then Dask can probably call that function many times without much effort.

For groups looking for advice on which formats to use, we recommend Parquet for tables and Zarr or HDF5 for arrays.

Does Dask have a SQL interface?

No. Dask provides no SQL support. Dask dataframe looks like and uses Pandas for these sorts of operations. It would be great to see someone build a SQL interface on top of Pandas, which Dask could then use, but this is out of scope for the core Dask project itself.

As with Pandas though, we do support a `dask.dataframe.from_sql` command for efficiently pulling data out of SQL databases for Pandas computations.

3.6 User Interfaces

Dask supports several user interfaces:

- **High-Level**
  - *Arrays*: Parallel NumPy
  - *Bags*: Parallel lists
  - *DataFrames*: Parallel Pandas
  - Machine Learning : Parallel Scikit-Learn
  - Others from external projects, like XArray
- **Low-Level**
  - *Delayed*: Parallel function evaluation
  - *Futures*: Real-time parallel function evaluation

Each of these user interfaces employs the same underlying parallel computing machinery, and so has the same scaling, diagnostics, resilience, and so on, but each provides a different set of parallel algorithms and programming style.

This document helps you to decide which user interface best suits your needs, and gives some general information that applies to all interfaces. The pages linked above give more information about each interface in greater depth.

3.6.1 High-Level Collections

Many people who start using Dask are explicitly looking for a scalable version of NumPy, Pandas, or Scikit-Learn. For these situations, the starting point within Dask is usually fairly clear. If you want scalable NumPy arrays, then start with Dask array; if you want scalable Pandas DataFrames, then start with Dask DataFrame, and so on.

These high-level interfaces copy the standard interface with slight variations. These interfaces automatically parallelize over larger datasets for you for a large subset of the API from the original project.

```
# Arrays
import dask.array as da
x = da.random.uniform(low=0, high=10, size=(10000, 10000),  # normal numpy code
                      chunks=(1000, 1000))  # break into chunks of size 1000x1000

y = x + x.T - x.mean(axis=0)  # Use normal syntax for high level algorithms

# DataFrames
import dask.dataframe as dd
df = dd.read_csv('2018-*-*.csv', parse_dates='timestamp',  # normal Pandas code
                 blocksize=64000000)  # break text into 64MB chunks

s = df.groupby('name').balance.mean()  # Use normal syntax for high level algorithms

# Bags / lists
import dask.bag as db
b = db.read_text('*.json').map(json.loads)
total = (b.filter(lambda d: d['name'] == 'Alice')
          .map(lambda d: d['balance'])
          .sum())
```

It is important to remember that, while APIs may be similar, some differences do exist. Additionally, the performance of some algorithms may differ from their in-memory counterparts due to the advantages and disadvantages of parallel programming. Some thought and attention is still required when using Dask.

3.6.2 Low-Level Interfaces

Often when parallelizing existing code bases or building custom algorithms, you run into code that is parallelizable, but isn't just a big DataFrame or array. Consider the for-loopy code below:

```
results = []
for a in A:
    for b in B:
        if a < b:
            c = f(a, b)
        else:
            c = g(a, b)
        results.append(c)
```

There is potential parallelism in this code (the many calls to `f` and `g` can be done in parallel), but it's not clear how to rewrite it into a big array or DataFrame so that it can use a higher-level API. Even if you could rewrite it into one of these paradigms, it's not clear that this would be a good idea. Much of the meaning would likely be lost in translation, and this process would become much more difficult for more complex systems.

Instead, Dask's lower-level APIs let you write parallel code one function call at a time within the context of your existing for loops. A common solution here is to use *Dask delayed* to wrap individual function calls into a lazily constructed task graph:

```
import dask

lazy_results = []
for a in A:
    for b in B:
        if a < b:
            c = dask.delayed(f)(a, b)  # add lazy task
        else:
            c = dask.delayed(g)(a, b)  # add lazy task
        lazy_results.append(c)

results = dask.compute(*lazy_results)  # compute all in parallel
```

3.6.3 Combining High- and Low-Level Interfaces

It is common to combine high- and low-level interfaces. For example, you might use Dask array/bag/dataframe to load in data and do initial pre-processing, then switch to Dask delayed for a custom algorithm that is specific to your domain, then switch back to Dask array/dataframe to clean up and store results. Understanding both sets of user interfaces, and how to switch between them, can be a productive combination.

```
# Convert to a list of delayed Pandas dataframes
delayed_values = df.to_delayed()

# Manipulate delayed values arbitrarily as you like

# Convert many delayed Pandas DataFrames back to a single Dask DataFrame
df = dd.from_delayed(delayed_values)
```

3.6.4 Laziness and Computing

Most Dask user interfaces are *lazy*, meaning that they do not evaluate until you explicitly ask for a result using the `compute` method:

```
# This array syntax doesn't cause computation
y = x + x.T - x.mean(axis=0)

# Trigger computation by explicitly calling the compute method
y = y.compute()
```

If you have multiple results that you want to compute at the same time, use the `dask.compute` function. This can share intermediate results and so be more efficient:

```
# compute multiple results at the same time with the compute function
min, max = dask.compute(y.min(), y.max())
```

Note that the `compute()` function returns in-memory results. It converts Dask DataFrames to Pandas DataFrames, Dask arrays to NumPy arrays, and Dask bags to lists. *You should only call compute on results that will fit comfortably in memory*. If your result does not fit in memory, then you might consider writing it to disk instead.

```
# Write larger results out to disk rather than store them in memory
my_dask_dataframe.to_parquet('myfile.parquet')
my_dask_array.to_hdf5('myfile.hdf5')
my_dask_bag.to_textfiles('myfile.*.txt')
```

3.6.5 Persist into Distributed Memory

Alternatively, if you are on a cluster, then you may want to trigger a computation and store the results in distributed memory. In this case you do not want to call `compute`, which would create a single Pandas, NumPy, or list result. Instead, you want to call `persist`, which returns a new Dask object that points to actively computing, or already computed results spread around your cluster's memory.

```
# Compute returns an in-memory non-Dask object
y = y.compute()

# Persist returns an in-memory Dask object that uses distributed storage if available
y = y.persist()
```

This is common to see after data loading an preprocessing steps, but before rapid iteration, exploration, or complex algorithms. For example, we might read in a lot of data, filter down to a more manageable subset, and then persist data into memory so that we can iterate quickly.

```
import dask.dataframe as dd
df = dd.read_parquet('...')
df = df[df.name == 'Alice']  # select important subset of data
df = df.persist()  # trigger computation in the background

# These are all relatively fast now that the relevant data is in memory
df.groupby(df.id).balance.sum().compute()   # explore data quickly
df.groupby(df.id).balance.mean().compute()  # explore data quickly
df.id.nunique()                             # explore data quickly
```

3.6.6 Lazy vs Immediate

As mentioned above, most Dask workloads are lazy, that is, they don't start any work until you explicitly trigger them with a call to `compute()`. However, sometimes you *do* want to submit work as quickly as possible, track it over time, submit new work or cancel work depending on partial results, and so on. This can be useful when tracking or responding to real-time events, handling streaming data, or when building complex and adaptive algorithms.

For these situations, people typically turn to the *futures interface* which is a low-level interface like Dask delayed, but operates immediately rather than lazily.

Here is the same example with Dask delayed and Dask futures to illustrate the difference.

Delayed: Lazy

```
@dask.delayed
def inc(x):
    return x + 1

@dask.delayed
def add(x, y):
    return x + y

a = inc(1)       # no work has happened yet
b = inc(2)       # no work has happened yet
c = add(a, b)    # no work has happened yet

c = c.compute()  # This triggers all of the above computations
```

Futures: Immediate

```
from dask.distributed import Client
client = Client()

def inc(x):
    return x + 1

def add(x, y):
    return x + y

a = client.submit(inc, 1)      # work starts immediately
b = client.submit(inc, 2)      # work starts immediately
c = client.submit(add, a, b)   # work starts immediately

c = c.result()                 # block until work finishes, then gather result
```

You can also trigger work with the high-level collections using the `persist` function. This will cause work to happen in the background when using the distributed scheduler.

3.6.7 Combining Interfaces

There are established ways to combine the interfaces above:

1. The high-level interfaces (array, bag, dataframe) have a `to_delayed` method that can convert to a sequence (or grid) of Dask delayed objects

   ```
   delayeds = df.to_delayed()
   ```

2. The high-level interfaces (array, bag, dataframe) have a `from_delayed` method that can convert from either Delayed *or* Future objects

   ```
   df = dd.from_delayed(delayeds)
   df = dd.from_delayed(futures)
   ```

3. The `Client.compute` method converts Delayed objects into Futures

   ```
   futures = client.compute(delayeds)
   ```

4. The `dask.distributed.futures_of` function gathers futures from persisted collections

   ```
   from dask.distributed import futures_of

   df = df.persist()  # start computation in the background
   futures = futures_of(df)
   ```

5. The Dask.delayed object converts Futures into delayed objects

   ```
   delayed_value = dask.delayed(future)
   ```

The approaches above should suffice to convert any interface into any other. We often see some anti-patterns that do not work as well:

1. Calling low-level APIs (delayed or futures) on high-level objects (like Dask arrays or DataFrames). This downgrades those objects to their NumPy or Pandas equivalents, which may not be desired. Often people are looking for APIs like `dask.array.map_blocks` or `dask.dataframe.map_partitions` instead.

2. Calling `compute()` on Future objects. Often people want the `.result()` method instead.
3. Calling NumPy/Pandas functions on high-level Dask objects or high-level Dask functions on NumPy/Pandas objects

3.6.8 Conclusion

Most people who use Dask start with only one of the interfaces above but eventually learn how to use a few interfaces together. This helps them leverage the sophisticated algorithms in the high-level interfaces while also working around tricky problems with the low-level interfaces.

For more information, see the documentation for the particular user interfaces below:

- **High Level**
  - *Arrays*: Parallel NumPy
  - *Bags*: Parallel lists
  - *DataFrames*: Parallel Pandas
  - Machine Learning : Parallel Scikit-Learn
  - Others from external projects, like XArray
- **Low Level**
  - *Delayed*: Parallel function evaluation
  - *Futures*: Real-time parallel function evaluation

3.7 Array

3.7.1 API

Top level user functions:

`all`(a[, axis, out, keepdims])	Test whether all array elements along a given axis evaluate to True.
`allclose`(arr1, arr2[, rtol, atol, equal_nan])	Returns True if two arrays are element-wise equal within a tolerance.
`angle`(x[, deg])	Return the angle of the complex argument.
`any`(a[, axis, out, keepdims])	Test whether any array element along a given axis evaluates to True.
`apply_along_axis`(func1d, axis, arr, *args[, . . .])	Apply a function to 1-D slices along the given axis.
`apply_over_axes`(func, a, axes)	Apply a function repeatedly over multiple axes.
`arange`(*args, **kwargs)	Return evenly spaced values from *start* to *stop* with step size *step*.
`arccos`(x, /[, out, where, casting, order, . . .])	Trigonometric inverse cosine, element-wise.
`arccosh`(x, /[, out, where, casting, order, . . .])	Inverse hyperbolic cosine, element-wise.
`arcsin`(x, /[, out, where, casting, order, . . .])	Inverse sine, element-wise.
`arcsinh`(x, /[, out, where, casting, order, . . .])	Inverse hyperbolic sine element-wise.
`arctan`(x, /[, out, where, casting, order, . . .])	Trigonometric inverse tangent, element-wise.
`arctan2`(x1, x2, /[, out, where, casting, . . .])	Element-wise arc tangent of `x1/x2` choosing the quadrant correctly.

Continued on next page

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`arctanh`(x, /[, out, where, casting, order, . . .])	Inverse hyperbolic tangent element-wise.
`argmax`(a[, axis, out])	Returns the indices of the maximum values along an axis.
`argmin`(a[, axis, out])	Returns the indices of the minimum values along an axis.
`argtopk`(a, k[, axis, split_every])	Extract the indices of the k largest elements from a on the given axis, and return them sorted from largest to smallest.
`argwhere`(a)	Find the indices of array elements that are non-zero, grouped by element.
`around`(x[, decimals])	Evenly round to the given number of decimals.
`array`(object[, dtype, copy, order, subok, ndmin])	This docstring was copied from numpy.array.
`asanyarray`(a)	Convert the input to a dask array.
`asarray`(a, **kwargs)	Convert the input to a dask array.
`atleast_1d`(*arys)	Convert inputs to arrays with at least one dimension.
`atleast_2d`(*arys)	View inputs as arrays with at least two dimensions.
`atleast_3d`(*arys)	View inputs as arrays with at least three dimensions.
`average`(a[, axis, weights, returned])	Compute the weighted average along the specified axis.
`bincount`(x[, weights, minlength])	This docstring was copied from numpy.bincount.
`bitwise_and`(x1, x2, /[, out, where, . . .])	Compute the bit-wise AND of two arrays element-wise.
`bitwise_not`(x, /[, out, where, casting, . . .])	Compute bit-wise inversion, or bit-wise NOT, element-wise.
`bitwise_or`(x1, x2, /[, out, where, casting, . . .])	Compute the bit-wise OR of two arrays element-wise.
`bitwise_xor`(x1, x2, /[, out, where, . . .])	Compute the bit-wise XOR of two arrays element-wise.
`block`(arrays[, allow_unknown_chunksizes])	Assemble an nd-array from nested lists of blocks.
`blockwise`(func, out_ind, *args[, name, . . .])	Tensor operation: Generalized inner and outer products
`broadcast_arrays`(*args, **kwargs)	Broadcast any number of arrays against each other.
`broadcast_to`(x, shape[, chunks])	Broadcast an array to a new shape.
`coarsen`(reduction, x, axes[, trim_excess])	Coarsen array by applying reduction to fixed size neighborhoods
`ceil`(x, /[, out, where, casting, order, . . .])	Return the ceiling of the input, element-wise.
`choose`(a, choices)	Construct an array from an index array and a set of arrays to choose from.
`clip`(*args, **kwargs)	Clip (limit) the values in an array.
`compress`(condition, a[, axis])	Return selected slices of an array along given axis.
`concatenate`(seq[, axis, . . .])	Concatenate arrays along an existing axis
`conj`(x, /[, out, where, casting, order, . . .])	Return the complex conjugate, element-wise.
`copysign`(x1, x2, /[, out, where, casting, . . .])	Change the sign of x1 to that of x2, element-wise.
`corrcoef`(x[, y, rowvar])	Return Pearson product-moment correlation coefficients.
`cos`(x, /[, out, where, casting, order, . . .])	Cosine element-wise.
`cosh`(x, /[, out, where, casting, order, . . .])	Hyperbolic cosine, element-wise.
`count_nonzero`(a[, axis])	Counts the number of non-zero values in the array `a`.
`cov`(m[, y, rowvar, bias, ddof])	Estimate a covariance matrix, given data and weights.
`cumprod`(a[, axis, dtype, out])	Return the cumulative product of elements along a given axis.
`cumsum`(a[, axis, dtype, out])	Return the cumulative sum of the elements along a given axis.
`deg2rad`(x, /[, out, where, casting, order, . . .])	Convert angles from degrees to radians.
`degrees`(x, /[, out, where, casting, order, . . .])	Convert angles from radians to degrees.
`diag`(v)	Extract a diagonal or construct a diagonal array.

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diagonal(a[, offset, axis1, axis2])	Return specified diagonals.
diff(a[, n, axis])	Calculate the n-th discrete difference along the given axis.
divmod(x1, x2[, out1, out2], / [[, out, . . .])	Return element-wise quotient and remainder simultaneously.
digitize(a, bins[, right])	Return the indices of the bins to which each value in input array belongs.
dot(a, b[, out])	This docstring was copied from numpy.dot.
dstack(tup[, allow_unknown_chunksizes])	Stack arrays in sequence depth wise (along third axis).
ediff1d(ary[, to_end, to_begin])	The differences between consecutive elements of an array.
einsum(subscripts, *operands[, out, dtype, . . .])	This docstring was copied from numpy.einsum.
empty(*args, **kwargs)	Blocked variant of empty
empty_like(a[, dtype, chunks])	Return a new array with the same shape and type as a given array.
exp(x, /[, out, where, casting, order, . . .])	Calculate the exponential of all elements in the input array.
expm1(x, /[, out, where, casting, order, . . .])	Calculate `exp(x) - 1` for all elements in the array.
eye(N[, chunks, M, k, dtype])	Return a 2-D Array with ones on the diagonal and zeros elsewhere.
fabs(x, /[, out, where, casting, order, . . .])	Compute the absolute values element-wise.
fix(*args, **kwargs)	Round to nearest integer towards zero.
flatnonzero(a)	Return indices that are non-zero in the flattened version of a.
flip(m, axis)	Reverse element order along axis.
flipud(m)	Flip array in the up/down direction.
fliplr(m)	Flip array in the left/right direction.
floor(x, /[, out, where, casting, order, . . .])	Return the floor of the input, element-wise.
fmax(x1, x2, /[, out, where, casting, . . .])	Element-wise maximum of array elements.
fmin(x1, x2, /[, out, where, casting, . . .])	Element-wise minimum of array elements.
fmod(x1, x2, /[, out, where, casting, . . .])	Return the element-wise remainder of division.
frexp(x[, out1, out2], / [[, out, where, . . .])	Decompose the elements of x into mantissa and twos exponent.
fromfunction(func[, chunks, shape, dtype])	Construct an array by executing a function over each coordinate.
frompyfunc(func, nin, nout)	This docstring was copied from numpy.frompyfunc.
full(*args, **kwargs)	Blocked variant of full
full_like(a, fill_value[, dtype, chunks])	Return a full array with the same shape and type as a given array.
gradient(f, *varargs, **kwargs)	Return the gradient of an N-dimensional array.
histogram(a[, bins, range, normed, weights, . . .])	Blocked variant of `numpy.histogram()`.
hstack(tup[, allow_unknown_chunksizes])	Stack arrays in sequence horizontally (column wise).
hypot(x1, x2, /[, out, where, casting, . . .])	Given the “legs” of a right triangle, return its hypotenuse.
imag(*args, **kwargs)	Return the imaginary part of the complex argument.
indices(dimensions[, dtype, chunks])	Implements NumPy’s `indices` for Dask Arrays.
insert(arr, obj, values, axis)	Insert values along the given axis before the given indices.
invert(x, /[, out, where, casting, order, . . .])	Compute bit-wise inversion, or bit-wise NOT, element-wise.

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`isclose`(arr1, arr2[, rtol, atol, equal_nan])	Returns a boolean array where two arrays are element-wise equal within a tolerance.
`iscomplex`(*args, **kwargs)	Returns a bool array, where True if input element is complex.
`isfinite`(x, /[, out, where, casting, order, . . .])	Test element-wise for finiteness (not infinity or not Not a Number).
`isin`(element, test_elements[, . . .])	Calculates *element in test_elements*, broadcasting over *element* only.
`isinf`(x, /[, out, where, casting, order, . . .])	Test element-wise for positive or negative infinity.
`isneginf`	Return (x1 == x2) element-wise.
`isnan`(x, /[, out, where, casting, order, . . .])	Test element-wise for NaN and return result as a boolean array.
`isnull`(values)	pandas.isnull for dask arrays
`isposinf`	Return (x1 == x2) element-wise.
`isreal`(*args, **kwargs)	Returns a bool array, where True if input element is real.
`ldexp`(x1, x2, /[, out, where, casting, . . .])	Returns x1 * 2**x2, element-wise.
`linspace`(start, stop[, num, endpoint, . . .])	Return *num* evenly spaced values over the closed interval [*start*, *stop*].
`log`(x, /[, out, where, casting, order, . . .])	Natural logarithm, element-wise.
`log10`(x, /[, out, where, casting, order, . . .])	Return the base 10 logarithm of the input array, element-wise.
`log1p`(x, /[, out, where, casting, order, . . .])	Return the natural logarithm of one plus the input array, element-wise.
`log2`(x, /[, out, where, casting, order, . . .])	Base-2 logarithm of *x*.
`logaddexp`(x1, x2, /[, out, where, casting, . . .])	Logarithm of the sum of exponentiations of the inputs.
`logaddexp2`(x1, x2, /[, out, where, casting, . . .])	Logarithm of the sum of exponentiations of the inputs in base-2.
`logical_and`(x1, x2, /[, out, where, . . .])	Compute the truth value of x1 AND x2 element-wise.
`logical_not`(x, /[, out, where, casting, . . .])	Compute the truth value of NOT x element-wise.
`logical_or`(x1, x2, /[, out, where, casting, . . .])	Compute the truth value of x1 OR x2 element-wise.
`logical_xor`(x1, x2, /[, out, where, . . .])	Compute the truth value of x1 XOR x2, element-wise.
`map_overlap`(x, func, depth[, boundary, trim])	Map a function over blocks of the array with some overlap
`map_blocks`(func, *args[, name, token, . . .])	Map a function across all blocks of a dask array.
`matmul`(x1, x2, /[, out, casting, order, . . .])	This docstring was copied from numpy.matmul.
`max`(a[, axis, out, keepdims, initial])	Return the maximum of an array or maximum along an axis.
`maximum`(x1, x2, /[, out, where, casting, . . .])	Element-wise maximum of array elements.
`mean`(a[, axis, dtype, out, keepdims])	Compute the arithmetic mean along the specified axis.
`meshgrid`(*xi, **kwargs)	Return coordinate matrices from coordinate vectors.
`min`(a[, axis, out, keepdims, initial])	Return the minimum of an array or minimum along an axis.
`minimum`(x1, x2, /[, out, where, casting, . . .])	Element-wise minimum of array elements.
`modf`(x[, out1, out2], / [[, out, where, . . .])	Return the fractional and integral parts of an array, element-wise.
`moment`(a, order[, axis, dtype, keepdims, . . .])	
`moveaxis`(a, source, destination)	Move axes of an array to new positions.
`nanargmax`(x, axis, **kwargs)	
`nanargmin`(x, axis, **kwargs)	
`nancumprod`(a[, axis, dtype, out])	Return the cumulative product of array elements over a given axis treating Not a Numbers (NaNs) as one.

Continued on next page

Table 9 – continued from previous page

nancumsum(a[, axis, dtype, out])	Return the cumulative sum of array elements over a given axis treating Not a Numbers (NaNs) as zero.
nanmax(a[, axis, out, keepdims])	Return the maximum of an array or maximum along an axis, ignoring any NaNs.
nanmean(a[, axis, dtype, out, keepdims])	Compute the arithmetic mean along the specified axis, ignoring NaNs.
nanmin(a[, axis, out, keepdims])	Return minimum of an array or minimum along an axis, ignoring any NaNs.
nanprod(a[, axis, dtype, out, keepdims])	Return the product of array elements over a given axis treating Not a Numbers (NaNs) as ones.
nanstd(a[, axis, dtype, out, ddof, keepdims])	Compute the standard deviation along the specified axis, while ignoring NaNs.
nansum(a[, axis, dtype, out, keepdims])	Return the sum of array elements over a given axis treating Not a Numbers (NaNs) as zero.
nanvar(a[, axis, dtype, out, ddof, keepdims])	Compute the variance along the specified axis, while ignoring NaNs.
nan_to_num(*args, **kwargs)	Replace NaN with zero and infinity with large finite numbers.
nextafter(x1, x2, /[, out, where, casting, . . .])	Return the next floating-point value after x1 towards x2, element-wise.
nonzero(a)	Return the indices of the elements that are non-zero.
notnull(values)	pandas.notnull for dask arrays
ones(*args, **kwargs)	Blocked variant of ones
ones_like(a[, dtype, chunks])	Return an array of ones with the same shape and type as a given array.
outer(a, b)	Compute the outer product of two vectors.
pad(array, pad_width, mode, **kwargs)	Pads an array.
percentile(a, q[, interpolation, method])	Approximate percentile of 1-D array
PerformanceWarning	A warning given when bad chunking may cause poor performance
piecewise(x, condlist, funclist, *args, **kw)	Evaluate a piecewise-defined function.
prod(a[, axis, dtype, out, keepdims, initial])	Return the product of array elements over a given axis.
ptp(a[, axis])	Range of values (maximum - minimum) along an axis.
rad2deg(x, /[, out, where, casting, order, . . .])	Convert angles from radians to degrees.
radians(x, /[, out, where, casting, order, . . .])	Convert angles from degrees to radians.
ravel(array)	Return a contiguous flattened array.
real(*args, **kwargs)	Return the real part of the complex argument.
rechunk(x, chunks[, threshold, block_size_limit])	Convert blocks in dask array x for new chunks.
reduction(x, chunk, aggregate[, axis, . . .])	General version of reductions
repeat(a, repeats[, axis])	Repeat elements of an array.
reshape(x, shape)	Reshape array to new shape
result_type(*arrays_and_dtypes)	This docstring was copied from numpy.result_type.
rint(x, /[, out, where, casting, order, . . .])	Round elements of the array to the nearest integer.
roll(array, shift[, axis])	Roll array elements along a given axis.
rollaxis(a, axis[, start])	
round(a[, decimals])	Round an array to the given number of decimals.
sign(x, /[, out, where, casting, order, . . .])	Returns an element-wise indication of the sign of a number.
signbit(x, /[, out, where, casting, order, . . .])	Returns element-wise True where signbit is set (less than zero).
sin(x, /[, out, where, casting, order, . . .])	Trigonometric sine, element-wise.

Continued on next page

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sinh(x, /[, out, where, casting, order, ...])	Hyperbolic sine, element-wise.
sqrt(x, /[, out, where, casting, order, ...])	Return the non-negative square-root of an array, element-wise.
square(x, /[, out, where, casting, order, ...])	Return the element-wise square of the input.
squeeze(a[, axis])	Remove single-dimensional entries from the shape of an array.
stack(seq[, axis])	Stack arrays along a new axis
std(a[, axis, dtype, out, ddof, keepdims])	Compute the standard deviation along the specified axis.
sum(a[, axis, dtype, out, keepdims, initial])	Sum of array elements over a given axis.
take(a, indices[, axis])	Take elements from an array along an axis.
tan(x, /[, out, where, casting, order, ...])	Compute tangent element-wise.
tanh(x, /[, out, where, casting, order, ...])	Compute hyperbolic tangent element-wise.
tensordot(lhs, rhs[, axes])	Compute tensor dot product along specified axes for arrays >= 1-D.
tile(A, reps)	Construct an array by repeating A the number of times given by reps.
topk(a, k[, axis, split_every])	Extract the k largest elements from a on the given axis, and return them sorted from largest to smallest.
trace(a[, offset, axis1, axis2, dtype, out])	Return the sum along diagonals of the array.
transpose(a[, axes])	Permute the dimensions of an array.
tril(m[, k])	Lower triangle of an array with elements above the *k*-th diagonal zeroed.
triu(m[, k])	Upper triangle of an array with elements above the *k*-th diagonal zeroed.
trunc(x, /[, out, where, casting, order, ...])	Return the truncated value of the input, element-wise.
unify_chunks(*args, **kwargs)	Unify chunks across a sequence of arrays
unique(ar[, return_index, return_inverse, ...])	Find the unique elements of an array.
unravel_index(indices, shape[, order])	This docstring was copied from numpy.unravel_index.
var(a[, axis, dtype, out, ddof, keepdims])	Compute the variance along the specified axis.
vdot(a, b)	This docstring was copied from numpy.vdot.
vstack(tup[, allow_unknown_chunksizes])	Stack arrays in sequence vertically (row wise).
where(condition, [x, y])	This docstring was copied from numpy.where.
zeros(*args, **kwargs)	Blocked variant of zeros
zeros_like(a[, dtype, chunks])	Return an array of zeros with the same shape and type as a given array.

Fast Fourier Transforms

fft.fft_wrap(fft_func[, kind, dtype])	Wrap 1D, 2D, and ND real and complex FFT functions
fft.fft(a[, n, axis])	Wrapping of numpy.fft.fft
fft.fft2(a[, s, axes])	Wrapping of numpy.fft.fft2
fft.fftn(a[, s, axes])	Wrapping of numpy.fft.fftn
fft.ifft(a[, n, axis])	Wrapping of numpy.fft.ifft
fft.ifft2(a[, s, axes])	Wrapping of numpy.fft.ifft2
fft.ifftn(a[, s, axes])	Wrapping of numpy.fft.ifftn
fft.rfft(a[, n, axis])	Wrapping of numpy.fft.rfft
fft.rfft2(a[, s, axes])	Wrapping of numpy.fft.rfft2
fft.rfftn(a[, s, axes])	Wrapping of numpy.fft.rfftn
fft.irfft(a[, n, axis])	Wrapping of numpy.fft.irfft

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`fft.irfft2`(a[, s, axes])	Wrapping of numpy.fft.irfft2
`fft.irfftn`(a[, s, axes])	Wrapping of numpy.fft.irfftn
`fft.hfft`(a[, n, axis])	Wrapping of numpy.fft.hfft
`fft.ihfft`(a[, n, axis])	Wrapping of numpy.fft.ihfft
`fft.fftfreq`(n[, d, chunks])	Return the Discrete Fourier Transform sample frequencies.
`fft.rfftfreq`(n[, d, chunks])	Return the Discrete Fourier Transform sample frequencies (for usage with rfft, irfft).
`fft.fftshift`(x[, axes])	Shift the zero-frequency component to the center of the spectrum.
`fft.ifftshift`(x[, axes])	The inverse of *fftshift*.

Linear Algebra

`linalg.cholesky`(a[, lower])	Returns the Cholesky decomposition, $A = LL^*$ or $A = U^*U$ of a Hermitian positive-definite matrix A.
`linalg.inv`(a)	Compute the inverse of a matrix with LU decomposition and forward / backward substitutions.
`linalg.lstsq`(a, b)	Return the least-squares solution to a linear matrix equation using QR decomposition.
`linalg.lu`(a)	Compute the lu decomposition of a matrix.
`linalg.norm`(x[, ord, axis, keepdims])	Matrix or vector norm.
`linalg.qr`(a)	Compute the qr factorization of a matrix.
`linalg.solve`(a, b[, sym_pos])	Solve the equation `a x = b` for `x`.
`linalg.solve_triangular`(a, b[, lower])	Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.
`linalg.svd`(a)	Compute the singular value decomposition of a matrix.
`linalg.svd_compressed`(a, k[, n_power_iter, . . .])	Randomly compressed rank-k thin Singular Value Decomposition.
`linalg.sfqr`(data[, name])	Direct Short-and-Fat QR
`linalg.tsqr`(data[, compute_svd, . . .])	Direct Tall-and-Skinny QR algorithm

Masked Arrays

`ma.average`(a[, axis, weights, returned])	Return the weighted average of array over the given axis.
`ma.filled`(a[, fill_value])	Return input as an array with masked data replaced by a fill value.
`ma.fix_invalid`(a[, fill_value])	Return input with invalid data masked and replaced by a fill value.
`ma.getdata`(a)	Return the data of a masked array as an ndarray.
`ma.getmaskarray`(a)	Return the mask of a masked array, or full boolean array of False.
`ma.masked_array`(data[, mask, fill_value])	An array class with possibly masked values.
`ma.masked_equal`(a, value)	Mask an array where equal to a given value.
`ma.masked_greater`(x, value[, copy])	Mask an array where greater than a given value.
`ma.masked_greater_equal`(x, value[, copy])	Mask an array where greater than or equal to a given value.
`ma.masked_inside`(x, v1, v2)	Mask an array inside a given interval.

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ma.masked_invalid(a)	Mask an array where invalid values occur (NaNs or infs).
ma.masked_less(x, value[, copy])	Mask an array where less than a given value.
ma.masked_less_equal(x, value[, copy])	Mask an array where less than or equal to a given value.
ma.masked_not_equal(x, value[, copy])	Mask an array where *not* equal to a given value.
ma.masked_outside(x, v1, v2)	Mask an array outside a given interval.
ma.masked_values(x, value[, rtol, atol, shrink])	Mask using floating point equality.
ma.masked_where(condition, a)	Mask an array where a condition is met.
ma.set_fill_value(a, fill_value)	Set the filling value of a, if a is a masked array.

Random

random.beta(a, b[, size])	Draw samples from a Beta distribution.
random.binomial(n, p[, size])	Draw samples from a binomial distribution.
random.chisquare(df[, size])	Draw samples from a chi-square distribution.
random.choice(a[, size, replace, p])	Generates a random sample from a given 1-D array
random.exponential([scale, size])	Draw samples from an exponential distribution.
random.f(dfnum, dfden[, size])	Draw samples from an F distribution.
random.gamma(shape[, scale, size])	Draw samples from a Gamma distribution.
random.geometric(p[, size])	Draw samples from the geometric distribution.
random.gumbel([loc, scale, size])	Draw samples from a Gumbel distribution.
random.hypergeometric(ngood, nbad, nsample)	Draw samples from a Hypergeometric distribution.
random.laplace([loc, scale, size])	Draw samples from the Laplace or double exponential distribution with specified location (or mean) and scale (decay).
random.logistic([loc, scale, size])	Draw samples from a logistic distribution.
random.lognormal([mean, sigma, size])	Draw samples from a log-normal distribution.
random.logseries(p[, size])	Draw samples from a logarithmic series distribution.
random.negative_binomial(n, p[, size])	Draw samples from a negative binomial distribution.
random.noncentral_chisquare(df, nonc[, size])	Draw samples from a noncentral chi-square distribution.
random.noncentral_f(dfnum, dfden, nonc[, size])	Draw samples from the noncentral F distribution.
random.normal([loc, scale, size])	Draw random samples from a normal (Gaussian) distribution.
random.pareto(a[, size])	Draw samples from a Pareto II or Lomax distribution with specified shape.
random.permutation(x)	Randomly permute a sequence, or return a permuted range.
random.poisson([lam, size])	Draw samples from a Poisson distribution.
random.power(a[, size])	Draws samples in [0, 1] from a power distribution with positive exponent a - 1.
random.randint(low[, high, size, dtype])	Return random integers from *low* (inclusive) to *high* (exclusive).
random.random([size])	Return random floats in the half-open interval [0.0, 1.0).
random.random_sample([size])	Return random floats in the half-open interval [0.0, 1.0).
random.rayleigh([scale, size])	Draw samples from a Rayleigh distribution.
random.standard_cauchy([size])	Draw samples from a standard Cauchy distribution with mode = 0.

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random.standard_exponential([size])	Draw samples from the standard exponential distribution.
random.standard_gamma(shape[, size])	Draw samples from a standard Gamma distribution.
random.standard_normal([size])	Draw samples from a standard Normal distribution (mean=0, stdev=1).
random.standard_t(df[, size])	Draw samples from a standard Student's t distribution with *df* degrees of freedom.
random.triangular(left, mode, right[, size])	Draw samples from the triangular distribution over the interval `[left, right]`.
random.uniform([low, high, size])	Draw samples from a uniform distribution.
random.vonmises(mu, kappa[, size])	Draw samples from a von Mises distribution.
random.wald(mean, scale[, size])	Draw samples from a Wald, or inverse Gaussian, distribution.
random.weibull(a[, size])	Draw samples from a Weibull distribution.
random.zipf(a[, size])	Standard distributions

Stats

stats.ttest_ind(a, b[, axis, equal_var])	Calculate the T-test for the means of *two independent* samples of scores.
stats.ttest_1samp(a, popmean[, axis, nan_policy])	Calculate the T-test for the mean of ONE group of scores.
stats.ttest_rel(a, b[, axis, nan_policy])	Calculate the T-test on TWO RELATED samples of scores, a and b.
stats.chisquare(f_obs[, f_exp, ddof, axis])	Calculate a one-way chi square test.
stats.power_divergence(f_obs[, f_exp, ddof, . . .])	Cressie-Read power divergence statistic and goodness of fit test.
stats.skew(a[, axis, bias, nan_policy])	Compute the skewness of a data set.
stats.skewtest(a[, axis, nan_policy])	Test whether the skew is different from the normal distribution.
stats.kurtosis(a[, axis, fisher, bias, . . .])	Compute the kurtosis (Fisher or Pearson) of a dataset.
stats.kurtosistest(a[, axis, nan_policy])	Test whether a dataset has normal kurtosis.
stats.normaltest(a[, axis, nan_policy])	Test whether a sample differs from a normal distribution.
stats.f_oneway(*args)	Performs a 1-way ANOVA.
stats.moment(a[, moment, axis, nan_policy])	Calculate the nth moment about the mean for a sample.

Image Support

image.imread(filename[, imread, preprocess])	Read a stack of images into a dask array

Slightly Overlapping Computations

overlap.overlap(x, depth, boundary)	Share boundaries between neighboring blocks
overlap.map_overlap(x, func, depth[, . . .])	Map a function over blocks of the array with some overlap
overlap.trim_internal(x, axes[, boundary])	Trim sides from each block
overlap.trim_overlap(x, depth[, boundary])	Trim sides from each block.

Create and Store Arrays

`from_array`(x[, chunks, name, lock, asarray, . . .])	Create dask array from something that looks like an array
`from_delayed`(value, shape[, dtype, meta, name])	Create a dask array from a dask delayed value
`from_npy_stack`(dirname[, mmap_mode])	Load dask array from stack of npy files
`from_zarr`(url[, component, storage_options, . . .])	Load array from the zarr storage format
`from_tiledb`(uri[, attribute, chunks, . . .])	Load array from the TileDB storage format
`store`(sources, targets[, lock, regions, . . .])	Store dask arrays in array-like objects, overwrite data in target
`to_hdf5`(filename, *args, **kwargs)	Store arrays in HDF5 file
`to_zarr`(arr, url[, component, . . .])	Save array to the zarr storage format
`to_npy_stack`(dirname, x[, axis])	Write dask array to a stack of .npy files
`to_tiledb`(darray, uri[, compute, . . .])	Save array to the TileDB storage format

Generalized Ufuncs

`apply_gufunc`(func, signature, *args, **kwargs)	Apply a generalized ufunc or similar python function to arrays.
`as_gufunc`([signature])	Decorator for `dask.array.gufunc`.
`gufunc`(pyfunc, **kwargs)	Binds *pyfunc* into `dask.array.apply_gufunc` when called.

Internal functions

`blockwise`(func, out_ind, *args[, name, . . .])	Tensor operation: Generalized inner and outer products
`normalize_chunks`(chunks[, shape, limit, . . .])	Normalize chunks to tuple of tuples

Other functions

`dask.array.`**`from_array`**`(`*x*, *chunks='auto'*, *name=None*, *lock=False*, *asarray=None*, *fancy=True*, *getitem=None*, *meta=None*`)`

Create dask array from something that looks like an array

Input must have a `.shape`, `.ndim`, `.dtype` and support numpy-style slicing.

Parameters

x [array_like]

chunks [int, tuple] How to chunk the array. Must be one of the following forms: - A blocksize like 1000. - A blockshape like (1000, 1000). - Explicit sizes of all blocks along all dimensions like

((1000, 1000, 500), (400, 400)).

- A size in bytes, like "100 MiB" which will choose a uniform block-like shape
- The word "auto" which acts like the above, but uses a configuration value `array.chunk-size` for the chunk size

-1 or None as a blocksize indicate the size of the corresponding dimension.

name [str, optional] The key name to use for the array. Defaults to a hash of `x`. By default, hash uses python's standard sha1. This behaviour can be changed by installing cityhash, xxhash or murmurhash. If installed, a large-factor speedup can be obtained in the tokenisation step. Use `name=False` to generate a random name instead of hashing (fast)

lock [bool or Lock, optional] If `x` doesn't support concurrent reads then provide a lock here, or pass in True to have dask.array create one for you.

asarray [bool, optional] If True then call np.asarray on chunks to convert them to numpy arrays. If False then chunks are passed through unchanged. If None (default) then we use True if the `__array_function__` method is undefined.

fancy [bool, optional] If `x` doesn't support fancy indexing (e.g. indexing with lists or arrays) then set to False. Default is True.

meta [Array-like, optional] The metadata for the resulting dask array. This is the kind of array that will result from slicing the input array. Defaults to the input array.

Examples

```
>>> x = h5py.File('...')['/data/path']  # doctest: +SKIP
>>> a = da.from_array(x, chunks=(1000, 1000))  # doctest: +SKIP
```

If your underlying datastore does not support concurrent reads then include the `lock=True` keyword argument or `lock=mylock` if you want multiple arrays to coordinate around the same lock.

```
>>> a = da.from_array(x, chunks=(1000, 1000), lock=True)  # doctest: +SKIP
```

If your underlying datastore has a `.chunks` attribute (as h5py and zarr datasets do) then a multiple of that chunk shape will be used if you do not provide a chunk shape.

```
>>> a = da.from_array(x, chunks='auto')  # doctest: +SKIP
>>> a = da.from_array(x, chunks='100 MiB')  # doctest: +SKIP
>>> a = da.from_array(x)  # doctest: +SKIP
```

`dask.array.`**`from_delayed`**(*value*, *shape*, *dtype=None*, *meta=None*, *name=None*)

Create a dask array from a dask delayed value

This routine is useful for constructing dask arrays in an ad-hoc fashion using dask delayed, particularly when combined with stack and concatenate.

The dask array will consist of a single chunk.

Examples

```
>>> import dask
>>> import dask.array as da
>>> value = dask.delayed(np.ones)(5)
>>> array = da.from_delayed(value, (5,), dtype=float)
>>> array
dask.array<from-value, shape=(5,), dtype=float64, chunksize=(5,), chunktype=numpy.
↪ndarray>
>>> array.compute()
array([1., 1., 1., 1., 1.])
```

`dask.array.`**`store`**`(`*sources*, *targets*, *lock=True*, *regions=None*, *compute=True*, *return_stored=False*, ***kwargs*`)`

Store dask arrays in array-like objects, overwrite data in target

This stores dask arrays into object that supports numpy-style setitem indexing. It stores values chunk by chunk so that it does not have to fill up memory. For best performance you can align the block size of the storage target with the block size of your array.

If your data fits in memory then you may prefer calling `np.array(myarray)` instead.

Parameters

sources: Array or iterable of Arrays

targets: array-like or Delayed or iterable of array-likes and/or Delayeds These should support setitem syntax `target[10:20] = ...`

lock: boolean or threading.Lock, optional Whether or not to lock the data stores while storing. Pass True (lock each file individually), False (don't lock) or a particular `threading.Lock` object to be shared among all writes.

regions: tuple of slices or list of tuples of slices Each `region` tuple in `regions` should be such that `target[region].shape = source.shape` for the corresponding source and target in sources and targets, respectively. If this is a tuple, the contents will be assumed to be slices, so do not provide a tuple of tuples.

compute: boolean, optional If true compute immediately, return `dask.delayed.Delayed` otherwise

return_stored: boolean, optional Optionally return the stored result (default False).

Examples

```
>>> x = ...  # doctest: +SKIP
```

```
>>> import h5py  # doctest: +SKIP
>>> f = h5py.File('myfile.hdf5', mode='a')  # doctest: +SKIP
>>> dset = f.create_dataset('/data', shape=x.shape,
...                                  chunks=x.chunks,
...                                  dtype='f8')  # doctest: +SKIP
```

```
>>> store(x, dset)  # doctest: +SKIP
```

Alternatively store many arrays at the same time

```
>>> store([x, y, z], [dset1, dset2, dset3])  # doctest: +SKIP
```

`dask.array.`**`coarsen`**`(`*reduction*, *x*, *axes*, *trim_excess=False*`)`

Coarsen array by applying reduction to fixed size neighborhoods

Parameters

reduction: function Function like np.sum, np.mean, etc…

x: np.ndarray Array to be coarsened

axes: dict Mapping of axis to coarsening factor

Examples

```
>>> x = np.array([1, 2, 3, 4, 5, 6])
>>> coarsen(np.sum, x, {0: 2})
array([ 3,  7, 11])
>>> coarsen(np.max, x, {0: 3})
array([3, 6])
```

Provide dictionary of scale per dimension

```
>>> x = np.arange(24).reshape((4, 6))
>>> x
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20, 21, 22, 23]])
```

```
>>> coarsen(np.min, x, {0: 2, 1: 3})
array([[ 0,  3],
       [12, 15]])
```

You must avoid excess elements explicitly

```
>>> x = np.array([1, 2, 3, 4, 5, 6, 7, 8])
>>> coarsen(np.min, x, {0: 3}, trim_excess=True)
array([1, 4])
```

`dask.array.`**`stack`**(*seq*, *axis=0*)

Stack arrays along a new axis

Given a sequence of dask arrays, form a new dask array by stacking them along a new dimension (axis=0 by default)

See also:

concatenate

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...           for i in range(3)]
```

```
>>> x = da.stack(data, axis=0)
>>> x.shape
(3, 4, 4)
```

```
>>> da.stack(data, axis=1).shape
(4, 3, 4)
```

```
>>> da.stack(data, axis=-1).shape
(4, 4, 3)
```

Result is a new dask Array

`dask.array.`**`concatenate`**`(`*seq*, *axis=0*, *allow_unknown_chunksizes=False*`)`

Concatenate arrays along an existing axis

Given a sequence of dask Arrays form a new dask Array by stacking them along an existing dimension (axis=0 by default)

Parameters

seq: list of dask.arrays

axis: int Dimension along which to align all of the arrays

allow_unknown_chunksizes: bool Allow unknown chunksizes, such as come from converting from dask dataframes. Dask.array is unable to verify that chunks line up. If data comes from differently aligned sources then this can cause unexpected results.

See also:

`stack`

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...           for i in range(3)]
```

```
>>> x = da.concatenate(data, axis=0)
>>> x.shape
(12, 4)
```

```
>>> da.concatenate(data, axis=1).shape
(4, 12)
```

Result is a new dask Array

`dask.array.`**`all`**`(`*a*, *axis=None*, *out=None*, *keepdims=<no value>*`)`

Test whether all array elements along a given axis evaluate to True.

Parameters

a [array_like] Input array or object that can be converted to an array.

axis [None or int or tuple of ints, optional] Axis or axes along which a logical AND reduction is performed. The default (*axis* = *None*) is to perform a logical AND over all the dimensions of the input array. *axis* may be negative, in which case it counts from the last to the first axis.

New in version 1.7.0.

If this is a tuple of ints, a reduction is performed on multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output and its type is preserved (e.g., if `dtype(out)` is float, the result will consist of 0.0's and 1.0's). See *doc.ufuncs* (Section "Output arguments") for more details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *all* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

Returns

all [ndarray, bool] A new boolean or array is returned unless *out* is specified, in which case a reference to *out* is returned.

See also:

`ndarray.all` equivalent method

`any` Test whether any element along a given axis evaluates to True.

Notes

Not a Number (NaN), positive infinity and negative infinity evaluate to *True* because these are not equal to zero.

Examples

```
>>> np.all([[True,False],[True,True]])
False
```

```
>>> np.all([[True,False],[True,True]], axis=0)
array([ True, False])
```

```
>>> np.all([-1, 4, 5])
True
```

```
>>> np.all([1.0, np.nan])
True
```

```
>>> o=np.array([False])
>>> z=np.all([-1, 4, 5], out=o)
>>> id(z), id(o), z                               # doctest: +SKIP
(28293632, 28293632, array([ True]))
```

`dask.array.`**`allclose`**(*arr1*, *arr2*, *rtol=1e-05*, *atol=1e-08*, *equal_nan=False*)

Returns True if two arrays are element-wise equal within a tolerance.

This docstring was copied from numpy.allclose.

Some inconsistencies with the Dask version may exist.

The tolerance values are positive, typically very small numbers. The relative difference (*rtol* * abs(*b*)) and the absolute difference *atol* are added together to compare against the absolute difference between *a* and *b*.

If either array contains one or more NaNs, False is returned. Infs are treated as equal if they are in the same place and of the same sign in both arrays.

Parameters

a, b [array_like] Input arrays to compare.

rtol [float] The relative tolerance parameter (see Notes).

atol [float] The absolute tolerance parameter (see Notes).

equal_nan [bool] Whether to compare NaN's as equal. If True, NaN's in *a* will be considered equal to NaN's in *b* in the output array.

New in version 1.10.0.

Returns

allclose [bool] Returns True if the two arrays are equal within the given tolerance; False otherwise.

See also:

isclose, *all*, *any*, equal

Notes

If the following equation is element-wise True, then allclose returns True.

absolute(*a* - *b*) <= (*atol* + *rtol* * absolute(*b*))

The above equation is not symmetric in *a* and *b*, so that `allclose(a, b)` might be different from `allclose(b, a)` in some rare cases.

The comparison of *a* and *b* uses standard broadcasting, which means that *a* and *b* need not have the same shape in order for `allclose(a, b)` to evaluate to True. The same is true for *equal* but not *array_equal*.

Examples

```
>>> np.allclose([1e10,1e-7], [1.00001e10,1e-8])  # doctest: +SKIP
False
>>> np.allclose([1e10,1e-8], [1.00001e10,1e-9])  # doctest: +SKIP
True
>>> np.allclose([1e10,1e-8], [1.0001e10,1e-9])  # doctest: +SKIP
False
>>> np.allclose([1.0, np.nan], [1.0, np.nan])  # doctest: +SKIP
False
>>> np.allclose([1.0, np.nan], [1.0, np.nan], equal_nan=True)  # doctest: +SKIP
True
```

`dask.array.`**`angle`**(*x*, *deg=0*)

Return the angle of the complex argument.

Parameters

z [array_like] A complex number or sequence of complex numbers.

deg [bool, optional] Return angle in degrees if True, radians if False (default).

Returns

angle [ndarray or scalar] The counterclockwise angle from the positive real axis on the complex plane, with dtype as numpy.float64.

..versionchanged:: 1.16.0 This function works on subclasses of ndarray like *ma.array*.

See also:

arctan2, absolute

Examples

```
>>> np.angle([1.0, 1.0j, 1+1j])               # in radians  # doctest: +SKIP
array([ 0.        ,  1.57079633,  0.78539816])
>>> np.angle(1+1j, deg=True)                  # in degrees  # doctest: +SKIP
45.0
```

`dask.array.`**`any`**(*a*, *axis=None*, *out=None*, *keepdims=<no value>*)

Test whether any array element along a given axis evaluates to True.

Returns single boolean unless *axis* is not `None`

Parameters

a [array_like] Input array or object that can be converted to an array.

axis [None or int or tuple of ints, optional] Axis or axes along which a logical OR reduction is performed. The default (*axis* = *None*) is to perform a logical OR over all the dimensions of the input array. *axis* may be negative, in which case it counts from the last to the first axis.

New in version 1.7.0.

If this is a tuple of ints, a reduction is performed on multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output and its type is preserved (e.g., if it is of type float, then it will remain so, returning 1.0 for True and 0.0 for False, regardless of the type of *a*). See *doc.ufuncs* (Section "Output arguments") for details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *any* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

Returns

any [bool or ndarray] A new boolean or *ndarray* is returned unless *out* is specified, in which case a reference to *out* is returned.

See also:

`ndarray.any` equivalent method

`all` Test whether all elements along a given axis evaluate to True.

Notes

Not a Number (NaN), positive infinity and negative infinity evaluate to *True* because these are not equal to zero.

Examples

```
>>> np.any([[True, False], [True, True]])
True
```

```
>>> np.any([[True, False], [False, False]], axis=0)
array([ True, False])
```

```
>>> np.any([-1, 0, 5])
True
```

```
>>> np.any(np.nan)
True
```

```
>>> o=np.array([False])
>>> z=np.any([-1, 4, 5], out=o)
>>> z, o
(array([ True]), array([ True]))
>>> # Check now that z is a reference to o
>>> z is o
True
>>> id(z), id(o) # identity of z and o              # doctest: +SKIP
(191614240, 191614240)
```

`dask.array.apply_along_axis`(*func1d*, *axis*, *arr*, **args*, *dtype=None*, *shape=None*, ***kwargs*)

Apply a function to 1-D slices along the given axis.

This docstring was copied from numpy.apply_along_axis.

Some inconsistencies with the Dask version may exist.

Apply a function to 1-D slices along the given axis. This is a blocked variant of `numpy.apply_along_axis()` implemented via `dask.array.map_blocks()`

func1d [callable] Function to apply to 1-D slices of the array along the given axis

axis [int] Axis along which func1d will be applied

arr [dask array] Dask array to which `func1d` will be applied

args [any] Additional arguments to `func1d`.

dtype [str or dtype, optional] The dtype of the output of `func1d`.

shape [tuple, optional] The shape of the output of `func1d`.

kwargs [any] Additional keyword arguments for `func1d`.

Parameters

func1d [function (M,) -> (Nj. . .)] This function should accept 1-D arrays. It is applied to 1-D slices of *arr* along the specified axis.

axis [integer] Axis along which *arr* is sliced.

arr [ndarray (Ni. . . , M, Nk. . .)] Input array.

args [any] Additional arguments to *func1d*.

kwargs [any] Additional named arguments to *func1d*.

New in version 1.9.0.

Returns

out [ndarray (Ni. . . , Nj. . . , Nk. . .)] The output array. The shape of *out* is identical to the shape of *arr*, except along the *axis* dimension. This axis is removed, and replaced with new dimensions equal to the shape of the return value of *func1d*. So if *func1d* returns a scalar *out* will have one fewer dimensions than *arr*.

See also:

`apply_over_axes` Apply a function repeatedly over multiple axes.

Notes

If either of *dtype* or *shape* are not provided, Dask attempts to determine them by calling *func1d* on a dummy array. This may produce incorrect values for *dtype* or *shape*, so we recommend providing them.

Execute *func1d(a, *args)* where *func1d* operates on 1-D arrays and *a* is a 1-D slice of *arr* along *axis*.

This is equivalent to (but faster than) the following use of *ndindex* and *s_*, which sets each of `ii`, `jj`, and `kk` to a tuple of indices:

```
Ni, Nk = a.shape[:axis], a.shape[axis+1:]
for ii in ndindex(Ni):
    for kk in ndindex(Nk):
        f = func1d(arr[ii + s_[:,] + kk])
        Nj = f.shape
        for jj in ndindex(Nj):
            out[ii + jj + kk] = f[jj]
```

Equivalently, eliminating the inner loop, this can be expressed as:

```
Ni, Nk = a.shape[:axis], a.shape[axis+1:]
for ii in ndindex(Ni):
    for kk in ndindex(Nk):
        out[ii + s_[...,] + kk] = func1d(arr[ii + s_[:,] + kk])
```

Examples

```
>>> def my_func(a):  # doctest: +SKIP
...     """Average first and last element of a 1-D array"""
...     return (a[0] + a[-1]) * 0.5
>>> b = np.array([[1,2,3], [4,5,6], [7,8,9]])  # doctest: +SKIP
>>> np.apply_along_axis(my_func, 0, b)  # doctest: +SKIP
array([ 4.,  5.,  6.])
>>> np.apply_along_axis(my_func, 1, b)  # doctest: +SKIP
array([ 2.,  5.,  8.])
```

For a function that returns a 1D array, the number of dimensions in *outarr* is the same as *arr*.

```
>>> b = np.array([[8,1,7], [4,3,9], [5,2,6]])  # doctest: +SKIP
>>> np.apply_along_axis(sorted, 1, b)  # doctest: +SKIP
array([[1, 7, 8],
       [3, 4, 9],
       [2, 5, 6]])
```

For a function that returns a higher dimensional array, those dimensions are inserted in place of the *axis* dimension.

```
>>> b = np.array([[1,2,3], [4,5,6], [7,8,9]])  # doctest: +SKIP
>>> np.apply_along_axis(np.diag, -1, b)  # doctest: +SKIP
array([[[1, 0, 0],
        [0, 2, 0],
        [0, 0, 3]],
       [[4, 0, 0],
        [0, 5, 0],
        [0, 0, 6]],
       [[7, 0, 0],
        [0, 8, 0],
        [0, 0, 9]]])
```

`dask.array.`**`apply_over_axes`**(*func*, *a*, *axes*)

Apply a function repeatedly over multiple axes.

This docstring was copied from numpy.apply_over_axes.

Some inconsistencies with the Dask version may exist.

func is called as *res = func(a, axis)*, where *axis* is the first element of *axes*. The result *res* of the function call must have either the same dimensions as *a* or one less dimension. If *res* has one less dimension than *a*, a dimension is inserted before *axis*. The call to *func* is then repeated for each axis in *axes*, with *res* as the first argument.

Parameters

func [function] This function must take two arguments, *func(a, axis)*.

a [array_like] Input array.

axes [array_like] Axes over which *func* is applied; the elements must be integers.

Returns

apply_over_axis [ndarray] The output array. The number of dimensions is the same as *a*, but the shape can be different. This depends on whether *func* changes the shape of its output with respect to its input.

See also:

`apply_along_axis` Apply a function to 1-D slices of an array along the given axis.

Notes

This function is equivalent to tuple axis arguments to reorderable ufuncs with keepdims=True. Tuple axis arguments to ufuncs have been available since version 1.7.0.

Examples

```
>>> a = np.arange(24).reshape(2,3,4)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([[[ 0,  1,  2,  3],
        [ 4,  5,  6,  7],
        [ 8,  9, 10, 11]],
       [[12, 13, 14, 15],
        [16, 17, 18, 19],
        [20, 21, 22, 23]]])
```

Sum over axes 0 and 2. The result has same number of dimensions as the original array:

```
>>> np.apply_over_axes(np.sum, a, [0,2])  # doctest: +SKIP
array([[[ 60],
        [ 92],
        [124]]])
```

Tuple axis arguments to ufuncs are equivalent:

```
>>> np.sum(a, axis=(0,2), keepdims=True)  # doctest: +SKIP
array([[[ 60],
        [ 92],
        [124]]])
```

`dask.array.`**`arange`**`(`**args*, ***kwargs*`)`

Return evenly spaced values from *start* to *stop* with step size *step*.

The values are half-open [start, stop), so including start and excluding stop. This is basically the same as python's range function but for dask arrays.

When using a non-integer step, such as 0.1, the results will often not be consistent. It is better to use linspace for these cases.

Parameters

start [int, optional] The starting value of the sequence. The default is 0.

stop [int] The end of the interval, this value is excluded from the interval.

step [int, optional] The spacing between the values. The default is 1 when not specified. The last value of the sequence.

chunks [int] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

dtype [numpy.dtype] Output dtype. Omit to infer it from start, stop, step

Returns

samples [dask array]

See also:

`dask.array.linspace`

`dask.array.`**`arccos`**`(`*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*]`)`

Trigonometric inverse cosine, element-wise.

The inverse of *cos* so that, if `y = cos(x)`, then `x = arccos(y)`.

Parameters

x [array_like] *x*-coordinate on the unit circle. For real arguments, the domain is [-1, 1].

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

angle [ndarray] The angle of the ray intersecting the unit circle at the given *x*-coordinate in radians [0, pi]. This is a scalar if *x* is a scalar.

See also:

`cos`, `arctan`, `arcsin`, `emath.arccos`

Notes

arccos is a multivalued function: for each *x* there are infinitely many numbers *z* such that *cos(z) = x*. The convention is to return the angle *z* whose real part lies in *[0, pi]*.

For real-valued input data types, *arccos* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arccos* is a complex analytic function that has branch cuts *[-inf, -1]* and *[1, inf]* and is continuous from above on the former and from below on the latter.

The inverse *cos* is also known as *acos* or cos^-1.

References

M. Abramowitz and I.A. Stegun, "Handbook of Mathematical Functions", 10th printing, 1964, pp. 79. http://www.math.sfu.ca/~cbm/aands/

Examples

We expect the arccos of 1 to be 0, and of -1 to be pi:

```
>>> np.arccos([1, -1])  # doctest: +SKIP
array([ 0.        ,  3.14159265])
```

Plot arccos:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> x = np.linspace(-1, 1, num=100)  # doctest: +SKIP
>>> plt.plot(x, np.arccos(x))  # doctest: +SKIP
>>> plt.axis('tight')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.`**`arccosh`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Inverse hyperbolic cosine, element-wise.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

arccosh [ndarray] Array of the same shape as *x*. This is a scalar if *x* is a scalar.

See also:

`cosh`, `arcsinh`, `sinh`, `arctanh`, `tanh`

Notes

arccosh is a multivalued function: for each *x* there are infinitely many numbers *z* such that *cosh(z) = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]* and the real part in `[0, inf]`.

For real-valued input data types, *arccosh* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arccosh* is a complex analytical function that has a branch cut *[-inf, 1]* and is continuous from above on it.

References

[1], [2]

Examples

```
>>> np.arccosh([np.e, 10.0])  # doctest: +SKIP
array([ 1.65745445,  2.99322285])
>>> np.arccosh(1)  # doctest: +SKIP
0.0
```

`dask.array.`**`arcsin`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Inverse sine, element-wise.

Parameters

x [array_like] *y*-coordinate on the unit circle.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

angle [ndarray] The inverse sine of each element in *x*, in radians and in the closed interval `[-pi/2, pi/2]`. This is a scalar if *x* is a scalar.

See also:

`sin`, `cos`, `arccos`, `tan`, `arctan`, `arctan2`, `emath.arcsin`

Notes

arcsin is a multivalued function: for each x there are infinitely many numbers z such that $sin(z) = x$. The convention is to return the angle z whose real part lies in [-pi/2, pi/2].

For real-valued input data types, *arcsin* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arcsin* is a complex analytic function that has, by convention, the branch cuts [-inf, -1] and [1, inf] and is continuous from above on the former and from below on the latter.

The inverse sine is also known as *asin* or sin^{-1}.

References

Abramowitz, M. and Stegun, I. A., *Handbook of Mathematical Functions*, 10th printing, New York: Dover, 1964, pp. 79ff. http://www.math.sfu.ca/~cbm/aands/

Examples

```
>>> np.arcsin(1)     # pi/2  # doctest: +SKIP
1.5707963267948966
>>> np.arcsin(-1)    # -pi/2  # doctest: +SKIP
-1.5707963267948966
>>> np.arcsin(0)  # doctest: +SKIP
0.0
```

`dask.array.`**`arcsinh`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Inverse hyperbolic sine element-wise.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Array of the same shape as *x*. This is a scalar if *x* is a scalar.

Notes

arcsinh is a multivalued function: for each x there are infinitely many numbers z such that *sinh(z) = x*. The convention is to return the z whose imaginary part lies in *[-pi/2, pi/2]*.

For real-valued input data types, *arcsinh* always returns real output. For each value that cannot be expressed as a real number or infinity, it returns `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arccos* is a complex analytical function that has branch cuts *[1j, infj]* and *[-1j, -infj]* and is continuous from the right on the former and from the left on the latter.

The inverse hyperbolic sine is also known as *asinh* or `sinh^-1`.

References

[1], [2]

Examples

```
>>> np.arcsinh(np.array([np.e, 10.0]))  # doctest: +SKIP
array([ 1.72538256,  2.99822295])
```

`dask.array.`**`arctan`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Trigonometric inverse tangent, element-wise.

The inverse of tan, so that if `y = tan(x)` then `x = arctan(y)`.

Parameters

x [array_like]

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Out has the same shape as *x*. Its real part is in `[-pi/2, pi/2]` (`arctan(+/-inf)` returns `+/-pi/2`). This is a scalar if *x* is a scalar.

See also:

`arctan2` The "four quadrant" arctan of the angle formed by (*x*, *y*) and the positive *x*-axis.

`angle` Argument of complex values.

Notes

arctan is a multi-valued function: for each *x* there are infinitely many numbers *z* such that tan(*z*) = *x*. The convention is to return the angle *z* whose real part lies in [-pi/2, pi/2].

For real-valued input data types, *arctan* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arctan* is a complex analytic function that has [*1j, infj*] and [*-1j, -infj*] as branch cuts, and is continuous from the left on the former and from the right on the latter.

The inverse tangent is also known as *atan* or tan^{-1}.

References

Abramowitz, M. and Stegun, I. A., *Handbook of Mathematical Functions*, 10th printing, New York: Dover, 1964, pp. 79. http://www.math.sfu.ca/~cbm/aands/

Examples

We expect the arctan of 0 to be 0, and of 1 to be pi/4:

```
>>> np.arctan([0, 1])  # doctest: +SKIP
array([ 0.        ,  0.78539816])
```

```
>>> np.pi/4  # doctest: +SKIP
0.78539816339744828
```

Plot arctan:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> x = np.linspace(-10, 10)  # doctest: +SKIP
>>> plt.plot(x, np.arctan(x))  # doctest: +SKIP
>>> plt.axis('tight')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.`**`arctan2`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Element-wise arc tangent of `x1/x2` choosing the quadrant correctly.

The quadrant (i.e., branch) is chosen so that `arctan2(x1, x2)` is the signed angle in radians between the ray ending at the origin and passing through the point (1,0), and the ray ending at the origin and passing through the point (*x2*, *x1*). (Note the role reversal: the "*y*-coordinate" is the first function parameter, the "*x*-coordinate" is the second.) By IEEE convention, this function is defined for *x2* = +/-0 and for either or both of *x1* and *x2* = +/-inf (see Notes for specific values).

This function is not defined for complex-valued arguments; for the so-called argument of complex values, use *angle*.

Parameters

x1 [array_like, real-valued] *y*-coordinates.

x2 [array_like, real-valued] *x*-coordinates. *x2* must be broadcastable to match the shape of *x1* or vice versa.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

angle [ndarray] Array of angles in radians, in the range `[-pi, pi]`. This is a scalar if both *x1* and *x2* are scalars.

See also:

arctan, *tan*, *angle*

Notes

arctan2 is identical to the *atan2* function of the underlying C library. The following special values are defined in the C standard: [1]

x1	*x2*	*arctan2(x1,x2)*
+/- 0	+0	+/- 0
+/- 0	-0	+/- pi
> 0	+/-inf	+0 / +pi
< 0	+/-inf	-0 / -pi
+/-inf	+inf	+/- (pi/4)
+/-inf	-inf	+/- (3*pi/4)

Note that +0 and -0 are distinct floating point numbers, as are +inf and -inf.

References

[1]

Examples

Consider four points in different quadrants:

```
>>> x = np.array([-1, +1, +1, -1])  # doctest: +SKIP
>>> y = np.array([-1, -1, +1, +1])  # doctest: +SKIP
>>> np.arctan2(y, x) * 180 / np.pi  # doctest: +SKIP
array([-135.,  -45.,   45.,  135.])
```

Note the order of the parameters. *arctan2* is defined also when *x2* = 0 and at several other special points, obtaining values in the range `[-pi, pi]`:

```
>>> np.arctan2([1., -1.], [0., 0.])  # doctest: +SKIP
array([ 1.57079633, -1.57079633])
>>> np.arctan2([0., 0., np.inf], [+0., -0., np.inf])  # doctest: +SKIP
array([ 0.        ,  3.14159265,  0.78539816])
```

`dask.array.`**`arctanh`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Inverse hyperbolic tangent element-wise.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Array of the same shape as *x*. This is a scalar if *x* is a scalar.

See also:

`emath.arctanh`

Notes

arctanh is a multivalued function: for each *x* there are infinitely many numbers *z* such that *tanh(z) = x*. The convention is to return the *z* whose imaginary part lies in *[-pi/2, pi/2]*.

For real-valued input data types, *arctanh* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *arctanh* is a complex analytical function that has branch cuts *[-1, -inf]* and *[1, inf]* and is continuous from above on the former and from below on the latter.

The inverse hyperbolic tangent is also known as *atanh* or `tanh^-1`.

References

[1], [2]

Examples

```
>>> np.arctanh([0, -0.5])  # doctest: +SKIP
array([ 0.        , -0.54930614])
```

`dask.array.`**`argmax`**`(`*a*, *axis=None*, *out=None*`)`

Returns the indices of the maximum values along an axis.

Parameters

a [array_like] Input array.

axis [int, optional] By default, the index is into the flattened array, otherwise along the specified axis.

out [array, optional] If provided, the result will be inserted into this array. It should be of the appropriate shape and dtype.

Returns

index_array [ndarray of ints] Array of indices into the array. It has the same shape as *a.shape* with the dimension along *axis* removed.

See also:

`ndarray.argmax`, *`argmin`*

`amax` The maximum value along a given axis.

`unravel_index` Convert a flat index into an index tuple.

Notes

In case of multiple occurrences of the maximum values, the indices corresponding to the first occurrence are returned.

Examples

```
>>> a = np.arange(6).reshape(2,3) + 10
>>> a
array([[10, 11, 12],
       [13, 14, 15]])
>>> np.argmax(a)
5
>>> np.argmax(a, axis=0)
array([1, 1, 1])
>>> np.argmax(a, axis=1)
array([2, 2])
```

Indexes of the maximal elements of a N-dimensional array:

```
>>> ind = np.unravel_index(np.argmax(a, axis=None), a.shape)
>>> ind
(1, 2)
>>> a[ind]
15
```

```
>>> b = np.arange(6)
>>> b[1] = 5
>>> b
array([0, 5, 2, 3, 4, 5])
>>> np.argmax(b)  # Only the first occurrence is returned.
1
```

`dask.array.`**`argmin`**`(`*a*, *axis=None*, *out=None*`)`

Returns the indices of the minimum values along an axis.

Parameters

a [array_like] Input array.

axis [int, optional] By default, the index is into the flattened array, otherwise along the specified axis.

out [array, optional] If provided, the result will be inserted into this array. It should be of the appropriate shape and dtype.

Returns

index_array [ndarray of ints] Array of indices into the array. It has the same shape as *a.shape* with the dimension along *axis* removed.

See also:

`ndarray.argmin`, *`argmax`*

`amin` The minimum value along a given axis.

`unravel_index` Convert a flat index into an index tuple.

Notes

In case of multiple occurrences of the minimum values, the indices corresponding to the first occurrence are returned.

Examples

```
>>> a = np.arange(6).reshape(2,3) + 10
>>> a
array([[10, 11, 12],
       [13, 14, 15]])
>>> np.argmin(a)
0
>>> np.argmin(a, axis=0)
array([0, 0, 0])
>>> np.argmin(a, axis=1)
array([0, 0])
```

Indices of the minimum elements of a N-dimensional array:

```
>>> ind = np.unravel_index(np.argmin(a, axis=None), a.shape)
>>> ind
(0, 0)
>>> a[ind]
10
```

```
>>> b = np.arange(6) + 10
>>> b[4] = 10
>>> b
array([10, 11, 12, 13, 10, 15])
>>> np.argmin(b)  # Only the first occurrence is returned.
0
```

`dask.array.`**`argtopk`**`(`*a*, *k*, *axis=-1*, *split_every=None*`)`

Extract the indices of the k largest elements from a on the given axis, and return them sorted from largest to smallest. If k is negative, extract the indices of the -k smallest elements instead, and return them sorted from smallest to largest.

This performs best when `k` is much smaller than the chunk size. All results will be returned in a single chunk along the given axis.

Parameters

x: Array Data being sorted

k: int

axis: int, optional

split_every: int >=2, optional See `topk()`. The performance considerations for topk also apply here.

Returns

Selection of np.intp indices of x with size abs(k) along the given axis.

Examples

```
>>> import dask.array as da
>>> x = np.array([5, 1, 3, 6])
>>> d = da.from_array(x, chunks=2)
>>> d.argtopk(2).compute()
array([3, 0])
>>> d.argtopk(-2).compute()
array([1, 2])
```

`dask.array.argwhere(a)`

Find the indices of array elements that are non-zero, grouped by element.

This docstring was copied from numpy.argwhere.

Some inconsistencies with the Dask version may exist.

Parameters

a [array_like] Input data.

Returns

index_array [ndarray] Indices of elements that are non-zero. Indices are grouped by element.

See also:

where, *nonzero*

Notes

`np.argwhere(a)` is the same as `np.transpose(np.nonzero(a))`.

The output of `argwhere` is not suitable for indexing arrays. For this purpose use `nonzero(a)` instead.

Examples

```
>>> x = np.arange(6).reshape(2,3)  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([[0, 1, 2],
       [3, 4, 5]])
>>> np.argwhere(x>1)  # doctest: +SKIP
array([[0, 2],
       [1, 0],
       [1, 1],
       [1, 2]])
```

`dask.array.around(x, decimals=0)`

Evenly round to the given number of decimals.

This docstring was copied from numpy.around.

Some inconsistencies with the Dask version may exist.

Parameters

a [array_like (Not supported in Dask)] Input data.

decimals [int, optional] Number of decimal places to round to (default: 0). If decimals is negative, it specifies the number of positions to the left of the decimal point.

out [ndarray, optional (Not supported in Dask)] Alternative output array in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary. See *doc.ufuncs* (Section "Output arguments") for details.

Returns

rounded_array [ndarray] An array of the same type as *a*, containing the rounded values. Unless *out* was specified, a new array is created. A reference to the result is returned.

The real and imaginary parts of complex numbers are rounded separately. The result of rounding a float is a float.

See also:

`ndarray.round` equivalent method

`ceil`, `fix`, `floor`, `rint`, `trunc`

Notes

For values exactly halfway between rounded decimal values, NumPy rounds to the nearest even value. Thus 1.5 and 2.5 round to 2.0, -0.5 and 0.5 round to 0.0, etc. Results may also be surprising due to the inexact representation of decimal fractions in the IEEE floating point standard [1] and errors introduced when scaling by powers of ten.

References

[1], [2]

Examples

```
>>> np.around([0.37, 1.64])  # doctest: +SKIP
array([ 0.,  2.])
>>> np.around([0.37, 1.64], decimals=1)  # doctest: +SKIP
array([ 0.4,  1.6])
>>> np.around([.5, 1.5, 2.5, 3.5, 4.5]) # rounds to nearest even value  #␣
↪doctest: +SKIP
array([ 0.,  2.,  2.,  4.,  4.])
>>> np.around([1,2,3,11], decimals=1) # ndarray of ints is returned  # doctest:␣
↪+SKIP
array([ 1,  2,  3, 11])
>>> np.around([1,2,3,11], decimals=-1)  # doctest: +SKIP
array([ 0,  0,  0, 10])
```

`dask.array.`**`array`**(*object*, *dtype=None*, *copy=True*, *order='K'*, *subok=False*, *ndmin=0*)

This docstring was copied from numpy.array.

Some inconsistencies with the Dask version may exist.

Create an array.

Parameters

object [array_like] An array, any object exposing the array interface, an object whose __array__ method returns an array, or any (nested) sequence.

dtype [data-type, optional] The desired data-type for the array. If not given, then the type will be determined as the minimum type required to hold the objects in the sequence. This argument can only be used to 'upcast' the array. For downcasting, use the .astype(t) method.

copy [bool, optional] If true (default), then the object is copied. Otherwise, a copy will only be made if __array__ returns a copy, if obj is a nested sequence, or if a copy is needed to satisfy any of the other requirements (*dtype*, *order*, etc.).

order [{'K', 'A', 'C', 'F'}, optional] Specify the memory layout of the array. If object is not an array, the newly created array will be in C order (row major) unless 'F' is specified, in which case it will be in Fortran order (column major). If object is an array the following holds.

order	no copy	copy=True
'K'	unchanged	F & C order preserved, otherwise most similar order
'A'	unchanged	F order if input is F and not C, otherwise C order
'C'	C order	C order
'F'	F order	F order

When `copy=False` and a copy is made for other reasons, the result is the same as if `copy=True`, with some exceptions for *A*, see the Notes section. The default order is 'K'.

subok [bool, optional] If True, then sub-classes will be passed-through, otherwise the returned array will be forced to be a base-class array (default).

ndmin [int, optional] Specifies the minimum number of dimensions that the resulting array should have. Ones will be pre-pended to the shape as needed to meet this requirement.

Returns

out [ndarray] An array object satisfying the specified requirements.

See also:

`empty_like` Return an empty array with shape and type of input.

`ones_like` Return an array of ones with shape and type of input.

`zeros_like` Return an array of zeros with shape and type of input.

`full_like` Return a new array with shape of input filled with value.

`empty` Return a new uninitialized array.

`ones` Return a new array setting values to one.

`zeros` Return a new array setting values to zero.

`full` Return a new array of given shape filled with value.

Notes

When order is 'A' and *object* is an array in neither 'C' nor 'F' order, and a copy is forced by a change in dtype, then the order of the result is not necessarily 'C' as expected. This is likely a bug.

Examples

```
>>> np.array([1, 2, 3])  # doctest: +SKIP
array([1, 2, 3])
```

Upcasting:

```
>>> np.array([1, 2, 3.0])  # doctest: +SKIP
array([ 1.,  2.,  3.])
```

More than one dimension:

```
>>> np.array([[1, 2], [3, 4]])  # doctest: +SKIP
array([[1, 2],
       [3, 4]])
```

Minimum dimensions 2:

```
>>> np.array([1, 2, 3], ndmin=2)  # doctest: +SKIP
array([[1, 2, 3]])
```

Type provided:

```
>>> np.array([1, 2, 3], dtype=complex)  # doctest: +SKIP
array([ 1.+0.j,  2.+0.j,  3.+0.j])
```

Data-type consisting of more than one element:

```
>>> x = np.array([(1,2),(3,4)],dtype=[('a','<i4'),('b','<i4')])  # doctest: +SKIP
>>> x['a']  # doctest: +SKIP
array([1, 3])
```

Creating an array from sub-classes:

```
>>> np.array(np.mat('1 2; 3 4'))  # doctest: +SKIP
array([[1, 2],
       [3, 4]])
```

```
>>> np.array(np.mat('1 2; 3 4'), subok=True)  # doctest: +SKIP
matrix([[1, 2],
        [3, 4]])
```

`dask.array.`**`asanyarray`**(*a*)

Convert the input to a dask array.

Subclasses of `np.ndarray` will be passed through as chunks unchanged.

Parameters

a [array-like] Input data, in any form that can be converted to a dask array.

Returns

out [dask array] Dask array interpretation of a.

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> x = np.arange(3)
>>> da.asanyarray(x)
dask.array<array, shape=(3,), dtype=int64, chunksize=(3,), chunktype=numpy.
↪ndarray>
```

```
>>> y = [[1, 2, 3], [4, 5, 6]]
>>> da.asanyarray(y)
dask.array<array, shape=(2, 3), dtype=int64, chunksize=(2, 3), chunktype=numpy.
↪ndarray>
```

`dask.array.`**`asarray`**`(`*a*, ***kwargs*`)`

Convert the input to a dask array.

Parameters

a [array-like] Input data, in any form that can be converted to a dask array.

Returns

out [dask array] Dask array interpretation of a.

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> x = np.arange(3)
>>> da.asarray(x)
dask.array<array, shape=(3,), dtype=int64, chunksize=(3,), chunktype=numpy.
↪ndarray>
```

```
>>> y = [[1, 2, 3], [4, 5, 6]]
>>> da.asarray(y)
dask.array<array, shape=(2, 3), dtype=int64, chunksize=(2, 3), chunktype=numpy.
↪ndarray>
```

`dask.array.`**`atleast_1d`**`(`**arys*`)`

Convert inputs to arrays with at least one dimension.

This docstring was copied from numpy.atleast_1d.

Some inconsistencies with the Dask version may exist.

Scalar inputs are converted to 1-dimensional arrays, whilst higher-dimensional inputs are preserved.

Parameters

arys1, arys2, … [array_like] One or more input arrays.

Returns

ret [ndarray] An array, or list of arrays, each with `a.ndim >= 1`. Copies are made only if necessary.

See also:

`atleast_2d`, `atleast_3d`

Examples

```
>>> np.atleast_1d(1.0)  # doctest: +SKIP
array([ 1.])
```

```
>>> x = np.arange(9.0).reshape(3,3)  # doctest: +SKIP
>>> np.atleast_1d(x)  # doctest: +SKIP
array([[ 0.,  1.,  2.],
       [ 3.,  4.,  5.],
       [ 6.,  7.,  8.]])
>>> np.atleast_1d(x) is x  # doctest: +SKIP
True
```

```
>>> np.atleast_1d(1, [3, 4])  # doctest: +SKIP
[array([1]), array([3, 4])]
```

`dask.array.atleast_2d(*arys)`

View inputs as arrays with at least two dimensions.

This docstring was copied from numpy.atleast_2d.

Some inconsistencies with the Dask version may exist.

Parameters

arys1, arys2, ... [array_like] One or more array-like sequences. Non-array inputs are converted to arrays. Arrays that already have two or more dimensions are preserved.

Returns

res, res2, ... [ndarray] An array, or list of arrays, each with `a.ndim >= 2`. Copies are avoided where possible, and views with two or more dimensions are returned.

See also:

atleast_1d, *atleast_3d*

Examples

```
>>> np.atleast_2d(3.0)  # doctest: +SKIP
array([[ 3.]])
```

```
>>> x = np.arange(3.0)  # doctest: +SKIP
>>> np.atleast_2d(x)  # doctest: +SKIP
array([[ 0.,  1.,  2.]])
>>> np.atleast_2d(x).base is x  # doctest: +SKIP
True
```

```
>>> np.atleast_2d(1, [1, 2], [[1, 2]])  # doctest: +SKIP
[array([[1]]), array([[1, 2]]), array([[1, 2]])]
```

`dask.array.atleast_3d(*arys)`

View inputs as arrays with at least three dimensions.

This docstring was copied from numpy.atleast_3d.

Some inconsistencies with the Dask version may exist.

Parameters

arys1, arys2, . . . [array_like] One or more array-like sequences. Non-array inputs are converted to arrays. Arrays that already have three or more dimensions are preserved.

Returns

res1, res2, . . . [ndarray] An array, or list of arrays, each with `a.ndim >= 3`. Copies are avoided where possible, and views with three or more dimensions are returned. For example, a 1-D array of shape `(N,)` becomes a view of shape `(1, N, 1)`, and a 2-D array of shape `(M, N)` becomes a view of shape `(M, N, 1)`.

See also:

atleast_1d, *atleast_2d*

Examples

```
>>> np.atleast_3d(3.0)  # doctest: +SKIP
array([[[ 3.]]])
```

```
>>> x = np.arange(3.0)  # doctest: +SKIP
>>> np.atleast_3d(x).shape  # doctest: +SKIP
(1, 3, 1)
```

```
>>> x = np.arange(12.0).reshape(4,3)  # doctest: +SKIP
>>> np.atleast_3d(x).shape  # doctest: +SKIP
(4, 3, 1)
>>> np.atleast_3d(x).base is x.base  # x is a reshape, so not base itself  #␣
↪doctest: +SKIP
True
```

```
>>> for arr in np.atleast_3d([1, 2], [[1, 2]], [[[1, 2]]]):  # doctest: +SKIP
...     print(arr, arr.shape)
...
[[[1]
  [2]]] (1, 2, 1)
[[[1]
  [2]]] (1, 2, 1)
[[[1 2]]] (1, 1, 2)
```

`dask.array.`**`average`**(*a*, *axis=None*, *weights=None*, *returned=False*)

Compute the weighted average along the specified axis.

This docstring was copied from numpy.average.

Some inconsistencies with the Dask version may exist.

Parameters

a [array_like] Array containing data to be averaged. If *a* is not an array, a conversion is attempted.

axis [None or int or tuple of ints, optional] Axis or axes along which to average *a*. The default, axis=None, will average over all of the elements of the input array. If axis is negative it counts from the last to the first axis.

New in version 1.7.0.

If axis is a tuple of ints, averaging is performed on all of the axes specified in the tuple instead of a single axis or all the axes as before.

weights [array_like, optional] An array of weights associated with the values in *a*. Each value in *a* contributes to the average according to its associated weight. The weights array can either be 1-D (in which case its length must be the size of *a* along the given axis) or of the same shape as *a*. If *weights=None*, then all data in *a* are assumed to have a weight equal to one.

returned [bool, optional] Default is *False*. If *True*, the tuple (*average*, *sum_of_weights*) is returned, otherwise only the average is returned. If *weights=None*, *sum_of_weights* is equivalent to the number of elements over which the average is taken.

Returns

retval, [sum_of_weights] [array_type or double] Return the average along the specified axis. When *returned* is *True*, return a tuple with the average as the first element and the sum of the weights as the second element. *sum_of_weights* is of the same type as *retval*. The result dtype follows a genereal pattern. If *weights* is None, the result dtype will be that of *a* , or `float64` if *a* is integral. Otherwise, if *weights* is not None and *a* is non- integral, the result type will be the type of lowest precision capable of representing values of both *a* and *weights*. If *a* happens to be integral, the previous rules still applies but the result dtype will at least be `float64`.

Raises

ZeroDivisionError When all weights along axis are zero. See *numpy.ma.average* for a version robust to this type of error.

TypeError When the length of 1D *weights* is not the same as the shape of *a* along axis.

See also:

`mean`

`ma.average` average for masked arrays – useful if your data contains "missing" values

`numpy.result_type` Returns the type that results from applying the numpy type promotion rules to the arguments.

Examples

```
>>> data = range(1,5)  # doctest: +SKIP
>>> data  # doctest: +SKIP
[1, 2, 3, 4]
>>> np.average(data)  # doctest: +SKIP
2.5
>>> np.average(range(1,11), weights=range(10,0,-1))  # doctest: +SKIP
4.0
```

```
>>> data = np.arange(6).reshape((3,2))  # doctest: +SKIP
>>> data  # doctest: +SKIP
array([[0, 1],
       [2, 3],
       [4, 5]])
>>> np.average(data, axis=1, weights=[1./4, 3./4])  # doctest: +SKIP
array([ 0.75,  2.75,  4.75])
>>> np.average(data, weights=[1./4, 3./4])  # doctest: +SKIP
```

Traceback (most recent call last): . . . TypeError: Axis must be specified when shapes of a and weights differ.

```
>>> a = np.ones(5, dtype=np.float128)  # doctest: +SKIP
>>> w = np.ones(5, dtype=np.complex64)  # doctest: +SKIP
>>> avg = np.average(a, weights=w)  # doctest: +SKIP
>>> print(avg.dtype)  # doctest: +SKIP
complex256
```

`dask.array.bincount`(*x*, *weights=None*, *minlength=0*)

This docstring was copied from numpy.bincount.

Some inconsistencies with the Dask version may exist.

Count number of occurrences of each value in array of non-negative ints.

The number of bins (of size 1) is one larger than the largest value in *x*. If *minlength* is specified, there will be at least this number of bins in the output array (though it will be longer if necessary, depending on the contents of *x*). Each bin gives the number of occurrences of its index value in *x*. If *weights* is specified the input array is weighted by it, i.e. if a value `n` is found at position `i`, `out[n] += weight[i]` instead of `out[n] += 1`.

Parameters

x [array_like, 1 dimension, nonnegative ints] Input array.

weights [array_like, optional] Weights, array of the same shape as *x*.

minlength [int, optional] A minimum number of bins for the output array.

New in version 1.6.0.

Returns

out [ndarray of ints] The result of binning the input array. The length of *out* is equal to `np.amax(x)+1`.

Raises

ValueError If the input is not 1-dimensional, or contains elements with negative values, or if *minlength* is negative.

TypeError If the type of the input is float or complex.

See also:

histogram, *digitize*, *unique*

Examples

```
>>> np.bincount(np.arange(5))  # doctest: +SKIP
array([1, 1, 1, 1, 1])
>>> np.bincount(np.array([0, 1, 1, 3, 2, 1, 7]))  # doctest: +SKIP
array([1, 3, 1, 1, 0, 0, 0, 1])
```

```
>>> x = np.array([0, 1, 1, 3, 2, 1, 7, 23])  # doctest: +SKIP
>>> np.bincount(x).size == np.amax(x)+1  # doctest: +SKIP
True
```

The input array needs to be of integer dtype, otherwise a TypeError is raised:

```
>>> np.bincount(np.arange(5, dtype=float))  # doctest: +SKIP
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
TypeError: array cannot be safely cast to required type
```

A possible use of `bincount` is to perform sums over variable-size chunks of an array, using the `weights` keyword.

```
>>> w = np.array([0.3, 0.5, 0.2, 0.7, 1., -0.6]) # weights  # doctest: +SKIP
>>> x = np.array([0, 1, 1, 2, 2, 2])  # doctest: +SKIP
>>> np.bincount(x,  weights=w)  # doctest: +SKIP
array([ 0.3,  0.7,  1.1])
```

`dask.array.`**`bitwise_and`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the bit-wise AND of two arrays element-wise.

Computes the bit-wise AND of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator `&`.

Parameters

x1, x2 [array_like] Only integer and boolean types are handled.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Result. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logical_and`, *`bitwise_or`*, *`bitwise_xor`*

`binary_repr` Return the binary representation of the input number as a string.

Examples

The number 13 is represented by `00001101`. Likewise, 17 is represented by `00010001`. The bit-wise AND of 13 and 17 is therefore `000000001`, or 1:

```
>>> np.bitwise_and(13, 17)  # doctest: +SKIP
1
```

```
>>> np.bitwise_and(14, 13)  # doctest: +SKIP
12
>>> np.binary_repr(12)  # doctest: +SKIP
'1100'
>>> np.bitwise_and([14,3], 13)  # doctest: +SKIP
array([12,  1])
```

```
>>> np.bitwise_and([11,7], [4,25])  # doctest: +SKIP
array([0, 1])
>>> np.bitwise_and(np.array([2,5,255]), np.array([3,14,16]))  # doctest: +SKIP
array([ 2,  4, 16])
>>> np.bitwise_and([True, True], [False, True])  # doctest: +SKIP
array([False,  True])
```

`dask.array.`**`bitwise_not`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute bit-wise inversion, or bit-wise NOT, element-wise.

Computes the bit-wise NOT of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator ~.

For signed integer inputs, the two's complement is returned. In a two's-complement system negative numbers are represented by the two's complement of the absolute value. This is the most common method of representing signed integers on computers [1]. A N-bit two's-complement system can represent every integer in the range -2^{N-1} to $+2^{N-1} - 1$.

Parameters

x [array_like] Only integer and boolean types are handled.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Result. This is a scalar if *x* is a scalar.

See also:

`bitwise_and`, *`bitwise_or`*, *`bitwise_xor`*, *`logical_not`*

`binary_repr` Return the binary representation of the input number as a string.

Notes

bitwise_not is an alias for *invert*:

```
>>> np.bitwise_not is np.invert  # doctest: +SKIP
True
```

References

[1]

Examples

We've seen that 13 is represented by `00001101`. The invert or bit-wise NOT of 13 is then:

```
>>> np.invert(np.array([13], dtype=uint8))  # doctest: +SKIP
array([242], dtype=uint8)
>>> np.binary_repr(x, width=8)  # doctest: +SKIP
'00001101'
>>> np.binary_repr(242, width=8)  # doctest: +SKIP
'11110010'
```

The result depends on the bit-width:

```
>>> np.invert(np.array([13], dtype=uint16))  # doctest: +SKIP
array([65522], dtype=uint16)
>>> np.binary_repr(x, width=16)  # doctest: +SKIP
'0000000000001101'
>>> np.binary_repr(65522, width=16)  # doctest: +SKIP
'1111111111110010'
```

When using signed integer types the result is the two's complement of the result for the unsigned type:

```
>>> np.invert(np.array([13], dtype=int8))  # doctest: +SKIP
array([-14], dtype=int8)
>>> np.binary_repr(-14, width=8)  # doctest: +SKIP
'11110010'
```

Booleans are accepted as well:

```
>>> np.invert(array([True, False]))  # doctest: +SKIP
array([False,  True])
```

`dask.array.`**`bitwise_or`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the bit-wise OR of two arrays element-wise.

Computes the bit-wise OR of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator `|`.

Parameters

x1, x2 [array_like] Only integer and boolean types are handled.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Result. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logical_or`, `bitwise_and`, `bitwise_xor`

`binary_repr` Return the binary representation of the input number as a string.

Examples

The number 13 has the binaray representation `00001101`. Likewise, 16 is represented by `00010000`. The bit-wise OR of 13 and 16 is then `000111011`, or 29:

```
>>> np.bitwise_or(13, 16)  # doctest: +SKIP
29
>>> np.binary_repr(29)  # doctest: +SKIP
'11101'
```

```
>>> np.bitwise_or(32, 2)  # doctest: +SKIP
34
>>> np.bitwise_or([33, 4], 1)  # doctest: +SKIP
array([33,  5])
>>> np.bitwise_or([33, 4], [1, 2])  # doctest: +SKIP
array([33,  6])
```

```
>>> np.bitwise_or(np.array([2, 5, 255]), np.array([4, 4, 4]))  # doctest: +SKIP
array([  6,   5, 255])
>>> np.array([2, 5, 255]) | np.array([4, 4, 4])  # doctest: +SKIP
array([  6,   5, 255])
>>> np.bitwise_or(np.array([2, 5, 255, 2147483647L], dtype=np.int32),  # doctest:␣
↪+SKIP
...               np.array([4, 4, 4, 2147483647L], dtype=np.int32))
array([         6,          5,        255, 2147483647])
>>> np.bitwise_or([True, True], [False, True])  # doctest: +SKIP
array([ True,  True])
```

`dask.array.`**`bitwise_xor`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the bit-wise XOR of two arrays element-wise.

Computes the bit-wise XOR of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator ^.

Parameters

x1, x2 [array_like] Only integer and boolean types are handled.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Result. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logical_xor`, `bitwise_and`, `bitwise_or`

`binary_repr` Return the binary representation of the input number as a string.

Examples

The number 13 is represented by `00001101`. Likewise, 17 is represented by `00010001`. The bit-wise XOR of 13 and 17 is therefore `00011100`, or 28:

```
>>> np.bitwise_xor(13, 17)  # doctest: +SKIP
28
>>> np.binary_repr(28)  # doctest: +SKIP
'11100'
```

```
>>> np.bitwise_xor(31, 5)  # doctest: +SKIP
26
>>> np.bitwise_xor([31,3], 5)  # doctest: +SKIP
array([26,  6])
```

```
>>> np.bitwise_xor([31,3], [5,6])  # doctest: +SKIP
array([26,  5])
>>> np.bitwise_xor([True, True], [False, True])  # doctest: +SKIP
array([ True, False])
```

`dask.array.block`(*arrays*, *allow_unknown_chunksizes=False*)

Assemble an nd-array from nested lists of blocks.

Blocks in the innermost lists are concatenated along the last dimension (-1), then these are concatenated along the second-last dimension (-2), and so on until the outermost list is reached

Blocks can be of any dimension, but will not be broadcasted using the normal rules. Instead, leading axes of size 1 are inserted, to make `block.ndim` the same for all blocks. This is primarily useful for working with scalars, and means that code like `block([v, 1])` is valid, where `v.ndim == 1`.

When the nested list is two levels deep, this allows block matrices to be constructed from their components.

Parameters

arrays [nested list of array_like or scalars (but not tuples)] If passed a single ndarray or scalar (a nested list of depth 0), this is returned unmodified (and not copied).

Elements shapes must match along the appropriate axes (without broadcasting), but leading 1s will be prepended to the shape as necessary to make the dimensions match.

allow_unknown_chunksizes: bool Allow unknown chunksizes, such as come from converting from dask dataframes. Dask.array is unable to verify that chunks line up. If data comes from differently aligned sources then this can cause unexpected results.

Returns

block_array [ndarray] The array assembled from the given blocks.

The dimensionality of the output is equal to the greatest of: * the dimensionality of all the inputs * the depth to which the input list is nested

Raises

ValueError

- If list depths are mismatched - for instance, `[[a, b], c]` is illegal, and should be spelt `[[a, b], [c]]`
- If lists are empty - for instance, `[[a, b], []]`

See also:

`concatenate` Join a sequence of arrays together.

`stack` Stack arrays in sequence along a new dimension.

`hstack` Stack arrays in sequence horizontally (column wise).

`vstack` Stack arrays in sequence vertically (row wise).

`dstack` Stack arrays in sequence depth wise (along third dimension).

`vsplit` Split array into a list of multiple sub-arrays vertically.

Notes

When called with only scalars, `block` is equivalent to an ndarray call. So `block([[1, 2], [3, 4]])` is equivalent to `array([[1, 2], [3, 4]])`.

This function does not enforce that the blocks lie on a fixed grid. `block([[a, b], [c, d]])` is not restricted to arrays of the form:

```
AAAbb
AAAbb
cccDD
```

But is also allowed to produce, for some `a, b, c, d`:

```
AAAbb
AAAbb
cDDDD
```

Since concatenation happens along the last axis first, *block* is _not_ capable of producing the following directly:

```
AAAbb
cccbb
cccDD
```

Matlab's "square bracket stacking", `[A, B, ...; p, q, ...]`, is equivalent to `block([[A, B, ...], [p, q, ...]])`.

`dask.array.`**`blockwise`**(*func, out_ind, *args, name=None, token=None, dtype=None, adjust_chunks=None, new_axes=None, align_arrays=True, concatenate=None, meta=None, **kwargs*)

Tensor operation: Generalized inner and outer products

A broad class of blocked algorithms and patterns can be specified with a concise multi-index notation. The `blockwise` function applies an in-memory function across multiple blocks of multiple inputs in a variety of ways. Many dask.array operations are special cases of blockwise including elementwise, broadcasting, reductions, tensordot, and transpose.

Parameters

func [callable] Function to apply to individual tuples of blocks

out_ind [iterable] Block pattern of the output, something like 'ijk' or (1, 2, 3)

***args** [sequence of Array, index pairs] Sequence like (x, 'ij', y, 'jk', z, 'i')

****kwargs** [dict] Extra keyword arguments to pass to function

dtype [np.dtype] Datatype of resulting array.

concatenate [bool, keyword only] If true concatenate arrays along dummy indices, else provide lists

adjust_chunks [dict] Dictionary mapping index to function to be applied to chunk sizes

new_axes [dict, keyword only] New indexes and their dimension lengths

Examples

2D embarrassingly parallel operation from two arrays, x, and y.

```
>>> z = blockwise(operator.add, 'ij', x, 'ij', y, 'ij', dtype='f8')  # z = x + y
↪# doctest: +SKIP
```

Outer product multiplying x by y, two 1-d vectors

```
>>> z = blockwise(operator.mul, 'ij', x, 'i', y, 'j', dtype='f8')  # doctest:␣
↪+SKIP
```

z = x.T

```
>>> z = blockwise(np.transpose, 'ji', x, 'ij', dtype=x.dtype)  # doctest: +SKIP
```

The transpose case above is illustrative because it does same transposition both on each in-memory block by calling `np.transpose` and on the order of the blocks themselves, by switching the order of the index `ij -> ji`.

We can compose these same patterns with more variables and more complex in-memory functions

z = X + Y.T

```
>>> z = blockwise(lambda x, y: x + y.T, 'ij', x, 'ij', y, 'ji', dtype='f8')  #␣
↪doctest: +SKIP
```

Any index, like `i` missing from the output index is interpreted as a contraction (note that this differs from Einstein convention; repeated indices do not imply contraction.) In the case of a contraction the passed function should expect an iterable of blocks on any array that holds that index. To receive arrays concatenated along contracted dimensions instead pass `concatenate=True`.

Inner product multiplying x by y, two 1-d vectors

```
>>> def sequence_dot(x_blocks, y_blocks):
...     result = 0
...     for x, y in zip(x_blocks, y_blocks):
...         result += x.dot(y)
...     return result
```

```
>>> z = blockwise(sequence_dot, '', x, 'i', y, 'i', dtype='f8')  # doctest: +SKIP
```

Add new single-chunk dimensions with the `new_axes=` keyword, including the length of the new dimension. New dimensions will always be in a single chunk.

```
>>> def f(x):
...     return x[:, None] * np.ones((1, 5))
```

```
>>> z = blockwise(f, 'az', x, 'a', new_axes={'z': 5}, dtype=x.dtype)  # doctest:␣
↪+SKIP
```

New dimensions can also be multi-chunk by specifying a tuple of chunk sizes. This has limited utility as is (because the chunks are all the same), but the resulting graph can be modified to achieve more useful results (see `da.map_blocks`).

```
>>> z = blockwise(f, 'az', x, 'a', new_axes={'z': (5, 5)}, dtype=x.dtype)  #␣
↪doctest: +SKIP
```

If the applied function changes the size of each chunk you can specify this with a `adjust_chunks={...}` dictionary holding a function for each index that modifies the dimension size in that index.

```
>>> def double(x):
...     return np.concatenate([x, x])
```

```
>>> y = blockwise(double, 'ij', x, 'ij',
...               adjust_chunks={'i': lambda n: 2 * n}, dtype=x.dtype)  #␣
↪doctest: +SKIP
```

Include literals by indexing with None

```
>>> y = blockwise(add, 'ij', x, 'ij', 1234, None, dtype=x.dtype)  # doctest: +SKIP
```

dask.array.**broadcast_arrays**(**args*, ***kwargs*)

Broadcast any number of arrays against each other.

This docstring was copied from numpy.broadcast_arrays.

Some inconsistencies with the Dask version may exist.

Parameters

‘*args‘ [array_likes] The arrays to broadcast.

subok [bool, optional] If True, then sub-classes will be passed-through, otherwise the returned arrays will be forced to be a base-class array (default).

Returns

broadcasted [list of arrays] These arrays are views on the original arrays. They are typically not contiguous. Furthermore, more than one element of a broadcasted array may refer to a single memory location. If you need to write to the arrays, make copies first.

Examples

```
>>> x = np.array([[1,2,3]])  # doctest: +SKIP
>>> y = np.array([[4],[5]])  # doctest: +SKIP
>>> np.broadcast_arrays(x, y)  # doctest: +SKIP
[array([[1, 2, 3],
       [1, 2, 3]]), array([[4, 4, 4],
       [5, 5, 5]])]
```

Here is a useful idiom for getting contiguous copies instead of non-contiguous views.

```
>>> [np.array(a) for a in np.broadcast_arrays(x, y)]  # doctest: +SKIP
[array([[1, 2, 3],
       [1, 2, 3]]), array([[4, 4, 4],
       [5, 5, 5]])]
```

dask.array.**broadcast_to**(*x*, *shape*, *chunks=None*)

Broadcast an array to a new shape.

Parameters

x [array_like] The array to broadcast.

shape [tuple] The shape of the desired array.

chunks [tuple, optional] If provided, then the result will use these chunks instead of the same chunks as the source array. Setting chunks explicitly as part of broadcast_to is more efficient than rechunking afterwards. Chunks are only allowed to differ from the original shape along dimensions that are new on the result or have size 1 the input array.

Returns

broadcast [dask array]

See also:

`numpy.broadcast_to()`

`dask.array.`**`coarsen`**(*reduction*, *x*, *axes*, *trim_excess=False*)

Coarsen array by applying reduction to fixed size neighborhoods

Parameters

reduction: function Function like np.sum, np.mean, etc...

x: np.ndarray Array to be coarsened

axes: dict Mapping of axis to coarsening factor

Examples

```
>>> x = np.array([1, 2, 3, 4, 5, 6])
>>> coarsen(np.sum, x, {0: 2})
array([ 3,  7, 11])
>>> coarsen(np.max, x, {0: 3})
array([3, 6])
```

Provide dictionary of scale per dimension

```
>>> x = np.arange(24).reshape((4, 6))
>>> x
array([[ 0,  1,  2,  3,  4,  5],
       [ 6,  7,  8,  9, 10, 11],
       [12, 13, 14, 15, 16, 17],
       [18, 19, 20, 21, 22, 23]])
```

```
>>> coarsen(np.min, x, {0: 2, 1: 3})
array([[ 0,  3],
       [12, 15]])
```

You must avoid excess elements explicitly

```
>>> x = np.array([1, 2, 3, 4, 5, 6, 7, 8])
>>> coarsen(np.min, x, {0: 3}, trim_excess=True)
array([1, 4])
```

`dask.array.`**`ceil`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the ceiling of the input, element-wise.

The ceil of the scalar *x* is the smallest integer *i*, such that *i* >= *x*. It is often denoted as $\lceil x \rceil$.

Parameters

x [array_like] Input data.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The ceiling of each element in *x*, with *float* dtype. This is a scalar if *x* is a scalar.

See also:

`floor`, `trunc`, `rint`

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])  # doctest: +SKIP
>>> np.ceil(a)  # doctest: +SKIP
array([-1., -1., -0.,  1.,  2.,  2.,  2.])
```

`dask.array.`**`choose`**`(`*a*, *choices*`)`

Construct an array from an index array and a set of arrays to choose from.

This docstring was copied from numpy.choose.

Some inconsistencies with the Dask version may exist.

First of all, if confused or uncertain, definitely look at the Examples - in its full generality, this function is less simple than it might seem from the following code description (below ndi = *numpy.lib.index_tricks*):

`np.choose(a,c) == np.array([c[a[I]][I] for I in ndi.ndindex(a.shape)])`.

But this omits some subtleties. Here is a fully general summary:

Given an "index" array (*a*) of integers and a sequence of *n* arrays (*choices*), *a* and each choice array are first broadcast, as necessary, to arrays of a common shape; calling these *Ba* and *Bchoices[i], i = 0,…,n-1* we have that, necessarily, `Ba.shape == Bchoices[i].shape` for each *i*. Then, a new array with shape `Ba.shape` is created as follows:

- if `mode=raise` (the default), then, first of all, each element of *a* (and thus *Ba*) must be in the range *[0, n-1]*; now, suppose that *i* (in that range) is the value at the *(j0, j1, ..., jm)* position in *Ba* - then the value at the same position in the new array is the value in *Bchoices[i]* at that same position;
- if `mode=wrap`, values in *a* (and thus *Ba*) may be any (signed) integer; modular arithmetic is used to map integers outside the range *[0, n-1]* back into that range; and then the new array is constructed as above;
- if `mode=clip`, values in *a* (and thus *Ba*) may be any (signed) integer; negative integers are mapped to 0; values greater than *n-1* are mapped to *n-1*; and then the new array is constructed as above.

Parameters

a [int array] This array must contain integers in *[0, n-1]*, where *n* is the number of choices, unless `mode=wrap` or `mode=clip`, in which cases any integers are permissible.

choices [sequence of arrays] Choice arrays. *a* and all of the choices must be broadcastable to the same shape. If *choices* is itself an array (not recommended), then its outermost dimension (i.e., the one corresponding to `choices.shape[0]`) is taken as defining the "sequence".

out [array, optional (Not supported in Dask)] If provided, the result will be inserted into this array. It should be of the appropriate shape and dtype.

mode [{'raise' (default), 'wrap', 'clip'}, optional (Not supported in Dask)] Specifies how indices outside *[0, n-1]* will be treated:

- 'raise' : an exception is raised
- 'wrap' : value becomes value mod *n*
- 'clip' : values < 0 are mapped to 0, values > n-1 are mapped to n-1

Returns

merged_array [array] The merged result.

Raises

ValueError: shape mismatch If *a* and each choice array are not all broadcastable to the same shape.

See also:

`ndarray.choose` equivalent method

Notes

To reduce the chance of misinterpretation, even though the following "abuse" is nominally supported, *choices* should neither be, nor be thought of as, a single array, i.e., the outermost sequence-like container should be either a list or a tuple.

Examples

```
>>> choices = [[0, 1, 2, 3], [10, 11, 12, 13],  # doctest: +SKIP
...   [20, 21, 22, 23], [30, 31, 32, 33]]
>>> np.choose([2, 3, 1, 0], choices  # doctest: +SKIP
... # the first element of the result will be the first element of the
... # third (2+1) "array" in choices, namely, 20; the second element
... # will be the second element of the fourth (3+1) choice array, i.e.,
... # 31, etc.
... )
array([20, 31, 12,  3])
>>> np.choose([2, 4, 1, 0], choices, mode='clip') # 4 goes to 3 (4-1)  # doctest:␣
↪+SKIP
array([20, 31, 12,  3])
>>> # because there are 4 choice arrays
>>> np.choose([2, 4, 1, 0], choices, mode='wrap') # 4 goes to (4 mod 4)  #␣
↪doctest: +SKIP
array([20,  1, 12,  3])
>>> # i.e., 0
```

A couple examples illustrating how choose broadcasts:

```
>>> a = [[1, 0, 1], [0, 1, 0], [1, 0, 1]]  # doctest: +SKIP
>>> choices = [-10, 10]  # doctest: +SKIP
>>> np.choose(a, choices)  # doctest: +SKIP
array([[ 10, -10,  10],
       [-10,  10, -10],
       [ 10, -10,  10]])
```

```
>>> # With thanks to Anne Archibald
>>> a = np.array([0, 1]).reshape((2,1,1))  # doctest: +SKIP
>>> c1 = np.array([1, 2, 3]).reshape((1,3,1))  # doctest: +SKIP
>>> c2 = np.array([-1, -2, -3, -4, -5]).reshape((1,1,5))  # doctest: +SKIP
>>> np.choose(a, (c1, c2)) # result is 2x3x5, res[0,:,:]=c1, res[1,:,:]=c2  #␣
↪doctest: +SKIP
array([[[ 1,  1,  1,  1,  1],
        [ 2,  2,  2,  2,  2],
        [ 3,  3,  3,  3,  3]],
       [[-1, -2, -3, -4, -5],
        [-1, -2, -3, -4, -5],
        [-1, -2, -3, -4, -5]]])
```

`dask.array.`**`clip`**(**args*, ***kwargs*)

Clip (limit) the values in an array.

Given an interval, values outside the interval are clipped to the interval edges. For example, if an interval of `[0, 1]` is specified, values smaller than 0 become 0, and values larger than 1 become 1.

Parameters

a [array_like] Array containing elements to clip.

a_min [scalar or array_like or *None*] Minimum value. If *None*, clipping is not performed on lower interval edge. Not more than one of *a_min* and *a_max* may be *None*.

a_max [scalar or array_like or *None*] Maximum value. If *None*, clipping is not performed on upper interval edge. Not more than one of *a_min* and *a_max* may be *None*. If *a_min* or *a_max* are array_like, then the three arrays will be broadcasted to match their shapes.

out [ndarray, optional] The results will be placed in this array. It may be the input array for in-place clipping. *out* must be of the right shape to hold the output. Its type is preserved.

Returns

clipped_array [ndarray] An array with the elements of *a*, but where values < *a_min* are replaced with *a_min*, and those > *a_max* with *a_max*.

See also:

`numpy.doc.ufuncs` Section “Output arguments”

Examples

```
>>> a = np.arange(10)  # doctest: +SKIP
>>> np.clip(a, 1, 8)  # doctest: +SKIP
array([1, 1, 2, 3, 4, 5, 6, 7, 8, 8])
>>> a  # doctest: +SKIP
array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
>>> np.clip(a, 3, 6, out=a)  # doctest: +SKIP
array([3, 3, 3, 3, 4, 5, 6, 6, 6, 6])
>>> a = np.arange(10)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
>>> np.clip(a, [3, 4, 1, 1, 1, 4, 4, 4, 4, 4], 8)  # doctest: +SKIP
array([3, 4, 2, 3, 4, 5, 6, 7, 8, 8])
```

`dask.array.`**`compress`**(*condition*, *a*, *axis=None*)

Return selected slices of an array along given axis.

This docstring was copied from numpy.compress.

Some inconsistencies with the Dask version may exist.

When working along a given axis, a slice along that axis is returned in *output* for each index where *condition* evaluates to True. When working on a 1-D array, *compress* is equivalent to *extract*.

Parameters

condition [1-D array of bools] Array that selects which entries to return. If len(condition) is less than the size of *a* along the given axis, then output is truncated to the length of the condition array.

a [array_like] Array from which to extract a part.

axis [int, optional] Axis along which to take slices. If None (default), work on the flattened array.

out [ndarray, optional (Not supported in Dask)] Output array. Its type is preserved and it must be of the right shape to hold the output.

Returns

compressed_array [ndarray] A copy of *a* without the slices along axis for which *condition* is false.

See also:

`take`, `choose`, `diag`, `diagonal`, `select`

`ndarray.compress` Equivalent method in ndarray

`np.extract` Equivalent method when working on 1-D arrays

`numpy.doc.ufuncs` Section "Output arguments"

Examples

```
>>> a = np.array([[1, 2], [3, 4], [5, 6]])  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([[1, 2],
       [3, 4],
       [5, 6]])
>>> np.compress([0, 1], a, axis=0)  # doctest: +SKIP
array([[3, 4]])
>>> np.compress([False, True, True], a, axis=0)  # doctest: +SKIP
array([[3, 4],
       [5, 6]])
>>> np.compress([False, True], a, axis=1)  # doctest: +SKIP
array([[2],
       [4],
       [6]])
```

Working on the flattened array does not return slices along an axis but selects elements.

```
>>> np.compress([False, True], a)  # doctest: +SKIP
array([2])
```

`dask.array.`**`concatenate`**(*seq*, *axis=0*, *allow_unknown_chunksizes=False*)

Concatenate arrays along an existing axis

Given a sequence of dask Arrays form a new dask Array by stacking them along an existing dimension (axis=0 by default)

Parameters

seq: list of dask.arrays

axis: int Dimension along which to align all of the arrays

allow_unknown_chunksizes: bool Allow unknown chunksizes, such as come from converting from dask dataframes. Dask.array is unable to verify that chunks line up. If data comes from differently aligned sources then this can cause unexpected results.

See also:

`stack`

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...          for i in range(3)]
```

```
>>> x = da.concatenate(data, axis=0)
>>> x.shape
(12, 4)
```

```
>>> da.concatenate(data, axis=1).shape
(4, 12)
```

Result is a new dask Array

`dask.array.conj`(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the complex conjugate, element-wise.

The complex conjugate of a complex number is obtained by changing the sign of its imaginary part.

Parameters

x [array_like] Input value.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The complex conjugate of *x*, with same dtype as *y*. This is a scalar if *x* is a scalar.

Examples

```
>>> np.conjugate(1+2j)  # doctest: +SKIP
(1-2j)
```

```
>>> x = np.eye(2) + 1j * np.eye(2)  # doctest: +SKIP
>>> np.conjugate(x)  # doctest: +SKIP
array([[ 1.-1.j,  0.-0.j],
       [ 0.-0.j,  1.-1.j]])
```

dask.array.**copysign**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Change the sign of x1 to that of x2, element-wise.

If both arguments are arrays or sequences, they have to be of the same length. If *x2* is a scalar, its sign will be copied to all elements of *x1*.

Parameters

x1 [array_like] Values to change the sign of.

x2 [array_like] The sign of *x2* is copied to *x1*.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] The values of *x1* with the sign of *x2*. This is a scalar if both *x1* and *x2* are scalars.

Examples

```
>>> np.copysign(1.3, -1)  # doctest: +SKIP
-1.3
>>> 1/np.copysign(0, 1)  # doctest: +SKIP
inf
>>> 1/np.copysign(0, -1)  # doctest: +SKIP
-inf
```

```
>>> np.copysign([-1, 0, 1], -1.1)  # doctest: +SKIP
array([-1., -0., -1.])
>>> np.copysign([-1, 0, 1], np.arange(3)-1)  # doctest: +SKIP
array([-1.,  0.,  1.])
```

dask.array.**corrcoef**(*x*, *y=None*, *rowvar=1*)

Return Pearson product-moment correlation coefficients.

This docstring was copied from numpy.corrcoef.

Some inconsistencies with the Dask version may exist.

Please refer to the documentation for *cov* for more detail. The relationship between the correlation coefficient matrix, *R*, and the covariance matrix, *C*, is

$$R_{ij} = \frac{C_{ij}}{\sqrt{C_{ii} * C_{jj}}}$$

The values of *R* are between -1 and 1, inclusive.

Parameters

x [array_like] A 1-D or 2-D array containing multiple variables and observations. Each row of *x* represents a variable, and each column a single observation of all those variables. Also see *rowvar* below.

y [array_like, optional] An additional set of variables and observations. *y* has the same shape as *x*.

rowvar [bool, optional] If *rowvar* is True (default), then each row represents a variable, with observations in the columns. Otherwise, the relationship is transposed: each column represents a variable, while the rows contain observations.

bias [_NoValue, optional (Not supported in Dask)] Has no effect, do not use.

Deprecated since version 1.10.0.

ddof [_NoValue, optional (Not supported in Dask)] Has no effect, do not use.

Deprecated since version 1.10.0.

Returns

R [ndarray] The correlation coefficient matrix of the variables.

See also:

`cov` Covariance matrix

Notes

Due to floating point rounding the resulting array may not be Hermitian, the diagonal elements may not be 1, and the elements may not satisfy the inequality abs(a) <= 1. The real and imaginary parts are clipped to the interval [-1, 1] in an attempt to improve on that situation but is not much help in the complex case.

This function accepts but discards arguments *bias* and *ddof*. This is for backwards compatibility with previous versions of this function. These arguments had no effect on the return values of the function and can be safely ignored in this and previous versions of numpy.

`dask.array.`**`cos`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Cosine element-wise.

Parameters

x [array_like] Input array in radians.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The corresponding cosine values. This is a scalar if *x* is a scalar.

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

M. Abramowitz and I. A. Stegun, Handbook of Mathematical Functions. New York, NY: Dover, 1972.

Examples

```
>>> np.cos(np.array([0, np.pi/2, np.pi]))  # doctest: +SKIP
array([  1.00000000e+00,   6.12303177e-17,  -1.00000000e+00])
>>>
>>> # Example of providing the optional output parameter
>>> out2 = np.cos([0.1], out1)  # doctest: +SKIP
>>> out2 is out1  # doctest: +SKIP
True
>>>
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.cos(np.zeros((3,3)),np.zeros((2,2)))  # doctest: +SKIP
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: operands could not be broadcast together with shapes (3,3) (2,2)
```

`dask.array.`**`cosh`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Hyperbolic cosine, element-wise.

Equivalent to `1/2 * (np.exp(x) + np.exp(-x))` and `np.cos(1j*x)`.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Output array of same shape as *x*. This is a scalar if *x* is a scalar.

Examples

```
>>> np.cosh(0)  # doctest: +SKIP
1.0
```

The hyperbolic cosine describes the shape of a hanging cable:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> x = np.linspace(-4, 4, 1000)  # doctest: +SKIP
>>> plt.plot(x, np.cosh(x))  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.`**`count_nonzero`**`(`*a*, *axis=None*`)`

Counts the number of non-zero values in the array `a`.

This docstring was copied from numpy.count_nonzero.

Some inconsistencies with the Dask version may exist.

The word "non-zero" is in reference to the Python 2.x built-in method `__nonzero__()` (renamed `__bool__()` in Python 3.x) of Python objects that tests an object's "truthfulness". For example, any number is considered truthful if it is nonzero, whereas any string is considered truthful if it is not the empty string. Thus, this function (recursively) counts how many elements in `a` (and in sub-arrays thereof) have their `__nonzero__()` or `__bool__()` method evaluated to `True`.

Parameters

a [array_like] The array for which to count non-zeros.

axis [int or tuple, optional] Axis or tuple of axes along which to count non-zeros. Default is None, meaning that non-zeros will be counted along a flattened version of `a`.

New in version 1.12.0.

Returns

count [int or array of int] Number of non-zero values in the array along a given axis. Otherwise, the total number of non-zero values in the array is returned.

See also:

`nonzero` Return the coordinates of all the non-zero values.

Examples

```
>>> np.count_nonzero(np.eye(4))  # doctest: +SKIP
4
>>> np.count_nonzero([[0,1,7,0,0],[3,0,0,2,19]])  # doctest: +SKIP
5
>>> np.count_nonzero([[0,1,7,0,0],[3,0,0,2,19]], axis=0)  # doctest: +SKIP
array([1, 1, 1, 1, 1])
>>> np.count_nonzero([[0,1,7,0,0],[3,0,0,2,19]], axis=1)  # doctest: +SKIP
array([2, 3])
```

`dask.array.`**`cov`**`(`*m*, *y=None*, *rowvar=1*, *bias=0*, *ddof=None*`)`

Estimate a covariance matrix, given data and weights.

This docstring was copied from numpy.cov.

Some inconsistencies with the Dask version may exist.

Covariance indicates the level to which two variables vary together. If we examine N-dimensional samples, $X = [x_1, x_2, ...x_N]^T$, then the covariance matrix element C_{ij} is the covariance of x_i and x_j. The element C_{ii} is the variance of x_i.

See the notes for an outline of the algorithm.

Parameters

m [array_like] A 1-D or 2-D array containing multiple variables and observations. Each row of *m* represents a variable, and each column a single observation of all those variables. Also see *rowvar* below.

y [array_like, optional] An additional set of variables and observations. *y* has the same form as that of *m*.

rowvar [bool, optional] If *rowvar* is True (default), then each row represents a variable, with observations in the columns. Otherwise, the relationship is transposed: each column represents a variable, while the rows contain observations.

bias [bool, optional] Default normalization (False) is by `(N - 1)`, where `N` is the number of observations given (unbiased estimate). If *bias* is True, then normalization is by `N`. These values can be overridden by using the keyword `ddof` in numpy versions >= 1.5.

ddof [int, optional] If not `None` the default value implied by *bias* is overridden. Note that `ddof=1` will return the unbiased estimate, even if both *fweights* and *aweights* are specified, and `ddof=0` will return the simple average. See the notes for the details. The default value is `None`.

New in version 1.5.

fweights [array_like, int, optional (Not supported in Dask)] 1-D array of integer frequency weights; the number of times each observation vector should be repeated.

New in version 1.10.

aweights [array_like, optional (Not supported in Dask)] 1-D array of observation vector weights. These relative weights are typically large for observations considered "important" and smaller for observations considered less "important". If `ddof=0` the array of weights can be used to assign probabilities to observation vectors.

New in version 1.10.

Returns

out [ndarray] The covariance matrix of the variables.

See also:

`corrcoef` Normalized covariance matrix

Notes

Assume that the observations are in the columns of the observation array *m* and let `f = fweights` and `a = aweights` for brevity. The steps to compute the weighted covariance are as follows:

```
>>> w = f * a
>>> v1 = np.sum(w)
>>> v2 = np.sum(w * a)
>>> m -= np.sum(m * w, axis=1, keepdims=True) / v1
>>> cov = np.dot(m * w, m.T) * v1 / (v1**2 - ddof * v2)
```

Note that when `a == 1`, the normalization factor `v1 / (v1**2 - ddof * v2)` goes over to `1 / (np.sum(f) - ddof)` as it should.

Examples

Consider two variables, x_0 and x_1, which correlate perfectly, but in opposite directions:

```
>>> x = np.array([[0, 2], [1, 1], [2, 0]]).T  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([[0, 1, 2],
       [2, 1, 0]])
```

Note how x_0 increases while x_1 decreases. The covariance matrix shows this clearly:

```
>>> np.cov(x)  # doctest: +SKIP
array([[ 1., -1.],
       [-1.,  1.]])
```

Note that element $C_{0,1}$, which shows the correlation between x_0 and x_1, is negative.

Further, note how *x* and *y* are combined:

```
>>> x = [-2.1, -1,  4.3]  # doctest: +SKIP
>>> y = [3,  1.1,  0.12]  # doctest: +SKIP
>>> X = np.stack((x, y), axis=0)  # doctest: +SKIP
>>> print(np.cov(X))  # doctest: +SKIP
[[ 11.71        -4.286     ]
 [ -4.286        2.14413333]]
>>> print(np.cov(x, y))  # doctest: +SKIP
[[ 11.71        -4.286     ]
 [ -4.286        2.14413333]]
>>> print(np.cov(x))  # doctest: +SKIP
11.71
```

`dask.array.`**`cumprod`**(*a*, *axis=None*, *dtype=None*, *out=None*)

Return the cumulative product of elements along a given axis.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative product is computed. By default the input is flattened.

dtype [dtype, optional] Type of the returned array, as well as of the accumulator in which the elements are multiplied. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used instead.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type of the resulting values will be cast if necessary.

Returns

cumprod [ndarray] A new array holding the result is returned unless *out* is specified, in which case a reference to out is returned.

See also:

numpy.doc.ufuncs Section "Output arguments"

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow.

Examples

```
>>> a = np.array([1,2,3])
>>> np.cumprod(a) # intermediate results 1, 1*2
...               # total product 1*2*3 = 6
array([1, 2, 6])
>>> a = np.array([[1, 2, 3], [4, 5, 6]])
>>> np.cumprod(a, dtype=float) # specify type of output
array([   1.,    2.,    6.,   24.,  120.,  720.])
```

The cumulative product for each column (i.e., over the rows) of *a*:

```
>>> np.cumprod(a, axis=0)
array([[ 1,  2,  3],
       [ 4, 10, 18]])
```

The cumulative product for each row (i.e. over the columns) of *a*:

```
>>> np.cumprod(a,axis=1)
array([[  1,   2,   6],
       [  4,  20, 120]])
```

dask.array.**cumsum**(*a*, *axis=None*, *dtype=None*, *out=None*)

Return the cumulative sum of the elements along a given axis.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative sum is computed. The default (None) is to compute the cumsum over the flattened array.

dtype [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type will be cast if necessary. See *doc.ufuncs* (Section "Output arguments") for more details.

Returns

cumsum_along_axis [ndarray.] A new array holding the result is returned unless *out* is specified, in which case a reference to *out* is returned. The result has the same size as *a*, and the same shape as *a* if *axis* is not None or *a* is a 1-d array.

See also:

sum Sum array elements.

trapz Integration of array values using the composite trapezoidal rule.

diff Calculate the n-th discrete difference along given axis.

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow.

Examples

```
>>> a = np.array([[1,2,3], [4,5,6]])
>>> a
array([[1, 2, 3],
       [4, 5, 6]])
>>> np.cumsum(a)
array([ 1,  3,  6, 10, 15, 21])
>>> np.cumsum(a, dtype=float)     # specifies type of output value(s)
array([  1.,   3.,   6.,  10.,  15.,  21.])
```

```
>>> np.cumsum(a,axis=0)      # sum over rows for each of the 3 columns
array([[1, 2, 3],
       [5, 7, 9]])
>>> np.cumsum(a,axis=1)      # sum over columns for each of the 2 rows
array([[ 1,  3,  6],
       [ 4,  9, 15]])
```

`dask.array.`**`deg2rad`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Convert angles from degrees to radians.

Parameters

x [array_like] Angles in degrees.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The corresponding angle in radians. This is a scalar if *x* is a scalar.

See also:

rad2deg Convert angles from radians to degrees.

unwrap Remove large jumps in angle by wrapping.

Notes

New in version 1.3.0.

`deg2rad(x)` is `x * pi / 180`.

Examples

```
>>> np.deg2rad(180)  # doctest: +SKIP
3.1415926535897931
```

`dask.array.degrees`(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Convert angles from radians to degrees.

Parameters

x [array_like] Input array in radians.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray of floats] The corresponding degree values; if *out* was supplied this is a reference to it. This is a scalar if *x* is a scalar.

See also:

`rad2deg` equivalent function

Examples

Convert a radian array to degrees

```
>>> rad = np.arange(12.)*np.pi/6  # doctest: +SKIP
>>> np.degrees(rad)  # doctest: +SKIP
array([   0.,   30.,   60.,   90.,  120.,  150.,  180.,  210.,  240.,
        270.,  300.,  330.])
```

```
>>> out = np.zeros((rad.shape))  # doctest: +SKIP
>>> r = degrees(rad, out)  # doctest: +SKIP
>>> np.all(r == out)  # doctest: +SKIP
True
```

`dask.array.diag`(*v*)

Extract a diagonal or construct a diagonal array.

This docstring was copied from numpy.diag.

Some inconsistencies with the Dask version may exist.

See the more detailed documentation for `numpy.diagonal` if you use this function to extract a diagonal and wish to write to the resulting array; whether it returns a copy or a view depends on what version of numpy you are using.

Parameters

v [array_like] If *v* is a 2-D array, return a copy of its *k*-th diagonal. If *v* is a 1-D array, return a 2-D array with *v* on the *k*-th diagonal.

k [int, optional (Not supported in Dask)] Diagonal in question. The default is 0. Use *k>0* for diagonals above the main diagonal, and *k<0* for diagonals below the main diagonal.

Returns

out [ndarray] The extracted diagonal or constructed diagonal array.

See also:

diagonal Return specified diagonals.

diagflat Create a 2-D array with the flattened input as a diagonal.

trace Sum along diagonals.

triu Upper triangle of an array.

tril Lower triangle of an array.

Examples

```
>>> x = np.arange(9).reshape((3,3))  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([[0, 1, 2],
       [3, 4, 5],
       [6, 7, 8]])
```

```
>>> np.diag(x)  # doctest: +SKIP
array([0, 4, 8])
>>> np.diag(x, k=1)  # doctest: +SKIP
array([1, 5])
>>> np.diag(x, k=-1)  # doctest: +SKIP
array([3, 7])
```

```
>>> np.diag(np.diag(x))  # doctest: +SKIP
array([[0, 0, 0],
       [0, 4, 0],
       [0, 0, 8]])
```

dask.array.**diagonal**(*a*, *offset=0*, *axis1=0*, *axis2=1*)

Return specified diagonals.

This docstring was copied from numpy.diagonal.

Some inconsistencies with the Dask version may exist.

If *a* is 2-D, returns the diagonal of *a* with the given offset, i.e., the collection of elements of the form `a[i, i+offset]`. If *a* has more than two dimensions, then the axes specified by *axis1* and *axis2* are used to determine the 2-D sub-array whose diagonal is returned. The shape of the resulting array can be determined by removing *axis1* and *axis2* and appending an index to the right equal to the size of the resulting diagonals.

In versions of NumPy prior to 1.7, this function always returned a new, independent array containing a copy of the values in the diagonal.

In NumPy 1.7 and 1.8, it continues to return a copy of the diagonal, but depending on this fact is deprecated. Writing to the resulting array continues to work as it used to, but a FutureWarning is issued.

Starting in NumPy 1.9 it returns a read-only view on the original array. Attempting to write to the resulting array will produce an error.

In some future release, it will return a read/write view and writing to the returned array will alter your original array. The returned array will have the same type as the input array.

If you don't write to the array returned by this function, then you can just ignore all of the above.

If you depend on the current behavior, then we suggest copying the returned array explicitly, i.e., use `np.diagonal(a).copy()` instead of just `np.diagonal(a)`. This will work with both past and future versions of NumPy.

Parameters

a [array_like] Array from which the diagonals are taken.

offset [int, optional] Offset of the diagonal from the main diagonal. Can be positive or negative. Defaults to main diagonal (0).

axis1 [int, optional] Axis to be used as the first axis of the 2-D sub-arrays from which the diagonals should be taken. Defaults to first axis (0).

axis2 [int, optional] Axis to be used as the second axis of the 2-D sub-arrays from which the diagonals should be taken. Defaults to second axis (1).

Returns

array_of_diagonals [ndarray] If *a* is 2-D, then a 1-D array containing the diagonal and of the same type as *a* is returned unless *a* is a *matrix*, in which case a 1-D array rather than a (2-D) *matrix* is returned in order to maintain backward compatibility.

If `a.ndim > 2`, then the dimensions specified by *axis1* and *axis2* are removed, and a new axis inserted at the end corresponding to the diagonal.

Raises

ValueError If the dimension of *a* is less than 2.

See also:

diag MATLAB work-a-like for 1-D and 2-D arrays.

diagflat Create diagonal arrays.

trace Sum along diagonals.

Examples

```
>>> a = np.arange(4).reshape(2,2)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([[0, 1],
       [2, 3]])
>>> a.diagonal()  # doctest: +SKIP
array([0, 3])
>>> a.diagonal(1)  # doctest: +SKIP
array([1])
```

A 3-D example:

```
>>> a = np.arange(8).reshape(2,2,2); a  # doctest: +SKIP
array([[[0, 1],
        [2, 3]],
       [[4, 5],
        [6, 7]]])
>>> a.diagonal(0, # Main diagonals of two arrays created by skipping  # doctest:␣
↪+SKIP
...            0, # across the outer(left)-most axis last and
...            1) # the "middle" (row) axis first.
array([[0, 6],
       [1, 7]])
```

The sub-arrays whose main diagonals we just obtained; note that each corresponds to fixing the right-most (column) axis, and that the diagonals are "packed" in rows.

```
>>> a[:,:,0] # main diagonal is [0 6]  # doctest: +SKIP
array([[0, 2],
       [4, 6]])
>>> a[:,:,1] # main diagonal is [1 7]  # doctest: +SKIP
array([[1, 3],
       [5, 7]])
```

dask.array.**diff**(*a*, *n=1*, *axis=-1*)

Calculate the n-th discrete difference along the given axis.

This docstring was copied from numpy.diff.

Some inconsistencies with the Dask version may exist.

The first difference is given by `out[n] = a[n+1] - a[n]` along the given axis, higher differences are calculated by using *diff* recursively.

Parameters

a [array_like] Input array

n [int, optional] The number of times values are differenced. If zero, the input is returned as-is.

axis [int, optional] The axis along which the difference is taken, default is the last axis.

prepend, append [array_like, optional] Values to prepend or append to "a" along axis prior to performing the difference. Scalar values are expanded to arrays with length 1 in the direction of axis and the shape of the input array in along all other axes. Otherwise the dimension and shape must match "a" except along axis.

Returns

diff [ndarray] The n-th differences. The shape of the output is the same as *a* except along *axis* where the dimension is smaller by *n*. The type of the output is the same as the type of the difference between any two elements of *a*. This is the same as the type of *a* in most cases. A notable exception is *datetime64*, which results in a *timedelta64* output array.

See also:

`gradient`, `ediff1d`, `cumsum`

Notes

Type is preserved for boolean arrays, so the result will contain *False* when consecutive elements are the same and *True* when they differ.

For unsigned integer arrays, the results will also be unsigned. This should not be surprising, as the result is consistent with calculating the difference directly:

```
>>> u8_arr = np.array([1, 0], dtype=np.uint8)  # doctest: +SKIP
>>> np.diff(u8_arr)  # doctest: +SKIP
array([255], dtype=uint8)
>>> u8_arr[1,...] - u8_arr[0,...]  # doctest: +SKIP
array(255, np.uint8)
```

If this is not desirable, then the array should be cast to a larger integer type first:

```
>>> i16_arr = u8_arr.astype(np.int16)  # doctest: +SKIP
>>> np.diff(i16_arr)  # doctest: +SKIP
array([-1], dtype=int16)
```

Examples

```
>>> x = np.array([1, 2, 4, 7, 0])  # doctest: +SKIP
>>> np.diff(x)  # doctest: +SKIP
array([ 1,  2,  3, -7])
>>> np.diff(x, n=2)  # doctest: +SKIP
array([  1,   1, -10])
```

```
>>> x = np.array([[1, 3, 6, 10], [0, 5, 6, 8]])  # doctest: +SKIP
>>> np.diff(x)  # doctest: +SKIP
array([[2, 3, 4],
       [5, 1, 2]])
>>> np.diff(x, axis=0)  # doctest: +SKIP
array([[-1,  2,  0, -2]])
```

```
>>> x = np.arange('1066-10-13', '1066-10-16', dtype=np.datetime64)  # doctest:␣
↪+SKIP
>>> np.diff(x)  # doctest: +SKIP
array([1, 1], dtype='timedelta64[D]')
```

`dask.array.`**`digitize`**`(`*a*, *bins*, *right=False*`)`

Return the indices of the bins to which each value in input array belongs.

This docstring was copied from numpy.digitize.

Some inconsistencies with the Dask version may exist.

right	order of bins	returned index *i* satisfies
`False`	increasing	`bins[i-1] <= x < bins[i]`
`True`	increasing	`bins[i-1] < x <= bins[i]`
`False`	decreasing	`bins[i-1] > x >= bins[i]`
`True`	decreasing	`bins[i-1] >= x > bins[i]`

If values in *x* are beyond the bounds of *bins*, 0 or `len(bins)` is returned as appropriate.

Parameters

x [array_like (Not supported in Dask)] Input array to be binned. Prior to NumPy 1.10.0, this array had to be 1-dimensional, but can now have any shape.

bins [array_like] Array of bins. It has to be 1-dimensional and monotonic.

right [bool, optional] Indicating whether the intervals include the right or the left bin edge. Default behavior is (right==False) indicating that the interval does not include the right edge. The left bin end is open in this case, i.e., bins[i-1] <= x < bins[i] is the default behavior for monotonically increasing bins.

Returns

indices [ndarray of ints] Output array of indices, of same shape as *x*.

Raises

ValueError If *bins* is not monotonic.

TypeError If the type of the input is complex.

See also:

bincount, *histogram*, *unique*, searchsorted

Notes

If values in *x* are such that they fall outside the bin range, attempting to index *bins* with the indices that *digitize* returns will result in an IndexError.

New in version 1.10.0.

np.digitize is implemented in terms of *np.searchsorted*. This means that a binary search is used to bin the values, which scales much better for larger number of bins than the previous linear search. It also removes the requirement for the input array to be 1-dimensional.

For monotonically _increasing_ *bins*, the following are equivalent:

```
np.digitize(x, bins, right=True)
np.searchsorted(bins, x, side='left')
```

Note that as the order of the arguments are reversed, the side must be too. The *searchsorted* call is marginally faster, as it does not do any monotonicity checks. Perhaps more importantly, it supports all dtypes.

Examples

```
>>> x = np.array([0.2, 6.4, 3.0, 1.6])  # doctest: +SKIP
>>> bins = np.array([0.0, 1.0, 2.5, 4.0, 10.0])  # doctest: +SKIP
>>> inds = np.digitize(x, bins)  # doctest: +SKIP
>>> inds  # doctest: +SKIP
array([1, 4, 3, 2])
>>> for n in range(x.size):  # doctest: +SKIP
...   print(bins[inds[n]-1], "<=", x[n], "<", bins[inds[n]])
...
0.0 <= 0.2 < 1.0
4.0 <= 6.4 < 10.0
2.5 <= 3.0 < 4.0
1.0 <= 1.6 < 2.5
```

```
>>> x = np.array([1.2, 10.0, 12.4, 15.5, 20.])  # doctest: +SKIP
>>> bins = np.array([0, 5, 10, 15, 20])  # doctest: +SKIP
>>> np.digitize(x,bins,right=True)  # doctest: +SKIP
array([1, 2, 3, 4, 4])
```

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```
>>> np.digitize(x,bins,right=False)  # doctest: +SKIP
array([1, 3, 3, 4, 5])
```

`dask.array.dot` (*a*, *b*, *out=None*)

This docstring was copied from numpy.dot.

Some inconsistencies with the Dask version may exist.

Dot product of two arrays. Specifically,

- If both *a* and *b* are 1-D arrays, it is inner product of vectors (without complex conjugation).
- If both *a* and *b* are 2-D arrays, it is matrix multiplication, but using `matmul()` or `a @ b` is preferred.
- If either *a* or *b* is 0-D (scalar), it is equivalent to `multiply()` and using `numpy.multiply(a, b)` or `a * b` is preferred.
- If *a* is an N-D array and *b* is a 1-D array, it is a sum product over the last axis of *a* and *b*.
- If *a* is an N-D array and *b* is an M-D array (where `M>=2`), it is a sum product over the last axis of *a* and the second-to-last axis of *b*:

```
dot(a, b)[i,j,k,m] = sum(a[i,j,:] * b[k,:,m])
```

Parameters

a [array_like] First argument.

b [array_like] Second argument.

out [ndarray, optional] Output argument. This must have the exact kind that would be returned if it was not used. In particular, it must have the right type, must be C-contiguous, and its dtype must be the dtype that would be returned for *dot(a,b)*. This is a performance feature. Therefore, if these conditions are not met, an exception is raised, instead of attempting to be flexible.

Returns

output [ndarray] Returns the dot product of *a* and *b*. If *a* and *b* are both scalars or both 1-D arrays then a scalar is returned; otherwise an array is returned. If *out* is given, then it is returned.

Raises

ValueError If the last dimension of *a* is not the same size as the second-to-last dimension of *b*.

See also:

`vdot` Complex-conjugating dot product.

`tensordot` Sum products over arbitrary axes.

`einsum` Einstein summation convention.

`matmul` '@' operator as method with out parameter.

Examples

```
>>> np.dot(3, 4)  # doctest: +SKIP
12
```

Neither argument is complex-conjugated:

```
>>> np.dot([2j, 3j], [2j, 3j])  # doctest: +SKIP
(-13+0j)
```

For 2-D arrays it is the matrix product:

```
>>> a = [[1, 0], [0, 1]]  # doctest: +SKIP
>>> b = [[4, 1], [2, 2]]  # doctest: +SKIP
>>> np.dot(a, b)  # doctest: +SKIP
array([[4, 1],
       [2, 2]])
```

```
>>> a = np.arange(3*4*5*6).reshape((3,4,5,6))  # doctest: +SKIP
>>> b = np.arange(3*4*5*6)[::-1].reshape((5,4,6,3))  # doctest: +SKIP
>>> np.dot(a, b)[2,3,2,1,2,2]  # doctest: +SKIP
499128
>>> sum(a[2,3,2,:] * b[1,2,:,2])  # doctest: +SKIP
499128
```

`dask.array.`**`dstack`**`(`*tup*, *allow_unknown_chunksizes=False*`)`

Stack arrays in sequence depth wise (along third axis).

This docstring was copied from numpy.dstack.

Some inconsistencies with the Dask version may exist.

This is equivalent to concatenation along the third axis after 2-D arrays of shape *(M,N)* have been reshaped to *(M,N,1)* and 1-D arrays of shape *(N,)* have been reshaped to *(1,N,1)*. Rebuilds arrays divided by *dsplit*.

This function makes most sense for arrays with up to 3 dimensions. For instance, for pixel-data with a height (first axis), width (second axis), and r/g/b channels (third axis). The functions *concatenate*, *stack* and *block* provide more general stacking and concatenation operations.

Parameters

tup [sequence of arrays] The arrays must have the same shape along all but the third axis. 1-D or 2-D arrays must have the same shape.

Returns

stacked [ndarray] The array formed by stacking the given arrays, will be at least 3-D.

See also:

`stack` Join a sequence of arrays along a new axis.

`vstack` Stack along first axis.

`hstack` Stack along second axis.

`concatenate` Join a sequence of arrays along an existing axis.

`dsplit` Split array along third axis.

Examples

```
>>> a = np.array((1,2,3))  # doctest: +SKIP
>>> b = np.array((2,3,4))  # doctest: +SKIP
>>> np.dstack((a,b))  # doctest: +SKIP
```

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```
array([[[1, 2],
        [2, 3],
        [3, 4]]])
```

```
>>> a = np.array([[1],[2],[3]])  # doctest: +SKIP
>>> b = np.array([[2],[3],[4]])  # doctest: +SKIP
>>> np.dstack((a,b))  # doctest: +SKIP
array([[[1, 2]],
       [[2, 3]],
       [[3, 4]]])
```

`dask.array.`**`ediff1d`**(*ary*, *to_end=None*, *to_begin=None*)

The differences between consecutive elements of an array.

This docstring was copied from numpy.ediff1d.

Some inconsistencies with the Dask version may exist.

Parameters

ary [array_like] If necessary, will be flattened before the differences are taken.

to_end [array_like, optional] Number(s) to append at the end of the returned differences.

to_begin [array_like, optional] Number(s) to prepend at the beginning of the returned differences.

Returns

ediff1d [ndarray] The differences. Loosely, this is `ary.flat[1:] - ary.flat[:-1]`.

See also:

`diff`, *`gradient`*

Notes

When applied to masked arrays, this function drops the mask information if the *to_begin* and/or *to_end* parameters are used.

Examples

```
>>> x = np.array([1, 2, 4, 7, 0])  # doctest: +SKIP
>>> np.ediff1d(x)  # doctest: +SKIP
array([ 1,  2,  3, -7])
```

```
>>> np.ediff1d(x, to_begin=-99, to_end=np.array([88, 99]))  # doctest: +SKIP
array([-99,   1,   2,   3,  -7,  88,  99])
```

The returned array is always 1D.

```
>>> y = [[1, 2, 4], [1, 6, 24]]  # doctest: +SKIP
>>> np.ediff1d(y)  # doctest: +SKIP
array([ 1,  2, -3,  5, 18])
```

`dask.array.empty(*args, **kwargs)`

Blocked variant of empty

Follows the signature of empty exactly except that it also requires a keyword argument chunks=(…)

Original signature follows below. empty(shape, dtype=float, order='C')

Return a new array of given shape and type, without initializing entries.

Parameters

shape [int or tuple of int] Shape of the empty array, e.g., `(2, 3)` or `2`.

dtype [data-type, optional] Desired output data-type for the array, e.g, *numpy.int8*. Default is *numpy.float64*.

order [{'C', 'F'}, optional, default: 'C'] Whether to store multi-dimensional data in row-major (C-style) or column-major (Fortran-style) order in memory.

Returns

out [ndarray] Array of uninitialized (arbitrary) data of the given shape, dtype, and order. Object arrays will be initialized to None.

See also:

`empty_like` Return an empty array with shape and type of input.

`ones` Return a new array setting values to one.

`zeros` Return a new array setting values to zero.

`full` Return a new array of given shape filled with value.

Notes

empty, unlike *zeros*, does not set the array values to zero, and may therefore be marginally faster. On the other hand, it requires the user to manually set all the values in the array, and should be used with caution.

Examples

```
>>> np.empty([2, 2])
array([[ -9.74499359e+001,   6.69583040e-309],
       [  2.13182611e-314,   3.06959433e-309]])         #random
```

```
>>> np.empty([2, 2], dtype=int)
array([[-1073741821, -1067949133],
       [  496041986,    19249760]])                     #random
```

`dask.array.empty_like(a, dtype=None, chunks=None)`

Return a new array with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of uninitialized (arbitrary) data with the same shape and type as *a*.

See also:

`ones_like` Return an array of ones with shape and type of input.

`zeros_like` Return an array of zeros with shape and type of input.

`empty` Return a new uninitialized array.

`ones` Return a new array setting values to one.

`zeros` Return a new array setting values to zero.

Notes

This function does *not* initialize the returned array; to do that use *zeros_like* or *ones_like* instead. It may be marginally faster than the functions that do set the array values.

`dask.array.`**`einsum`**`(`*subscripts*, **operands*, *out=None*, *dtype=None*, *order='K'*, *casting='safe'*, *optimize=False*`)`

This docstring was copied from numpy.einsum.

Some inconsistencies with the Dask version may exist.

Evaluates the Einstein summation convention on the operands.

Using the Einstein summation convention, many common multi-dimensional, linear algebraic array operations can be represented in a simple fashion. In *implicit* mode *einsum* computes these values.

In *explicit* mode, *einsum* provides further flexibility to compute other array operations that might not be considered classical Einstein summation operations, by disabling, or forcing summation over specified subscript labels.

See the notes and examples for clarification.

Parameters

subscripts [str] Specifies the subscripts for summation as comma separated list of subscript labels. An implicit (classical Einstein summation) calculation is performed unless the explicit indicator '->' is included as well as subscript labels of the precise output form.

operands [list of array_like] These are the arrays for the operation.

out [ndarray, optional] If provided, the calculation is done into this array.

dtype [{data-type, None}, optional] If provided, forces the calculation to use the data type specified. Note that you may have to also give a more liberal *casting* parameter to allow the conversions. Default is None.

order [{'C', 'F', 'A', 'K'}, optional] Controls the memory layout of the output. 'C' means it should be C contiguous. 'F' means it should be Fortran contiguous, 'A' means it should be 'F' if the inputs are all 'F', 'C' otherwise. 'K' means it should be as close to the layout as the inputs as is possible, including arbitrarily permuted axes. Default is 'K'.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Setting this to 'unsafe' is not recommended, as it can adversely affect accumulations.

- 'no' means the data types should not be cast at all.
- 'equiv' means only byte-order changes are allowed.

- 'safe' means only casts which can preserve values are allowed.
- 'same_kind' means only safe casts or casts within a kind, like float64 to float32, are allowed.
- 'unsafe' means any data conversions may be done.

Default is 'safe'.

optimize [{False, True, 'greedy', 'optimal'}, optional] Controls if intermediate optimization should occur. No optimization will occur if False and True will default to the 'greedy' algorithm. Also accepts an explicit contraction list from the `np.einsum_path` function. See `np.einsum_path` for more details. Defaults to False.

Returns

output [ndarray] The calculation based on the Einstein summation convention.

See also:

`einsum_path`, *`dot`*, `inner`, *`outer`*, *`tensordot`*, `linalg.multi_dot`

Notes

New in version 1.6.0.

The Einstein summation convention can be used to compute many multi-dimensional, linear algebraic array operations. *einsum* provides a succinct way of representing these.

A non-exhaustive list of these operations, which can be computed by *einsum*, is shown below along with examples:

- Trace of an array, `numpy.trace()`.
- Return a diagonal, `numpy.diag()`.
- Array axis summations, `numpy.sum()`.
- Transpositions and permutations, `numpy.transpose()`.
- Matrix multiplication and dot product, `numpy.matmul()` `numpy.dot()`.
- Vector inner and outer products, `numpy.inner()` `numpy.outer()`.
- Broadcasting, element-wise and scalar multiplication, `numpy.multiply()`.
- Tensor contractions, `numpy.tensordot()`.
- Chained array operations, in efficient calculation order, `numpy.einsum_path()`.

The subscripts string is a comma-separated list of subscript labels, where each label refers to a dimension of the corresponding operand. Whenever a label is repeated it is summed, so `np.einsum('i,i', a, b)` is equivalent to `np.inner(a,b)`. If a label appears only once, it is not summed, so `np.einsum('i', a)` produces a view of `a` with no changes. A further example `np.einsum('ij,jk', a, b)` describes traditional matrix multiplication and is equivalent to `np.matmul(a,b)`. Repeated subscript labels in one operand take the diagonal. For example, `np.einsum('ii', a)` is equivalent to `np.trace(a)`.

In *implicit mode*, the chosen subscripts are important since the axes of the output are reordered alphabetically. This means that `np.einsum('ij', a)` doesn't affect a 2D array, while `np.einsum('ji', a)` takes its transpose. Additionally, `np.einsum('ij,jk', a, b)` returns a matrix multiplication, while, `np.einsum('ij,jh', a, b)` returns the transpose of the multiplication since subscript 'h' precedes subscript 'i'.

In *explicit mode* the output can be directly controlled by specifying output subscript labels. This requires the identifier '->' as well as the list of output subscript labels. This feature increases the flexibility of the function since summing can be disabled or forced when required. The call `np.einsum('i->', a)` is like `np.sum(a, axis=-1)`, and `np.einsum('ii->i', a)` is like `np.diag(a)`. The difference is that *einsum* does not allow broadcasting by default. Additionally `np.einsum('ij,jh->ih', a, b)` directly specifies the order of the output subscript labels and therefore returns matrix multiplication, unlike the example above in implicit mode.

To enable and control broadcasting, use an ellipsis. Default NumPy-style broadcasting is done by adding an ellipsis to the left of each term, like `np.einsum('...ii->...i', a)`. To take the trace along the first and last axes, you can do `np.einsum('i...i', a)`, or to do a matrix-matrix product with the left-most indices instead of rightmost, one can do `np.einsum('ij...,jk...->ik...', a, b)`.

When there is only one operand, no axes are summed, and no output parameter is provided, a view into the operand is returned instead of a new array. Thus, taking the diagonal as `np.einsum('ii->i', a)` produces a view (changed in version 1.10.0).

einsum also provides an alternative way to provide the subscripts and operands as `einsum(op0, sublist0, op1, sublist1, ..., [sublistout])`. If the output shape is not provided in this format *einsum* will be calculated in implicit mode, otherwise it will be performed explicitly. The examples below have corresponding *einsum* calls with the two parameter methods.

New in version 1.10.0.

Views returned from einsum are now writeable whenever the input array is writeable. For example, `np.einsum('ijk...->kji...', a)` will now have the same effect as `np.swapaxes(a, 0, 2)` and `np.einsum('ii->i', a)` will return a writeable view of the diagonal of a 2D array.

New in version 1.12.0.

Added the `optimize` argument which will optimize the contraction order of an einsum expression. For a contraction with three or more operands this can greatly increase the computational efficiency at the cost of a larger memory footprint during computation.

Typically a 'greedy' algorithm is applied which empirical tests have shown returns the optimal path in the majority of cases. In some cases 'optimal' will return the superlative path through a more expensive, exhaustive search. For iterative calculations it may be advisable to calculate the optimal path once and reuse that path by supplying it as an argument. An example is given below.

See `numpy.einsum_path()` for more details.

Examples

```
>>> a = np.arange(25).reshape(5,5)  # doctest: +SKIP
>>> b = np.arange(5)  # doctest: +SKIP
>>> c = np.arange(6).reshape(2,3)  # doctest: +SKIP
```

Trace of a matrix:

```
>>> np.einsum('ii', a)  # doctest: +SKIP
60
>>> np.einsum(a, [0,0])  # doctest: +SKIP
60
>>> np.trace(a)  # doctest: +SKIP
60
```

Extract the diagonal (requires explicit form):

```
>>> np.einsum('ii->i', a)  # doctest: +SKIP
array([ 0,  6, 12, 18, 24])
>>> np.einsum(a, [0,0], [0])  # doctest: +SKIP
array([ 0,  6, 12, 18, 24])
>>> np.diag(a)  # doctest: +SKIP
array([ 0,  6, 12, 18, 24])
```

Sum over an axis (requires explicit form):

```
>>> np.einsum('ij->i', a)  # doctest: +SKIP
array([ 10,  35,  60,  85, 110])
>>> np.einsum(a, [0,1], [0])  # doctest: +SKIP
array([ 10,  35,  60,  85, 110])
>>> np.sum(a, axis=1)  # doctest: +SKIP
array([ 10,  35,  60,  85, 110])
```

For higher dimensional arrays summing a single axis can be done with ellipsis:

```
>>> np.einsum('...j->...', a)  # doctest: +SKIP
array([ 10,  35,  60,  85, 110])
>>> np.einsum(a, [Ellipsis,1], [Ellipsis])  # doctest: +SKIP
array([ 10,  35,  60,  85, 110])
```

Compute a matrix transpose, or reorder any number of axes:

```
>>> np.einsum('ji', c)  # doctest: +SKIP
array([[0, 3],
       [1, 4],
       [2, 5]])
>>> np.einsum('ij->ji', c)  # doctest: +SKIP
array([[0, 3],
       [1, 4],
       [2, 5]])
>>> np.einsum(c, [1,0])  # doctest: +SKIP
array([[0, 3],
       [1, 4],
       [2, 5]])
>>> np.transpose(c)  # doctest: +SKIP
array([[0, 3],
       [1, 4],
       [2, 5]])
```

Vector inner products:

```
>>> np.einsum('i,i', b, b)  # doctest: +SKIP
30
>>> np.einsum(b, [0], b, [0])  # doctest: +SKIP
30
>>> np.inner(b,b)  # doctest: +SKIP
30
```

Matrix vector multiplication:

```
>>> np.einsum('ij,j', a, b)  # doctest: +SKIP
array([ 30,  80, 130, 180, 230])
>>> np.einsum(a, [0,1], b, [1])  # doctest: +SKIP
array([ 30,  80, 130, 180, 230])
```

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```
>>> np.dot(a, b)  # doctest: +SKIP
array([ 30,  80, 130, 180, 230])
>>> np.einsum('...j,j', a, b)  # doctest: +SKIP
array([ 30,  80, 130, 180, 230])
```

Broadcasting and scalar multiplication:

```
>>> np.einsum('..., ...', 3, c)  # doctest: +SKIP
array([[ 0,  3,  6],
       [ 9, 12, 15]])
>>> np.einsum(',ij', 3, c)  # doctest: +SKIP
array([[ 0,  3,  6],
       [ 9, 12, 15]])
>>> np.einsum(3, [Ellipsis], c, [Ellipsis])  # doctest: +SKIP
array([[ 0,  3,  6],
       [ 9, 12, 15]])
>>> np.multiply(3, c)  # doctest: +SKIP
array([[ 0,  3,  6],
       [ 9, 12, 15]])
```

Vector outer product:

```
>>> np.einsum('i,j', np.arange(2)+1, b)  # doctest: +SKIP
array([[0, 1, 2, 3, 4],
       [0, 2, 4, 6, 8]])
>>> np.einsum(np.arange(2)+1, [0], b, [1])  # doctest: +SKIP
array([[0, 1, 2, 3, 4],
       [0, 2, 4, 6, 8]])
>>> np.outer(np.arange(2)+1, b)  # doctest: +SKIP
array([[0, 1, 2, 3, 4],
       [0, 2, 4, 6, 8]])
```

Tensor contraction:

```
>>> a = np.arange(60.).reshape(3,4,5)  # doctest: +SKIP
>>> b = np.arange(24.).reshape(4,3,2)  # doctest: +SKIP
>>> np.einsum('ijk,jil->kl', a, b)  # doctest: +SKIP
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
>>> np.einsum(a, [0,1,2], b, [1,0,3], [2,3])  # doctest: +SKIP
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
>>> np.tensordot(a,b, axes=([1,0],[0,1]))  # doctest: +SKIP
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
```

Writeable returned arrays (since version 1.10.0):

```
>>> a = np.zeros((3, 3))  # doctest: +SKIP
>>> np.einsum('ii->i', a)[:] = 1  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([[ 1.,  0.,  0.],
       [ 0.,  1.,  0.],
       [ 0.,  0.,  1.]])
```

Example of ellipsis use:

```
>>> a = np.arange(6).reshape((3,2))  # doctest: +SKIP
>>> b = np.arange(12).reshape((4,3))  # doctest: +SKIP
>>> np.einsum('ki,jk->ij', a, b)  # doctest: +SKIP
array([[10, 28, 46, 64],
       [13, 40, 67, 94]])
>>> np.einsum('ki,...k->i...', a, b)  # doctest: +SKIP
array([[10, 28, 46, 64],
       [13, 40, 67, 94]])
>>> np.einsum('k...,jk', a, b)  # doctest: +SKIP
array([[10, 28, 46, 64],
       [13, 40, 67, 94]])
```

Chained array operations. For more complicated contractions, speed ups might be achieved by repeatedly computing a 'greedy' path or pre-computing the 'optimal' path and repeatedly applying it, using an *einsum_path* insertion (since version 1.12.0). Performance improvements can be particularly significant with larger arrays:

```
>>> a = np.ones(64).reshape(2,4,8)  # doctest: +SKIP
# Basic `einsum`: ~1520ms  (benchmarked on 3.1GHz Intel i5.)
>>> for iteration in range(500):  # doctest: +SKIP
...     np.einsum('ijk,ilm,njm,nlk,abc->',a,a,a,a,a)
# Sub-optimal `einsum` (due to repeated path calculation time): ~330ms
>>> for iteration in range(500):  # doctest: +SKIP
...     np.einsum('ijk,ilm,njm,nlk,abc->',a,a,a,a,a, optimize='optimal')
# Greedy `einsum` (faster optimal path approximation): ~160ms
>>> for iteration in range(500):  # doctest: +SKIP
...     np.einsum('ijk,ilm,njm,nlk,abc->',a,a,a,a,a, optimize='greedy')
# Optimal `einsum` (best usage pattern in some use cases): ~110ms
>>> path = np.einsum_path('ijk,ilm,njm,nlk,abc->',a,a,a,a,a, optimize='optimal
↪')[0]  # doctest: +SKIP
>>> for iteration in range(500):  # doctest: +SKIP
...     np.einsum('ijk,ilm,njm,nlk,abc->',a,a,a,a,a, optimize=path)
```

`dask.array.exp`(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Calculate the exponential of all elements in the input array.

Parameters

x [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Output array, element-wise exponential of *x*. This is a scalar if *x* is a scalar.

See also:

expm1 Calculate `exp(x) - 1` for all elements in the array.

`exp2` Calculate `2**x` for all elements in the array.

Notes

The irrational number `e` is also known as Euler's number. It is approximately 2.718281, and is the base of the natural logarithm, `ln` (this means that, if $x = \ln y = \log_e y$, then $e^x = y$. For real input, `exp(x)` is always positive.

For complex arguments, `x = a + ib`, we can write $e^x = e^a e^{ib}$. The first term, e^a, is already known (it is the real argument, described above). The second term, e^{ib}, is $\cos b + i \sin b$, a function with magnitude 1 and a periodic phase.

References

[1], [2]

Examples

Plot the magnitude and phase of `exp(x)` in the complex plane:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
```

```
>>> x = np.linspace(-2*np.pi, 2*np.pi, 100)  # doctest: +SKIP
>>> xx = x + 1j * x[:, np.newaxis] # a + ib over complex plane  # doctest: +SKIP
>>> out = np.exp(xx)  # doctest: +SKIP
```

```
>>> plt.subplot(121)  # doctest: +SKIP
>>> plt.imshow(np.abs(out),  # doctest: +SKIP
...            extent=[-2*np.pi, 2*np.pi, -2*np.pi, 2*np.pi], cmap='gray')
>>> plt.title('Magnitude of exp(x)')  # doctest: +SKIP
```

```
>>> plt.subplot(122)  # doctest: +SKIP
>>> plt.imshow(np.angle(out),  # doctest: +SKIP
...            extent=[-2*np.pi, 2*np.pi, -2*np.pi, 2*np.pi], cmap='hsv')
>>> plt.title('Phase (angle) of exp(x)')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.`**`expm1`**`(`*x, /, out=None, *, where=True, casting='same_kind', order='K', dtype=None, subok=True*[*, signature, extobj*]`)`

Calculate `exp(x) - 1` for all elements in the array.

Parameters

x [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Element-wise exponential minus one: `out = exp(x) - 1`. This is a scalar if *x* is a scalar.

See also:

log1p `log(1 + x)`, the inverse of expm1.

Notes

This function provides greater precision than `exp(x) - 1` for small values of `x`.

Examples

The true value of `exp(1e-10) - 1` is `1.00000000005e-10` to about 32 significant digits. This example shows the superiority of expm1 in this case.

```
>>> np.expm1(1e-10)  # doctest: +SKIP
1.00000000005e-10
>>> np.exp(1e-10) - 1  # doctest: +SKIP
1.000000082740371e-10
```

`dask.array.`**`eye`**(*N*, *chunks='auto'*, *M=None*, *k=0*, *dtype=<class 'float'>*)

Return a 2-D Array with ones on the diagonal and zeros elsewhere.

Parameters

N [int] Number of rows in the output.

chunks [int, str] How to chunk the array. Must be one of the following forms:

- A blocksize like 1000.
- A size in bytes, like "100 MiB" which will choose a uniform block-like shape
- The word "auto" which acts like the above, but uses a configuration value `array.chunk-size` for the chunk size

M [int, optional] Number of columns in the output. If None, defaults to *N*.

k [int, optional] Index of the diagonal: 0 (the default) refers to the main diagonal, a positive value refers to an upper diagonal, and a negative value to a lower diagonal.

dtype [data-type, optional] Data-type of the returned array.

Returns

I [Array of shape (N,M)] An array where all elements are equal to zero, except for the *k*-th diagonal, whose values are equal to one.

`dask.array.`**`fabs`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the absolute values element-wise.

This function returns the absolute values (positive magnitude) of the data in *x*. Complex values are not handled, use *absolute* to find the absolute values of complex data.

Parameters

x [array_like] The array of numbers for which the absolute values are required. If *x* is a scalar, the result *y* will also be a scalar.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The absolute values of *x*, the returned values are always floats. This is a scalar if *x* is a scalar.

See also:

absolute Absolute values including *complex* types.

Examples

```
>>> np.fabs(-1)  # doctest: +SKIP
1.0
>>> np.fabs([-1.2, 1.2])  # doctest: +SKIP
array([ 1.2,  1.2])
```

`dask.array.fix(*args, **kwargs)`

Round to nearest integer towards zero.

Round an array of floats element-wise to nearest integer towards zero. The rounded values are returned as floats.

Parameters

x [array_like] An array of floats to be rounded

y [ndarray, optional] Output array

Returns

out [ndarray of floats] The array of rounded numbers

See also:

`trunc`, `floor`, `ceil`

around Round to given number of decimals

Examples

```
>>> np.fix(3.14)  # doctest: +SKIP
3.0
>>> np.fix(3)  # doctest: +SKIP
3.0
>>> np.fix([2.1, 2.9, -2.1, -2.9])  # doctest: +SKIP
array([ 2.,  2., -2., -2.])
```

`dask.array.`**`flatnonzero`**`(`*a*`)`

Return indices that are non-zero in the flattened version of a.

This docstring was copied from numpy.flatnonzero.

Some inconsistencies with the Dask version may exist.

This is equivalent to np.nonzero(np.ravel(a))[0].

Parameters

a [array_like] Input data.

Returns

res [ndarray] Output array, containing the indices of the elements of *a.ravel()* that are non-zero.

See also:

`nonzero` Return the indices of the non-zero elements of the input array.

`ravel` Return a 1-D array containing the elements of the input array.

Examples

```
>>> x = np.arange(-2, 3)  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([-2, -1,  0,  1,  2])
>>> np.flatnonzero(x)  # doctest: +SKIP
array([0, 1, 3, 4])
```

Use the indices of the non-zero elements as an index array to extract these elements:

```
>>> x.ravel()[np.flatnonzero(x)]  # doctest: +SKIP
array([-2, -1,  1,  2])
```

`dask.array.`**`flip`**`(`*m, axis*`)`

Reverse element order along axis.

Parameters

axis [int] Axis to reverse element order of.

Returns

reversed array [ndarray]

`dask.array.`**`flipud`**`(`*m*`)`

Flip array in the up/down direction.

This docstring was copied from numpy.flipud.

Some inconsistencies with the Dask version may exist.

Flip the entries in each column in the up/down direction. Rows are preserved, but appear in a different order than before.

Parameters

m [array_like] Input array.

Returns

out [array_like] A view of *m* with the rows reversed. Since a view is returned, this operation is $\mathcal{O}(1)$.

See also:

`fliplr` Flip array in the left/right direction.

`rot90` Rotate array counterclockwise.

Notes

Equivalent to `m[::-1,...]`. Does not require the array to be two-dimensional.

Examples

```
>>> A = np.diag([1.0, 2, 3])  # doctest: +SKIP
>>> A  # doctest: +SKIP
array([[ 1.,  0.,  0.],
       [ 0.,  2.,  0.],
       [ 0.,  0.,  3.]])
>>> np.flipud(A)  # doctest: +SKIP
array([[ 0.,  0.,  3.],
       [ 0.,  2.,  0.],
       [ 1.,  0.,  0.]])
```

```
>>> A = np.random.randn(2,3,5)  # doctest: +SKIP
>>> np.all(np.flipud(A) == A[::-1,...])  # doctest: +SKIP
True
```

```
>>> np.flipud([1,2])  # doctest: +SKIP
array([2, 1])
```

`dask.array.`**`fliplr`**`(`*m*`)`

Flip array in the left/right direction.

This docstring was copied from numpy.fliplr.

Some inconsistencies with the Dask version may exist.

Flip the entries in each row in the left/right direction. Columns are preserved, but appear in a different order than before.

Parameters

m [array_like] Input array, must be at least 2-D.

Returns

f [ndarray] A view of *m* with the columns reversed. Since a view is returned, this operation is $\mathcal{O}(1)$.

See also:

`flipud` Flip array in the up/down direction.

`rot90` Rotate array counterclockwise.

Notes

Equivalent to m[:,::-1]. Requires the array to be at least 2-D.

Examples

```
>>> A = np.diag([1.,2.,3.])  # doctest: +SKIP
>>> A  # doctest: +SKIP
array([[ 1.,  0.,  0.],
       [ 0.,  2.,  0.],
       [ 0.,  0.,  3.]])
>>> np.fliplr(A)  # doctest: +SKIP
array([[ 0.,  0.,  1.],
       [ 0.,  2.,  0.],
       [ 3.,  0.,  0.]])
```

```
>>> A = np.random.randn(2,3,5)  # doctest: +SKIP
>>> np.all(np.fliplr(A) == A[:,::-1,...])  # doctest: +SKIP
True
```

`dask.array.floor`(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the floor of the input, element-wise.

The floor of the scalar *x* is the largest integer *i*, such that *i* <= *x*. It is often denoted as $\lfloor x \rfloor$.

Parameters

x [array_like] Input data.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The floor of each element in *x*. This is a scalar if *x* is a scalar.

See also:

`ceil`, `trunc`, `rint`

Notes

Some spreadsheet programs calculate the "floor-towards-zero", in other words `floor(-2.5) == -2`. NumPy instead uses the definition of *floor* where *floor(-2.5) == -3*.

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])  # doctest: +SKIP
>>> np.floor(a)  # doctest: +SKIP
array([-2., -2., -1.,  0.,  1.,  1.,  2.])
```

`dask.array.`**`fmax`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Element-wise maximum of array elements.

Compare two arrays and returns a new array containing the element-wise maxima. If one of the elements being compared is a NaN, then the non-nan element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are ignored when possible.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The maximum of *x1* and *x2*, element-wise. This is a scalar if both *x1* and *x2* are scalars.

See also:

`fmin` Element-wise minimum of two arrays, ignores NaNs.

`maximum` Element-wise maximum of two arrays, propagates NaNs.

`amax` The maximum value of an array along a given axis, propagates NaNs.

`nanmax` The maximum value of an array along a given axis, ignores NaNs.

`minimum`, `amin`, `nanmin`

Notes

New in version 1.3.0.

The fmax is equivalent to `np.where(x1 >= x2, x1, x2)` when neither x1 nor x2 are NaNs, but it is faster and does proper broadcasting.

Examples

```
>>> np.fmax([2, 3, 4], [1, 5, 2])  # doctest: +SKIP
array([ 2.,  5.,  4.])
```

```
>>> np.fmax(np.eye(2), [0.5, 2])  # doctest: +SKIP
array([[ 1. ,  2. ],
       [ 0.5,  2. ]])
```

```
>>> np.fmax([np.nan, 0, np.nan],[0, np.nan, np.nan])  # doctest: +SKIP
array([  0.,   0.,  NaN])
```

`dask.array.`**`fmin`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Element-wise minimum of array elements.

Compare two arrays and returns a new array containing the element-wise minima. If one of the elements being compared is a NaN, then the non-nan element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are ignored when possible.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The minimum of *x1* and *x2*, element-wise. This is a scalar if both *x1* and *x2* are scalars.

See also:

`fmax` Element-wise maximum of two arrays, ignores NaNs.

`minimum` Element-wise minimum of two arrays, propagates NaNs.

`amin` The minimum value of an array along a given axis, propagates NaNs.

`nanmin` The minimum value of an array along a given axis, ignores NaNs.

`maximum`, `amax`, `nanmax`

Notes

New in version 1.3.0.

The fmin is equivalent to `np.where(x1 <= x2, x1, x2)` when neither x1 nor x2 are NaNs, but it is faster and does proper broadcasting.

Examples

```
>>> np.fmin([2, 3, 4], [1, 5, 2])  # doctest: +SKIP
array([1, 3, 2])
```

```
>>> np.fmin(np.eye(2), [0.5, 2])  # doctest: +SKIP
array([[ 0.5,  0. ],
       [ 0. ,  1. ]])
```

```
>>> np.fmin([np.nan, 0, np.nan],[0, np.nan, np.nan])  # doctest: +SKIP
array([  0.,   0.,  NaN])
```

`dask.array.`**`fmod`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the element-wise remainder of division.

This is the NumPy implementation of the C library function fmod, the remainder has the same sign as the dividend *x1*. It is equivalent to the Matlab(TM) `rem` function and should not be confused with the Python modulus operator `x1 % x2`.

Parameters

x1 [array_like] Dividend.

x2 [array_like] Divisor.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [array_like] The remainder of the division of *x1* by *x2*. This is a scalar if both *x1* and *x2* are scalars.

See also:

`remainder` Equivalent to the Python `%` operator.

`divide`

Notes

The result of the modulo operation for negative dividend and divisors is bound by conventions. For *fmod*, the sign of result is the sign of the dividend, while for *remainder* the sign of the result is the sign of the divisor. The *fmod* function is equivalent to the Matlab(TM) `rem` function.

Examples

```
>>> np.fmod([-3, -2, -1, 1, 2, 3], 2)  # doctest: +SKIP
array([-1,  0, -1,  1,  0,  1])
>>> np.remainder([-3, -2, -1, 1, 2, 3], 2)  # doctest: +SKIP
array([1, 0, 1, 1, 0, 1])
```

```
>>> np.fmod([5, 3], [2, 2.])  # doctest: +SKIP
array([ 1.,  1.])
>>> a = np.arange(-3, 3).reshape(3, 2)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([[-3, -2],
       [-1,  0],
       [ 1,  2]])
>>> np.fmod(a, [2,2])  # doctest: +SKIP
array([[-1,  0],
       [-1,  0],
       [ 1,  0]])
```

`dask.array.`**`frexp`**(*x*[, *out1*, *out2*], /[, *out=(None*, *None)*], *, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Decompose the elements of x into mantissa and twos exponent.

Returns (*mantissa*, *exponent*), where *x = mantissa * 2**exponent*`. The mantissa is lies in the open interval(-1, 1), while the twos exponent is a signed integer.

Parameters

x [array_like] Array of numbers to be decomposed.

out1 [ndarray, optional] Output array for the mantissa. Must have the same shape as *x*.

out2 [ndarray, optional] Output array for the exponent. Must have the same shape as *x*.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

mantissa [ndarray] Floating values between -1 and 1. This is a scalar if *x* is a scalar.

exponent [ndarray] Integer exponents of 2. This is a scalar if *x* is a scalar.

See also:

`ldexp` Compute `y = x1 * 2**x2`, the inverse of *frexp*.

Notes

Complex dtypes are not supported, they will raise a TypeError.

Examples

```
>>> x = np.arange(9)  # doctest: +SKIP
>>> y1, y2 = np.frexp(x)  # doctest: +SKIP
>>> y1  # doctest: +SKIP
array([ 0.   ,  0.5  ,  0.5  ,  0.75 ,  0.5  ,  0.625,  0.75 ,  0.875,
        0.5  ])
>>> y2  # doctest: +SKIP
array([0, 1, 2, 2, 3, 3, 3, 3, 4])
>>> y1 * 2**y2  # doctest: +SKIP
array([ 0.,  1.,  2.,  3.,  4.,  5.,  6.,  7.,  8.])
```

`dask.array.`**`fromfunction`**(*func*, *chunks='auto'*, *shape=None*, *dtype=None*, ***kwargs*)

Construct an array by executing a function over each coordinate.

This docstring was copied from numpy.fromfunction.

Some inconsistencies with the Dask version may exist.

The resulting array therefore has a value `fn(x, y, z)` at coordinate `(x, y, z)`.

Parameters

function [callable (Not supported in Dask)] The function is called with N parameters, where N is the rank of *shape*. Each parameter represents the coordinates of the array varying along a specific axis. For example, if *shape* were `(2, 2)`, then the parameters would be `array([[0, 0], [1, 1]])` and `array([[0, 1], [0, 1]])`

shape [(N,) tuple of ints] Shape of the output array, which also determines the shape of the coordinate arrays passed to *function*.

dtype [data-type, optional] Data-type of the coordinate arrays passed to *function*. By default, *dtype* is float.

Returns

fromfunction [any] The result of the call to *function* is passed back directly. Therefore the shape of *fromfunction* is completely determined by *function*. If *function* returns a scalar value, the shape of *fromfunction* would not match the *shape* parameter.

See also:

`indices`, *`meshgrid`*

Notes

Keywords other than *dtype* are passed to *function*.

Examples

```
>>> np.fromfunction(lambda i, j: i == j, (3, 3), dtype=int)  # doctest: +SKIP
array([[ True, False, False],
       [False,  True, False],
       [False, False,  True]])
```

```
>>> np.fromfunction(lambda i, j: i + j, (3, 3), dtype=int)  # doctest: +SKIP
array([[0, 1, 2],
       [1, 2, 3],
       [2, 3, 4]])
```

dask.array.**frompyfunc**(*func*, *nin*, *nout*)

This docstring was copied from numpy.frompyfunc.

Some inconsistencies with the Dask version may exist.

Takes an arbitrary Python function and returns a NumPy ufunc.

Can be used, for example, to add broadcasting to a built-in Python function (see Examples section).

Parameters

func [Python function object] An arbitrary Python function.

nin [int] The number of input arguments.

nout [int] The number of objects returned by *func*.

Returns

out [ufunc] Returns a NumPy universal function (`ufunc`) object.

See also:

vectorize evaluates pyfunc over input arrays using broadcasting rules of numpy

Notes

The returned ufunc always returns PyObject arrays.

Examples

Use frompyfunc to add broadcasting to the Python function `oct`:

```
>>> oct_array = np.frompyfunc(oct, 1, 1)  # doctest: +SKIP
>>> oct_array(np.array((10, 30, 100)))  # doctest: +SKIP
array([012, 036, 0144], dtype=object)
>>> np.array((oct(10), oct(30), oct(100))) # for comparison  # doctest: +SKIP
array(['012', '036', '0144'],
      dtype='|S4')
```

dask.array.**full**(**args*, ***kwargs*)

Blocked variant of full

Follows the signature of full exactly except that it also requires a keyword argument chunks=(. . .)

Original signature follows below.

Return a new array of given shape and type, filled with *fill_value*.

Parameters

shape [int or sequence of ints] Shape of the new array, e.g., `(2, 3)` or `2`.

fill_value [scalar] Fill value.

dtype [data-type, optional]

The desired data-type for the array The default, *None*, means
np.array(fill_value).dtype.

order [{'C', 'F'}, optional] Whether to store multidimensional data in C- or Fortran-contiguous (row- or column-wise) order in memory.

Returns

out [ndarray] Array of *fill_value* with the given shape, dtype, and order.

See also:

`full_like` Return a new array with shape of input filled with value.

`empty` Return a new uninitialized array.

`ones` Return a new array setting values to one.

`zeros` Return a new array setting values to zero.

Examples

```
>>> np.full((2, 2), np.inf)
array([[ inf,  inf],
       [ inf,  inf]])
>>> np.full((2, 2), 10)
array([[10, 10],
       [10, 10]])
```

`dask.array.full_like`(*a*, *fill_value*, *dtype=None*, *chunks=None*)
Return a full array with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

fill_value [scalar] Fill value.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of *fill_value* with the same shape and type as *a*.

See also:

`zeros_like` Return an array of zeros with shape and type of input.

`ones_like` Return an array of ones with shape and type of input.

`empty_like` Return an empty array with shape and type of input.

`zeros` Return a new array setting values to zero.

`ones` Return a new array setting values to one.

`empty` Return a new uninitialized array.

`full` Fill a new array.

`dask.array.gradient` (*f*, **varargs*, ***kwargs*)

Return the gradient of an N-dimensional array.

This docstring was copied from numpy.gradient.

Some inconsistencies with the Dask version may exist.

The gradient is computed using second order accurate central differences in the interior points and either first or second order accurate one-sides (forward or backwards) differences at the boundaries. The returned gradient hence has the same shape as the input array.

Parameters

f [array_like] An N-dimensional array containing samples of a scalar function.

varargs [list of scalar or array, optional] Spacing between f values. Default unitary spacing for all dimensions. Spacing can be specified using:

1. single scalar to specify a sample distance for all dimensions.
2. N scalars to specify a constant sample distance for each dimension. i.e. *dx*, *dy*, *dz*, ...
3. N arrays to specify the coordinates of the values along each dimension of F. The length of the array must match the size of the corresponding dimension
4. Any combination of N scalars/arrays with the meaning of 2. and 3.

If *axis* is given, the number of varargs must equal the number of axes. Default: 1.

edge_order [{1, 2}, optional] Gradient is calculated using N-th order accurate differences at the boundaries. Default: 1.

New in version 1.9.1.

axis [None or int or tuple of ints, optional] Gradient is calculated only along the given axis or axes The default (axis = None) is to calculate the gradient for all the axes of the input array. axis may be negative, in which case it counts from the last to the first axis.

New in version 1.11.0.

Returns

gradient [ndarray or list of ndarray] A set of ndarrays (or a single ndarray if there is only one dimension) corresponding to the derivatives of f with respect to each dimension. Each derivative has the same shape as f.

Notes

Assuming that $f \in C^3$ (i.e., f has at least 3 continuous derivatives) and let h_* be a non-homogeneous stepsize, we minimize the "consistency error" η_i between the true gradient and its estimate from a linear combination of the neighboring grid-points:

$$\eta_i = f_i^{(1)} - \left[\alpha f(x_i) + \beta f(x_i + h_d) + \gamma f(x_i - h_s) \right]$$

By substituting $f(x_i + h_d)$ and $f(x_i - h_s)$ with their Taylor series expansion, this translates into solving the following the linear system:

$$\left\{ \begin{array}{r} \alpha + \beta + \gamma = 0 \\ \beta h_d - \gamma h_s = 1 \\ \beta h_d^2 + \gamma h_s^2 = 0 \end{array} \right.$$

The resulting approximation of $f_i^{(1)}$ is the following:

$$\hat f_i^{(1)} = \frac{h_s^2 f\left(x_i + h_d\right) + \left(h_d^2 - h_s^2\right) f\left(x_i\right) - h_d^2 f\left(x_i - h_s\right)}{h_s h_d\left(h_d + h_s\right)} + \mathcal{O}\left(\frac{h_d h_s^2 + h_s h_d^2}{h_d + h_s}\right)$$

It is worth noting that if $h_s = h_d$ (i.e., data are evenly spaced) we find the standard second order approximation:

$$\hat f_i^{(1)} = \frac{f\left(x_{i+1}\right) - f\left(x_{i-1}\right)}{2h} + \mathcal{O}\left(h^2\right)$$

With a similar procedure the forward/backward approximations used for boundaries can be derived.

References

[1], [2], [3]

Examples

```
>>> f = np.array([1, 2, 4, 7, 11, 16], dtype=float)  # doctest: +SKIP
>>> np.gradient(f)  # doctest: +SKIP
array([ 1. ,  1.5,  2.5,  3.5,  4.5,  5. ])
>>> np.gradient(f, 2)  # doctest: +SKIP
array([ 0.5 ,  0.75,  1.25,  1.75,  2.25,  2.5 ])
```

Spacing can be also specified with an array that represents the coordinates of the values F along the dimensions. For instance a uniform spacing:

```
>>> x = np.arange(f.size)  # doctest: +SKIP
>>> np.gradient(f, x)  # doctest: +SKIP
array([ 1. ,  1.5,  2.5,  3.5,  4.5,  5. ])
```

Or a non uniform one:

```
>>> x = np.array([0., 1., 1.5, 3.5, 4., 6.], dtype=float)  # doctest: +SKIP
>>> np.gradient(f, x)  # doctest: +SKIP
array([ 1. ,  3. ,  3.5,  6.7,  6.9,  2.5])
```

For two dimensional arrays, the return will be two arrays ordered by axis. In this example the first array stands for the gradient in rows and the second one in columns direction:

```
>>> np.gradient(np.array([[1, 2, 6], [3, 4, 5]], dtype=float))  # doctest: +SKIP
[array([[ 2.,  2., -1.],
        [ 2.,  2., -1.]]), array([[ 1. ,  2.5,  4. ],
        [ 1. ,  1. ,  1. ]])]
```

In this example the spacing is also specified: uniform for axis=0 and non uniform for axis=1

```
>>> dx = 2.  # doctest: +SKIP
>>> y = [1., 1.5, 3.5]  # doctest: +SKIP
>>> np.gradient(np.array([[1, 2, 6], [3, 4, 5]], dtype=float), dx, y)  # doctest:␣
↪+SKIP
[array([[ 1. ,  1. , -0.5],
        [ 1. ,  1. , -0.5]]), array([[ 2. ,  2. ,  2. ],
        [ 2. ,  1.7,  0.5]])]
```

It is possible to specify how boundaries are treated using *edge_order*

```
>>> x = np.array([0, 1, 2, 3, 4])  # doctest: +SKIP
>>> f = x**2  # doctest: +SKIP
>>> np.gradient(f, edge_order=1)  # doctest: +SKIP
array([ 1.,  2.,  4.,  6.,  7.])
>>> np.gradient(f, edge_order=2)  # doctest: +SKIP
array([-0.,  2.,  4.,  6.,  8.])
```

The *axis* keyword can be used to specify a subset of axes of which the gradient is calculated

```
>>> np.gradient(np.array([[1, 2, 6], [3, 4, 5]], dtype=float), axis=0)  #␣
↪doctest: +SKIP
array([[ 2.,  2., -1.],
       [ 2.,  2., -1.]])
```

`dask.array.`**`histogram`**(*a*, *bins=None*, *range=None*, *normed=False*, *weights=None*, *density=None*)
Blocked variant of `numpy.histogram()`.

Follows the signature of `numpy.histogram()` exactly with the following exceptions:

- Either an iterable specifying the `bins` or the number of `bins` and a `range` argument is required as computing `min` and `max` over blocked arrays is an expensive operation that must be performed explicitly.
- `weights` must be a dask.array.Array with the same block structure as `a`.

Examples

Using number of bins and range:

```
>>> import dask.array as da
>>> import numpy as np
>>> x = da.from_array(np.arange(10000), chunks=10)
>>> h, bins = da.histogram(x, bins=10, range=[0, 10000])
>>> bins
array([    0.,  1000.,  2000.,  3000.,  4000.,  5000.,  6000.,  7000.,
        8000.,  9000., 10000.])
>>> h.compute()
array([1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000, 1000])
```

Explicitly specifying the bins:

```
>>> h, bins = da.histogram(x, bins=np.array([0, 5000, 10000]))
>>> bins
array([    0,  5000, 10000])
>>> h.compute()
array([5000, 5000])
```

`dask.array.`**`hstack`**(*tup*, *allow_unknown_chunksizes=False*)
Stack arrays in sequence horizontally (column wise).

This docstring was copied from numpy.hstack.

Some inconsistencies with the Dask version may exist.

This is equivalent to concatenation along the second axis, except for 1-D arrays where it concatenates along the first axis. Rebuilds arrays divided by *hsplit*.

This function makes most sense for arrays with up to 3 dimensions. For instance, for pixel-data with a height (first axis), width (second axis), and r/g/b channels (third axis). The functions *concatenate*, *stack* and *block* provide more general stacking and concatenation operations.

Parameters

tup [sequence of ndarrays] The arrays must have the same shape along all but the second axis, except 1-D arrays which can be any length.

Returns

stacked [ndarray] The array formed by stacking the given arrays.

See also:

`stack` Join a sequence of arrays along a new axis.

`vstack` Stack arrays in sequence vertically (row wise).

`dstack` Stack arrays in sequence depth wise (along third axis).

`concatenate` Join a sequence of arrays along an existing axis.

`hsplit` Split array along second axis.

`block` Assemble arrays from blocks.

Examples

```
>>> a = np.array((1,2,3))  # doctest: +SKIP
>>> b = np.array((2,3,4))  # doctest: +SKIP
>>> np.hstack((a,b))  # doctest: +SKIP
array([1, 2, 3, 2, 3, 4])
>>> a = np.array([[1],[2],[3]])  # doctest: +SKIP
>>> b = np.array([[2],[3],[4]])  # doctest: +SKIP
>>> np.hstack((a,b))  # doctest: +SKIP
array([[1, 2],
       [2, 3],
       [3, 4]])
```

`dask.array.`**`hypot`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Given the "legs" of a right triangle, return its hypotenuse.

Equivalent to `sqrt(x1**2 + x2**2)`, element-wise. If *x1* or *x2* is scalar_like (i.e., unambiguously cast-able to a scalar type), it is broadcast for use with each element of the other argument. (See Examples)

Parameters

x1, x2 [array_like] Leg of the triangle(s).

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

z [ndarray] The hypotenuse of the triangle(s). This is a scalar if both *x1* and *x2* are scalars.

Examples

```
>>> np.hypot(3*np.ones((3, 3)), 4*np.ones((3, 3)))  # doctest: +SKIP
array([[ 5.,  5.,  5.],
       [ 5.,  5.,  5.],
       [ 5.,  5.,  5.]])
```

Example showing broadcast of scalar_like argument:

```
>>> np.hypot(3*np.ones((3, 3)), [4])  # doctest: +SKIP
array([[ 5.,  5.,  5.],
       [ 5.,  5.,  5.],
       [ 5.,  5.,  5.]])
```

`dask.array.`**`imag`**`(`**args*, ***kwargs*`)`

Return the imaginary part of the complex argument.

Parameters

val [array_like] Input array.

Returns

out [ndarray or scalar] The imaginary component of the complex argument. If *val* is real, the type of *val* is used for the output. If *val* has complex elements, the returned type is float.

See also:

`real`, *`angle`*, `real_if_close`

Examples

```
>>> a = np.array([1+2j, 3+4j, 5+6j])  # doctest: +SKIP
>>> a.imag  # doctest: +SKIP
array([ 2.,  4.,  6.])
>>> a.imag = np.array([8, 10, 12])  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([ 1. +8.j,  3.+10.j,  5.+12.j])
>>> np.imag(1 + 1j)  # doctest: +SKIP
1.0
```

`dask.array.`**`indices`**`(`*dimensions*, *dtype=<class 'int'>*, *chunks='auto'*`)`

Implements NumPy's `indices` for Dask Arrays.

Generates a grid of indices covering the dimensions provided.

The final array has the shape `(len(dimensions), *dimensions)`. The chunks are used to specify the chunking for axis 1 up to `len(dimensions)`. The 0th axis always has chunks of length 1.

Parameters

dimensions [sequence of ints] The shape of the index grid.

dtype [dtype, optional] Type to use for the array. Default is `int`.

chunks [sequence of ints, str] The size of each block. Must be one of the following forms:

- A blocksize like (500, 1000)
- A size in bytes, like "100 MiB" which will choose a uniform block-like shape

- The word "auto" which acts like the above, but uses a configuration value `array.chunk-size` for the chunk size

Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

grid [dask array]

`dask.array.insert`(*arr*, *obj*, *values*, *axis*)

Insert values along the given axis before the given indices.

This docstring was copied from numpy.insert.

Some inconsistencies with the Dask version may exist.

Parameters

arr [array_like] Input array.

obj [int, slice or sequence of ints] Object that defines the index or indices before which *values* is inserted.

New in version 1.8.0.

Support for multiple insertions when *obj* is a single scalar or a sequence with one element (similar to calling insert multiple times).

values [array_like] Values to insert into *arr*. If the type of *values* is different from that of *arr*, *values* is converted to the type of *arr*. *values* should be shaped so that `arr[...,obj,...] = values` is legal.

axis [int, optional] Axis along which to insert *values*. If *axis* is None then *arr* is flattened first.

Returns

out [ndarray] A copy of *arr* with *values* inserted. Note that *insert* does not occur in-place: a new array is returned. If *axis* is None, *out* is a flattened array.

See also:

`append` Append elements at the end of an array.

`concatenate` Join a sequence of arrays along an existing axis.

`delete` Delete elements from an array.

Notes

Note that for higher dimensional inserts *obj=0* behaves very different from *obj=[0]* just like *arr[:,0,:] = values* is different from *arr[:,[0],:] = values*.

Examples

```
>>> a = np.array([[1, 1], [2, 2], [3, 3]])  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([[1, 1],
       [2, 2],
       [3, 3]])
>>> np.insert(a, 1, 5)  # doctest: +SKIP
array([1, 5, 1, 2, 2, 3, 3])
```

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```
>>> np.insert(a, 1, 5, axis=1)  # doctest: +SKIP
array([[1, 5, 1],
       [2, 5, 2],
       [3, 5, 3]])
```

Difference between sequence and scalars:

```
>>> np.insert(a, [1], [[1],[2],[3]], axis=1)  # doctest: +SKIP
array([[1, 1, 1],
       [2, 2, 2],
       [3, 3, 3]])
>>> np.array_equal(np.insert(a, 1, [1, 2, 3], axis=1),  # doctest: +SKIP
...                np.insert(a, [1], [[1],[2],[3]], axis=1))
True
```

```
>>> b = a.flatten()  # doctest: +SKIP
>>> b  # doctest: +SKIP
array([1, 1, 2, 2, 3, 3])
>>> np.insert(b, [2, 2], [5, 6])  # doctest: +SKIP
array([1, 1, 5, 6, 2, 2, 3, 3])
```

```
>>> np.insert(b, slice(2, 4), [5, 6])  # doctest: +SKIP
array([1, 1, 5, 2, 6, 2, 3, 3])
```

```
>>> np.insert(b, [2, 2], [7.13, False]) # type casting  # doctest: +SKIP
array([1, 1, 7, 0, 2, 2, 3, 3])
```

```
>>> x = np.arange(8).reshape(2, 4)  # doctest: +SKIP
>>> idx = (1, 3)  # doctest: +SKIP
>>> np.insert(x, idx, 999, axis=1)  # doctest: +SKIP
array([[  0, 999,   1,   2, 999,   3],
       [  4, 999,   5,   6, 999,   7]])
```

dask.array.**invert**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute bit-wise inversion, or bit-wise NOT, element-wise.

Computes the bit-wise NOT of the underlying binary representation of the integers in the input arrays. This ufunc implements the C/Python operator ~.

For signed integer inputs, the two's complement is returned. In a two's-complement system negative numbers are represented by the two's complement of the absolute value. This is the most common method of representing signed integers on computers [1]. A N-bit two's-complement system can represent every integer in the range -2^{N-1} to $+2^{N-1}-1$.

Parameters

x [array_like] Only integer and boolean types are handled.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Result. This is a scalar if *x* is a scalar.

See also:

`bitwise_and`, `bitwise_or`, `bitwise_xor`, `logical_not`

`binary_repr` Return the binary representation of the input number as a string.

Notes

bitwise_not is an alias for *invert*:

```
>>> np.bitwise_not is np.invert  # doctest: +SKIP
True
```

References

[1]

Examples

We've seen that 13 is represented by `00001101`. The invert or bit-wise NOT of 13 is then:

```
>>> np.invert(np.array([13], dtype=uint8))  # doctest: +SKIP
array([242], dtype=uint8)
>>> np.binary_repr(x, width=8)  # doctest: +SKIP
'00001101'
>>> np.binary_repr(242, width=8)  # doctest: +SKIP
'11110010'
```

The result depends on the bit-width:

```
>>> np.invert(np.array([13], dtype=uint16))  # doctest: +SKIP
array([65522], dtype=uint16)
>>> np.binary_repr(x, width=16)  # doctest: +SKIP
'0000000000001101'
>>> np.binary_repr(65522, width=16)  # doctest: +SKIP
'1111111111110010'
```

When using signed integer types the result is the two's complement of the result for the unsigned type:

```
>>> np.invert(np.array([13], dtype=int8))  # doctest: +SKIP
array([-14], dtype=int8)
>>> np.binary_repr(-14, width=8)  # doctest: +SKIP
'11110010'
```

Booleans are accepted as well:

```
>>> np.invert(array([True, False]))  # doctest: +SKIP
array([False,  True])
```

`dask.array.`**`isclose`**(*arr1*, *arr2*, *rtol=1e-05*, *atol=1e-08*, *equal_nan=False*)

Returns a boolean array where two arrays are element-wise equal within a tolerance.

This docstring was copied from numpy.isclose.

Some inconsistencies with the Dask version may exist.

The tolerance values are positive, typically very small numbers. The relative difference (*rtol* * abs(*b*)) and the absolute difference *atol* are added together to compare against the absolute difference between *a* and *b*.

Warning: The default *atol* is not appropriate for comparing numbers that are much smaller than one (see Notes).

Parameters

a, b [array_like] Input arrays to compare.

rtol [float] The relative tolerance parameter (see Notes).

atol [float] The absolute tolerance parameter (see Notes).

equal_nan [bool] Whether to compare NaN's as equal. If True, NaN's in *a* will be considered equal to NaN's in *b* in the output array.

Returns

y [array_like] Returns a boolean array of where *a* and *b* are equal within the given tolerance. If both *a* and *b* are scalars, returns a single boolean value.

See also:

`allclose`

Notes

New in version 1.7.0.

For finite values, isclose uses the following equation to test whether two floating point values are equivalent.

absolute(*a* - *b*) <= (*atol* + *rtol* * absolute(*b*))

Unlike the built-in *math.isclose*, the above equation is not symmetric in *a* and *b* – it assumes *b* is the reference value – so that *isclose(a, b)* might be different from *isclose(b, a)*. Furthermore, the default value of atol is not zero, and is used to determine what small values should be considered close to zero. The default value is appropriate for expected values of order unity: if the expected values are significantly smaller than one, it can result in false positives. *atol* should be carefully selected for the use case at hand. A zero value for *atol* will result in *False* if either *a* or *b* is zero.

Examples

```
>>> np.isclose([1e10,1e-7], [1.00001e10,1e-8])  # doctest: +SKIP
array([True, False])
>>> np.isclose([1e10,1e-8], [1.00001e10,1e-9])  # doctest: +SKIP
array([True, True])
>>> np.isclose([1e10,1e-8], [1.0001e10,1e-9])  # doctest: +SKIP
array([False, True])
>>> np.isclose([1.0, np.nan], [1.0, np.nan])  # doctest: +SKIP
array([True, False])
>>> np.isclose([1.0, np.nan], [1.0, np.nan], equal_nan=True)  # doctest: +SKIP
array([True, True])
>>> np.isclose([1e-8, 1e-7], [0.0, 0.0])  # doctest: +SKIP
```

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```
array([ True, False], dtype=bool)
>>> np.isclose([1e-100, 1e-7], [0.0, 0.0], atol=0.0)  # doctest: +SKIP
array([False, False], dtype=bool)
>>> np.isclose([1e-10, 1e-10], [1e-20, 0.0])  # doctest: +SKIP
array([ True,  True], dtype=bool)
>>> np.isclose([1e-10, 1e-10], [1e-20, 0.999999e-10], atol=0.0)  # doctest: +SKIP
array([False,  True], dtype=bool)
```

`dask.array.`**`iscomplex`**(**args*, ***kwargs*)

Returns a bool array, where True if input element is complex.

What is tested is whether the input has a non-zero imaginary part, not if the input type is complex.

Parameters

x [array_like] Input array.

Returns

out [ndarray of bools] Output array.

See also:

isreal

iscomplexobj Return True if x is a complex type or an array of complex numbers.

Examples

```
>>> np.iscomplex([1+1j, 1+0j, 4.5, 3, 2, 2j])  # doctest: +SKIP
array([ True, False, False, False, False,  True])
```

`dask.array.`**`isfinite`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Test element-wise for finiteness (not infinity or not Not a Number).

The result is returned as a boolean array.

Parameters

x [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray, bool] True where `x` is not positive infinity, negative infinity, or NaN; false otherwise. This is a scalar if *x* is a scalar.

See also:

isinf, *isneginf*, *isposinf*, *isnan*

Notes

Not a Number, positive infinity and negative infinity are considered to be non-finite.

NumPy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity. Also that positive infinity is not equivalent to negative infinity. But infinity is equivalent to positive infinity. Errors result if the second argument is also supplied when *x* is a scalar input, or if first and second arguments have different shapes.

Examples

```
>>> np.isfinite(1)  # doctest: +SKIP
True
>>> np.isfinite(0)  # doctest: +SKIP
True
>>> np.isfinite(np.nan)  # doctest: +SKIP
False
>>> np.isfinite(np.inf)  # doctest: +SKIP
False
>>> np.isfinite(np.NINF)  # doctest: +SKIP
False
>>> np.isfinite([np.log(-1.),1.,np.log(0)])  # doctest: +SKIP
array([False,  True, False])
```

```
>>> x = np.array([-np.inf, 0., np.inf])  # doctest: +SKIP
>>> y = np.array([2, 2, 2])  # doctest: +SKIP
>>> np.isfinite(x, y)  # doctest: +SKIP
array([0, 1, 0])
>>> y  # doctest: +SKIP
array([0, 1, 0])
```

`dask.array.isin`(*element*, *test_elements*, *assume_unique=False*, *invert=False*)

Calculates *element in test_elements*, broadcasting over *element* only. Returns a boolean array of the same shape as *element* that is True where an element of *element* is in *test_elements* and False otherwise.

Parameters

element [array_like] Input array.

test_elements [array_like] The values against which to test each value of *element*. This argument is flattened if it is an array or array_like. See notes for behavior with non-array-like parameters.

assume_unique [bool, optional] If True, the input arrays are both assumed to be unique, which can speed up the calculation. Default is False.

invert [bool, optional] If True, the values in the returned array are inverted, as if calculating *element not in test_elements*. Default is False. `np.isin(a, b, invert=True)` is equivalent to (but faster than) `np.invert(np.isin(a, b))`.

Returns

isin [ndarray, bool] Has the same shape as *element*. The values *element[isin]* are in *test_elements*.

See also:

`in1d` Flattened version of this function.

numpy.lib.arraysetops Module with a number of other functions for performing set operations on arrays.

Notes

isin is an element-wise function version of the python keyword *in*. `isin(a, b)` is roughly equivalent to `np.array([item in b for item in a])` if *a* and *b* are 1-D sequences.

element and *test_elements* are converted to arrays if they are not already. If *test_elements* is a set (or other non-sequence collection) it will be converted to an object array with one element, rather than an array of the values contained in *test_elements*. This is a consequence of the *array* constructor's way of handling non-sequence collections. Converting the set to a list usually gives the desired behavior.

New in version 1.13.0.

Examples

```
>>> element = 2*np.arange(4).reshape((2, 2))
>>> element
array([[0, 2],
       [4, 6]])
>>> test_elements = [1, 2, 4, 8]
>>> mask = np.isin(element, test_elements)
>>> mask
array([[ False,  True],
       [ True,  False]])
>>> element[mask]
array([2, 4])
```

The indices of the matched values can be obtained with *nonzero*:

```
>>> np.nonzero(mask)
(array([0, 1]), array([1, 0]))
```

The test can also be inverted:

```
>>> mask = np.isin(element, test_elements, invert=True)
>>> mask
array([[ True, False],
       [ False, True]])
>>> element[mask]
array([0, 6])
```

Because of how *array* handles sets, the following does not work as expected:

```
>>> test_set = {1, 2, 4, 8}
>>> np.isin(element, test_set)
array([[ False, False],
       [ False, False]])
```

Casting the set to a list gives the expected result:

```
>>> np.isin(element, list(test_set))
array([[ False,  True],
       [ True,  False]])
```

`dask.array.isinf`(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Test element-wise for positive or negative infinity.

Returns a boolean array of the same shape as *x*, True where `x == +/-inf`, otherwise False.

Parameters

x [array_like] Input values

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [bool (scalar) or boolean ndarray] True where `x` is positive or negative infinity, false otherwise. This is a scalar if *x* is a scalar.

See also:

`isneginf`, `isposinf`, `isnan`, `isfinite`

Notes

NumPy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754).

Errors result if the second argument is supplied when the first argument is a scalar, or if the first and second arguments have different shapes.

Examples

```
>>> np.isinf(np.inf)  # doctest: +SKIP
True
>>> np.isinf(np.nan)  # doctest: +SKIP
False
>>> np.isinf(np.NINF)  # doctest: +SKIP
True
>>> np.isinf([np.inf, -np.inf, 1.0, np.nan])  # doctest: +SKIP
array([ True,  True, False, False])
```

```
>>> x = np.array([-np.inf, 0., np.inf])  # doctest: +SKIP
>>> y = np.array([2, 2, 2])  # doctest: +SKIP
>>> np.isinf(x, y)  # doctest: +SKIP
array([1, 0, 1])
>>> y  # doctest: +SKIP
array([1, 0, 1])
```

`dask.array.isneginf`(**args*, ***kwargs*)

Return (x1 == x2) element-wise.

Parameters

x1, x2 [array_like] Input arrays of the same shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Output array, element-wise comparison of *x1* and *x2*. Typically of type bool, unless `dtype=object` is passed. This is a scalar if both *x1* and *x2* are scalars.

See also:

`not_equal`, `greater_equal`, `less_equal`, `greater`, `less`

Examples

```
>>> np.equal([0, 1, 3], np.arange(3))  # doctest: +SKIP
array([ True,  True, False])
```

What is compared are values, not types. So an int (1) and an array of length one can evaluate as True:

```
>>> np.equal(1, np.ones(1))  # doctest: +SKIP
array([ True])
```

`dask.array.`**`isnan`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Test element-wise for NaN and return result as a boolean array.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or bool] True where `x` is NaN, false otherwise. This is a scalar if *x* is a scalar.

See also:

`isinf`, *`isneginf`*, *`isposinf`*, *`isfinite`*, `isnat`

Notes

NumPy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity.

Examples

```
>>> np.isnan(np.nan)  # doctest: +SKIP
True
>>> np.isnan(np.inf)  # doctest: +SKIP
False
>>> np.isnan([np.log(-1.),1.,np.log(0)])  # doctest: +SKIP
array([ True, False, False])
```

`dask.array.`**`isnull`**`(`*values*`)`

pandas.isnull for dask arrays

`dask.array.`**`isposinf`**`(`**args*, ***kwargs*`)`

Return (x1 == x2) element-wise.

Parameters

x1, x2 [array_like] Input arrays of the same shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Output array, element-wise comparison of *x1* and *x2*. Typically of type bool, unless `dtype=object` is passed. This is a scalar if both *x1* and *x2* are scalars.

See also:

`not_equal`, `greater_equal`, `less_equal`, `greater`, `less`

Examples

```
>>> np.equal([0, 1, 3], np.arange(3))  # doctest: +SKIP
array([ True,  True, False])
```

What is compared are values, not types. So an int (1) and an array of length one can evaluate as True:

```
>>> np.equal(1, np.ones(1))  # doctest: +SKIP
array([ True])
```

`dask.array.`**`isreal`**`(`**args*, ***kwargs*`)`

Returns a bool array, where True if input element is real.

If element has complex type with zero complex part, the return value for that element is True.

Parameters

x [array_like] Input array.

Returns

out [ndarray, bool] Boolean array of same shape as *x*.

See also:

iscomplex

isrealobj Return True if x is not a complex type.

Examples

```
>>> np.isreal([1+1j, 1+0j, 4.5, 3, 2, 2j])  # doctest: +SKIP
array([False,  True,  True,  True,  True, False])
```

dask.array.**ldexp**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Returns x1 * 2**x2, element-wise.

The mantissas *x1* and twos exponents *x2* are used to construct floating point numbers `x1 * 2**x2`.

Parameters

x1 [array_like] Array of multipliers.

x2 [array_like, int] Array of twos exponents.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The result of `x1 * 2**x2`. This is a scalar if both *x1* and *x2* are scalars.

See also:

frexp Return (y1, y2) from `x = y1 * 2**y2`, inverse to *ldexp*.

Notes

Complex dtypes are not supported, they will raise a TypeError.

ldexp is useful as the inverse of *frexp*, if used by itself it is more clear to simply use the expression `x1 * 2**x2`.

Examples

```
>>> np.ldexp(5, np.arange(4))  # doctest: +SKIP
array([  5.,  10.,  20.,  40.], dtype=float32)
```

```
>>> x = np.arange(6)  # doctest: +SKIP
>>> np.ldexp(*np.frexp(x))  # doctest: +SKIP
array([ 0.,  1.,  2.,  3.,  4.,  5.])
```

`dask.array.`**`linspace`**(*start*, *stop*, *num=50*, *endpoint=True*, *retstep=False*, *chunks='auto'*, *dtype=None*)

Return *num* evenly spaced values over the closed interval [*start*, *stop*].

Parameters

start [scalar] The starting value of the sequence.

stop [scalar] The last value of the sequence.

num [int, optional] Number of samples to include in the returned dask array, including the endpoints. Default is 50.

endpoint [bool, optional] If True, `stop` is the last sample. Otherwise, it is not included. Default is True.

retstep [bool, optional] If True, return (samples, step), where step is the spacing between samples. Default is False.

chunks [int] The number of samples on each block. Note that the last block will have fewer samples if *num % blocksize != 0*

dtype [dtype, optional] The type of the output array.

Returns

samples [dask array]

step [float, optional] Only returned if `retstep` is True. Size of spacing between samples.

See also:

`dask.array.arange`

`dask.array.`**`log`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Natural logarithm, element-wise.

The natural logarithm *log* is the inverse of the exponential function, so that *log(exp(x)) = x*. The natural logarithm is logarithm in base *e*.

Parameters

x [array_like] Input value.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The natural logarithm of *x*, element-wise. This is a scalar if *x* is a scalar.

See also:

`log10`, *`log2`*, *`log1p`*, `emath.log`

Notes

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *exp(z) = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log* is a complex analytical function that has a branch cut *[-inf, 0]* and is continuous from above on it. *log* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

References

[1], [2]

Examples

```
>>> np.log([1, np.e, np.e**2, 0])  # doctest: +SKIP
array([  0.,   1.,   2., -Inf])
```

`dask.array.`**`log10`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the base 10 logarithm of the input array, element-wise.

Parameters

x [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The logarithm to the base 10 of *x*, element-wise. NaNs are returned where x is negative. This is a scalar if *x* is a scalar.

See also:

`emath.log10`

Notes

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *10**z = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log10* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log10* is a complex analytical function that has a branch cut *[-inf, 0]* and is continuous from above on it. *log10* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

References

[1], [2]

Examples

```
>>> np.log10([1e-15, -3.])  # doctest: +SKIP
array([-15.,  NaN])
```

`dask.array.`**`log1p`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the natural logarithm of one plus the input array, element-wise.

Calculates `log(1 + x)`.

Parameters

x [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] Natural logarithm of *1 + x*, element-wise. This is a scalar if *x* is a scalar.

See also:

`expm1` `exp(x) - 1`, the inverse of *log1p*.

Notes

For real-valued input, *log1p* is accurate also for *x* so small that *1 + x == 1* in floating-point accuracy.

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *exp(z) = 1 + x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log1p* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log1p* is a complex analytical function that has a branch cut *[-inf, -1]* and is continuous from above on it. *log1p* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

References

[1], [2]

Examples

```
>>> np.log1p(1e-99)  # doctest: +SKIP
1e-99
>>> np.log(1 + 1e-99)  # doctest: +SKIP
0.0
```

`dask.array.log2`(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Base-2 logarithm of *x*.

Parameters

x [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] Base-2 logarithm of *x*. This is a scalar if *x* is a scalar.

See also:

log, *log10*, *log1p*, emath.log2

Notes

New in version 1.3.0.

Logarithm is a multivalued function: for each *x* there is an infinite number of *z* such that *2**z = x*. The convention is to return the *z* whose imaginary part lies in *[-pi, pi]*.

For real-valued input data types, *log2* always returns real output. For each value that cannot be expressed as a real number or infinity, it yields `nan` and sets the *invalid* floating point error flag.

For complex-valued input, *log2* is a complex analytical function that has a branch cut *[-inf, 0]* and is continuous from above on it. *log2* handles the floating-point negative zero as an infinitesimal negative number, conforming to the C99 standard.

Examples

```
>>> x = np.array([0, 1, 2, 2**4])  # doctest: +SKIP
>>> np.log2(x)  # doctest: +SKIP
array([-Inf,   0.,   1.,   4.])
```

```
>>> xi = np.array([0+1.j, 1, 2+0.j, 4.j])  # doctest: +SKIP
>>> np.log2(xi)  # doctest: +SKIP
array([ 0.+2.26618007j,  0.+0.j        ,  1.+0.j        ,  2.+2.26618007j])
```

`dask.array.`**`logaddexp`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Logarithm of the sum of exponentiations of the inputs.

Calculates `log(exp(x1) + exp(x2))`. This function is useful in statistics where the calculated probabilities of events may be so small as to exceed the range of normal floating point numbers. In such cases the logarithm of the calculated probability is stored. This function allows adding probabilities stored in such a fashion.

Parameters

x1, x2 [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

result [ndarray] Logarithm of `exp(x1) + exp(x2)`. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logaddexp2` Logarithm of the sum of exponentiations of inputs in base 2.

Notes

New in version 1.3.0.

Examples

```
>>> prob1 = np.log(1e-50)  # doctest: +SKIP
>>> prob2 = np.log(2.5e-50)  # doctest: +SKIP
>>> prob12 = np.logaddexp(prob1, prob2)  # doctest: +SKIP
>>> prob12  # doctest: +SKIP
-113.87649168120691
>>> np.exp(prob12)  # doctest: +SKIP
3.5000000000000057e-50
```

`dask.array.`**`logaddexp2`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Logarithm of the sum of exponentiations of the inputs in base-2.

Calculates `log2(2**x1 + 2**x2)`. This function is useful in machine learning when the calculated probabilities of events may be so small as to exceed the range of normal floating point numbers. In such cases the base-2 logarithm of the calculated probability can be used instead. This function allows adding probabilities stored in such a fashion.

Parameters

x1, x2 [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

result [ndarray] Base-2 logarithm of `2**x1 + 2**x2`. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logaddexp` Logarithm of the sum of exponentiations of the inputs.

Notes

New in version 1.3.0.

Examples

```
>>> prob1 = np.log2(1e-50)  # doctest: +SKIP
>>> prob2 = np.log2(2.5e-50)  # doctest: +SKIP
>>> prob12 = np.logaddexp2(prob1, prob2)  # doctest: +SKIP
>>> prob1, prob2, prob12  # doctest: +SKIP
(-166.09640474436813, -164.77447664948076, -164.28904982231052)
>>> 2**prob12  # doctest: +SKIP
3.4999999999999914e-50
```

`dask.array.`**`logical_and`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the truth value of x1 AND x2 element-wise.

Parameters

x1, x2 [array_like] Input arrays. *x1* and *x2* must be of the same shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or bool] Boolean result with the same shape as *x1* and *x2* of the logical AND operation on corresponding elements of *x1* and *x2*. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logical_or`, *`logical_not`*, *`logical_xor`*, *`bitwise_and`*

Examples

```
>>> np.logical_and(True, False)  # doctest: +SKIP
False
>>> np.logical_and([True, False], [False, False])  # doctest: +SKIP
array([False, False])
```

```
>>> x = np.arange(5)  # doctest: +SKIP
>>> np.logical_and(x>1, x<4)  # doctest: +SKIP
array([False, False,  True,  True, False])
```

dask.array.**logical_not**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the truth value of NOT x element-wise.

Parameters

x [array_like] Logical NOT is applied to the elements of *x*.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [bool or ndarray of bool] Boolean result with the same shape as *x* of the NOT operation on elements of *x*. This is a scalar if *x* is a scalar.

See also:

logical_and, *logical_or*, *logical_xor*

Examples

```
>>> np.logical_not(3)  # doctest: +SKIP
False
>>> np.logical_not([True, False, 0, 1])  # doctest: +SKIP
array([False,  True,  True, False])
```

```
>>> x = np.arange(5)  # doctest: +SKIP
>>> np.logical_not(x<3)  # doctest: +SKIP
array([False, False, False,  True,  True])
```

dask.array.**logical_or**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the truth value of x1 OR x2 element-wise.

Parameters

x1, x2 [array_like] Logical OR is applied to the elements of *x1* and *x2*. They have to be of the same shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or bool] Boolean result with the same shape as *x1* and *x2* of the logical OR operation on elements of *x1* and *x2*. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logical_and`, `logical_not`, `logical_xor`, `bitwise_or`

Examples

```
>>> np.logical_or(True, False)  # doctest: +SKIP
True
>>> np.logical_or([True, False], [False, False])  # doctest: +SKIP
array([ True, False])
```

```
>>> x = np.arange(5)  # doctest: +SKIP
>>> np.logical_or(x < 1, x > 3)  # doctest: +SKIP
array([ True, False, False, False,  True])
```

`dask.array.`**`logical_xor`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute the truth value of x1 XOR x2, element-wise.

Parameters

x1, x2 [array_like] Logical XOR is applied to the elements of *x1* and *x2*. They must be broadcastable to the same shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [bool or ndarray of bool] Boolean result of the logical XOR operation applied to the elements of *x1* and *x2*; the shape is determined by whether or not broadcasting of one or both arrays was required. This is a scalar if both *x1* and *x2* are scalars.

See also:

`logical_and`, `logical_or`, `logical_not`, `bitwise_xor`

Examples

```
>>> np.logical_xor(True, False)  # doctest: +SKIP
True
>>> np.logical_xor([True, True, False, False], [True, False, True, False])  #␣
↪doctest: +SKIP
array([False,  True,  True, False])
```

```
>>> x = np.arange(5)  # doctest: +SKIP
>>> np.logical_xor(x < 1, x > 3)  # doctest: +SKIP
array([ True, False, False, False,  True])
```

Simple example showing support of broadcasting

```
>>> np.logical_xor(0, np.eye(2))  # doctest: +SKIP
array([[ True, False],
       [False,  True]])
```

dask.array.**map_blocks**(*func*, **args*, *name=None*, *token=None*, *dtype=None*, *chunks=None*, *drop_axis=[]*, *new_axis=None*, *meta=None*, ***kwargs*)

Map a function across all blocks of a dask array.

Parameters

func [callable] Function to apply to every block in the array.

args [dask arrays or other objects]

dtype [np.dtype, optional] The `dtype` of the output array. It is recommended to provide this. If not provided, will be inferred by applying the function to a small set of fake data.

chunks [tuple, optional] Chunk shape of resulting blocks if the function does not preserve shape. If not provided, the resulting array is assumed to have the same block structure as the first input array.

drop_axis [number or iterable, optional] Dimensions lost by the function.

new_axis [number or iterable, optional] New dimensions created by the function. Note that these are applied after `drop_axis` (if present).

token [string, optional] The key prefix to use for the output array. If not provided, will be determined from the function name.

name [string, optional] The key name to use for the output array. Note that this fully specifies the output key name, and must be unique. If not provided, will be determined by a hash of the arguments.

****kwargs :** Other keyword arguments to pass to function. Values must be constants (not dask.arrays)

Examples

```
>>> import dask.array as da
>>> x = da.arange(6, chunks=3)
```

```
>>> x.map_blocks(lambda x: x * 2).compute()
array([ 0,  2,  4,  6,  8, 10])
```

The `da.map_blocks` function can also accept multiple arrays.

```
>>> d = da.arange(5, chunks=2)
>>> e = da.arange(5, chunks=2)
```

```
>>> f = map_blocks(lambda a, b: a + b**2, d, e)
>>> f.compute()
array([ 0,  2,  6, 12, 20])
```

If the function changes shape of the blocks then you must provide chunks explicitly.

```
>>> y = x.map_blocks(lambda x: x[::2], chunks=((2, 2),))
```

You have a bit of freedom in specifying chunks. If all of the output chunk sizes are the same, you can provide just that chunk size as a single tuple.

```
>>> a = da.arange(18, chunks=(6,))
>>> b = a.map_blocks(lambda x: x[:3], chunks=(3,))
```

If the function changes the dimension of the blocks you must specify the created or destroyed dimensions.

```
>>> b = a.map_blocks(lambda x: x[None, :, None], chunks=(1, 6, 1),
...                  new_axis=[0, 2])
```

If `chunks` is specified but `new_axis` is not, then it is inferred to add the necessary number of axes on the left.

Map_blocks aligns blocks by block positions without regard to shape. In the following example we have two arrays with the same number of blocks but with different shape and chunk sizes.

```
>>> x = da.arange(1000, chunks=(100,))
>>> y = da.arange(100, chunks=(10,))
```

The relevant attribute to match is numblocks.

```
>>> x.numblocks
(10,)
>>> y.numblocks
(10,)
```

If these match (up to broadcasting rules) then we can map arbitrary functions across blocks

```
>>> def func(a, b):
...     return np.array([a.max(), b.max()])
```

```
>>> da.map_blocks(func, x, y, chunks=(2,), dtype='i8')
dask.array<func, shape=(20,), dtype=int64, chunksize=(2,), chunktype=numpy.
↪ndarray>
```

```
>>> _.compute()
array([ 99,   9, 199,  19, 299,  29, 399,  39, 499,  49, 599,  59, 699,
        69, 799,  79, 899,  89, 999,  99])
```

Your block function get information about where it is in the array by accepting a special `block_info` keyword argument.

```
>>> def func(block, block_info=None):
...     pass
```

This will receive the following information:

```
>>> block_info  # doctest: +SKIP
{0: {'shape': (1000,),
     'num-chunks': (10,),
     'chunk-location': (4,),
     'array-location': [(400, 500)]},
 None: {'shape': (1000,),
        'num-chunks': (10,),
        'chunk-location': (4,),
        'array-location': [(400, 500)],
        'chunk-shape': (100,),
        'dtype': dtype('float64')}}
```

For each argument and keyword arguments that are dask arrays (the positions of which are the first index), you will receive the shape of the full array, the number of chunks of the full array in each dimension, the chunk location (for example the fourth chunk over in the first dimension), and the array location (for example the slice corresponding to `40:50`). The same information is provided for the output, with the key `None`, plus the shape and dtype that should be returned.

These features can be combined to synthesize an array from scratch, for example:

```
>>> def func(block_info=None):
...     loc = block_info[None]['array-location'][0]
...     return np.arange(loc[0], loc[1])
```

```
>>> da.map_blocks(func, chunks=((4, 4),), dtype=np.float_)
dask.array<func, shape=(8,), dtype=float64, chunksize=(4,), chunktype=numpy.
↪ndarray>
```

```
>>> _.compute()
array([0, 1, 2, 3, 4, 5, 6, 7])
```

You may specify the key name prefix of the resulting task in the graph with the optional `token` keyword argument.

```
>>> x.map_blocks(lambda x: x + 1, name='increment')  # doctest: +SKIP
dask.array<increment, shape=(100,), dtype=int64, chunksize=(10,), chunktype=numpy.
↪ndarray>
```

`dask.array.`**`matmul`**(*x1*, *x2*, */*, *out=None*, ***, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

This docstring was copied from numpy.matmul.

Some inconsistencies with the Dask version may exist.

Matrix product of two arrays.

Parameters

x1, x2 [array_like] Input arrays, scalars not allowed.

out [ndarray, optional] A location into which the result is stored. If provided, it must have a shape that matches the signature *(n,k),(k,m)->(n,m)*. If not provided or *None*, a freshly-allocated array is returned.

****kwargs** For other keyword-only arguments, see the ufunc docs.

..versionadded:: 1.16 Now handles ufunc kwargs

Returns

y [ndarray] The matrix product of the inputs. This is a scalar only when both x1, x2 are 1-d vectors.

Raises

ValueError If the last dimension of *a* is not the same size as the second-to-last dimension of *b*.

If a scalar value is passed in.

See also:

vdot Complex-conjugating dot product.

tensordot Sum products over arbitrary axes.

einsum Einstein summation convention.

dot alternative matrix product with different broadcasting rules.

Notes

The behavior depends on the arguments in the following way.

- If both arguments are 2-D they are multiplied like conventional matrices.
- If either argument is N-D, N > 2, it is treated as a stack of matrices residing in the last two indexes and broadcast accordingly.
- If the first argument is 1-D, it is promoted to a matrix by prepending a 1 to its dimensions. After matrix multiplication the prepended 1 is removed.
- If the second argument is 1-D, it is promoted to a matrix by appending a 1 to its dimensions. After matrix multiplication the appended 1 is removed.

`matmul` differs from `dot` in two important ways:

- Multiplication by scalars is not allowed, use `*` instead.
- Stacks of matrices are broadcast together as if the matrices were elements, respecting the signature `(n,k),(k,m)->(n,m)`:

```
>>> a = np.ones([9, 5, 7, 4])  # doctest: +SKIP
>>> c = np.ones([9, 5, 4, 3])  # doctest: +SKIP
>>> np.dot(a, c).shape  # doctest: +SKIP
(9, 5, 7, 9, 5, 3)
>>> np.matmul(a, c).shape  # doctest: +SKIP
(9, 5, 7, 3)
>>> # n is 7, k is 4, m is 3
```

The matmul function implements the semantics of the @ operator introduced in Python 3.5 following PEP465.

Examples

For 2-D arrays it is the matrix product:

```
>>> a = np.array([[1, 0],  # doctest: +SKIP
...               [0, 1]])
>>> b = np.array([[4, 1],  # doctest: +SKIP
...               [2, 2]])
>>> np.matmul(a, b)  # doctest: +SKIP
```

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```
array([[4, 1],
       [2, 2]])
```

For 2-D mixed with 1-D, the result is the usual.

```
>>> a = np.array([[1, 0],  # doctest: +SKIP
...               [0, 1]]
>>> b = np.array([1, 2])  # doctest: +SKIP
>>> np.matmul(a, b)  # doctest: +SKIP
array([1, 2])
>>> np.matmul(b, a)  # doctest: +SKIP
array([1, 2])
```

Broadcasting is conventional for stacks of arrays

```
>>> a = np.arange(2 * 2 * 4).reshape((2, 2, 4))  # doctest: +SKIP
>>> b = np.arange(2 * 2 * 4).reshape((2, 4, 2))  # doctest: +SKIP
>>> np.matmul(a,b).shape  # doctest: +SKIP
(2, 2, 2)
>>> np.matmul(a, b)[0, 1, 1]  # doctest: +SKIP
98
>>> sum(a[0, 1, :] * b[0 , :, 1])  # doctest: +SKIP
98
```

Vector, vector returns the scalar inner product, but neither argument is complex-conjugated:

```
>>> np.matmul([2j, 3j], [2j, 3j])  # doctest: +SKIP
(-13+0j)
```

Scalar multiplication raises an error.

```
>>> np.matmul([1,2], 3)  # doctest: +SKIP
Traceback (most recent call last):
...
ValueError: matmul: Input operand 1 does not have enough dimensions ...
```

New in version 1.10.0.

`dask.array.`**`max`**(*a*, *axis=None*, *out=None*, *keepdims=<no value>*, *initial=<no value>*)

Return the maximum of an array or maximum along an axis.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] Axis or axes along which to operate. By default, flattened input is used.

New in version 1.7.0.

If this is a tuple of ints, the maximum is selected over multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternative output array in which to place the result. Must be of the same shape and buffer length as the expected output. See *doc.ufuncs* (Section "Output arguments") for more details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *amax* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

initial [scalar, optional] The minimum value of an output element. Must be present to allow computation on empty slice. See *~numpy.ufunc.reduce* for details.

New in version 1.15.0.

Returns

amax [ndarray or scalar] Maximum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is an array of dimension `a.ndim - 1`.

See also:

`amin` The minimum value of an array along a given axis, propagating any NaNs.

`nanmax` The maximum value of an array along a given axis, ignoring any NaNs.

`maximum` Element-wise maximum of two arrays, propagating any NaNs.

`fmax` Element-wise maximum of two arrays, ignoring any NaNs.

`argmax` Return the indices of the maximum values.

`nanmin`, `minimum`, `fmin`

Notes

NaN values are propagated, that is if at least one item is NaN, the corresponding max value will be NaN as well. To ignore NaN values (MATLAB behavior), please use nanmax.

Don't use *amax* for element-wise comparison of 2 arrays; when `a.shape[0]` is 2, `maximum(a[0], a[1])` is faster than `amax(a, axis=0)`.

Examples

```
>>> a = np.arange(4).reshape((2,2))
>>> a
array([[0, 1],
       [2, 3]])
>>> np.amax(a)           # Maximum of the flattened array
3
>>> np.amax(a, axis=0)   # Maxima along the first axis
array([2, 3])
>>> np.amax(a, axis=1)   # Maxima along the second axis
array([1, 3])
```

```
>>> b = np.arange(5, dtype=float)
>>> b[2] = np.NaN
>>> np.amax(b)
nan
>>> np.nanmax(b)
4.0
```

You can use an initial value to compute the maximum of an empty slice, or to initialize it to a different value:

```
>>> np.max([[-50], [10]], axis=-1, initial=0)
array([ 0, 10])
```

Notice that the initial value is used as one of the elements for which the maximum is determined, unlike for the default argument Python's max function, which is only used for empty iterables.

```
>>> np.max([5], initial=6)
6
>>> max([5], default=6)
5
```

dask.array.**maximum**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Element-wise maximum of array elements.

Compare two arrays and returns a new array containing the element-wise maxima. If one of the elements being compared is a NaN, then that element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are propagated.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape, or shapes that can be broadcast to a single shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The maximum of *x1* and *x2*, element-wise. This is a scalar if both *x1* and *x2* are scalars.

See also:

minimum Element-wise minimum of two arrays, propagates NaNs.

fmax Element-wise maximum of two arrays, ignores NaNs.

amax The maximum value of an array along a given axis, propagates NaNs.

nanmax The maximum value of an array along a given axis, ignores NaNs.

fmin, amin, *nanmin*

Notes

The maximum is equivalent to `np.where(x1 >= x2, x1, x2)` when neither x1 nor x2 are nans, but it is faster and does proper broadcasting.

Examples

```
>>> np.maximum([2, 3, 4], [1, 5, 2])  # doctest: +SKIP
array([2, 5, 4])
```

```
>>> np.maximum(np.eye(2), [0.5, 2]) # broadcasting  # doctest: +SKIP
array([[ 1. ,  2. ],
       [ 0.5,  2. ]])
```

```
>>> np.maximum([np.nan, 0, np.nan], [0, np.nan, np.nan])  # doctest: +SKIP
array([ NaN,  NaN,  NaN])
>>> np.maximum(np.Inf, 1)  # doctest: +SKIP
inf
```

`dask.array.`**`mean`**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=<no value>*)

Compute the arithmetic mean along the specified axis.

Returns the average of the array elements. The average is taken over the flattened array by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

Parameters

a [array_like] Array containing numbers whose mean is desired. If *a* is not an array, a conversion is attempted.

axis [None or int or tuple of ints, optional] Axis or axes along which the means are computed. The default is to compute the mean of the flattened array.

New in version 1.7.0.

If this is a tuple of ints, a mean is performed over multiple axes, instead of a single axis or all the axes as before.

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for floating point inputs, it is the same as the input dtype.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *mean* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

Returns

m [ndarray, see dtype parameter above] If *out=None*, returns a new array containing the mean values, otherwise a reference to the output array is returned.

See also:

`average` Weighted average

`std`, `var`, `nanmean`, `nanstd`, `nanvar`

Notes

The arithmetic mean is the sum of the elements along the axis divided by the number of elements.

Note that for floating-point input, the mean is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32* (see example below). Specifying a higher-precision accumulator using the *dtype* keyword can alleviate this issue.

By default, *float16* results are computed using *float32* intermediates for extra precision.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])
>>> np.mean(a)
2.5
>>> np.mean(a, axis=0)
array([ 2.,  3.])
>>> np.mean(a, axis=1)
array([ 1.5,  3.5])
```

In single precision, *mean* can be inaccurate:

```
>>> a = np.zeros((2, 512*512), dtype=np.float32)
>>> a[0, :] = 1.0
>>> a[1, :] = 0.1
>>> np.mean(a)
0.54999924
```

Computing the mean in float64 is more accurate:

```
>>> np.mean(a, dtype=np.float64)
0.55000000074505806
```

`dask.array.`**`meshgrid`**`(`**xi*, ***kwargs*`)`

Return coordinate matrices from coordinate vectors.

This docstring was copied from numpy.meshgrid.

Some inconsistencies with the Dask version may exist.

Make N-D coordinate arrays for vectorized evaluations of N-D scalar/vector fields over N-D grids, given one-dimensional coordinate arrays x1, x2,. . . , xn.

Changed in version 1.9: 1-D and 0-D cases are allowed.

Parameters

x1, x2,. . . , xn [array_like] 1-D arrays representing the coordinates of a grid.

indexing [{‘xy’, ‘ij’}, optional] Cartesian (‘xy’, default) or matrix (‘ij’) indexing of output. See Notes for more details.

New in version 1.7.0.

sparse [bool, optional] If True a sparse grid is returned in order to conserve memory. Default is False.

New in version 1.7.0.

copy [bool, optional] If False, a view into the original arrays are returned in order to conserve memory. Default is True. Please note that `sparse=False, copy=False` will likely return non-contiguous arrays. Furthermore, more than one element of a broadcast array may refer to a single memory location. If you need to write to the arrays, make copies first.

New in version 1.7.0.

Returns

X1, X2,..., XN [ndarray] For vectors *x1*, *x2*,..., 'xn' with lengths `Ni=len(xi)` , return `(N1, N2, N3,...Nn)` shaped arrays if indexing='ij' or `(N2, N1, N3,...Nn)` shaped arrays if indexing='xy' with the elements of *xi* repeated to fill the matrix along the first dimension for *x1*, the second for *x2* and so on.

See also:

`index_tricks.mgrid` Construct a multi-dimensional "meshgrid" using indexing notation.

`index_tricks.ogrid` Construct an open multi-dimensional "meshgrid" using indexing notation.

Notes

This function supports both indexing conventions through the indexing keyword argument. Giving the string 'ij' returns a meshgrid with matrix indexing, while 'xy' returns a meshgrid with Cartesian indexing. In the 2-D case with inputs of length M and N, the outputs are of shape (N, M) for 'xy' indexing and (M, N) for 'ij' indexing. In the 3-D case with inputs of length M, N and P, outputs are of shape (N, M, P) for 'xy' indexing and (M, N, P) for 'ij' indexing. The difference is illustrated by the following code snippet:

```
xv, yv = np.meshgrid(x, y, sparse=False, indexing='ij')
for i in range(nx):
    for j in range(ny):
        # treat xv[i,j], yv[i,j]

xv, yv = np.meshgrid(x, y, sparse=False, indexing='xy')
for i in range(nx):
    for j in range(ny):
        # treat xv[j,i], yv[j,i]
```

In the 1-D and 0-D case, the indexing and sparse keywords have no effect.

Examples

```
>>> nx, ny = (3, 2)  # doctest: +SKIP
>>> x = np.linspace(0, 1, nx)  # doctest: +SKIP
>>> y = np.linspace(0, 1, ny)  # doctest: +SKIP
>>> xv, yv = np.meshgrid(x, y)  # doctest: +SKIP
>>> xv  # doctest: +SKIP
array([[ 0. ,  0.5,  1. ],
       [ 0. ,  0.5,  1. ]])
>>> yv  # doctest: +SKIP
array([[ 0.,  0.,  0.],
       [ 1.,  1.,  1.]])
>>> xv, yv = np.meshgrid(x, y, sparse=True)  # make sparse output arrays  #␣
↪doctest: +SKIP
>>> xv  # doctest: +SKIP
array([[ 0. ,  0.5,  1. ]])
```

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```
>>> yv  # doctest: +SKIP
array([[ 0.],
       [ 1.]])
```

meshgrid is very useful to evaluate functions on a grid.

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> x = np.arange(-5, 5, 0.1)  # doctest: +SKIP
>>> y = np.arange(-5, 5, 0.1)  # doctest: +SKIP
>>> xx, yy = np.meshgrid(x, y, sparse=True)  # doctest: +SKIP
>>> z = np.sin(xx**2 + yy**2) / (xx**2 + yy**2)  # doctest: +SKIP
>>> h = plt.contourf(x,y,z)  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.`**`min`**(*a*, *axis=None*, *out=None*, *keepdims=<no value>*, *initial=<no value>*)

Return the minimum of an array or minimum along an axis.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] Axis or axes along which to operate. By default, flattened input is used.

New in version 1.7.0.

If this is a tuple of ints, the minimum is selected over multiple axes, instead of a single axis or all the axes as before.

out [ndarray, optional] Alternative output array in which to place the result. Must be of the same shape and buffer length as the expected output. See *doc.ufuncs* (Section "Output arguments") for more details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *amin* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

initial [scalar, optional] The maximum value of an output element. Must be present to allow computation on empty slice. See *~numpy.ufunc.reduce* for details.

New in version 1.15.0.

Returns

amin [ndarray or scalar] Minimum of *a*. If *axis* is None, the result is a scalar value. If *axis* is given, the result is an array of dimension `a.ndim - 1`.

See also:

`amax` The maximum value of an array along a given axis, propagating any NaNs.

`nanmin` The minimum value of an array along a given axis, ignoring any NaNs.

`minimum` Element-wise minimum of two arrays, propagating any NaNs.

`fmin` Element-wise minimum of two arrays, ignoring any NaNs.

`argmin` Return the indices of the minimum values.

nanmax, *maximum*, *fmax*

Notes

NaN values are propagated, that is if at least one item is NaN, the corresponding min value will be NaN as well. To ignore NaN values (MATLAB behavior), please use nanmin.

Don't use *amin* for element-wise comparison of 2 arrays; when `a.shape[0]` is 2, `minimum(a[0], a[1])` is faster than `amin(a, axis=0)`.

Examples

```
>>> a = np.arange(4).reshape((2,2))
>>> a
array([[0, 1],
       [2, 3]])
>>> np.amin(a)           # Minimum of the flattened array
0
>>> np.amin(a, axis=0)   # Minima along the first axis
array([0, 1])
>>> np.amin(a, axis=1)   # Minima along the second axis
array([0, 2])
```

```
>>> b = np.arange(5, dtype=float)
>>> b[2] = np.NaN
>>> np.amin(b)
nan
>>> np.nanmin(b)
0.0
```

```
>>> np.min([[-50], [10]], axis=-1, initial=0)
array([-50,   0])
```

Notice that the initial value is used as one of the elements for which the minimum is determined, unlike for the default argument Python's max function, which is only used for empty iterables.

Notice that this isn't the same as Python's `default` argument.

```
>>> np.min([6], initial=5)
5
>>> min([6], default=5)
6
```

`dask.array.`**`minimum`**(*x1*, *x2*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Element-wise minimum of array elements.

Compare two arrays and returns a new array containing the element-wise minima. If one of the elements being compared is a NaN, then that element is returned. If both elements are NaNs then the first is returned. The latter distinction is important for complex NaNs, which are defined as at least one of the real or imaginary parts being a NaN. The net effect is that NaNs are propagated.

Parameters

x1, x2 [array_like] The arrays holding the elements to be compared. They must have the same shape, or shapes that can be broadcast to a single shape.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The minimum of *x1* and *x2*, element-wise. This is a scalar if both *x1* and *x2* are scalars.

See also:

`maximum` Element-wise maximum of two arrays, propagates NaNs.

`fmin` Element-wise minimum of two arrays, ignores NaNs.

`amin` The minimum value of an array along a given axis, propagates NaNs.

`nanmin` The minimum value of an array along a given axis, ignores NaNs.

`fmax`, `amax`, `nanmax`

Notes

The minimum is equivalent to `np.where(x1 <= x2, x1, x2)` when neither x1 nor x2 are NaNs, but it is faster and does proper broadcasting.

Examples

```
>>> np.minimum([2, 3, 4], [1, 5, 2])  # doctest: +SKIP
array([1, 3, 2])
```

```
>>> np.minimum(np.eye(2), [0.5, 2]) # broadcasting  # doctest: +SKIP
array([[ 0.5,  0. ],
       [ 0. ,  1. ]])
```

```
>>> np.minimum([np.nan, 0, np.nan],[0, np.nan, np.nan])  # doctest: +SKIP
array([ NaN,  NaN,  NaN])
>>> np.minimum(-np.Inf, 1)  # doctest: +SKIP
-inf
```

`dask.array.`**`modf`**(*x*[, *out1*, *out2*], / [, *out=(None, None)*], *, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the fractional and integral parts of an array, element-wise.

The fractional and integral parts are negative if the given number is negative.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y1 [ndarray] Fractional part of *x*. This is a scalar if *x* is a scalar.

y2 [ndarray] Integral part of *x*. This is a scalar if *x* is a scalar.

See also:

`divmod` `divmod(x, 1)` is equivalent to `modf` with the return values switched, except it always has a positive remainder.

Notes

For integer input the return values are floats.

Examples

```
>>> np.modf([0, 3.5])  # doctest: +SKIP
(array([ 0. ,  0.5]), array([ 0.,  3.]))
>>> np.modf(-0.5)  # doctest: +SKIP
(-0.5, -0)
```

`dask.array.`**`moment`**(*a*, *order*, *axis=None*, *dtype=None*, *keepdims=False*, *ddof=0*, *split_every=None*, *out=None*)

`dask.array.`**`moveaxis`**(*a*, *source*, *destination*)

Move axes of an array to new positions.

This docstring was copied from numpy.moveaxis.

Some inconsistencies with the Dask version may exist.

Other axes remain in their original order.

New in version 1.11.0.

Parameters

a [np.ndarray] The array whose axes should be reordered.

source [int or sequence of int] Original positions of the axes to move. These must be unique.

destination [int or sequence of int] Destination positions for each of the original axes. These must also be unique.

Returns

result [np.ndarray] Array with moved axes. This array is a view of the input array.

See also:

`transpose` Permute the dimensions of an array.

swapaxes Interchange two axes of an array.

Examples

```
>>> x = np.zeros((3, 4, 5))  # doctest: +SKIP
>>> np.moveaxis(x, 0, -1).shape  # doctest: +SKIP
(4, 5, 3)
>>> np.moveaxis(x, -1, 0).shape  # doctest: +SKIP
(5, 3, 4)
```

These all achieve the same result:

```
>>> np.transpose(x).shape  # doctest: +SKIP
(5, 4, 3)
>>> np.swapaxes(x, 0, -1).shape  # doctest: +SKIP
(5, 4, 3)
>>> np.moveaxis(x, [0, 1], [-1, -2]).shape  # doctest: +SKIP
(5, 4, 3)
>>> np.moveaxis(x, [0, 1, 2], [-1, -2, -3]).shape  # doctest: +SKIP
(5, 4, 3)
```

dask.array.**nanargmax**(*x*, *axis*, ***kwargs*)

dask.array.**nanargmin**(*x*, *axis*, ***kwargs*)

dask.array.**nancumprod**(*a*, *axis=None*, *dtype=None*, *out=None*)

Return the cumulative product of array elements over a given axis treating Not a Numbers (NaNs) as one. The cumulative product does not change when NaNs are encountered and leading NaNs are replaced by ones.

Ones are returned for slices that are all-NaN or empty.

New in version 1.12.0.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative product is computed. By default the input is flattened.

dtype [dtype, optional] Type of the returned array, as well as of the accumulator in which the elements are multiplied. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used instead.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type of the resulting values will be cast if necessary.

Returns

nancumprod [ndarray] A new array holding the result is returned unless *out* is specified, in which case it is returned.

See also:

numpy.cumprod Cumulative product across array propagating NaNs.

isnan Show which elements are NaN.

Examples

```
>>> np.nancumprod(1)
array([1])
>>> np.nancumprod([1])
array([1])
>>> np.nancumprod([1, np.nan])
array([ 1.,  1.])
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nancumprod(a)
array([ 1.,  2.,  6.,  6.])
>>> np.nancumprod(a, axis=0)
array([[ 1.,  2.],
       [ 3.,  2.]])
>>> np.nancumprod(a, axis=1)
array([[ 1.,  2.],
       [ 3.,  3.]])
```

`dask.array.`**`nancumsum`**(*a*, *axis=None*, *dtype=None*, *out=None*)

Return the cumulative sum of array elements over a given axis treating Not a Numbers (NaNs) as zero. The cumulative sum does not change when NaNs are encountered and leading NaNs are replaced by zeros.

Zeros are returned for slices that are all-NaN or empty.

New in version 1.12.0.

Parameters

a [array_like] Input array.

axis [int, optional] Axis along which the cumulative sum is computed. The default (None) is to compute the cumsum over the flattened array.

dtype [dtype, optional] Type of the returned array and of the accumulator in which the elements are summed. If *dtype* is not specified, it defaults to the dtype of *a*, unless *a* has an integer dtype with a precision less than that of the default platform integer. In that case, the default platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output but the type will be cast if necessary. See *doc.ufuncs* (Section "Output arguments") for more details.

Returns

nancumsum [ndarray.] A new array holding the result is returned unless *out* is specified, in which it is returned. The result has the same size as *a*, and the same shape as *a* if *axis* is not None or *a* is a 1-d array.

See also:

`numpy.cumsum` Cumulative sum across array propagating NaNs.

`isnan` Show which elements are NaN.

Examples

```
>>> np.nancumsum(1)
array([1])
>>> np.nancumsum([1])
```

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```
array([1])
>>> np.nancumsum([1, np.nan])
array([ 1.,  1.])
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nancumsum(a)
array([ 1.,  3.,  6.,  6.])
>>> np.nancumsum(a, axis=0)
array([[ 1.,  2.],
       [ 4.,  2.]])
>>> np.nancumsum(a, axis=1)
array([[ 1.,  3.],
       [ 3.,  3.]])
```

`dask.array.nanmax`(*a*, *axis=None*, *out=None*, *keepdims=<no value>*)

Return the maximum of an array or maximum along an axis, ignoring any NaNs. When all-NaN slices are encountered a `RuntimeWarning` is raised and NaN is returned for that slice.

Parameters

a [array_like] Array containing numbers whose maximum is desired. If *a* is not an array, a conversion is attempted.

axis [{int, tuple of int, None}, optional] Axis or axes along which the maximum is computed. The default is to compute the maximum of the flattened array.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

New in version 1.8.0.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

If the value is anything but the default, then *keepdims* will be passed through to the *max* method of sub-classes of *ndarray*. If the sub-classes methods does not implement *keepdims* any exceptions will be raised.

New in version 1.8.0.

Returns

nanmax [ndarray] An array with the same shape as *a*, with the specified axis removed. If *a* is a 0-d array, or if axis is None, an ndarray scalar is returned. The same dtype as *a* is returned.

See also:

nanmin The minimum value of an array along a given axis, ignoring any NaNs.

amax The maximum value of an array along a given axis, propagating any NaNs.

fmax Element-wise maximum of two arrays, ignoring any NaNs.

maximum Element-wise maximum of two arrays, propagating any NaNs.

isnan Shows which elements are Not a Number (NaN).

isfinite Shows which elements are neither NaN nor infinity.

`amin`, *`fmin`*, *`minimum`*

Notes

NumPy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity. Positive infinity is treated as a very large number and negative infinity is treated as a very small (i.e. negative) number.

If the input has a integer type the function is equivalent to np.max.

Examples

```
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nanmax(a)
3.0
>>> np.nanmax(a, axis=0)
array([ 3.,  2.])
>>> np.nanmax(a, axis=1)
array([ 2.,  3.])
```

When positive infinity and negative infinity are present:

```
>>> np.nanmax([1, 2, np.nan, np.NINF])
2.0
>>> np.nanmax([1, 2, np.nan, np.inf])
inf
```

`dask.array.`**`nanmean`**(*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=<no value>*)

Compute the arithmetic mean along the specified axis, ignoring NaNs.

Returns the average of the array elements. The average is taken over the flattened array by default, otherwise over the specified axis. *float64* intermediate and return values are used for integer inputs.

For all-NaN slices, NaN is returned and a *RuntimeWarning* is raised.

New in version 1.8.0.

Parameters

a [array_like] Array containing numbers whose mean is desired. If *a* is not an array, a conversion is attempted.

axis [{int, tuple of int, None}, optional] Axis or axes along which the means are computed. The default is to compute the mean of the flattened array.

dtype [data-type, optional] Type to use in computing the mean. For integer inputs, the default is *float64*; for inexact inputs, it is the same as the input dtype.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

If the value is anything but the default, then *keepdims* will be passed through to the *mean* or *sum* methods of sub-classes of *ndarray*. If the sub-classes methods does not implement *keepdims* any exceptions will be raised.

Returns

m [ndarray, see dtype parameter above] If *out=None*, returns a new array containing the mean values, otherwise a reference to the output array is returned. Nan is returned for slices that contain only NaNs.

See also:

average Weighted average

mean Arithmetic mean taken while not ignoring NaNs

var, *nanvar*

Notes

The arithmetic mean is the sum of the non-NaN elements along the axis divided by the number of non-NaN elements.

Note that for floating-point input, the mean is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32*. Specifying a higher-precision accumulator using the *dtype* keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, np.nan], [3, 4]])
>>> np.nanmean(a)
2.6666666666666665
>>> np.nanmean(a, axis=0)
array([ 2.,  4.])
>>> np.nanmean(a, axis=1)
array([ 1.,  3.5])
```

`dask.array.`**`nanmin`**`(`*a*, *axis=None*, *out=None*, *keepdims=<no value>*`)`

Return minimum of an array or minimum along an axis, ignoring any NaNs. When all-NaN slices are encountered a `RuntimeWarning` is raised and Nan is returned for that slice.

Parameters

a [array_like] Array containing numbers whose minimum is desired. If *a* is not an array, a conversion is attempted.

axis [{int, tuple of int, None}, optional] Axis or axes along which the minimum is computed. The default is to compute the minimum of the flattened array.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`; if provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details.

New in version 1.8.0.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

If the value is anything but the default, then *keepdims* will be passed through to the *min* method of sub-classes of *ndarray*. If the sub-classes methods does not implement *keepdims* any exceptions will be raised.

New in version 1.8.0.

Returns

nanmin [ndarray] An array with the same shape as *a*, with the specified axis removed. If *a* is a 0-d array, or if axis is None, an ndarray scalar is returned. The same dtype as *a* is returned.

See also:

`nanmax` The maximum value of an array along a given axis, ignoring any NaNs.

`amin` The minimum value of an array along a given axis, propagating any NaNs.

`fmin` Element-wise minimum of two arrays, ignoring any NaNs.

`minimum` Element-wise minimum of two arrays, propagating any NaNs.

`isnan` Shows which elements are Not a Number (NaN).

`isfinite` Shows which elements are neither NaN nor infinity.

`amax`, `fmax`, `maximum`

Notes

NumPy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity. Positive infinity is treated as a very large number and negative infinity is treated as a very small (i.e. negative) number.

If the input has a integer type the function is equivalent to np.min.

Examples

```
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nanmin(a)
1.0
>>> np.nanmin(a, axis=0)
array([ 1.,  2.])
>>> np.nanmin(a, axis=1)
array([ 1.,  3.])
```

When positive infinity and negative infinity are present:

```
>>> np.nanmin([1, 2, np.nan, np.inf])
1.0
>>> np.nanmin([1, 2, np.nan, np.NINF])
-inf
```

`dask.array.`**`nanprod`**`(`*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=<no value>*`)`

Return the product of array elements over a given axis treating Not a Numbers (NaNs) as ones.

One is returned for slices that are all-NaN or empty.

New in version 1.10.0.

Parameters

a [array_like] Array containing numbers whose product is desired. If *a* is not an array, a conversion is attempted.

axis [{int, tuple of int, None}, optional] Axis or axes along which the product is computed. The default is to compute the product of the flattened array.

dtype [data-type, optional] The type of the returned array and of the accumulator in which the elements are summed. By default, the dtype of *a* is used. An exception is when *a* has an integer type with less precision than the platform (u)intp. In that case, the default will be either (u)int32 or (u)int64 depending on whether the platform is 32 or 64 bits. For inexact inputs, dtype must be inexact.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`. If provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details. The casting of NaN to integer can yield unexpected results.

keepdims [bool, optional] If True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *arr*.

Returns

nanprod [ndarray] A new array holding the result is returned unless *out* is specified, in which case it is returned.

See also:

`numpy.prod` Product across array propagating NaNs.

`isnan` Show which elements are NaN.

Examples

```
>>> np.nanprod(1)
1
>>> np.nanprod([1])
1
>>> np.nanprod([1, np.nan])
1.0
>>> a = np.array([[1, 2], [3, np.nan]])
>>> np.nanprod(a)
6.0
>>> np.nanprod(a, axis=0)
array([ 3.,  2.])
```

`dask.array.`**`nanstd`**(*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=<no value>*)

Compute the standard deviation along the specified axis, while ignoring NaNs.

Returns the standard deviation, a measure of the spread of a distribution, of the non-NaN array elements. The standard deviation is computed for the flattened array by default, otherwise over the specified axis.

For all-NaN slices or slices with zero degrees of freedom, NaN is returned and a *RuntimeWarning* is raised.

New in version 1.8.0.

Parameters

a [array_like] Calculate the standard deviation of the non-NaN values.

axis [{int, tuple of int, None}, optional] Axis or axes along which the standard deviation is computed. The default is to compute the standard deviation of the flattened array.

dtype [dtype, optional] Type to use in computing the standard deviation. For arrays of integer type the default is float64, for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output but the type (of the calculated values) will be cast if necessary.

ddof [int, optional] Means Delta Degrees of Freedom. The divisor used in calculations is `N - ddof`, where `N` represents the number of non-NaN elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

If this value is anything but the default it is passed through as-is to the relevant functions of the sub-classes. If these functions do not have a *keepdims* kwarg, a RuntimeError will be raised.

Returns

standard_deviation [ndarray, see dtype parameter above.] If *out* is None, return a new array containing the standard deviation, otherwise return a reference to the output array. If ddof is >= the number of non-NaN elements in a slice or the slice contains only NaNs, then the result for that slice is NaN.

See also:

var, *mean*, *std*, *nanvar*, *nanmean*

numpy.doc.ufuncs Section "Output arguments"

Notes

The standard deviation is the square root of the average of the squared deviations from the mean: `std = sqrt(mean(abs(x - x.mean())**2))`.

The average squared deviation is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of the infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables. The standard deviation computed in this function is the square root of the estimated variance, so even with `ddof=1`, it will not be an unbiased estimate of the standard deviation per se.

Note that, for complex numbers, *std* takes the absolute value before squaring, so that the result is always real and nonnegative.

For floating-point input, the *std* is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for float32 (see example below). Specifying a higher-accuracy accumulator using the *dtype* keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, np.nan], [3, 4]])
>>> np.nanstd(a)
1.247219128924647
>>> np.nanstd(a, axis=0)
array([ 1.,  0.])
>>> np.nanstd(a, axis=1)
array([ 0.,  0.5])
```

`dask.array.nansum(a, axis=None, dtype=None, out=None, keepdims=<no value>)`

Return the sum of array elements over a given axis treating Not a Numbers (NaNs) as zero.

In NumPy versions <= 1.9.0 Nan is returned for slices that are all-NaN or empty. In later versions zero is returned.

Parameters

a [array_like] Array containing numbers whose sum is desired. If *a* is not an array, a conversion is attempted.

axis [{int, tuple of int, None}, optional] Axis or axes along which the sum is computed. The default is to compute the sum of the flattened array.

dtype [data-type, optional] The type of the returned array and of the accumulator in which the elements are summed. By default, the dtype of *a* is used. An exception is when *a* has an integer type with less precision than the platform (u)intp. In that case, the default will be either (u)int32 or (u)int64 depending on whether the platform is 32 or 64 bits. For inexact inputs, dtype must be inexact.

New in version 1.8.0.

out [ndarray, optional] Alternate output array in which to place the result. The default is `None`. If provided, it must have the same shape as the expected output, but the type will be cast if necessary. See *doc.ufuncs* for details. The casting of NaN to integer can yield unexpected results.

New in version 1.8.0.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

If the value is anything but the default, then *keepdims* will be passed through to the *mean* or *sum* methods of sub-classes of *ndarray*. If the sub-classes methods does not implement *keepdims* any exceptions will be raised.

New in version 1.8.0.

Returns

nansum [ndarray.] A new array holding the result is returned unless *out* is specified, in which it is returned. The result has the same size as *a*, and the same shape as *a* if *axis* is not None or *a* is a 1-d array.

See also:

`numpy.sum` Sum across array propagating NaNs.

`isnan` Show which elements are NaN.

`isfinite` Show which elements are not NaN or +/-inf.

Notes

If both positive and negative infinity are present, the sum will be Not A Number (NaN).

Examples

```
>>> np.nansum(1)
1
>>> np.nansum([1])
1
>>> np.nansum([1, np.nan])
1.0
>>> a = np.array([[1, 1], [1, np.nan]])
>>> np.nansum(a)
3.0
>>> np.nansum(a, axis=0)
array([ 2.,  1.])
>>> np.nansum([1, np.nan, np.inf])
inf
>>> np.nansum([1, np.nan, np.NINF])
-inf
>>> np.nansum([1, np.nan, np.inf, -np.inf]) # both +/- infinity present
nan
```

`dask.array.`**`nanvar`**(*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=<no value>*)

Compute the variance along the specified axis, while ignoring NaNs.

Returns the variance of the array elements, a measure of the spread of a distribution. The variance is computed for the flattened array by default, otherwise over the specified axis.

For all-NaN slices or slices with zero degrees of freedom, NaN is returned and a *RuntimeWarning* is raised.

New in version 1.8.0.

Parameters

a [array_like] Array containing numbers whose variance is desired. If *a* is not an array, a conversion is attempted.

axis [{int, tuple of int, None}, optional] Axis or axes along which the variance is computed. The default is to compute the variance of the flattened array.

dtype [data-type, optional] Type to use in computing the variance. For arrays of integer type the default is *float32*; for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output, but the type is cast if necessary.

ddof [int, optional] "Delta Degrees of Freedom": the divisor used in the calculation is `N - ddof`, where `N` represents the number of non-NaN elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original *a*.

Returns

variance [ndarray, see dtype parameter above] If *out* is None, return a new array containing the variance, otherwise return a reference to the output array. If ddof is >= the number of non-NaN elements in a slice or the slice contains only NaNs, then the result for that slice is NaN.

See also:

`std` Standard deviation

mean Average

var Variance while not ignoring NaNs

nanstd, *nanmean*

numpy.doc.ufuncs Section "Output arguments"

Notes

The variance is the average of the squared deviations from the mean, i.e., `var = mean(abs(x - x.mean())**2)`.

The mean is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of a hypothetical infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables.

Note that for complex numbers, the absolute value is taken before squaring, so that the result is always real and nonnegative.

For floating-point input, the variance is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32* (see example below). Specifying a higher-accuracy accumulator using the `dtype` keyword can alleviate this issue.

For this function to work on sub-classes of ndarray, they must define *sum* with the kwarg *keepdims*

Examples

```
>>> a = np.array([[1, np.nan], [3, 4]])
>>> np.var(a)
1.5555555555555554
>>> np.nanvar(a, axis=0)
array([ 1.,  0.])
>>> np.nanvar(a, axis=1)
array([ 0.,  0.25])
```

`dask.array.`**`nan_to_num`**`(`**args*, ***kwargs*`)`

Replace NaN with zero and infinity with large finite numbers.

If *x* is inexact, NaN is replaced by zero, and infinity and -infinity replaced by the respectively largest and most negative finite floating point values representable by `x.dtype`.

For complex dtypes, the above is applied to each of the real and imaginary components of *x* separately.

If *x* is not inexact, then no replacements are made.

Parameters

x [scalar or array_like] Input data.

copy [bool, optional] Whether to create a copy of *x* (True) or to replace values in-place (False). The in-place operation only occurs if casting to an array does not require a copy. Default is True.

New in version 1.13.

Returns

out [ndarray] *x*, with the non-finite values replaced. If *copy* is False, this may be *x* itself.

See also:

isinf Shows which elements are positive or negative infinity.

isneginf Shows which elements are negative infinity.

isposinf Shows which elements are positive infinity.

isnan Shows which elements are Not a Number (NaN).

isfinite Shows which elements are finite (not NaN, not infinity)

Notes

NumPy uses the IEEE Standard for Binary Floating-Point for Arithmetic (IEEE 754). This means that Not a Number is not equivalent to infinity.

Examples

```
>>> np.nan_to_num(np.inf)  # doctest: +SKIP
1.7976931348623157e+308
>>> np.nan_to_num(-np.inf)  # doctest: +SKIP
-1.7976931348623157e+308
>>> np.nan_to_num(np.nan)  # doctest: +SKIP
0.0
>>> x = np.array([np.inf, -np.inf, np.nan, -128, 128])  # doctest: +SKIP
>>> np.nan_to_num(x)  # doctest: +SKIP
array([  1.79769313e+308,  -1.79769313e+308,   0.00000000e+000,
        -1.28000000e+002,   1.28000000e+002])
>>> y = np.array([complex(np.inf, np.nan), np.nan, complex(np.nan, np.inf)])  #␣
↪doctest: +SKIP
>>> np.nan_to_num(y)  # doctest: +SKIP
array([  1.79769313e+308 +0.00000000e+000j,
         0.00000000e+000 +0.00000000e+000j,
         0.00000000e+000 +1.79769313e+308j])
```

`dask.array.`**`nextafter`**(*x1*, *x2*, /, *out=None*, *, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the next floating-point value after x1 towards x2, element-wise.

Parameters

x1 [array_like] Values to find the next representable value of.

x2 [array_like] The direction where to look for the next representable value of *x1*.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] The next representable values of *x1* in the direction of *x2*. This is a scalar if both *x1* and *x2* are scalars.

Examples

```
>>> eps = np.finfo(np.float64).eps  # doctest: +SKIP
>>> np.nextafter(1, 2) == eps + 1  # doctest: +SKIP
True
>>> np.nextafter([1, 2], [2, 1]) == [eps + 1, 2 - eps]  # doctest: +SKIP
array([ True,  True])
```

`dask.array.`**`nonzero`**`(`*a*`)`

Return the indices of the elements that are non-zero.

This docstring was copied from numpy.nonzero.

Some inconsistencies with the Dask version may exist.

Returns a tuple of arrays, one for each dimension of *a*, containing the indices of the non-zero elements in that dimension. The values in *a* are always tested and returned in row-major, C-style order. The corresponding non-zero values can be obtained with:

```
a[nonzero(a)]
```

To group the indices by element, rather than dimension, use:

```
transpose(nonzero(a))
```

The result of this is always a 2-D array, with a row for each non-zero element.

Parameters

a [array_like] Input array.

Returns

tuple_of_arrays [tuple] Indices of elements that are non-zero.

See also:

`flatnonzero` Return indices that are non-zero in the flattened version of the input array.

`ndarray.nonzero` Equivalent ndarray method.

`count_nonzero` Counts the number of non-zero elements in the input array.

Examples

```
>>> x = np.array([[3, 0, 0], [0, 4, 0], [5, 6, 0]])  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([[3, 0, 0],
       [0, 4, 0],
       [5, 6, 0]])
>>> np.nonzero(x)  # doctest: +SKIP
(array([0, 1, 2, 2]), array([0, 1, 0, 1]))
```

```
>>> x[np.nonzero(x)]  # doctest: +SKIP
array([3, 4, 5, 6])
>>> np.transpose(np.nonzero(x))  # doctest: +SKIP
array([[0, 0],
       [1, 1],
```

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```
       [2, 0],
       [2, 1])
```

A common use for `nonzero` is to find the indices of an array, where a condition is True. Given an array *a*, the condition *a* > 3 is a boolean array and since False is interpreted as 0, np.nonzero(a > 3) yields the indices of the *a* where the condition is true.

```
>>> a = np.array([[1, 2, 3], [4, 5, 6], [7, 8, 9]])  # doctest: +SKIP
>>> a > 3  # doctest: +SKIP
array([[False, False, False],
       [ True,  True,  True],
       [ True,  True,  True]])
>>> np.nonzero(a > 3)  # doctest: +SKIP
(array([1, 1, 1, 2, 2, 2]), array([0, 1, 2, 0, 1, 2]))
```

Using this result to index *a* is equivalent to using the mask directly:

```
>>> a[np.nonzero(a > 3)]  # doctest: +SKIP
array([4, 5, 6, 7, 8, 9])
>>> a[a > 3]  # prefer this spelling  # doctest: +SKIP
array([4, 5, 6, 7, 8, 9])
```

`nonzero` can also be called as a method of the array.

```
>>> (a > 3).nonzero()  # doctest: +SKIP
(array([1, 1, 1, 2, 2, 2]), array([0, 1, 2, 0, 1, 2]))
```

`dask.array.`**`notnull`**`(`*values*`)`

pandas.notnull for dask arrays

`dask.array.`**`ones`**`(`**args*, ***kwargs*`)`

Blocked variant of ones

Follows the signature of ones exactly except that it also requires a keyword argument chunks=(. . .)

Original signature follows below.

Return a new array of given shape and type, filled with ones.

Parameters

shape [int or sequence of ints] Shape of the new array, e.g., `(2, 3)` or `2`.

dtype [data-type, optional] The desired data-type for the array, e.g., *numpy.int8*. Default is *numpy.float64*.

order [{'C', 'F'}, optional, default: C] Whether to store multi-dimensional data in row-major (C-style) or column-major (Fortran-style) order in memory.

Returns

out [ndarray] Array of ones with the given shape, dtype, and order.

See also:

`ones_like` Return an array of ones with shape and type of input.

`empty` Return a new uninitialized array.

`zeros` Return a new array setting values to zero.

`full` Return a new array of given shape filled with value.

Examples

```
>>> np.ones(5)
array([ 1.,  1.,  1.,  1.,  1.])
```

```
>>> np.ones((5,), dtype=int)
array([1, 1, 1, 1, 1])
```

```
>>> np.ones((2, 1))
array([[ 1.],
       [ 1.]])
```

```
>>> s = (2,2)
>>> np.ones(s)
array([[ 1.,  1.],
       [ 1.,  1.]])
```

`dask.array.`**`ones_like`**(*a*, *dtype=None*, *chunks=None*)

Return an array of ones with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of ones with the same shape and type as *a*.

See also:

zeros_like Return an array of zeros with shape and type of input.

empty_like Return an empty array with shape and type of input.

zeros Return a new array setting values to zero.

ones Return a new array setting values to one.

empty Return a new uninitialized array.

`dask.array.`**`outer`**(*a*, *b*)

Compute the outer product of two vectors.

This docstring was copied from numpy.outer.

Some inconsistencies with the Dask version may exist.

Given two vectors, `a = [a0, a1, ..., aM]` and `b = [b0, b1, ..., bN]`, the outer product [1] is:

```
[[a0*b0  a0*b1 ... a0*bN ]
 [a1*b0    .
 [ ...          .
 [aM*b0            aM*bN ]]
```

Parameters

a [(M,) array_like] First input vector. Input is flattened if not already 1-dimensional.

b [(N,) array_like] Second input vector. Input is flattened if not already 1-dimensional.

out [(M, N) ndarray, optional] A location where the result is stored

New in version 1.9.0.

Returns

out [(M, N) ndarray] `out[i, j] = a[i] * b[j]`

See also:

`inner`

einsum `einsum('i,j->ij', a.ravel(), b.ravel())` is the equivalent.

`ufunc.outer` A generalization to N dimensions and other operations. `np.multiply.outer(a.ravel(), b.ravel())` is the equivalent.

References

[1]

Examples

Make a (*very* coarse) grid for computing a Mandelbrot set:

```
>>> rl = np.outer(np.ones((5,)), np.linspace(-2, 2, 5))  # doctest: +SKIP
>>> rl  # doctest: +SKIP
array([[-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.],
       [-2., -1.,  0.,  1.,  2.]])
>>> im = np.outer(1j*np.linspace(2, -2, 5), np.ones((5,)))  # doctest: +SKIP
>>> im  # doctest: +SKIP
array([[ 0.+2.j,  0.+2.j,  0.+2.j,  0.+2.j,  0.+2.j],
       [ 0.+1.j,  0.+1.j,  0.+1.j,  0.+1.j,  0.+1.j],
       [ 0.+0.j,  0.+0.j,  0.+0.j,  0.+0.j,  0.+0.j],
       [ 0.-1.j,  0.-1.j,  0.-1.j,  0.-1.j,  0.-1.j],
       [ 0.-2.j,  0.-2.j,  0.-2.j,  0.-2.j,  0.-2.j]])
>>> grid = rl + im  # doctest: +SKIP
>>> grid  # doctest: +SKIP
array([[-2.+2.j, -1.+2.j,  0.+2.j,  1.+2.j,  2.+2.j],
       [-2.+1.j, -1.+1.j,  0.+1.j,  1.+1.j,  2.+1.j],
       [-2.+0.j, -1.+0.j,  0.+0.j,  1.+0.j,  2.+0.j],
       [-2.-1.j, -1.-1.j,  0.-1.j,  1.-1.j,  2.-1.j],
       [-2.-2.j, -1.-2.j,  0.-2.j,  1.-2.j,  2.-2.j]])
```

An example using a "vector" of letters:

```
>>> x = np.array(['a', 'b', 'c'], dtype=object)  # doctest: +SKIP
>>> np.outer(x, [1, 2, 3])  # doctest: +SKIP
array([[a, aa, aaa],
       [b, bb, bbb],
       [c, cc, ccc]], dtype=object)
```

`dask.array.`**`pad`**(*array*, *pad_width*, *mode*, ***kwargs*)

Pads an array.

This docstring was copied from numpy.pad.

Some inconsistencies with the Dask version may exist.

Parameters

array [array_like of rank N] Input array

pad_width [{sequence, array_like, int}] Number of values padded to the edges of each axis. ((before_1, after_1), … (before_N, after_N)) unique pad widths for each axis. ((before, after),) yields same before and after pad for each axis. (pad,) or int is a shortcut for before = after = pad width for all axes.

mode [str or function] One of the following string values or a user supplied function.

'constant' Pads with a constant value.

'edge' Pads with the edge values of array.

'linear_ramp' Pads with the linear ramp between end_value and the array edge value.

'maximum' Pads with the maximum value of all or part of the vector along each axis.

'mean' Pads with the mean value of all or part of the vector along each axis.

'median' Pads with the median value of all or part of the vector along each axis.

'minimum' Pads with the minimum value of all or part of the vector along each axis.

'reflect' Pads with the reflection of the vector mirrored on the first and last values of the vector along each axis.

'symmetric' Pads with the reflection of the vector mirrored along the edge of the array.

'wrap' Pads with the wrap of the vector along the axis. The first values are used to pad the end and the end values are used to pad the beginning.

<function> Padding function, see Notes.

stat_length [sequence or int, optional] Used in 'maximum', 'mean', 'median', and 'minimum'. Number of values at edge of each axis used to calculate the statistic value.

((before_1, after_1), … (before_N, after_N)) unique statistic lengths for each axis.

((before, after),) yields same before and after statistic lengths for each axis.

(stat_length,) or int is a shortcut for before = after = statistic length for all axes.

Default is `None`, to use the entire axis.

constant_values [sequence or int, optional] Used in 'constant'. The values to set the padded values for each axis.

((before_1, after_1), … (before_N, after_N)) unique pad constants for each axis.

((before, after),) yields same before and after constants for each axis.

(constant,) or int is a shortcut for before = after = constant for all axes.

Default is 0.

end_values [sequence or int, optional] Used in 'linear_ramp'. The values used for the ending value of the linear_ramp and that will form the edge of the padded array.

((before_1, after_1), … (before_N, after_N)) unique end values for each axis.

((before, after),) yields same before and after end values for each axis.

(constant,) or int is a shortcut for before = after = end value for all axes.

Default is 0.

reflect_type [{'even', 'odd'}, optional] Used in 'reflect', and 'symmetric'. The 'even' style is the default with an unaltered reflection around the edge value. For the 'odd' style, the extended part of the array is created by subtracting the reflected values from two times the edge value.

Returns

pad [ndarray] Padded array of rank equal to *array* with shape increased according to *pad_width*.

Notes

New in version 1.7.0.

For an array with rank greater than 1, some of the padding of later axes is calculated from padding of previous axes. This is easiest to think about with a rank 2 array where the corners of the padded array are calculated by using padded values from the first axis.

The padding function, if used, should return a rank 1 array equal in length to the vector argument with padded values replaced. It has the following signature:

```
padding_func(vector, iaxis_pad_width, iaxis, kwargs)
```

where

vector [ndarray] A rank 1 array already padded with zeros. Padded values are vector[:pad_tuple[0]] and vector[-pad_tuple[1]:].

iaxis_pad_width [tuple] A 2-tuple of ints, iaxis_pad_width[0] represents the number of values padded at the beginning of vector where iaxis_pad_width[1] represents the number of values padded at the end of vector.

iaxis [int] The axis currently being calculated.

kwargs [dict] Any keyword arguments the function requires.

Examples

```
>>> a = [1, 2, 3, 4, 5]  # doctest: +SKIP
>>> np.pad(a, (2,3), 'constant', constant_values=(4, 6))  # doctest: +SKIP
array([4, 4, 1, 2, 3, 4, 5, 6, 6, 6])
```

```
>>> np.pad(a, (2, 3), 'edge')  # doctest: +SKIP
array([1, 1, 1, 2, 3, 4, 5, 5, 5, 5])
```

```
>>> np.pad(a, (2, 3), 'linear_ramp', end_values=(5, -4))  # doctest: +SKIP
array([ 5,  3,  1,  2,  3,  4,  5,  2, -1, -4])
```

```
>>> np.pad(a, (2,), 'maximum')  # doctest: +SKIP
array([5, 5, 1, 2, 3, 4, 5, 5, 5])
```

```
>>> np.pad(a, (2,), 'mean')  # doctest: +SKIP
array([3, 3, 1, 2, 3, 4, 5, 3, 3])
```

```
>>> np.pad(a, (2,), 'median')  # doctest: +SKIP
array([3, 3, 1, 2, 3, 4, 5, 3, 3])
```

```
>>> a = [[1, 2], [3, 4]]  # doctest: +SKIP
>>> np.pad(a, ((3, 2), (2, 3)), 'minimum')  # doctest: +SKIP
array([[1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1],
       [3, 3, 3, 4, 3, 3, 3],
       [1, 1, 1, 2, 1, 1, 1],
       [1, 1, 1, 2, 1, 1, 1]])
```

```
>>> a = [1, 2, 3, 4, 5]  # doctest: +SKIP
>>> np.pad(a, (2, 3), 'reflect')  # doctest: +SKIP
array([3, 2, 1, 2, 3, 4, 5, 4, 3, 2])
```

```
>>> np.pad(a, (2, 3), 'reflect', reflect_type='odd')  # doctest: +SKIP
array([-1,  0,  1,  2,  3,  4,  5,  6,  7,  8])
```

```
>>> np.pad(a, (2, 3), 'symmetric')  # doctest: +SKIP
array([2, 1, 1, 2, 3, 4, 5, 5, 4, 3])
```

```
>>> np.pad(a, (2, 3), 'symmetric', reflect_type='odd')  # doctest: +SKIP
array([0, 1, 1, 2, 3, 4, 5, 5, 6, 7])
```

```
>>> np.pad(a, (2, 3), 'wrap')  # doctest: +SKIP
array([4, 5, 1, 2, 3, 4, 5, 1, 2, 3])
```

```
>>> def pad_with(vector, pad_width, iaxis, kwargs):  # doctest: +SKIP
...     pad_value = kwargs.get('padder', 10)
...     vector[:pad_width[0]] = pad_value
...     vector[-pad_width[1]:] = pad_value
...     return vector
>>> a = np.arange(6)  # doctest: +SKIP
>>> a = a.reshape((2, 3))  # doctest: +SKIP
>>> np.pad(a, 2, pad_with)  # doctest: +SKIP
array([[10, 10, 10, 10, 10, 10, 10],
       [10, 10, 10, 10, 10, 10, 10],
       [10, 10,  0,  1,  2, 10, 10],
       [10, 10,  3,  4,  5, 10, 10],
       [10, 10, 10, 10, 10, 10, 10],
       [10, 10, 10, 10, 10, 10, 10]])
>>> np.pad(a, 2, pad_with, padder=100)  # doctest: +SKIP
array([[100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100],
       [100, 100,   0,   1,   2, 100, 100],
       [100, 100,   3,   4,   5, 100, 100],
       [100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100]])
```

`dask.array.`**`percentile`**(*a, q, interpolation='linear', method='default'*)

Approximate percentile of 1-D array

Parameters

a [Array]

q [array_like of float] Percentile or sequence of percentiles to compute, which must be between 0 and 100 inclusive.

interpolation [{'linear', 'lower', 'higher', 'midpoint', 'nearest'}, optional] The interpolation method to use when the desired percentile lies between two data points `i < j`. Only valid for `method='dask'`.

- 'linear': `i + (j - i) * fraction`, where `fraction`

is the fractional part of the index surrounded by `i` and `j`. * 'lower': `i`. * 'higher': `j`. * 'nearest': `i` or `j`, whichever is nearest. * 'midpoint': `(i + j) / 2`.

method [{'default', 'dask', 'tdigest'}, optional] What method to use. By default will use dask's internal custom algorithm (`'dask'`). If set to `'tdigest'` will use tdigest for floats and ints and fallback to the `'dask'` otherwise.

See also:

`numpy.percentile` Numpy's equivalent Percentile function

`dask.array.`**`piecewise`**(*x*, *condlist*, *funclist*, **args*, ***kw*)

Evaluate a piecewise-defined function.

This docstring was copied from numpy.piecewise.

Some inconsistencies with the Dask version may exist.

Given a set of conditions and corresponding functions, evaluate each function on the input data wherever its condition is true.

Parameters

x [ndarray or scalar] The input domain.

condlist [list of bool arrays or bool scalars] Each boolean array corresponds to a function in *funclist*. Wherever *condlist[i]* is True, *funclist[i](x)* is used as the output value.

Each boolean array in *condlist* selects a piece of *x*, and should therefore be of the same shape as *x*.

The length of *condlist* must correspond to that of *funclist*. If one extra function is given, i.e. if `len(funclist) == len(condlist) + 1`, then that extra function is the default value, used wherever all conditions are false.

funclist [list of callables, f(x,*args,**kw), or scalars] Each function is evaluated over *x* wherever its corresponding condition is True. It should take a 1d array as input and give an 1d array or a scalar value as output. If, instead of a callable, a scalar is provided then a constant function (`lambda x: scalar`) is assumed.

args [tuple, optional] Any further arguments given to *piecewise* are passed to the functions upon execution, i.e., if called `piecewise(..., ..., 1, 'a')`, then each function is called as `f(x, 1, 'a')`.

kw [dict, optional] Keyword arguments used in calling *piecewise* are passed to the functions upon execution, i.e., if called `piecewise(..., ..., alpha=1)`, then each function is called as `f(x, alpha=1)`.

Returns

out [ndarray] The output is the same shape and type as x and is found by calling the functions in *funclist* on the appropriate portions of *x*, as defined by the boolean arrays in *condlist*. Portions not covered by any condition have a default value of 0.

See also:

choose, select, where

Notes

This is similar to choose or select, except that functions are evaluated on elements of *x* that satisfy the corresponding condition from *condlist*.

The result is:

```
      |--
      |funclist[0](x[condlist[0]])
out = |funclist[1](x[condlist[1]])
      |...
      |funclist[n2](x[condlist[n2]])
      |--
```

Examples

Define the sigma function, which is -1 for `x < 0` and +1 for `x >= 0`.

```
>>> x = np.linspace(-2.5, 2.5, 6)  # doctest: +SKIP
>>> np.piecewise(x, [x < 0, x >= 0], [-1, 1])  # doctest: +SKIP
array([-1., -1., -1.,  1.,  1.,  1.])
```

Define the absolute value, which is `-x` for `x <0` and `x` for `x >= 0`.

```
>>> np.piecewise(x, [x < 0, x >= 0], [lambda x: -x, lambda x: x])  # doctest:␣
↪+SKIP
array([ 2.5,  1.5,  0.5,  0.5,  1.5,  2.5])
```

Apply the same function to a scalar value.

```
>>> y = -2  # doctest: +SKIP
>>> np.piecewise(y, [y < 0, y >= 0], [lambda x: -x, lambda x: x])  # doctest:␣
↪+SKIP
array(2)
```

`dask.array.`**`prod`**`(`*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=<no value>*, *initial=<no value>*`)`

Return the product of array elements over a given axis.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] Axis or axes along which a product is performed. The default, axis=None, will calculate the product of all the elements in the input array. If axis is negative it counts from the last to the first axis.

New in version 1.7.0.

If axis is a tuple of ints, a product is performed on all of the axes specified in the tuple instead of a single axis or all the axes as before.

dtype [dtype, optional] The type of the returned array, as well as of the accumulator in which the elements are multiplied. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *prod* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

initial [scalar, optional] The starting value for this product. See *~numpy.ufunc.reduce* for details.

New in version 1.15.0.

Returns

product_along_axis [ndarray, see *dtype* parameter above.] An array shaped as *a* but with the specified axis removed. Returns a reference to *out* if specified.

See also:

`ndarray.prod` equivalent method

`numpy.doc.ufuncs` Section "Output arguments"

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow. That means that, on a 32-bit platform:

```
>>> x = np.array([536870910, 536870910, 536870910, 536870910])
>>> np.prod(x)  # random
16
```

The product of an empty array is the neutral element 1:

```
>>> np.prod([])
1.0
```

Examples

By default, calculate the product of all elements:

```
>>> np.prod([1.,2.])
2.0
```

Even when the input array is two-dimensional:

```
>>> np.prod([[1.,2.],[3.,4.]])
24.0
```

But we can also specify the axis over which to multiply:

```
>>> np.prod([[1.,2.],[3.,4.]], axis=1)
array([  2.,  12.])
```

If the type of *x* is unsigned, then the output type is the unsigned platform integer:

```
>>> x = np.array([1, 2, 3], dtype=np.uint8)
>>> np.prod(x).dtype == np.uint
True
```

If *x* is of a signed integer type, then the output type is the default platform integer:

```
>>> x = np.array([1, 2, 3], dtype=np.int8)
>>> np.prod(x).dtype == int
True
```

You can also start the product with a value other than one:

```
>>> np.prod([1, 2], initial=5)
10
```

`dask.array.`**`ptp`**(*a*, *axis=None*)

Range of values (maximum - minimum) along an axis.

This docstring was copied from numpy.ptp.

Some inconsistencies with the Dask version may exist.

The name of the function comes from the acronym for 'peak to peak'.

Parameters

a [array_like] Input values.

axis [None or int or tuple of ints, optional] Axis along which to find the peaks. By default, flatten the array. *axis* may be negative, in which case it counts from the last to the first axis.

New in version 1.15.0.

If this is a tuple of ints, a reduction is performed on multiple axes, instead of a single axis or all the axes as before.

out [array_like (Not supported in Dask)] Alternative output array in which to place the result. It must have the same shape and buffer length as the expected output, but the type of the output values will be cast if necessary.

keepdims [bool, optional (Not supported in Dask)] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *ptp* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

Returns

ptp [ndarray] A new array holding the result, unless *out* was specified, in which case a reference to *out* is returned.

Examples

```
>>> x = np.arange(4).reshape((2,2))  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([[0, 1],
       [2, 3]])
```

```
>>> np.ptp(x, axis=0)  # doctest: +SKIP
array([2, 2])
```

```
>>> np.ptp(x, axis=1)  # doctest: +SKIP
array([1, 1])
```

`dask.array.`**`rad2deg`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Convert angles from radians to degrees.

Parameters

x [array_like] Angle in radians.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The corresponding angle in degrees. This is a scalar if *x* is a scalar.

See also:

`deg2rad` Convert angles from degrees to radians.

`unwrap` Remove large jumps in angle by wrapping.

Notes

New in version 1.3.0.

rad2deg(x) is `180 * x / pi`.

Examples

```
>>> np.rad2deg(np.pi/2)  # doctest: +SKIP
90.0
```

`dask.array.`**`radians`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Convert angles from degrees to radians.

Parameters

x [array_like] Input array in degrees.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The corresponding radian values. This is a scalar if *x* is a scalar.

See also:

`deg2rad` equivalent function

Examples

Convert a degree array to radians

```
>>> deg = np.arange(12.) * 30.  # doctest: +SKIP
>>> np.radians(deg)  # doctest: +SKIP
array([ 0.        ,  0.52359878,  1.04719755,  1.57079633,  2.0943951 ,
        2.61799388,  3.14159265,  3.66519143,  4.1887902 ,  4.71238898,
        5.23598776,  5.75958653])
```

```
>>> out = np.zeros((deg.shape))  # doctest: +SKIP
>>> ret = np.radians(deg, out)  # doctest: +SKIP
>>> ret is out  # doctest: +SKIP
True
```

dask.array.**ravel**(*array*)

Return a contiguous flattened array.

This docstring was copied from numpy.ravel.

Some inconsistencies with the Dask version may exist.

A 1-D array, containing the elements of the input, is returned. A copy is made only if needed.

As of NumPy 1.10, the returned array will have the same type as the input array. (for example, a masked array will be returned for a masked array input)

Parameters

a [array_like (Not supported in Dask)] Input array. The elements in *a* are read in the order specified by *order*, and packed as a 1-D array.

order [{'C','F', 'A', 'K'}, optional (Not supported in Dask)] The elements of *a* are read using this index order. 'C' means to index the elements in row-major, C-style order, with the last axis index changing fastest, back to the first axis index changing slowest. 'F' means to index the elements in column-major, Fortran-style order, with the first index changing fastest, and the last index changing slowest. Note that the 'C' and 'F' options take no account of the memory layout of the underlying array, and only refer to the order of axis indexing. 'A' means to read the elements in Fortran-like index order if *a* is Fortran *contiguous* in memory, C-like order otherwise. 'K' means to read the elements in the order they occur in memory, except for reversing the data when strides are negative. By default, 'C' index order is used.

Returns

y [array_like] y is an array of the same subtype as *a*, with shape `(a.size,)`. Note that matrices are special cased for backward compatibility, if *a* is a matrix, then y is a 1-D ndarray.

See also:

`ndarray.flat` 1-D iterator over an array.

`ndarray.flatten` 1-D array copy of the elements of an array in row-major order.

`ndarray.reshape` Change the shape of an array without changing its data.

Notes

In row-major, C-style order, in two dimensions, the row index varies the slowest, and the column index the quickest. This can be generalized to multiple dimensions, where row-major order implies that the index along the first axis varies slowest, and the index along the last quickest. The opposite holds for column-major, Fortran-style index ordering.

When a view is desired in as many cases as possible, `arr.reshape(-1)` may be preferable.

Examples

It is equivalent to `reshape(-1, order=order)`.

```
>>> x = np.array([[1, 2, 3], [4, 5, 6]])  # doctest: +SKIP
>>> print(np.ravel(x))  # doctest: +SKIP
[1 2 3 4 5 6]
```

```
>>> print(x.reshape(-1))  # doctest: +SKIP
[1 2 3 4 5 6]
```

```
>>> print(np.ravel(x, order='F'))  # doctest: +SKIP
[1 4 2 5 3 6]
```

When `order` is 'A', it will preserve the array's 'C' or 'F' ordering:

```
>>> print(np.ravel(x.T))  # doctest: +SKIP
[1 4 2 5 3 6]
>>> print(np.ravel(x.T, order='A'))  # doctest: +SKIP
[1 2 3 4 5 6]
```

When `order` is 'K', it will preserve orderings that are neither 'C' nor 'F', but won't reverse axes:

```
>>> a = np.arange(3)[::-1]; a  # doctest: +SKIP
array([2, 1, 0])
>>> a.ravel(order='C')  # doctest: +SKIP
array([2, 1, 0])
>>> a.ravel(order='K')  # doctest: +SKIP
array([2, 1, 0])
```

```
>>> a = np.arange(12).reshape(2,3,2).swapaxes(1,2); a  # doctest: +SKIP
array([[[ 0,  2,  4],
        [ 1,  3,  5]],
       [[ 6,  8, 10],
        [ 7,  9, 11]]])
>>> a.ravel(order='C')  # doctest: +SKIP
array([ 0,  2,  4,  1,  3,  5,  6,  8, 10,  7,  9, 11])
>>> a.ravel(order='K')  # doctest: +SKIP
array([ 0,  1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11])
```

`dask.array.`**`real`**(**args*, ***kwargs*)

Return the real part of the complex argument.

Parameters

val [array_like] Input array.

Returns

out [ndarray or scalar] The real component of the complex argument. If *val* is real, the type of *val* is used for the output. If *val* has complex elements, the returned type is float.

See also:

`real_if_close`, *`imag`*, *`angle`*

Examples

```
>>> a = np.array([1+2j, 3+4j, 5+6j])  # doctest: +SKIP
>>> a.real  # doctest: +SKIP
array([ 1.,  3.,  5.])
>>> a.real = 9  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([ 9.+2.j,  9.+4.j,  9.+6.j])
>>> a.real = np.array([9, 8, 7])  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([ 9.+2.j,  8.+4.j,  7.+6.j])
>>> np.real(1 + 1j)  # doctest: +SKIP
1.0
```

`dask.array.`**`rechunk`**(*x*, *chunks*, *threshold=None*, *block_size_limit=None*)

Convert blocks in dask array x for new chunks.

Parameters

x: dask array Array to be rechunked.

chunks: int, tuple or dict The new block dimensions to create. -1 indicates the full size of the corresponding dimension.

threshold: int The graph growth factor under which we don't bother introducing an intermediate step.

block_size_limit: int The maximum block size (in bytes) we want to produce Defaults to the configuration value `array.chunk-size`

Examples

```
>>> import dask.array as da
>>> x = da.ones((1000, 1000), chunks=(100, 100))
```

Specify uniform chunk sizes with a tuple

```
>>> y = x.rechunk((1000, 10))
```

Or chunk only specific dimensions with a dictionary

```
>>> y = x.rechunk({0: 1000})
```

Use the value `-1` to specify that you want a single chunk along a dimension or the value `"auto"` to specify that dask can freely rechunk a dimension to attain blocks of a uniform block size

```
>>> y = x.rechunk({0: -1, 1: 'auto'}, block_size_limit=1e8)
```

`dask.array.`**`reduction`**(*x*, *chunk*, *aggregate*, *axis=None*, *keepdims=False*, *dtype=None*, *split_every=None*, *combine=None*, *name=None*, *out=None*, *concatenate=True*, *output_size=1*, *meta=None*)

General version of reductions

Parameters

x: Array Data being reduced along one or more axes

chunk: callable(x_chunk, axis, keepdims) First function to be executed when resolving the dask graph. This function is applied in parallel to all original chunks of x. See below for function parameters.

combine: callable(x_chunk, axis, keepdims), optional Function used for intermediate recursive aggregation (see split_every below). If omitted, it defaults to aggregate. If the reduction can be performed in less than 3 steps, it will not be invoked at all.

aggregate: callable(x_chunk, axis, keepdims) Last function to be executed when resolving the dask graph, producing the final output. It is always invoked, even when the reduced Array counts a single chunk along the reduced axes.

axis: int or sequence of ints, optional Axis or axes to aggregate upon. If omitted, aggregate along all axes.

keepdims: boolean, optional Whether the reduction function should preserve the reduced axes, leaving them at size `output_size`, or remove them.

dtype: np.dtype, optional Force output dtype. Defaults to x.dtype if omitted.

split_every: int >= 2 or dict(axis: int), optional Determines the depth of the recursive aggregation. If set to or more than the number of input chunks, the aggregation will be performed in two steps, one `chunk` function per input chunk and a single `aggregate` function at the end. If set to less than that, an intermediate `combine` function will be used, so that any one `combine` or `aggregate` function has no more than `split_every` inputs. The depth of the aggregation graph will be $log_{split_every}(inputchunksalongreducedaxes)$. Setting to a low value can reduce cache size and network transfers, at the cost of more CPU and a larger dask graph.

Omit to let dask heuristically decide a good default. A default can also be set globally with the `split_every` key in `dask.config`.

name: str, optional Prefix of the keys of the intermediate and output nodes. If omitted it defaults to the function names.

out: Array, optional Another dask array whose contents will be replaced. Omit to create a new one. Note that, unlike in numpy, this setting gives no performance benefits whatsoever, but can still be useful if one needs to preserve the references to a previously existing Array.

concatenate: bool, optional If True (the default), the outputs of the `chunk`/`combine` functions are concatenated into a single np.array before being passed to the `combine`/`aggregate` functions. If False, the input of `combine` and `aggregate` will be either a list of the raw outputs of the previous step or a single output, and the function will have to concatenate it itself. It can be useful to set this to False if the chunk and/or combine steps do not produce np.arrays.

output_size: int >= 1, optional Size of the output of the `aggregate` function along the reduced axes. Ignored if keepdims is False.

Returns

dask array

****Function Parameters****

x_chunk: numpy.ndarray Individual input chunk. For `chunk` functions, it is one of the original chunks of x. For `combine` and `aggregate` functions, it's the concatenation of the outputs produced by the previous `chunk` or `combine` functions. If concatenate=False, it's a list of the raw outputs from the previous functions.

axis: tuple Normalized list of axes to reduce upon, e.g. `(0, )` Scalar, negative, and None axes have been normalized away. Note that some numpy reduction functions cannot reduce along multiple axes at once and strictly require an int in input. Such functions have to be wrapped to cope.

keepdims: bool Whether the reduction function should preserve the reduced axes or remove them.

`dask.array.`**`repeat`**(*a*, *repeats*, *axis=None*)

Repeat elements of an array.

This docstring was copied from numpy.repeat.

Some inconsistencies with the Dask version may exist.

Parameters

a [array_like] Input array.

repeats [int or array of ints] The number of repetitions for each element. *repeats* is broadcasted to fit the shape of the given axis.

axis [int, optional] The axis along which to repeat values. By default, use the flattened input array, and return a flat output array.

Returns

repeated_array [ndarray] Output array which has the same shape as *a*, except along the given axis.

See also:

`tile` Tile an array.

Examples

```
>>> np.repeat(3, 4)  # doctest: +SKIP
array([3, 3, 3, 3])
>>> x = np.array([[1,2],[3,4]])  # doctest: +SKIP
>>> np.repeat(x, 2)  # doctest: +SKIP
array([1, 1, 2, 2, 3, 3, 4, 4])
>>> np.repeat(x, 3, axis=1)  # doctest: +SKIP
array([[1, 1, 1, 2, 2, 2],
       [3, 3, 3, 4, 4, 4]])
>>> np.repeat(x, [1, 2], axis=0)  # doctest: +SKIP
array([[1, 2],
       [3, 4],
       [3, 4]])
```

`dask.array.`**`reshape`**`(`*x*, *shape*`)`

Reshape array to new shape

This is a parallelized version of the `np.reshape` function with the following limitations:

1. It assumes that the array is stored in row-major order
2. It only allows for reshapings that collapse or merge dimensions like `(1, 2, 3, 4) -> (1, 6, 4)` or `(64,) -> (4, 4, 4)`

When communication is necessary this algorithm depends on the logic within rechunk. It endeavors to keep chunk sizes roughly the same when possible.

See also:

`dask.array.rechunk`, `numpy.reshape`

`dask.array.`**`result_type`**`(`**arrays_and_dtypes*`)`

This docstring was copied from numpy.result_type.

Some inconsistencies with the Dask version may exist.

Returns the type that results from applying the NumPy type promotion rules to the arguments.

Type promotion in NumPy works similarly to the rules in languages like C++, with some slight differences. When both scalars and arrays are used, the array's type takes precedence and the actual value of the scalar is taken into account.

For example, calculating 3*a, where a is an array of 32-bit floats, intuitively should result in a 32-bit float output. If the 3 is a 32-bit integer, the NumPy rules indicate it can't convert losslessly into a 32-bit float, so a 64-bit float should be the result type. By examining the value of the constant, '3', we see that it fits in an 8-bit integer, which can be cast losslessly into the 32-bit float.

Parameters

arrays_and_dtypes [list of arrays and dtypes] The operands of some operation whose result type is needed.

Returns

out [dtype] The result type.

See also:

`dtype`, `promote_types`, `min_scalar_type`, `can_cast`

Notes

New in version 1.6.0.

The specific algorithm used is as follows.

Categories are determined by first checking which of boolean, integer (int/uint), or floating point (float/complex) the maximum kind of all the arrays and the scalars are.

If there are only scalars or the maximum category of the scalars is higher than the maximum category of the arrays, the data types are combined with `promote_types()` to produce the return value.

Otherwise, *min_scalar_type* is called on each array, and the resulting data types are all combined with `promote_types()` to produce the return value.

The set of int values is not a subset of the uint values for types with the same number of bits, something not reflected in `min_scalar_type()`, but handled as a special case in *result_type*.

Examples

```
>>> np.result_type(3, np.arange(7, dtype='i1'))  # doctest: +SKIP
dtype('int8')
```

```
>>> np.result_type('i4', 'c8')  # doctest: +SKIP
dtype('complex128')
```

```
>>> np.result_type(3.0, -2)  # doctest: +SKIP
dtype('float64')
```

`dask.array.`**`rint`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Round elements of the array to the nearest integer.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Output array is same shape and type as *x*. This is a scalar if *x* is a scalar.

See also:

`ceil`, *`floor`*, *`trunc`*

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])  # doctest: +SKIP
>>> np.rint(a)  # doctest: +SKIP
array([-2., -2., -0.,  0.,  2.,  2.,  2.])
```

`dask.array.roll(array, shift, axis=None)`

Roll array elements along a given axis.

This docstring was copied from numpy.roll.

Some inconsistencies with the Dask version may exist.

Elements that roll beyond the last position are re-introduced at the first.

Parameters

a [array_like (Not supported in Dask)] Input array.

shift [int or tuple of ints] The number of places by which elements are shifted. If a tuple, then *axis* must be a tuple of the same size, and each of the given axes is shifted by the corresponding number. If an int while *axis* is a tuple of ints, then the same value is used for all given axes.

axis [int or tuple of ints, optional] Axis or axes along which elements are shifted. By default, the array is flattened before shifting, after which the original shape is restored.

Returns

res [ndarray] Output array, with the same shape as *a*.

See also:

rollaxis Roll the specified axis backwards, until it lies in a given position.

Notes

New in version 1.12.0.

Supports rolling over multiple dimensions simultaneously.

Examples

```
>>> x = np.arange(10)  # doctest: +SKIP
>>> np.roll(x, 2)  # doctest: +SKIP
array([8, 9, 0, 1, 2, 3, 4, 5, 6, 7])
```

```
>>> x2 = np.reshape(x, (2,5))  # doctest: +SKIP
>>> x2  # doctest: +SKIP
array([[0, 1, 2, 3, 4],
       [5, 6, 7, 8, 9]])
>>> np.roll(x2, 1)  # doctest: +SKIP
array([[9, 0, 1, 2, 3],
       [4, 5, 6, 7, 8]])
>>> np.roll(x2, 1, axis=0)  # doctest: +SKIP
array([[5, 6, 7, 8, 9],
       [0, 1, 2, 3, 4]])
>>> np.roll(x2, 1, axis=1)  # doctest: +SKIP
array([[4, 0, 1, 2, 3],
       [9, 5, 6, 7, 8]])
```

`dask.array.`**`rollaxis`**(*a*, *axis*, *start=0*)

`dask.array.`**`round`**(*a*, *decimals=0*)

Round an array to the given number of decimals.

This docstring was copied from numpy.round.

Some inconsistencies with the Dask version may exist.

See also:

`around` equivalent function; see for details.

`dask.array.`**`sign`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Returns an element-wise indication of the sign of a number.

The *sign* function returns `-1 if x < 0, 0 if x==0, 1 if x > 0`. nan is returned for nan inputs.

For complex inputs, the *sign* function returns `sign(x.real) + 0j if x.real != 0 else sign(x.imag) + 0j`.

complex(nan, 0) is returned for complex nan inputs.

Parameters

x [array_like] Input values.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The sign of *x*. This is a scalar if *x* is a scalar.

Notes

There is more than one definition of sign in common use for complex numbers. The definition used here is equivalent to $x/\sqrt{x * x}$ which is different from a common alternative, $x/|x|$.

Examples

```
>>> np.sign([-5., 4.5])  # doctest: +SKIP
array([-1.,  1.])
>>> np.sign(0)  # doctest: +SKIP
0
>>> np.sign(5-2j)  # doctest: +SKIP
(1+0j)
```

`dask.array.`**`signbit`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Returns element-wise True where signbit is set (less than zero).

Parameters

x [array_like] The input value(s).

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

result [ndarray of bool] Output array, or reference to *out* if that was supplied. This is a scalar if *x* is a scalar.

Examples

```
>>> np.signbit(-1.2)  # doctest: +SKIP
True
>>> np.signbit(np.array([1, -2.3, 2.1]))  # doctest: +SKIP
array([False,  True, False])
```

`dask.array.`**`sin`**`(`*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*]`)`

Trigonometric sine, element-wise.

Parameters

x [array_like] Angle, in radians (2π rad equals 360 degrees).

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [array_like] The sine of each element of x. This is a scalar if *x* is a scalar.

See also:

`arcsin`, *`sinh`*, *`cos`*

Notes

The sine is one of the fundamental functions of trigonometry (the mathematical study of triangles). Consider a circle of radius 1 centered on the origin. A ray comes in from the $+x$ axis, makes an angle at the origin (measured counter-clockwise from that axis), and departs from the origin. The y coordinate of the outgoing ray's intersection with the unit circle is the sine of that angle. It ranges from -1 for $x = 3\pi/2$ to +1 for $\pi/2$. The function has zeroes where the angle is a multiple of π. Sines of angles between π and 2π are negative. The numerous properties of the sine and related functions are included in any standard trigonometry text.

Examples

Print sine of one angle:

```
>>> np.sin(np.pi/2.)  # doctest: +SKIP
1.0
```

Print sines of an array of angles given in degrees:

```
>>> np.sin(np.array((0., 30., 45., 60., 90.)) * np.pi / 180. )  # doctest: +SKIP
array([ 0.        ,  0.5       ,  0.70710678,  0.8660254 ,  1.        ])
```

Plot the sine function:

```
>>> import matplotlib.pylab as plt  # doctest: +SKIP
>>> x = np.linspace(-np.pi, np.pi, 201)  # doctest: +SKIP
>>> plt.plot(x, np.sin(x))  # doctest: +SKIP
>>> plt.xlabel('Angle [rad]')  # doctest: +SKIP
>>> plt.ylabel('sin(x)')  # doctest: +SKIP
>>> plt.axis('tight')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.`**`sinh`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Hyperbolic sine, element-wise.

Equivalent to `1/2 * (np.exp(x) - np.exp(-x))` or `-1j * np.sin(1j*x)`.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The corresponding hyperbolic sine values. This is a scalar if *x* is a scalar.

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

M. Abramowitz and I. A. Stegun, Handbook of Mathematical Functions. New York, NY: Dover, 1972, pg. 83.

Examples

```
>>> np.sinh(0)  # doctest: +SKIP
0.0
>>> np.sinh(np.pi*1j/2)  # doctest: +SKIP
1j
>>> np.sinh(np.pi*1j) # (exact value is 0)  # doctest: +SKIP
1.2246063538223773e-016j
>>> # Discrepancy due to vagaries of floating point arithmetic.
```

```
>>> # Example of providing the optional output parameter
>>> out2 = np.sinh([0.1], out1)  # doctest: +SKIP
>>> out2 is out1  # doctest: +SKIP
True
```

```
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.sinh(np.zeros((3,3)),np.zeros((2,2)))  # doctest: +SKIP
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: operands could not be broadcast together with shapes (3,3) (2,2)
```

`dask.array.`**`sqrt`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the non-negative square-root of an array, element-wise.

Parameters

x [array_like] The values whose square-roots are required.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] An array of the same shape as *x*, containing the positive square-root of each element in *x*. If any element in *x* is complex, a complex array is returned (and the square-roots of negative reals are calculated). If all of the elements in *x* are real, so is *y*, with negative elements returning `nan`. If *out* was provided, *y* is a reference to it. This is a scalar if *x* is a scalar.

See also:

`lib.scimath.sqrt` A version which returns complex numbers when given negative reals.

Notes

sqrt has–consistent with common convention–as its branch cut the real "interval" [*-inf*, 0), and is continuous from above on it. A branch cut is a curve in the complex plane across which a given complex function fails to be continuous.

Examples

```
>>> np.sqrt([1,4,9])  # doctest: +SKIP
array([ 1.,  2.,  3.])
```

```
>>> np.sqrt([4, -1, -3+4J])  # doctest: +SKIP
array([ 2.+0.j,  0.+1.j,  1.+2.j])
```

```
>>> np.sqrt([4, -1, numpy.inf])  # doctest: +SKIP
array([  2.,  NaN,  Inf])
```

`dask.array.`**`square`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Return the element-wise square of the input.

Parameters

x [array_like] Input data.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

out [ndarray or scalar] Element-wise *x***x*, of the same shape and dtype as *x*. This is a scalar if *x* is a scalar.

See also:

`numpy.linalg.matrix_power`, *`sqrt`*, `power`

Examples

```
>>> np.square([-1j, 1])  # doctest: +SKIP
array([-1.-0.j,  1.+0.j])
```

`dask.array.`**`squeeze`**(*a*, *axis=None*)

Remove single-dimensional entries from the shape of an array.

This docstring was copied from numpy.squeeze.

Some inconsistencies with the Dask version may exist.

Parameters

a [array_like] Input data.

axis [None or int or tuple of ints, optional] New in version 1.7.0.

Selects a subset of the single-dimensional entries in the shape. If an axis is selected with shape entry greater than one, an error is raised.

Returns

squeezed [ndarray] The input array, but with all or a subset of the dimensions of length 1 removed. This is always *a* itself or a view into *a*.

Raises

ValueError If *axis* is not *None*, and an axis being squeezed is not of length 1

See also:

expand_dims The inverse operation, adding singleton dimensions

reshape Insert, remove, and combine dimensions, and resize existing ones

Examples

```
>>> x = np.array([[[0], [1], [2]]])  # doctest: +SKIP
>>> x.shape  # doctest: +SKIP
(1, 3, 1)
>>> np.squeeze(x).shape  # doctest: +SKIP
(3,)
>>> np.squeeze(x, axis=0).shape  # doctest: +SKIP
(3, 1)
>>> np.squeeze(x, axis=1).shape  # doctest: +SKIP
Traceback (most recent call last):
...
ValueError: cannot select an axis to squeeze out which has size not equal to one
>>> np.squeeze(x, axis=2).shape  # doctest: +SKIP
(1, 3)
```

dask.array.**stack**(*seq*, *axis=0*)

Stack arrays along a new axis

Given a sequence of dask arrays, form a new dask array by stacking them along a new dimension (axis=0 by default)

See also:

concatenate

Examples

Create slices

```
>>> import dask.array as da
>>> import numpy as np
```

```
>>> data = [from_array(np.ones((4, 4)), chunks=(2, 2))
...          for i in range(3)]
```

```
>>> x = da.stack(data, axis=0)
>>> x.shape
(3, 4, 4)
```

```
>>> da.stack(data, axis=1).shape
(4, 3, 4)
```

```
>>> da.stack(data, axis=-1).shape
(4, 4, 3)
```

Result is a new dask Array

`dask.array.`**`std`**`(`*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=<no value>*`)`

Compute the standard deviation along the specified axis.

Returns the standard deviation, a measure of the spread of a distribution, of the array elements. The standard deviation is computed for the flattened array by default, otherwise over the specified axis.

Parameters

a [array_like] Calculate the standard deviation of these values.

axis [None or int or tuple of ints, optional] Axis or axes along which the standard deviation is computed. The default is to compute the standard deviation of the flattened array.

New in version 1.7.0.

If this is a tuple of ints, a standard deviation is performed over multiple axes, instead of a single axis or all the axes as before.

dtype [dtype, optional] Type to use in computing the standard deviation. For arrays of integer type the default is float64, for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output but the type (of the calculated values) will be cast if necessary.

ddof [int, optional] Means Delta Degrees of Freedom. The divisor used in calculations is `N - ddof`, where `N` represents the number of elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *std* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

Returns

standard_deviation [ndarray, see dtype parameter above.] If *out* is None, return a new array containing the standard deviation, otherwise return a reference to the output array.

See also:

`var`, *`mean`*, *`nanmean`*, *`nanstd`*, *`nanvar`*

`numpy.doc.ufuncs` Section "Output arguments"

Notes

The standard deviation is the square root of the average of the squared deviations from the mean, i.e., `std = sqrt(mean(abs(x - x.mean())**2))`.

The average squared deviation is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of the infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables. The standard deviation computed in this function is the square root of the estimated variance, so even with `ddof=1`, it will not be an unbiased estimate of the standard deviation per se.

Note that, for complex numbers, *std* takes the absolute value before squaring, so that the result is always real and nonnegative.

For floating-point input, the *std* is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for float32 (see example below). Specifying a higher-accuracy accumulator using the *dtype* keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])
>>> np.std(a)
1.1180339887498949
>>> np.std(a, axis=0)
array([ 1.,  1.])
>>> np.std(a, axis=1)
array([ 0.5,  0.5])
```

In single precision, std() can be inaccurate:

```
>>> a = np.zeros((2, 512*512), dtype=np.float32)
>>> a[0, :] = 1.0
>>> a[1, :] = 0.1
>>> np.std(a)
0.45000005
```

Computing the standard deviation in float64 is more accurate:

```
>>> np.std(a, dtype=np.float64)
0.44999999925494177
```

`dask.array.`**`sum`**`(`*a*, *axis=None*, *dtype=None*, *out=None*, *keepdims=<no value>*, *initial=<no value>*`)`

Sum of array elements over a given axis.

Parameters

a [array_like] Elements to sum.

axis [None or int or tuple of ints, optional] Axis or axes along which a sum is performed. The default, axis=None, will sum all of the elements of the input array. If axis is negative it counts from the last to the first axis.

New in version 1.7.0.

If axis is a tuple of ints, a sum is performed on all of the axes specified in the tuple instead of a single axis or all the axes as before.

dtype [dtype, optional] The type of the returned array and of the accumulator in which the elements are summed. The dtype of *a* is used by default unless *a* has an integer dtype of less precision than the default platform integer. In that case, if *a* is signed then the platform integer is used while if *a* is unsigned then an unsigned integer of the same precision as the platform integer is used.

out [ndarray, optional] Alternative output array in which to place the result. It must have the same shape as the expected output, but the type of the output values will be cast if necessary.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *sum* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

initial [scalar, optional] Starting value for the sum. See *~numpy.ufunc.reduce* for details.

New in version 1.15.0.

Returns

sum_along_axis [ndarray] An array with the same shape as *a*, with the specified axis removed. If *a* is a 0-d array, or if *axis* is None, a scalar is returned. If an output array is specified, a reference to *out* is returned.

See also:

`ndarray.sum` Equivalent method.

`cumsum` Cumulative sum of array elements.

`trapz` Integration of array values using the composite trapezoidal rule.

`mean`, `average`

Notes

Arithmetic is modular when using integer types, and no error is raised on overflow.

The sum of an empty array is the neutral element 0:

```
>>> np.sum([])
0.0
```

Examples

```
>>> np.sum([0.5, 1.5])
2.0
>>> np.sum([0.5, 0.7, 0.2, 1.5], dtype=np.int32)
1
>>> np.sum([[0, 1], [0, 5]])
6
>>> np.sum([[0, 1], [0, 5]], axis=0)
array([0, 6])
>>> np.sum([[0, 1], [0, 5]], axis=1)
array([1, 5])
```

If the accumulator is too small, overflow occurs:

```
>>> np.ones(128, dtype=np.int8).sum(dtype=np.int8)
-128
```

You can also start the sum with a value other than zero:

```
>>> np.sum([10], initial=5)
15
```

dask.array.**take**(*a*, *indices*, *axis=0*)

Take elements from an array along an axis.

This docstring was copied from numpy.take.

Some inconsistencies with the Dask version may exist.

When axis is not None, this function does the same thing as "fancy" indexing (indexing arrays using arrays); however, it can be easier to use if you need elements along a given axis. A call such as `np.take(arr, indices, axis=3)` is equivalent to `arr[:,:,:,indices,...]`.

Explained without fancy indexing, this is equivalent to the following use of *ndindex*, which sets each of `ii`, `jj`, and `kk` to a tuple of indices:

```
Ni, Nk = a.shape[:axis], a.shape[axis+1:]
Nj = indices.shape
for ii in ndindex(Ni):
    for jj in ndindex(Nj):
        for kk in ndindex(Nk):
            out[ii + jj + kk] = a[ii + (indices[jj],) + kk]
```

Parameters

a [array_like (Ni…, M, Nk…)] The source array.

indices [array_like (Nj…)] The indices of the values to extract.

New in version 1.8.0.

Also allow scalars for indices.

axis [int, optional] The axis over which to select values. By default, the flattened input array is used.

out [ndarray, optional (Ni…, Nj…, Nk…)] If provided, the result will be placed in this array. It should be of the appropriate shape and dtype.

mode [{'raise', 'wrap', 'clip'}, optional (Not supported in Dask)] Specifies how out-of-bounds indices will behave.

- 'raise' – raise an error (default)
- 'wrap' – wrap around
- 'clip' – clip to the range

'clip' mode means that all indices that are too large are replaced by the index that addresses the last element along that axis. Note that this disables indexing with negative numbers.

Returns

out [ndarray (Ni…, Nj…, Nk…)] The returned array has the same type as *a*.

See also:

compress Take elements using a boolean mask

ndarray.take equivalent method

take_along_axis Take elements by matching the array and the index arrays

Notes

By eliminating the inner loop in the description above, and using *s_* to build simple slice objects, *take* can be expressed in terms of applying fancy indexing to each 1-d slice:

```
Ni, Nk = a.shape[:axis], a.shape[axis+1:]
for ii in ndindex(Ni):
    for kk in ndindex(Nj):
        out[ii + s_[...,] + kk] = a[ii + s_[:,] + kk][indices]
```

For this reason, it is equivalent to (but faster than) the following use of *apply_along_axis*:

```
out = np.apply_along_axis(lambda a_1d: a_1d[indices], axis, a)
```

Examples

```
>>> a = [4, 3, 5, 7, 6, 8]  # doctest: +SKIP
>>> indices = [0, 1, 4]  # doctest: +SKIP
>>> np.take(a, indices)  # doctest: +SKIP
array([4, 3, 6])
```

In this example if *a* is an ndarray, "fancy" indexing can be used.

```
>>> a = np.array(a)  # doctest: +SKIP
>>> a[indices]  # doctest: +SKIP
array([4, 3, 6])
```

If *indices* is not one dimensional, the output also has these dimensions.

```
>>> np.take(a, [[0, 1], [2, 3]])  # doctest: +SKIP
array([[4, 3],
       [5, 7]])
```

`dask.array.tan`(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute tangent element-wise.

Equivalent to `np.sin(x)/np.cos(x)` element-wise.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The corresponding tangent values. This is a scalar if *x* is a scalar.

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

M. Abramowitz and I. A. Stegun, Handbook of Mathematical Functions. New York, NY: Dover, 1972.

Examples

```
>>> from math import pi  # doctest: +SKIP
>>> np.tan(np.array([-pi,pi/2,pi]))  # doctest: +SKIP
array([  1.22460635e-16,   1.63317787e+16,  -1.22460635e-16])
>>>
>>> # Example of providing the optional output parameter illustrating
>>> # that what is returned is a reference to said parameter
>>> out2 = np.cos([0.1], out1)  # doctest: +SKIP
>>> out2 is out1  # doctest: +SKIP
True
>>>
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.cos(np.zeros((3,3)),np.zeros((2,2)))  # doctest: +SKIP
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: operands could not be broadcast together with shapes (3,3) (2,2)
```

`dask.array.`**`tanh`**(*x*, */*, *out=None*, ***, *where=True*, *casting='same_kind'*, *order='K'*, *dtype=None*, *subok=True*[, *signature*, *extobj*])

Compute hyperbolic tangent element-wise.

Equivalent to `np.sinh(x)/np.cosh(x)` or `-1j * np.tan(1j*x)`.

Parameters

x [array_like] Input array.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray] The corresponding hyperbolic tangent values. This is a scalar if *x* is a scalar.

Notes

If *out* is provided, the function writes the result into it, and returns a reference to *out*. (See Examples)

References

[1], [2]

Examples

```
>>> np.tanh((0, np.pi*1j, np.pi*1j/2))  # doctest: +SKIP
array([ 0. +0.00000000e+00j,  0. -1.22460635e-16j,  0. +1.63317787e+16j])
```

```
>>> # Example of providing the optional output parameter illustrating
>>> # that what is returned is a reference to said parameter
>>> out2 = np.tanh([0.1], out1)  # doctest: +SKIP
>>> out2 is out1  # doctest: +SKIP
True
```

```
>>> # Example of ValueError due to provision of shape mis-matched `out`
>>> np.tanh(np.zeros((3,3)),np.zeros((2,2)))  # doctest: +SKIP
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
ValueError: operands could not be broadcast together with shapes (3,3) (2,2)
```

`dask.array.`**`tensordot`**(*lhs*, *rhs*, *axes=2*)

Compute tensor dot product along specified axes for arrays >= 1-D.

This docstring was copied from numpy.tensordot.

Some inconsistencies with the Dask version may exist.

Given two tensors (arrays of dimension greater than or equal to one), *a* and *b*, and an array_like object containing two array_like objects, `(a_axes, b_axes)`, sum the products of *a*'s and *b*'s elements (components) over the axes specified by `a_axes` and `b_axes`. The third argument can be a single non-negative integer_like scalar, `N`; if it is such, then the last `N` dimensions of *a* and the first `N` dimensions of *b* are summed over.

Parameters

a, b [array_like, len(shape) >= 1] Tensors to "dot".

axes [int or (2,) array_like]

- integer_like If an int N, sum over the last N axes of *a* and the first N axes of *b* in order. The sizes of the corresponding axes must match.
- (2,) array_like Or, a list of axes to be summed over, first sequence applying to *a*, second to *b*. Both elements array_like must be of the same length.

See also:

`dot`, *`einsum`*

Notes

Three common use cases are:

- `axes = 0` : tensor product $a \otimes b$
- `axes = 1` : tensor dot product $a \cdot b$
- `axes = 2` : (default) tensor double contraction $a : b$

When *axes* is integer_like, the sequence for evaluation will be: first the -Nth axis in *a* and 0th axis in *b*, and the -1th axis in *a* and Nth axis in *b* last.

When there is more than one axis to sum over - and they are not the last (first) axes of *a* (*b*) - the argument *axes* should consist of two sequences of the same length, with the first axis to sum over given first in both sequences, the second axis second, and so forth.

Examples

A "traditional" example:

```
>>> a = np.arange(60.).reshape(3,4,5)  # doctest: +SKIP
>>> b = np.arange(24.).reshape(4,3,2)  # doctest: +SKIP
>>> c = np.tensordot(a,b, axes=([1,0],[0,1]))  # doctest: +SKIP
>>> c.shape  # doctest: +SKIP
(5, 2)
>>> c  # doctest: +SKIP
array([[ 4400.,  4730.],
       [ 4532.,  4874.],
       [ 4664.,  5018.],
       [ 4796.,  5162.],
       [ 4928.,  5306.]])
>>> # A slower but equivalent way of computing the same...
>>> d = np.zeros((5,2))  # doctest: +SKIP
>>> for i in range(5):  # doctest: +SKIP
...   for j in range(2):
...     for k in range(3):
...       for n in range(4):
...         d[i,j] += a[k,n,i] * b[n,k,j]
>>> c == d  # doctest: +SKIP
array([[ True,  True],
       [ True,  True],
       [ True,  True],
       [ True,  True],
       [ True,  True]])
```

An extended example taking advantage of the overloading of + and *:

```
>>> a = np.array(range(1, 9))  # doctest: +SKIP
>>> a.shape = (2, 2, 2)  # doctest: +SKIP
>>> A = np.array(('a', 'b', 'c', 'd'), dtype=object)  # doctest: +SKIP
>>> A.shape = (2, 2)  # doctest: +SKIP
>>> a; A  # doctest: +SKIP
array([[[1, 2],
        [3, 4]],
       [[5, 6],
        [7, 8]]])
array([[a, b],
       [c, d]], dtype=object)
```

```
>>> np.tensordot(a, A) # third argument default is 2 for double-contraction  #␣
↪doctest: +SKIP
array([abbcccdddd, aaaaabbbbbbcccccccdddddddd], dtype=object)
```

```
>>> np.tensordot(a, A, 1)  # doctest: +SKIP
array([[[acc, bdd],
```

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```
        [aaacccc, bbbdddd]],
       [[aaaaacccccc, bbbbbdddddd],
        [aaaaaaacccccccc, bbbbbbbdddddddd]]], dtype=object)
```

```
>>> np.tensordot(a, A, 0) # tensor product (result too long to incl.)  # doctest:␣
↪+SKIP
array([[[[[a, b],
          [c, d]],
          ...
```

```
>>> np.tensordot(a, A, (0, 1))  # doctest: +SKIP
array([[[abbbbb, cddddd],
        [aabbbbbb, ccdddddd]],
       [[aaabbbbbbb, cccddddddd],
        [aaaabbbbbbbb, ccccdddddddd]]], dtype=object)
```

```
>>> np.tensordot(a, A, (2, 1))  # doctest: +SKIP
array([[[abb, cdd],
        [aaabbbb, cccdddd]],
       [[aaaaabbbbbb, cccccdddddd],
        [aaaaaaabbbbbbbb, cccccccdddddddd]]], dtype=object)
```

```
>>> np.tensordot(a, A, ((0, 1), (0, 1)))  # doctest: +SKIP
array([abbbcccccddddddd, aabbbbccccccdddddddd], dtype=object)
```

```
>>> np.tensordot(a, A, ((2, 1), (1, 0)))  # doctest: +SKIP
array([acccbbdddd, aaaaacccccccbbbbbbdddddddd], dtype=object)
```

`dask.array.`**`tile`**(*A*, *reps*)

Construct an array by repeating A the number of times given by reps.

This docstring was copied from numpy.tile.

Some inconsistencies with the Dask version may exist.

If *reps* has length `d`, the result will have dimension of `max(d, A.ndim)`.

If `A.ndim < d`, *A* is promoted to be d-dimensional by prepending new axes. So a shape (3,) array is promoted to (1, 3) for 2-D replication, or shape (1, 1, 3) for 3-D replication. If this is not the desired behavior, promote *A* to d-dimensions manually before calling this function.

If `A.ndim > d`, *reps* is promoted to *A*.ndim by pre-pending 1's to it. Thus for an *A* of shape (2, 3, 4, 5), a *reps* of (2, 2) is treated as (1, 1, 2, 2).

Note : Although tile may be used for broadcasting, it is strongly recommended to use numpy's broadcasting operations and functions.

Parameters

A [array_like] The input array.

reps [array_like] The number of repetitions of *A* along each axis.

Returns

c [ndarray] The tiled output array.

See also:

repeat Repeat elements of an array.

broadcast_to Broadcast an array to a new shape

Examples

```
>>> a = np.array([0, 1, 2])  # doctest: +SKIP
>>> np.tile(a, 2)  # doctest: +SKIP
array([0, 1, 2, 0, 1, 2])
>>> np.tile(a, (2, 2))  # doctest: +SKIP
array([[0, 1, 2, 0, 1, 2],
       [0, 1, 2, 0, 1, 2]])
>>> np.tile(a, (2, 1, 2))  # doctest: +SKIP
array([[[0, 1, 2, 0, 1, 2]],
       [[0, 1, 2, 0, 1, 2]]])
```

```
>>> b = np.array([[1, 2], [3, 4]])  # doctest: +SKIP
>>> np.tile(b, 2)  # doctest: +SKIP
array([[1, 2, 1, 2],
       [3, 4, 3, 4]])
>>> np.tile(b, (2, 1))  # doctest: +SKIP
array([[1, 2],
       [3, 4],
       [1, 2],
       [3, 4]])
```

```
>>> c = np.array([1,2,3,4])  # doctest: +SKIP
>>> np.tile(c,(4,1))  # doctest: +SKIP
array([[1, 2, 3, 4],
       [1, 2, 3, 4],
       [1, 2, 3, 4],
       [1, 2, 3, 4]])
```

dask.array.**topk**(*a*, *k*, *axis=-1*, *split_every=None*)

Extract the k largest elements from a on the given axis, and return them sorted from largest to smallest. If k is negative, extract the -k smallest elements instead, and return them sorted from smallest to largest.

This performs best when `k` is much smaller than the chunk size. All results will be returned in a single chunk along the given axis.

Parameters

x: Array Data being sorted

k: int

axis: int, optional

split_every: int >=2, optional See `reduce()`. This parameter becomes very important when k is on the same order of magnitude of the chunk size or more, as it prevents getting the whole or a significant portion of the input array in memory all at once, with a negative impact on network transfer too when running on distributed.

Returns

Selection of x with size abs(k) along the given axis.

Examples

```
>>> import dask.array as da
>>> x = np.array([5, 1, 3, 6])
>>> d = da.from_array(x, chunks=2)
>>> d.topk(2).compute()
array([6, 5])
>>> d.topk(-2).compute()
array([1, 3])
```

`dask.array.transpose`(*a*, *axes=None*)

Permute the dimensions of an array.

This docstring was copied from numpy.transpose.

Some inconsistencies with the Dask version may exist.

Parameters

a [array_like] Input array.

axes [list of ints, optional] By default, reverse the dimensions, otherwise permute the axes according to the values given.

Returns

p [ndarray] *a* with its axes permuted. A view is returned whenever possible.

See also:

moveaxis, argsort

Notes

Use *transpose(a, argsort(axes))* to invert the transposition of tensors when using the *axes* keyword argument.

Transposing a 1-D array returns an unchanged view of the original array.

Examples

```
>>> x = np.arange(4).reshape((2,2))  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([[0, 1],
       [2, 3]])
```

```
>>> np.transpose(x)  # doctest: +SKIP
array([[0, 2],
       [1, 3]])
```

```
>>> x = np.ones((1, 2, 3))  # doctest: +SKIP
>>> np.transpose(x, (1, 0, 2)).shape  # doctest: +SKIP
(2, 1, 3)
```

`dask.array.tril`(*m*, *k=0*)

Lower triangle of an array with elements above the *k*-th diagonal zeroed.

Parameters

m [array_like, shape (M, M)] Input array.

k [int, optional] Diagonal above which to zero elements. *k = 0* (the default) is the main diagonal, *k < 0* is below it and *k > 0* is above.

Returns

tril [ndarray, shape (M, M)] Lower triangle of *m*, of same shape and data-type as *m*.

See also:

`triu` upper triangle of an array

`dask.array.triu(m, k=0)`

Upper triangle of an array with elements above the *k*-th diagonal zeroed.

Parameters

m [array_like, shape (M, N)] Input array.

k [int, optional] Diagonal above which to zero elements. *k = 0* (the default) is the main diagonal, *k < 0* is below it and *k > 0* is above.

Returns

triu [ndarray, shape (M, N)] Upper triangle of *m*, of same shape and data-type as *m*.

See also:

`tril` lower triangle of an array

`dask.array.trunc(x, /, out=None, *, where=True, casting='same_kind', order='K', dtype=None, subok=True[, signature, extobj])`

Return the truncated value of the input, element-wise.

The truncated value of the scalar *x* is the nearest integer *i* which is closer to zero than *x* is. In short, the fractional part of the signed number *x* is discarded.

Parameters

x [array_like] Input data.

out [ndarray, None, or tuple of ndarray and None, optional] A location into which the result is stored. If provided, it must have a shape that the inputs broadcast to. If not provided or *None*, a freshly-allocated array is returned. A tuple (possible only as a keyword argument) must have length equal to the number of outputs.

where [array_like, optional] Values of True indicate to calculate the ufunc at that position, values of False indicate to leave the value in the output alone.

****kwargs** For other keyword-only arguments, see the ufunc docs.

Returns

y [ndarray or scalar] The truncated value of each element in *x*. This is a scalar if *x* is a scalar.

See also:

`ceil`, `floor`, `rint`

Notes

New in version 1.3.0.

Examples

```
>>> a = np.array([-1.7, -1.5, -0.2, 0.2, 1.5, 1.7, 2.0])  # doctest: +SKIP
>>> np.trunc(a)  # doctest: +SKIP
array([-1., -1., -0.,  0.,  1.,  1.,  2.])
```

`dask.array.unique`(*ar*, *return_index=False*, *return_inverse=False*, *return_counts=False*)

Find the unique elements of an array.

This docstring was copied from numpy.unique.

Some inconsistencies with the Dask version may exist.

Returns the sorted unique elements of an array. There are three optional outputs in addition to the unique elements:

- the indices of the input array that give the unique values
- the indices of the unique array that reconstruct the input array
- the number of times each unique value comes up in the input array

Parameters

ar [array_like] Input array. Unless *axis* is specified, this will be flattened if it is not already 1-D.

return_index [bool, optional] If True, also return the indices of *ar* (along the specified axis, if provided, or in the flattened array) that result in the unique array.

return_inverse [bool, optional] If True, also return the indices of the unique array (for the specified axis, if provided) that can be used to reconstruct *ar*.

return_counts [bool, optional] If True, also return the number of times each unique item appears in *ar*.

New in version 1.9.0.

axis [int or None, optional (Not supported in Dask)] The axis to operate on. If None, *ar* will be flattened. If an integer, the subarrays indexed by the given axis will be flattened and treated as the elements of a 1-D array with the dimension of the given axis, see the notes for more details. Object arrays or structured arrays that contain objects are not supported if the *axis* kwarg is used. The default is None.

New in version 1.13.0.

Returns

unique [ndarray] The sorted unique values.

unique_indices [ndarray, optional] The indices of the first occurrences of the unique values in the original array. Only provided if *return_index* is True.

unique_inverse [ndarray, optional] The indices to reconstruct the original array from the unique array. Only provided if *return_inverse* is True.

unique_counts [ndarray, optional] The number of times each of the unique values comes up in the original array. Only provided if *return_counts* is True.

New in version 1.9.0.

See also:

numpy.lib.arraysetops Module with a number of other functions for performing set operations on arrays.

Notes

When an axis is specified the subarrays indexed by the axis are sorted. This is done by making the specified axis the first dimension of the array and then flattening the subarrays in C order. The flattened subarrays are then viewed as a structured type with each element given a label, with the effect that we end up with a 1-D array of structured types that can be treated in the same way as any other 1-D array. The result is that the flattened subarrays are sorted in lexicographic order starting with the first element.

Examples

```
>>> np.unique([1, 1, 2, 2, 3, 3])  # doctest: +SKIP
array([1, 2, 3])
>>> a = np.array([[1, 1], [2, 3]])  # doctest: +SKIP
>>> np.unique(a)  # doctest: +SKIP
array([1, 2, 3])
```

Return the unique rows of a 2D array

```
>>> a = np.array([[1, 0, 0], [1, 0, 0], [2, 3, 4]])  # doctest: +SKIP
>>> np.unique(a, axis=0)  # doctest: +SKIP
array([[1, 0, 0], [2, 3, 4]])
```

Return the indices of the original array that give the unique values:

```
>>> a = np.array(['a', 'b', 'b', 'c', 'a'])  # doctest: +SKIP
>>> u, indices = np.unique(a, return_index=True)  # doctest: +SKIP
>>> u  # doctest: +SKIP
array(['a', 'b', 'c'],
       dtype='|S1')
>>> indices  # doctest: +SKIP
array([0, 1, 3])
>>> a[indices]  # doctest: +SKIP
array(['a', 'b', 'c'],
       dtype='|S1')
```

Reconstruct the input array from the unique values:

```
>>> a = np.array([1, 2, 6, 4, 2, 3, 2])  # doctest: +SKIP
>>> u, indices = np.unique(a, return_inverse=True)  # doctest: +SKIP
>>> u  # doctest: +SKIP
array([1, 2, 3, 4, 6])
>>> indices  # doctest: +SKIP
array([0, 1, 4, 3, 1, 2, 1])
>>> u[indices]  # doctest: +SKIP
array([1, 2, 6, 4, 2, 3, 2])
```

dask.array.**unravel_index**(*indices*, *shape*, *order='C'*)

This docstring was copied from numpy.unravel_index.

Some inconsistencies with the Dask version may exist.

Converts a flat index or array of flat indices into a tuple of coordinate arrays.

Parameters

indices [array_like] An integer array whose elements are indices into the flattened version of an array of dimensions `shape`. Before version 1.6.0, this function accepted just one index value.

shape [tuple of ints] The shape of the array to use for unraveling `indices`.

Changed in version 1.16.0: Renamed from `dims` to `shape`.

order [{'C', 'F'}, optional] Determines whether the indices should be viewed as indexing in row-major (C-style) or column-major (Fortran-style) order.

New in version 1.6.0.

Returns

unraveled_coords [tuple of ndarray] Each array in the tuple has the same shape as the `indices` array.

See also:

`ravel_multi_index`

Examples

```
>>> np.unravel_index([22, 41, 37], (7,6))  # doctest: +SKIP
(array([3, 6, 6]), array([4, 5, 1]))
>>> np.unravel_index([31, 41, 13], (7,6), order='F')  # doctest: +SKIP
(array([3, 6, 6]), array([4, 5, 1]))
```

```
>>> np.unravel_index(1621, (6,7,8,9))  # doctest: +SKIP
(3, 1, 4, 1)
```

`dask.array.`**`var`**(*a*, *axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=<no value>*)

Compute the variance along the specified axis.

Returns the variance of the array elements, a measure of the spread of a distribution. The variance is computed for the flattened array by default, otherwise over the specified axis.

Parameters

a [array_like] Array containing numbers whose variance is desired. If *a* is not an array, a conversion is attempted.

axis [None or int or tuple of ints, optional] Axis or axes along which the variance is computed. The default is to compute the variance of the flattened array.

New in version 1.7.0.

If this is a tuple of ints, a variance is performed over multiple axes, instead of a single axis or all the axes as before.

dtype [data-type, optional] Type to use in computing the variance. For arrays of integer type the default is *float32*; for arrays of float types it is the same as the array type.

out [ndarray, optional] Alternate output array in which to place the result. It must have the same shape as the expected output, but the type is cast if necessary.

ddof [int, optional] "Delta Degrees of Freedom": the divisor used in the calculation is `N - ddof`, where `N` represents the number of elements. By default *ddof* is zero.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the input array.

If the default value is passed, then *keepdims* will not be passed through to the *var* method of sub-classes of *ndarray*, however any non-default value will be. If the sub-class' method does not implement *keepdims* any exceptions will be raised.

Returns

variance [ndarray, see dtype parameter above] If `out=None`, returns a new array containing the variance; otherwise, a reference to the output array is returned.

See also:

`std`, `mean`, `nanmean`, `nanstd`, `nanvar`

`numpy.doc.ufuncs` Section "Output arguments"

Notes

The variance is the average of the squared deviations from the mean, i.e., `var = mean(abs(x - x.mean())**2)`.

The mean is normally calculated as `x.sum() / N`, where `N = len(x)`. If, however, *ddof* is specified, the divisor `N - ddof` is used instead. In standard statistical practice, `ddof=1` provides an unbiased estimator of the variance of a hypothetical infinite population. `ddof=0` provides a maximum likelihood estimate of the variance for normally distributed variables.

Note that for complex numbers, the absolute value is taken before squaring, so that the result is always real and nonnegative.

For floating-point input, the variance is computed using the same precision the input has. Depending on the input data, this can cause the results to be inaccurate, especially for *float32* (see example below). Specifying a higher-accuracy accumulator using the `dtype` keyword can alleviate this issue.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])
>>> np.var(a)
1.25
>>> np.var(a, axis=0)
array([ 1.,  1.])
>>> np.var(a, axis=1)
array([ 0.25,  0.25])
```

In single precision, var() can be inaccurate:

```
>>> a = np.zeros((2, 512*512), dtype=np.float32)
>>> a[0, :] = 1.0
>>> a[1, :] = 0.1
>>> np.var(a)
0.20250003
```

Computing the variance in float64 is more accurate:

```
>>> np.var(a, dtype=np.float64)
0.20249999932944759
>>> ((1-0.55)**2 + (0.1-0.55)**2)/2
0.2025
```

`dask.array.vdot(a, b)`

This docstring was copied from numpy.vdot.

Some inconsistencies with the Dask version may exist.

Return the dot product of two vectors.

The vdot(*a*, *b*) function handles complex numbers differently than dot(*a*, *b*). If the first argument is complex the complex conjugate of the first argument is used for the calculation of the dot product.

Note that *vdot* handles multidimensional arrays differently than *dot*: it does *not* perform a matrix product, but flattens input arguments to 1-D vectors first. Consequently, it should only be used for vectors.

Parameters

a [array_like] If *a* is complex the complex conjugate is taken before calculation of the dot product.

b [array_like] Second argument to the dot product.

Returns

output [ndarray] Dot product of *a* and *b*. Can be an int, float, or complex depending on the types of *a* and *b*.

See also:

`dot` Return the dot product without using the complex conjugate of the first argument.

Examples

```
>>> a = np.array([1+2j,3+4j])  # doctest: +SKIP
>>> b = np.array([5+6j,7+8j])  # doctest: +SKIP
>>> np.vdot(a, b)  # doctest: +SKIP
(70-8j)
>>> np.vdot(b, a)  # doctest: +SKIP
(70+8j)
```

Note that higher-dimensional arrays are flattened!

```
>>> a = np.array([[1, 4], [5, 6]])  # doctest: +SKIP
>>> b = np.array([[4, 1], [2, 2]])  # doctest: +SKIP
>>> np.vdot(a, b)  # doctest: +SKIP
30
>>> np.vdot(b, a)  # doctest: +SKIP
30
>>> 1*4 + 4*1 + 5*2 + 6*2  # doctest: +SKIP
30
```

`dask.array.vstack(tup, allow_unknown_chunksizes=False)`

Stack arrays in sequence vertically (row wise).

This docstring was copied from numpy.vstack.

Some inconsistencies with the Dask version may exist.

This is equivalent to concatenation along the first axis after 1-D arrays of shape *(N,)* have been reshaped to *(1,N)*. Rebuilds arrays divided by *vsplit*.

This function makes most sense for arrays with up to 3 dimensions. For instance, for pixel-data with a height (first axis), width (second axis), and r/g/b channels (third axis). The functions *concatenate*, *stack* and *block* provide more general stacking and concatenation operations.

Parameters

tup [sequence of ndarrays] The arrays must have the same shape along all but the first axis. 1-D arrays must have the same length.

Returns

stacked [ndarray] The array formed by stacking the given arrays, will be at least 2-D.

See also:

`stack` Join a sequence of arrays along a new axis.

`hstack` Stack arrays in sequence horizontally (column wise).

`dstack` Stack arrays in sequence depth wise (along third dimension).

`concatenate` Join a sequence of arrays along an existing axis.

`vsplit` Split array into a list of multiple sub-arrays vertically.

`block` Assemble arrays from blocks.

Examples

```
>>> a = np.array([1, 2, 3])  # doctest: +SKIP
>>> b = np.array([2, 3, 4])  # doctest: +SKIP
>>> np.vstack((a,b))  # doctest: +SKIP
array([[1, 2, 3],
       [2, 3, 4]])
```

```
>>> a = np.array([[1], [2], [3]])  # doctest: +SKIP
>>> b = np.array([[2], [3], [4]])  # doctest: +SKIP
>>> np.vstack((a,b))  # doctest: +SKIP
array([[1],
       [2],
       [3],
       [2],
       [3],
       [4]])
```

`dask.array.`**`where`**(*condition*[, *x*, *y*])

This docstring was copied from numpy.where.

Some inconsistencies with the Dask version may exist.

Return elements chosen from *x* or *y* depending on *condition*.

Note: When only *condition* is provided, this function is a shorthand for `np.asarray(condition).nonzero()`. Using *nonzero* directly should be preferred, as it behaves correctly for subclasses. The rest of this documentation covers only the case where all three arguments are provided.

Parameters

condition [array_like, bool] Where True, yield *x*, otherwise yield *y*.

x, y [array_like] Values from which to choose. *x*, *y* and *condition* need to be broadcastable to some shape.

Returns

out [ndarray] An array with elements from *x* where *condition* is True, and elements from *y* elsewhere.

See also:

choose

nonzero The function that is called when x and y are omitted

Notes

If all the arrays are 1-D, *where* is equivalent to:

```
[xv if c else yv
 for c, xv, yv in zip(condition, x, y)]
```

Examples

```
>>> a = np.arange(10)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
>>> np.where(a < 5, a, 10*a)  # doctest: +SKIP
array([ 0,  1,  2,  3,  4, 50, 60, 70, 80, 90])
```

This can be used on multidimensional arrays too:

```
>>> np.where([[True, False], [True, True]],  # doctest: +SKIP
...          [[1, 2], [3, 4]],
...          [[9, 8], [7, 6]])
array([[1, 8],
       [3, 4]])
```

The shapes of x, y, and the condition are broadcast together:

```
>>> x, y = np.ogrid[:3, :4]  # doctest: +SKIP
>>> np.where(x < y, x, 10 + y)  # both x and 10+y are broadcast  # doctest: +SKIP
array([[10,  0,  0,  0],
       [10, 11,  1,  1],
       [10, 11, 12,  2]])
```

```
>>> a = np.array([[0, 1, 2],  # doctest: +SKIP
...               [0, 2, 4],
...               [0, 3, 6]])
>>> np.where(a < 4, a, -1)  # -1 is broadcast  # doctest: +SKIP
array([[ 0,  1,  2],
       [ 0,  2, -1],
       [ 0,  3, -1]])
```

dask.array.**zeros**(**args*, ***kwargs*)
Blocked variant of zeros

Follows the signature of zeros exactly except that it also requires a keyword argument chunks=(. . .)

Original signature follows below. zeros(shape, dtype=float, order='C')

Return a new array of given shape and type, filled with zeros.

Parameters

shape [int or tuple of ints] Shape of the new array, e.g., `(2, 3)` or `2`.

dtype [data-type, optional] The desired data-type for the array, e.g., *numpy.int8*. Default is *numpy.float64*.

order [{'C', 'F'}, optional, default: 'C'] Whether to store multi-dimensional data in row-major (C-style) or column-major (Fortran-style) order in memory.

Returns

out [ndarray] Array of zeros with the given shape, dtype, and order.

See also:

zeros_like Return an array of zeros with shape and type of input.

empty Return a new uninitialized array.

ones Return a new array setting values to one.

full Return a new array of given shape filled with value.

Examples

```
>>> np.zeros(5)
array([ 0.,  0.,  0.,  0.,  0.])
```

```
>>> np.zeros((5,), dtype=int)
array([0, 0, 0, 0, 0])
```

```
>>> np.zeros((2, 1))
array([[ 0.],
       [ 0.]])
```

```
>>> s = (2,2)
>>> np.zeros(s)
array([[ 0.,  0.],
       [ 0.,  0.]])
```

```
>>> np.zeros((2,), dtype=[('x', 'i4'), ('y', 'i4')]) # custom dtype
array([(0, 0), (0, 0)],
      dtype=[('x', '<i4'), ('y', '<i4')])
```

dask.array.**zeros_like**(*a*, *dtype=None*, *chunks=None*)
Return an array of zeros with the same shape and type as a given array.

Parameters

a [array_like] The shape and data-type of *a* define these same attributes of the returned array.

dtype [data-type, optional] Overrides the data type of the result.

chunks [sequence of ints] The number of samples on each block. Note that the last block will have fewer samples if `len(array) % chunks != 0`.

Returns

out [ndarray] Array of zeros with the same shape and type as *a*.

See also:

ones_like Return an array of ones with shape and type of input.

empty_like Return an empty array with shape and type of input.

zeros Return a new array setting values to zero.

ones Return a new array setting values to one.

empty Return a new uninitialized array.

`dask.array.linalg.`**`cholesky`**`(`*a*, *lower=False*`)`

Returns the Cholesky decomposition, $A = LL^*$ or $A = U^*U$ of a Hermitian positive-definite matrix A.

Parameters

a [(M, M) array_like] Matrix to be decomposed

lower [bool, optional] Whether to compute the upper or lower triangular Cholesky factorization. Default is upper-triangular.

Returns

c [(M, M) Array] Upper- or lower-triangular Cholesky factor of *a*.

`dask.array.linalg.`**`inv`**`(`*a*`)`

Compute the inverse of a matrix with LU decomposition and forward / backward substitutions.

Parameters

a [array_like] Square matrix to be inverted.

Returns

ainv [Array] Inverse of the matrix *a*.

`dask.array.linalg.`**`lstsq`**`(`*a*, *b*`)`

Return the least-squares solution to a linear matrix equation using QR decomposition.

Solves the equation *a x* = *b* by computing a vector *x* that minimizes the Euclidean 2-norm || *b* - *a x* ||^2. The equation may be under-, well-, or over- determined (i.e., the number of linearly independent rows of *a* can be less than, equal to, or greater than its number of linearly independent columns). If *a* is square and of full rank, then *x* (but for round-off error) is the "exact" solution of the equation.

Parameters

a [(M, N) array_like] "Coefficient" matrix.

b [(M,) array_like] Ordinate or "dependent variable" values.

Returns

x [(N,) Array] Least-squares solution. If *b* is two-dimensional, the solutions are in the *K* columns of *x*.

residuals [(1,) Array] Sums of residuals; squared Euclidean 2-norm for each column in `b - a*x`.

rank [Array] Rank of matrix *a*.

s [(min(M, N),) Array] Singular values of *a*.

`dask.array.linalg.lu(a)`

Compute the lu decomposition of a matrix.

Returns

p: Array, permutation matrix

l: Array, lower triangular matrix with unit diagonal.

u: Array, upper triangular matrix

Examples

```
>>> p, l, u = da.linalg.lu(x)  # doctest: +SKIP
```

`dask.array.linalg.norm(x, ord=None, axis=None, keepdims=False)`

Matrix or vector norm.

This docstring was copied from numpy.linalg.norm.

Some inconsistencies with the Dask version may exist.

This function is able to return one of eight different matrix norms, or one of an infinite number of vector norms (described below), depending on the value of the `ord` parameter.

Parameters

x [array_like] Input array. If *axis* is None, *x* must be 1-D or 2-D.

ord [{non-zero int, inf, -inf, 'fro', 'nuc'}, optional] Order of the norm (see table under `Notes`). inf means numpy's *inf* object.

axis [{int, 2-tuple of ints, None}, optional] If *axis* is an integer, it specifies the axis of *x* along which to compute the vector norms. If *axis* is a 2-tuple, it specifies the axes that hold 2-D matrices, and the matrix norms of these matrices are computed. If *axis* is None then either a vector norm (when *x* is 1-D) or a matrix norm (when *x* is 2-D) is returned.

New in version 1.8.0.

keepdims [bool, optional] If this is set to True, the axes which are normed over are left in the result as dimensions with size one. With this option the result will broadcast correctly against the original *x*.

New in version 1.10.0.

Returns

n [float or ndarray] Norm of the matrix or vector(s).

Notes

For values of `ord <= 0`, the result is, strictly speaking, not a mathematical 'norm', but it may still be useful for various numerical purposes.

The following norms can be calculated:

ord	norm for matrices	norm for vectors
None	Frobenius norm	2-norm
'fro'	Frobenius norm	–
'nuc'	nuclear norm	–
inf	max(sum(abs(x), axis=1))	max(abs(x))
-inf	min(sum(abs(x), axis=1))	min(abs(x))
0	–	sum(x != 0)
1	max(sum(abs(x), axis=0))	as below
-1	min(sum(abs(x), axis=0))	as below
2	2-norm (largest sing. value)	as below
-2	smallest singular value	as below
other	–	sum(abs(x)**ord)**(1./ord)

The Frobenius norm is given by [1]:

$$||A||_F = [\sum_{i,j} abs(a_{i,j})^2]^{1/2}$$

The nuclear norm is the sum of the singular values.

References

[1]

Examples

```
>>> from numpy import linalg as LA  # doctest: +SKIP
>>> a = np.arange(9) - 4  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([-4, -3, -2, -1,  0,  1,  2,  3,  4])
>>> b = a.reshape((3, 3))  # doctest: +SKIP
>>> b  # doctest: +SKIP
array([[-4, -3, -2],
       [-1,  0,  1],
       [ 2,  3,  4]])
```

```
>>> LA.norm(a)  # doctest: +SKIP
7.745966692414834
>>> LA.norm(b)  # doctest: +SKIP
7.745966692414834
>>> LA.norm(b, 'fro')  # doctest: +SKIP
7.745966692414834
>>> LA.norm(a, np.inf)  # doctest: +SKIP
4.0
>>> LA.norm(b, np.inf)  # doctest: +SKIP
9.0
>>> LA.norm(a, -np.inf)  # doctest: +SKIP
0.0
>>> LA.norm(b, -np.inf)  # doctest: +SKIP
2.0
```

```
>>> LA.norm(a, 1)  # doctest: +SKIP
20.0
>>> LA.norm(b, 1)  # doctest: +SKIP
```

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```
7.0
>>> LA.norm(a, -1)  # doctest: +SKIP
-4.6566128774142013e-010
>>> LA.norm(b, -1)  # doctest: +SKIP
6.0
>>> LA.norm(a, 2)  # doctest: +SKIP
7.745966692414834
>>> LA.norm(b, 2)  # doctest: +SKIP
7.3484692283495345
```

```
>>> LA.norm(a, -2)  # doctest: +SKIP
nan
>>> LA.norm(b, -2)  # doctest: +SKIP
1.8570331885190563e-016
>>> LA.norm(a, 3)  # doctest: +SKIP
5.8480354764257312
>>> LA.norm(a, -3)  # doctest: +SKIP
nan
```

Using the *axis* argument to compute vector norms:

```
>>> c = np.array([[ 1, 2, 3],  # doctest: +SKIP
...               [-1, 1, 4]])
>>> LA.norm(c, axis=0)  # doctest: +SKIP
array([ 1.41421356,  2.23606798,  5.        ])
>>> LA.norm(c, axis=1)  # doctest: +SKIP
array([ 3.74165739,  4.24264069])
>>> LA.norm(c, ord=1, axis=1)  # doctest: +SKIP
array([ 6.,  6.])
```

Using the *axis* argument to compute matrix norms:

```
>>> m = np.arange(8).reshape(2,2,2)  # doctest: +SKIP
>>> LA.norm(m, axis=(1,2))  # doctest: +SKIP
array([  3.74165739,  11.22497216])
>>> LA.norm(m[0, :, :]), LA.norm(m[1, :, :])  # doctest: +SKIP
(3.7416573867739413, 11.224972160321824)
```

`dask.array.linalg.`**`qr`**`(`*a*`)`

Compute the qr factorization of a matrix.

Returns

q: Array, orthonormal

r: Array, upper-triangular

See also:

`np.linalg.qr` Equivalent NumPy Operation

`dask.array.linalg.tsqr` Implementation for tall-and-skinny arrays

`dask.array.linalg.sfqr` Implementation for short-and-fat arrays

Examples

```
>>> q, r = da.linalg.qr(x)  # doctest: +SKIP
```

`dask.array.linalg.`**`solve`**`(`*a*, *b*, *sym_pos=False*`)`

Solve the equation `a x = b` for `x`. By default, use LU decomposition and forward / backward substitutions. When `sym_pos` is `True`, use Cholesky decomposition.

Parameters

a [(M, M) array_like] A square matrix.

b [(M,) or (M, N) array_like] Right-hand side matrix in `a x = b`.

sym_pos [bool] Assume a is symmetric and positive definite. If `True`, use Cholesky decomposition.

Returns

x [(M,) or (M, N) Array] Solution to the system `a x = b`. Shape of the return matches the shape of *b*.

`dask.array.linalg.`**`solve_triangular`**`(`*a*, *b*, *lower=False*`)`

Solve the equation *a x = b* for *x*, assuming a is a triangular matrix.

Parameters

a [(M, M) array_like] A triangular matrix

b [(M,) or (M, N) array_like] Right-hand side matrix in *a x = b*

lower [bool, optional] Use only data contained in the lower triangle of *a*. Default is to use upper triangle.

Returns

x [(M,) or (M, N) array] Solution to the system *a x = b*. Shape of return matches *b*.

`dask.array.linalg.`**`svd`**`(`*a*`)`

Compute the singular value decomposition of a matrix.

Returns

u: Array, unitary / orthogonal

s: Array, singular values in decreasing order (largest first)

v: Array, unitary / orthogonal

See also:

`np.linalg.svd` Equivalent NumPy Operation

`dask.array.linalg.tsqr` Implementation for tall-and-skinny arrays

Examples

```
>>> u, s, v = da.linalg.svd(x)  # doctest: +SKIP
```

`dask.array.linalg.`**`svd_compressed`**`(`*a*, *k*, *n_power_iter=0*, *seed=None*, *compute=False*`)`

Randomly compressed rank-k thin Singular Value Decomposition.

This computes the approximate singular value decomposition of a large array. This algorithm is generally faster than the normal algorithm but does not provide exact results. One can balance between performance and accuracy with input parameters (see below).

Parameters

a: Array Input array

k: int Rank of the desired thin SVD decomposition.

n_power_iter: int Number of power iterations, useful when the singular values decay slowly. Error decreases exponentially as n_power_iter increases. In practice, set n_power_iter <= 4.

compute [bool] Whether or not to compute data at each use. Recomputing the input while performing several passes reduces memory pressure, but means that we have to compute the input multiple times. This is a good choice if the data is larger than memory and cheap to recreate.

Returns

u: Array, unitary / orthogonal

s: Array, singular values in decreasing order (largest first)

v: Array, unitary / orthogonal

References

N. Halko, P. G. Martinsson, and J. A. Tropp. Finding structure with randomness: Probabilistic algorithms for constructing approximate matrix decompositions. SIAM Rev., Survey and Review section, Vol. 53, num. 2, pp. 217-288, June 2011 https://arxiv.org/abs/0909.4061

Examples

```
>>> u, s, vt = svd_compressed(x, 20)  # doctest: +SKIP
```

`dask.array.linalg.`**`sfqr`**(*data*, *name=None*)

Direct Short-and-Fat QR

Currently, this is a quick hack for non-tall-and-skinny matrices which are one chunk tall and (unless they are one chunk wide) have chunks that are wider than they are tall

Q [R_1 R_2 . . .] = [A_1 A_2 . . .]

it computes the factorization Q R_1 = A_1, then computes the other R_k's in parallel.

Parameters

data: Array

See also:

`dask.array.linalg.qr`, *`dask.array.linalg.tsqr`*

`dask.array.linalg.`**`tsqr`**(*data*, *compute_svd=False*, *_max_vchunk_size=None*)

Direct Tall-and-Skinny QR algorithm

As presented in:

A. Benson, D. Gleich, and J. Demmel. Direct QR factorizations for tall-and-skinny matrices in MapReduce architectures. IEEE International Conference on Big Data, 2013. https://arxiv.org/abs/1301.1071

This algorithm is used to compute both the QR decomposition and the Singular Value Decomposition. It requires that the input array have a single column of blocks, each of which fit in memory.

Parameters

data: Array

compute_svd: bool Whether to compute the SVD rather than the QR decomposition

_max_vchunk_size: Integer Used internally in recursion to set the maximum row dimension of chunks in subsequent recursive calls.

See also:

`dask.array.linalg.qr`, *`dask.array.linalg.svd`*, *`dask.array.linalg.sfqr`*

Notes

With `k` blocks of size `(m, n)`, this algorithm has memory use that scales as `k * n * n`.

The implementation here is the recursive variant due to the ultimate need for one "single core" QR decomposition. In the non-recursive version of the algorithm, given `k` blocks, after `k m * n` QR decompositions, there will be a "single core" QR decomposition that will have to work with a `(k * n, n)` matrix.

Here, recursion is applied as necessary to ensure that `k * n` is not larger than `m` (if `m / n >= 2`). In particular, this is done to ensure that single core computations do not have to work on blocks larger than `(m, n)`.

Where blocks are irregular, the above logic is applied with the "height" of the "tallest" block used in place of `m`.

Consider use of the `rechunk` method to control this behavior. Taller blocks will reduce overall memory use (assuming that many of them still fit in memory at once).

`dask.array.ma.`**`average`**`(`*a*, *axis=None*, *weights=None*, *returned=False*`)`

Return the weighted average of array over the given axis.

This docstring was copied from numpy.ma.average.

Some inconsistencies with the Dask version may exist.

Parameters

a [array_like] Data to be averaged. Masked entries are not taken into account in the computation.

axis [int, optional] Axis along which to average *a*. If *None*, averaging is done over the flattened array.

weights [array_like, optional] The importance that each element has in the computation of the average. The weights array can either be 1-D (in which case its length must be the size of *a* along the given axis) or of the same shape as *a*. If `weights=None`, then all data in *a* are assumed to have a weight equal to one. If *weights* is complex, the imaginary parts are ignored.

returned [bool, optional] Flag indicating whether a tuple `(result, sum of weights)` should be returned as output (True), or just the result (False). Default is False.

Returns

average, [sum_of_weights] [(tuple of) scalar or MaskedArray] The average along the specified axis. When returned is *True*, return a tuple with the average as the first element and the sum of the weights as the second element. The return type is *np.float64* if *a* is of integer type and floats smaller than *float64*, or the input data-type, otherwise. If returned, *sum_of_weights* is always *float64*.

Examples

```
>>> a = np.ma.array([1., 2., 3., 4.], mask=[False, False, True, True])  #␣
↪doctest: +SKIP
>>> np.ma.average(a, weights=[3, 1, 0, 0])  # doctest: +SKIP
1.25
```

```
>>> x = np.ma.arange(6.).reshape(3, 2)  # doctest: +SKIP
>>> print(x)  # doctest: +SKIP
[[ 0.  1.]
 [ 2.  3.]
 [ 4.  5.]]
>>> avg, sumweights = np.ma.average(x, axis=0, weights=[1, 2, 3],  # doctest:␣
↪+SKIP
...                                 returned=True)
>>> print(avg)  # doctest: +SKIP
[2.66666666667 3.66666666667]
```

dask.array.ma.**filled**(*a*, *fill_value=None*)

Return input as an array with masked data replaced by a fill value.

This docstring was copied from numpy.ma.filled.

Some inconsistencies with the Dask version may exist.

If *a* is not a *MaskedArray*, *a* itself is returned. If *a* is a *MaskedArray* and *fill_value* is None, *fill_value* is set to `a.fill_value`.

Parameters

a [MaskedArray or array_like] An input object.

fill_value [scalar, optional] Filling value. Default is None.

Returns

a [ndarray] The filled array.

See also:

`compressed`

Examples

```
>>> x = np.ma.array(np.arange(9).reshape(3, 3), mask=[[1, 0, 0],  # doctest: +SKIP
...                                                    [1, 0, 0],
...                                                    [0, 0, 0]])
>>> x.filled()  # doctest: +SKIP
array([[999999,      1,      2],
       [999999,      4,      5],
       [     6,      7,      8]])
```

`dask.array.ma.`**`fix_invalid`**`(`*a*, *fill_value=None*`)`

Return input with invalid data masked and replaced by a fill value.

This docstring was copied from numpy.ma.fix_invalid.

Some inconsistencies with the Dask version may exist.

Invalid data means values of *nan*, *inf*, etc.

Parameters

a [array_like] Input array, a (subclass of) ndarray.

mask [sequence, optional (Not supported in Dask)] Mask. Must be convertible to an array of booleans with the same shape as *data*. True indicates a masked (i.e. invalid) data.

copy [bool, optional (Not supported in Dask)] Whether to use a copy of *a* (True) or to fix *a* in place (False). Default is True.

fill_value [scalar, optional] Value used for fixing invalid data. Default is None, in which case the `a.fill_value` is used.

Returns

b [MaskedArray] The input array with invalid entries fixed.

Notes

A copy is performed by default.

Examples

```
>>> x = np.ma.array([1., -1, np.nan, np.inf], mask=[1] + [0]*3)  # doctest: +SKIP
>>> x  # doctest: +SKIP
masked_array(data = [-- -1.0 nan inf],
             mask = [ True False False False],
       fill_value = 1e+20)
>>> np.ma.fix_invalid(x)  # doctest: +SKIP
masked_array(data = [-- -1.0 -- --],
             mask = [ True False  True  True],
       fill_value = 1e+20)
```

```
>>> fixed = np.ma.fix_invalid(x)  # doctest: +SKIP
>>> fixed.data  # doctest: +SKIP
array([  1.00000000e+00,  -1.00000000e+00,   1.00000000e+20,
         1.00000000e+20])
>>> x.data  # doctest: +SKIP
array([  1.,  -1.,  NaN,  Inf])
```

`dask.array.ma.`**`getdata`**`(`*a*`)`

Return the data of a masked array as an ndarray.

This docstring was copied from numpy.ma.getdata.

Some inconsistencies with the Dask version may exist.

Return the data of *a* (if any) as an ndarray if *a* is a `MaskedArray`, else return *a* as a ndarray or subclass (depending on *subok*) if not.

Parameters

a [array_like] Input `MaskedArray`, alternatively a ndarray or a subclass thereof.

subok [bool (Not supported in Dask)] Whether to force the output to be a *pure* ndarray (False) or to return a subclass of ndarray if appropriate (True, default).

See also:

`getmask` Return the mask of a masked array, or nomask.

`getmaskarray` Return the mask of a masked array, or full array of False.

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> a = ma.masked_equal([[1,2],[3,4]], 2)  # doctest: +SKIP
>>> a  # doctest: +SKIP
masked_array(data =
 [[1 --]
 [3 4]],
      mask =
 [[False  True]
 [False False]],
      fill_value=999999)
>>> ma.getdata(a)  # doctest: +SKIP
array([[1, 2],
       [3, 4]])
```

Equivalently use the `MaskedArray` *data* attribute.

```
>>> a.data  # doctest: +SKIP
array([[1, 2],
       [3, 4]])
```

`dask.array.ma.`**`getmaskarray`**`(a)`

Return the mask of a masked array, or full boolean array of False.

This docstring was copied from numpy.ma.getmaskarray.

Some inconsistencies with the Dask version may exist.

Return the mask of *arr* as an ndarray if *arr* is a *MaskedArray* and the mask is not *nomask*, else return a full boolean array of False of the same shape as *arr*.

Parameters

arr [array_like (Not supported in Dask)] Input *MaskedArray* for which the mask is required.

See also:

`getmask` Return the mask of a masked array, or nomask.

`getdata` Return the data of a masked array as an ndarray.

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> a = ma.masked_equal([[1,2],[3,4]], 2)  # doctest: +SKIP
>>> a  # doctest: +SKIP
```

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```
masked_array(data =
 [[1 --]
 [3 4]],
      mask =
 [[False  True]
 [False False]],
      fill_value=999999)
>>> ma.getmaskarray(a)  # doctest: +SKIP
array([[False,  True],
       [False, False]])
```

Result when mask == `nomask`

```
>>> b = ma.masked_array([[1,2],[3,4]])  # doctest: +SKIP
>>> b  # doctest: +SKIP
masked_array(data =
 [[1 2]
 [3 4]],
      mask =
 False,
      fill_value=999999)
>>> >ma.getmaskarray(b)  # doctest: +SKIP
array([[False, False],
       [False, False]])
```

`dask.array.ma.`**`masked_array`**(*data*, *mask=False*, *fill_value=None*, ***kwargs*)

An array class with possibly masked values.

This docstring was copied from numpy.ma.masked_array.

Some inconsistencies with the Dask version may exist.

Masked values of True exclude the corresponding element from any computation.

Construction:

```
x = MaskedArray(data, mask=nomask, dtype=None, copy=False, subok=True,
                ndmin=0, fill_value=None, keep_mask=True, hard_mask=None,
                shrink=True, order=None)
```

Parameters

data [array_like] Input data.

mask [sequence, optional] Mask. Must be convertible to an array of booleans with the same shape as *data*. True indicates a masked (i.e. invalid) data.

dtype [dtype, optional (Not supported in Dask)] Data type of the output. If *dtype* is None, the type of the data argument (`data.dtype`) is used. If *dtype* is not None and different from `data.dtype`, a copy is performed.

copy [bool, optional (Not supported in Dask)] Whether to copy the input data (True), or to use a reference instead. Default is False.

subok [bool, optional (Not supported in Dask)] Whether to return a subclass of *MaskedArray* if possible (True) or a plain *MaskedArray*. Default is True.

ndmin [int, optional (Not supported in Dask)] Minimum number of dimensions. Default is 0.

fill_value [scalar, optional] Value used to fill in the masked values when necessary. If None, a default based on the data-type is used.

keep_mask [bool, optional (Not supported in Dask)] Whether to combine *mask* with the mask of the input data, if any (True), or to use only *mask* for the output (False). Default is True.

hard_mask [bool, optional (Not supported in Dask)] Whether to use a hard mask or not. With a hard mask, masked values cannot be unmasked. Default is False.

shrink [bool, optional (Not supported in Dask)] Whether to force compression of an empty mask. Default is True.

order [{'C', 'F', 'A'}, optional (Not supported in Dask)] Specify the order of the array. If order is 'C', then the array will be in C-contiguous order (last-index varies the fastest). If order is 'F', then the returned array will be in Fortran-contiguous order (first-index varies the fastest). If order is 'A' (default), then the returned array may be in any order (either C-, Fortran-contiguous, or even discontiguous), unless a copy is required, in which case it will be C-contiguous.

`dask.array.ma.`**`masked_equal`**`(`*a*, *value*`)`

Mask an array where equal to a given value.

This docstring was copied from numpy.ma.masked_equal.

Some inconsistencies with the Dask version may exist.

This function is a shortcut to `masked_where`, with *condition* = (x == value). For floating point arrays, consider using `masked_values(x, value)`.

See also:

masked_where Mask where a condition is met.

masked_values Mask using floating point equality.

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> a = np.arange(4)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([0, 1, 2, 3])
>>> ma.masked_equal(a, 2)  # doctest: +SKIP
masked_array(data = [0 1 -- 3],
      mask = [False False  True False],
      fill_value=999999)
```

`dask.array.ma.`**`masked_greater`**`(`*x*, *value*, *copy=True*`)`

Mask an array where greater than a given value.

This function is a shortcut to `masked_where`, with *condition* = (x > value).

See also:

masked_where Mask where a condition is met.

Examples

```
>>> import numpy.ma as ma
>>> a = np.arange(4)
>>> a
array([0, 1, 2, 3])
>>> ma.masked_greater(a, 2)
masked_array(data = [0 1 2 --],
      mask = [False False False  True],
      fill_value=999999)
```

`dask.array.ma.`**`masked_greater_equal`**(*x*, *value*, *copy=True*)

Mask an array where greater than or equal to a given value.

This function is a shortcut to `masked_where`, with *condition* = (x >= value).

See also:

`masked_where` Mask where a condition is met.

Examples

```
>>> import numpy.ma as ma
>>> a = np.arange(4)
>>> a
array([0, 1, 2, 3])
>>> ma.masked_greater_equal(a, 2)
masked_array(data = [0 1 -- --],
      mask = [False False  True  True],
      fill_value=999999)
```

`dask.array.ma.`**`masked_inside`**(*x*, *v1*, *v2*)

Mask an array inside a given interval.

This docstring was copied from numpy.ma.masked_inside.

Some inconsistencies with the Dask version may exist.

Shortcut to `masked_where`, where *condition* is True for *x* inside the interval [v1,v2] (v1 <= x <= v2). The boundaries *v1* and *v2* can be given in either order.

See also:

`masked_where` Mask where a condition is met.

Notes

The array *x* is prefilled with its filling value.

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> x = [0.31, 1.2, 0.01, 0.2, -0.4, -1.1]  # doctest: +SKIP
>>> ma.masked_inside(x, -0.3, 0.3)  # doctest: +SKIP
masked_array(data = [0.31 1.2 -- -- -0.4 -1.1],
```

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```
      mask = [False False  True  True False False],
      fill_value=1e+20)
```

The order of *v1* and *v2* doesn't matter.

```
>>> ma.masked_inside(x, 0.3, -0.3)  # doctest: +SKIP
masked_array(data = [0.31 1.2 -- -- -0.4 -1.1],
      mask = [False False  True  True False False],
      fill_value=1e+20)
```

`dask.array.ma.`**`masked_invalid`**`(`*a*`)`

Mask an array where invalid values occur (NaNs or infs).

This docstring was copied from numpy.ma.masked_invalid.

Some inconsistencies with the Dask version may exist.

This function is a shortcut to `masked_where`, with *condition* = ~(np.isfinite(a)). Any pre-existing mask is conserved. Only applies to arrays with a dtype where NaNs or infs make sense (i.e. floating point types), but accepts any array_like object.

See also:

`masked_where` Mask where a condition is met.

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> a = np.arange(5, dtype=float)  # doctest: +SKIP
>>> a[2] = np.NaN  # doctest: +SKIP
>>> a[3] = np.PINF  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([  0.,   1.,  NaN,  Inf,   4.])
>>> ma.masked_invalid(a)  # doctest: +SKIP
masked_array(data = [0.0 1.0 -- -- 4.0],
      mask = [False False  True  True False],
      fill_value=1e+20)
```

`dask.array.ma.`**`masked_less`**`(`*x*, *value*, *copy=True*`)`

Mask an array where less than a given value.

This function is a shortcut to `masked_where`, with *condition* = (x < value).

See also:

`masked_where` Mask where a condition is met.

Examples

```
>>> import numpy.ma as ma
>>> a = np.arange(4)
>>> a
array([0, 1, 2, 3])
>>> ma.masked_less(a, 2)
masked_array(data = [-- -- 2 3],
```

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```
      mask = [ True  True False False],
      fill_value=999999)
```

dask.array.ma.**masked_less_equal**(*x*, *value*, *copy=True*)

Mask an array where less than or equal to a given value.

This function is a shortcut to `masked_where`, with *condition* = (x <= value).

See also:

masked_where Mask where a condition is met.

Examples

```
>>> import numpy.ma as ma
>>> a = np.arange(4)
>>> a
array([0, 1, 2, 3])
>>> ma.masked_less_equal(a, 2)
masked_array(data = [-- -- -- 3],
      mask = [ True  True  True False],
      fill_value=999999)
```

dask.array.ma.**masked_not_equal**(*x*, *value*, *copy=True*)

Mask an array where *not* equal to a given value.

This function is a shortcut to `masked_where`, with *condition* = (x != value).

See also:

masked_where Mask where a condition is met.

Examples

```
>>> import numpy.ma as ma
>>> a = np.arange(4)
>>> a
array([0, 1, 2, 3])
>>> ma.masked_not_equal(a, 2)
masked_array(data = [-- -- 2 --],
      mask = [ True  True False  True],
      fill_value=999999)
```

dask.array.ma.**masked_outside**(*x*, *v1*, *v2*)

Mask an array outside a given interval.

This docstring was copied from numpy.ma.masked_outside.

Some inconsistencies with the Dask version may exist.

Shortcut to `masked_where`, where *condition* is True for *x* outside the interval [v1,v2] (x < v1)|(x > v2). The boundaries *v1* and *v2* can be given in either order.

See also:

masked_where Mask where a condition is met.

Notes

The array *x* is prefilled with its filling value.

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> x = [0.31, 1.2, 0.01, 0.2, -0.4, -1.1]  # doctest: +SKIP
>>> ma.masked_outside(x, -0.3, 0.3)  # doctest: +SKIP
masked_array(data = [-- -- 0.01 0.2 -- --],
      mask = [ True  True False False  True  True],
      fill_value=1e+20)
```

The order of *v1* and *v2* doesn't matter.

```
>>> ma.masked_outside(x, 0.3, -0.3)  # doctest: +SKIP
masked_array(data = [-- -- 0.01 0.2 -- --],
      mask = [ True  True False False  True  True],
      fill_value=1e+20)
```

`dask.array.ma.`**`masked_values`**(*x*, *value*, *rtol=1e-05*, *atol=1e-08*, *shrink=True*)

Mask using floating point equality.

This docstring was copied from numpy.ma.masked_values.

Some inconsistencies with the Dask version may exist.

Return a MaskedArray, masked where the data in array *x* are approximately equal to *value*, determined using *isclose*. The default tolerances for *masked_values* are the same as those for *isclose*.

For integer types, exact equality is used, in the same way as *masked_equal*.

The fill_value is set to *value* and the mask is set to `nomask` if possible.

Parameters

x [array_like] Array to mask.

value [float] Masking value.

rtol, atol [float, optional] Tolerance parameters passed on to *isclose*

copy [bool, optional (Not supported in Dask)] Whether to return a copy of *x*.

shrink [bool, optional] Whether to collapse a mask full of False to `nomask`.

Returns

result [MaskedArray] The result of masking *x* where approximately equal to *value*.

See also:

`masked_where` Mask where a condition is met.

`masked_equal` Mask where equal to a given value (integers).

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> x = np.array([1, 1.1, 2, 1.1, 3])  # doctest: +SKIP
>>> ma.masked_values(x, 1.1)  # doctest: +SKIP
masked_array(data = [1.0 -- 2.0 -- 3.0],
      mask = [False  True False  True False],
      fill_value=1.1)
```

Note that *mask* is set to `nomask` if possible.

```
>>> ma.masked_values(x, 1.5)  # doctest: +SKIP
masked_array(data = [ 1.   1.1  2.   1.1  3. ],
      mask = False,
      fill_value=1.5)
```

For integers, the fill value will be different in general to the result of `masked_equal`.

```
>>> x = np.arange(5)  # doctest: +SKIP
>>> x  # doctest: +SKIP
array([0, 1, 2, 3, 4])
>>> ma.masked_values(x, 2)  # doctest: +SKIP
masked_array(data = [0 1 -- 3 4],
      mask = [False False  True False False],
      fill_value=2)
>>> ma.masked_equal(x, 2)  # doctest: +SKIP
masked_array(data = [0 1 -- 3 4],
      mask = [False False  True False False],
      fill_value=999999)
```

`dask.array.ma.`**`masked_where`**`(`*condition*, *a*`)`

Mask an array where a condition is met.

This docstring was copied from numpy.ma.masked_where.

Some inconsistencies with the Dask version may exist.

Return *a* as an array masked where *condition* is True. Any masked values of *a* or *condition* are also masked in the output.

Parameters

condition [array_like] Masking condition. When *condition* tests floating point values for equality, consider using `masked_values` instead.

a [array_like] Array to mask.

copy [bool (Not supported in Dask)] If True (default) make a copy of *a* in the result. If False modify *a* in place and return a view.

Returns

result [MaskedArray] The result of masking *a* where *condition* is True.

See also:

`masked_values` Mask using floating point equality.

`masked_equal` Mask where equal to a given value.

`masked_not_equal` Mask where *not* equal to a given value.

`masked_less_equal` Mask where less than or equal to a given value.

masked_greater_equal Mask where greater than or equal to a given value.

masked_less Mask where less than a given value.

masked_greater Mask where greater than a given value.

masked_inside Mask inside a given interval.

masked_outside Mask outside a given interval.

masked_invalid Mask invalid values (NaNs or infs).

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> a = np.arange(4)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([0, 1, 2, 3])
>>> ma.masked_where(a <= 2, a)  # doctest: +SKIP
masked_array(data = [-- -- -- 3],
      mask = [ True  True  True False],
      fill_value=999999)
```

Mask array *b* conditional on *a*.

```
>>> b = ['a', 'b', 'c', 'd']  # doctest: +SKIP
>>> ma.masked_where(a == 2, b)  # doctest: +SKIP
masked_array(data = [a b -- d],
      mask = [False False  True False],
      fill_value=N/A)
```

Effect of the *copy* argument.

```
>>> c = ma.masked_where(a <= 2, a)  # doctest: +SKIP
>>> c  # doctest: +SKIP
masked_array(data = [-- -- -- 3],
      mask = [ True  True  True False],
      fill_value=999999)
>>> c[0] = 99  # doctest: +SKIP
>>> c  # doctest: +SKIP
masked_array(data = [99 -- -- 3],
      mask = [False  True  True False],
      fill_value=999999)
>>> a  # doctest: +SKIP
array([0, 1, 2, 3])
>>> c = ma.masked_where(a <= 2, a, copy=False)  # doctest: +SKIP
>>> c[0] = 99  # doctest: +SKIP
>>> c  # doctest: +SKIP
masked_array(data = [99 -- -- 3],
      mask = [False  True  True False],
      fill_value=999999)
>>> a  # doctest: +SKIP
array([99,  1,  2,  3])
```

When *condition* or *a* contain masked values.

```
>>> a = np.arange(4)  # doctest: +SKIP
>>> a = ma.masked_where(a == 2, a)  # doctest: +SKIP
```

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```
>>> a  # doctest: +SKIP
masked_array(data = [0 1 -- 3],
      mask = [False False  True False],
      fill_value=999999)
>>> b = np.arange(4)  # doctest: +SKIP
>>> b = ma.masked_where(b == 0, b)  # doctest: +SKIP
>>> b  # doctest: +SKIP
masked_array(data = [-- 1 2 3],
      mask = [ True False False False],
      fill_value=999999)
>>> ma.masked_where(a == 3, b)  # doctest: +SKIP
masked_array(data = [-- 1 -- --],
      mask = [ True False  True  True],
      fill_value=999999)
```

`dask.array.ma.`**`set_fill_value`**(*a*, *fill_value*)

Set the filling value of a, if a is a masked array.

This docstring was copied from numpy.ma.set_fill_value.

Some inconsistencies with the Dask version may exist.

This function changes the fill value of the masked array *a* in place. If *a* is not a masked array, the function returns silently, without doing anything.

Parameters

a [array_like] Input array.

fill_value [dtype] Filling value. A consistency test is performed to make sure the value is compatible with the dtype of *a*.

Returns

None Nothing returned by this function.

See also:

`maximum_fill_value` Return the default fill value for a dtype.

`MaskedArray.fill_value` Return current fill value.

`MaskedArray.set_fill_value` Equivalent method.

Examples

```
>>> import numpy.ma as ma  # doctest: +SKIP
>>> a = np.arange(5)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([0, 1, 2, 3, 4])
>>> a = ma.masked_where(a < 3, a)  # doctest: +SKIP
>>> a  # doctest: +SKIP
masked_array(data = [-- -- -- 3 4],
      mask = [ True  True  True False False],
      fill_value=999999)
>>> ma.set_fill_value(a, -999)  # doctest: +SKIP
>>> a  # doctest: +SKIP
masked_array(data = [-- -- -- 3 4],
```

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```
      mask = [ True  True  True False False],
      fill_value=-999)
```

Nothing happens if *a* is not a masked array.

```
>>> a = range(5)  # doctest: +SKIP
>>> a  # doctest: +SKIP
[0, 1, 2, 3, 4]
>>> ma.set_fill_value(a, 100)  # doctest: +SKIP
>>> a  # doctest: +SKIP
[0, 1, 2, 3, 4]
>>> a = np.arange(5)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([0, 1, 2, 3, 4])
>>> ma.set_fill_value(a, 100)  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([0, 1, 2, 3, 4])
```

dask.array.overlap.**overlap**(*x*, *depth*, *boundary*)
Share boundaries between neighboring blocks

Parameters

x: da.Array A dask array

depth: dict The size of the shared boundary per axis

boundary: dict The boundary condition on each axis. Options are 'reflect', 'periodic', 'nearest', 'none', or an array value. Such a value will fill the boundary with that value.

The depth input informs how many cells to overlap between neighboring

blocks ''{0: 2, 2: 5}'' means share two cells in 0 axis, 5 cells in 2 axis.

Axes missing from this input will not be overlapped.

Examples

```
>>> import numpy as np
>>> import dask.array as da
```

```
>>> x = np.arange(64).reshape((8, 8))
>>> d = da.from_array(x, chunks=(4, 4))
>>> d.chunks
((4, 4), (4, 4))
```

```
>>> g = da.overlap.overlap(d, depth={0: 2, 1: 1},
...                        boundary={0: 100, 1: 'reflect'})
>>> g.chunks
((8, 8), (6, 6))
```

```
>>> np.array(g)
array([[100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [  0,   0,   1,   2,   3,   4,   3,   4,   5,   6,   7,   7],
       [  8,   8,   9,  10,  11,  12,  11,  12,  13,  14,  15,  15],
```

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```
        [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
        [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
        [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
        [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
        [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
        [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
        [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
        [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
        [ 48,  48,  49,  50,  51,  52,  51,  52,  53,  54,  55,  55],
        [ 56,  56,  57,  58,  59,  60,  59,  60,  61,  62,  63,  63],
        [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
        [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100]])
```

`dask.array.overlap.`**`map_overlap`**(*x*, *func*, *depth*, *boundary=None*, *trim=True*, ***kwargs*)

Map a function over blocks of the array with some overlap

We share neighboring zones between blocks of the array, then map a function, then trim away the neighboring strips.

Parameters

func: function The function to apply to each extended block

depth: int, tuple, or dict The number of elements that each block should share with its neighbors If a tuple or dict then this can be different per axis. Asymmetric depths may be specified using a dict value of (-/+) tuples. Note that asymmetric depths are currently only supported when `boundary` is 'none'.

boundary: str, tuple, dict How to handle the boundaries. Values include 'reflect', 'periodic', 'nearest', 'none', or any constant value like 0 or np.nan

trim: bool Whether or not to trim `depth` elements from each block after calling the map function. Set this to False if your mapping function already does this for you

****kwargs:** Other keyword arguments valid in `map_blocks`

Examples

```
>>> import numpy as np
>>> import dask.array as da
```

```
>>> x = np.array([1, 1, 2, 3, 3, 3, 2, 1, 1])
>>> x = da.from_array(x, chunks=5)
>>> def derivative(x):
...     return x - np.roll(x, 1)
```

```
>>> y = x.map_overlap(derivative, depth=1, boundary=0)
>>> y.compute()
array([ 1,  0,  1,  1,  0,  0, -1, -1,  0])
```

```
>>> x = np.arange(16).reshape((4, 4))
>>> d = da.from_array(x, chunks=(2, 2))
>>> d.map_overlap(lambda x: x + x.size, depth=1).compute()
array([[16, 17, 18, 19],
       [20, 21, 22, 23],
```

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```
         [24, 25, 26, 27],
         [28, 29, 30, 31]])
```

```
>>> func = lambda x: x + x.size
>>> depth = {0: 1, 1: 1}
>>> boundary = {0: 'reflect', 1: 'none'}
>>> d.map_overlap(func, depth, boundary).compute()  # doctest: +NORMALIZE_
↪WHITESPACE
array([[12,  13,  14,  15],
       [16,  17,  18,  19],
       [20,  21,  22,  23],
       [24,  25,  26,  27]])
```

`dask.array.overlap.`**`trim_internal`**(*x*, *axes*, *boundary=None*)

Trim sides from each block

This couples well with the overlap operation, which may leave excess data on each block

See also:

`dask.array.chunk.trim`, *`dask.array.map_blocks`*

`dask.array.overlap.`**`trim_overlap`**(*x*, *depth*, *boundary=None*)

Trim sides from each block.

This couples well with the `map_overlap` operation which may leave excess data on each block.

See also:

`dask.array.overlap.map_overlap`

`dask.array.`**`from_array`**(*x*, *chunks='auto'*, *name=None*, *lock=False*, *asarray=None*, *fancy=True*, *getitem=None*, *meta=None*)

Create dask array from something that looks like an array

Input must have a `.shape`, `.ndim`, `.dtype` and support numpy-style slicing.

Parameters

x [array_like]

chunks [int, tuple] How to chunk the array. Must be one of the following forms: - A blocksize like 1000. - A blockshape like (1000, 1000). - Explicit sizes of all blocks along all dimensions like

((1000, 1000, 500), (400, 400)).

- A size in bytes, like "100 MiB" which will choose a uniform block-like shape
- The word "auto" which acts like the above, but uses a configuration value `array.chunk-size` for the chunk size

-1 or None as a blocksize indicate the size of the corresponding dimension.

name [str, optional] The key name to use for the array. Defaults to a hash of `x`. By default, hash uses python's standard sha1. This behaviour can be changed by installing cityhash, xxhash or murmurhash. If installed, a large-factor speedup can be obtained in the tokenisation step. Use `name=False` to generate a random name instead of hashing (fast)

lock [bool or Lock, optional] If `x` doesn't support concurrent reads then provide a lock here, or pass in True to have dask.array create one for you.

asarray [bool, optional] If True then call np.asarray on chunks to convert them to numpy arrays. If False then chunks are passed through unchanged. If None (default) then we use True if the `__array_function__` method is undefined.

fancy [bool, optional] If `x` doesn't support fancy indexing (e.g. indexing with lists or arrays) then set to False. Default is True.

meta [Array-like, optional] The metadata for the resulting dask array. This is the kind of array that will result from slicing the input array. Defaults to the input array.

Examples

```
>>> x = h5py.File('...')['/data/path']  # doctest: +SKIP
>>> a = da.from_array(x, chunks=(1000, 1000))  # doctest: +SKIP
```

If your underlying datastore does not support concurrent reads then include the `lock=True` keyword argument or `lock=mylock` if you want multiple arrays to coordinate around the same lock.

```
>>> a = da.from_array(x, chunks=(1000, 1000), lock=True)  # doctest: +SKIP
```

If your underlying datastore has a `.chunks` attribute (as h5py and zarr datasets do) then a multiple of that chunk shape will be used if you do not provide a chunk shape.

```
>>> a = da.from_array(x, chunks='auto')  # doctest: +SKIP
>>> a = da.from_array(x, chunks='100 MiB')  # doctest: +SKIP
>>> a = da.from_array(x)  # doctest: +SKIP
```

`dask.array.`**`from_delayed`**(*value*, *shape*, *dtype=None*, *meta=None*, *name=None*)

Create a dask array from a dask delayed value

This routine is useful for constructing dask arrays in an ad-hoc fashion using dask delayed, particularly when combined with stack and concatenate.

The dask array will consist of a single chunk.

Examples

```
>>> import dask
>>> import dask.array as da
>>> value = dask.delayed(np.ones)(5)
>>> array = da.from_delayed(value, (5,), dtype=float)
>>> array
dask.array<from-value, shape=(5,), dtype=float64, chunksize=(5,), chunktype=numpy.
↪ndarray>
>>> array.compute()
array([1., 1., 1., 1., 1.])
```

`dask.array.`**`from_npy_stack`**(*dirname*, *mmap_mode='r'*)

Load dask array from stack of npy files

See `da.to_npy_stack` for docstring

Parameters

dirname: string Directory of .npy files

mmap_mode: (None or 'r') Read data in memory map mode `dask.array.from_zarr`(*url*, *component=None*, *storage_options=None*, *chunks=None*, *name=None*, ***kwargs*)

Load array from the zarr storage format

See https://zarr.readthedocs.io for details about the format.

Parameters

url: Zarr Array or str or MutableMapping Location of the data. A URL can include a protocol specifier like s3:// for remote data. Can also be any MutableMapping instance, which should be serializable if used in multiple processes.

component: str or None If the location is a zarr group rather than an array, this is the subcomponent that should be loaded, something like `'foo/bar'`.

storage_options: dict Any additional parameters for the storage backend (ignored for local paths)

chunks: tuple of ints or tuples of ints Passed to `da.from_array`, allows setting the chunks on initialisation, if the chunking scheme in the on-disc dataset is not optimal for the calculations to follow.

name [str, optional] An optional keyname for the array. Defaults to hashing the input

kwargs: passed to ‘‘zarr.Array‘‘.

`dask.array.from_tiledb`(*uri*, *attribute=None*, *chunks=None*, *storage_options=None*, ***kwargs*)

Load array from the TileDB storage format

See https://docs.tiledb.io for more information about TileDB.

Parameters

uri: TileDB array or str Location to save the data

attribute: str or None Attribute selection (single-attribute view on multi-attribute array)

Returns

A Dask Array

Examples

```
>>> # create a tiledb array
>>> import tiledb, numpy as np, tempfile  # doctest: +SKIP
>>> uri = tempfile.NamedTemporaryFile().name  # doctest: +SKIP
>>> tiledb.from_numpy(uri, np.arange(0,9).reshape(3,3))  # doctest: +SKIP
<tiledb.libtiledb.DenseArray object at 0x...>
>>> # read back the array
>>> import dask.array as da  # doctest: +SKIP
>>> tdb_ar = da.from_tiledb(uri)  # doctest: +SKIP
>>> tdb_ar.shape  # doctest: +SKIP
(3, 3)
>>> tdb_ar.mean().compute()  # doctest: +SKIP
4.0
```

`dask.array.store`(*sources*, *targets*, *lock=True*, *regions=None*, *compute=True*, *return_stored=False*, ***kwargs*)

Store dask arrays in array-like objects, overwrite data in target

This stores dask arrays into object that supports numpy-style setitem indexing. It stores values chunk by chunk so that it does not have to fill up memory. For best performance you can align the block size of the storage target with the block size of your array.

If your data fits in memory then you may prefer calling `np.array(myarray)` instead.

Parameters

sources: Array or iterable of Arrays

targets: array-like or Delayed or iterable of array-likes and/or Delayeds These should support setitem syntax `target[10:20] = ...`

lock: boolean or threading.Lock, optional Whether or not to lock the data stores while storing. Pass True (lock each file individually), False (don't lock) or a particular `threading.Lock` object to be shared among all writes.

regions: tuple of slices or list of tuples of slices Each `region` tuple in `regions` should be such that `target[region].shape = source.shape` for the corresponding source and target in sources and targets, respectively. If this is a tuple, the contents will be assumed to be slices, so do not provide a tuple of tuples.

compute: boolean, optional If true compute immediately, return `dask.delayed.Delayed` otherwise

return_stored: boolean, optional Optionally return the stored result (default False).

Examples

```
>>> x = ...  # doctest: +SKIP
```

```
>>> import h5py  # doctest: +SKIP
>>> f = h5py.File('myfile.hdf5', mode='a')  # doctest: +SKIP
>>> dset = f.create_dataset('/data', shape=x.shape,
...                                   chunks=x.chunks,
...                                   dtype='f8')  # doctest: +SKIP
```

```
>>> store(x, dset)  # doctest: +SKIP
```

Alternatively store many arrays at the same time

```
>>> store([x, y, z], [dset1, dset2, dset3])  # doctest: +SKIP
```

`dask.array.`**`to_hdf5`**(*filename*, **args*, ***kwargs*)
Store arrays in HDF5 file

This saves several dask arrays into several datapaths in an HDF5 file. It creates the necessary datasets and handles clean file opening/closing.

```
>>> da.to_hdf5('myfile.hdf5', '/x', x)  # doctest: +SKIP
```

or

```
>>> da.to_hdf5('myfile.hdf5', {'/x': x, '/y': y})  # doctest: +SKIP
```

Optionally provide arguments as though to `h5py.File.create_dataset`

```
>>> da.to_hdf5('myfile.hdf5', '/x', x, compression='lzf', shuffle=True)  #␣
↪doctest: +SKIP
```

This can also be used as a method on a single Array

```
>>> x.to_hdf5('myfile.hdf5', '/x')  # doctest: +SKIP
```

See also:

`da.store`, `h5py.File.create_dataset`

`dask.array.`**`to_zarr`**(*arr*, *url*, *component=None*, *storage_options=None*, *overwrite=False*, *compute=True*, *return_stored=False*, ***kwargs*)

Save array to the zarr storage format

See https://zarr.readthedocs.io for details about the format.

Parameters

arr: dask.array Data to store

url: Zarr Array or str or MutableMapping Location of the data. A URL can include a protocol specifier like s3:// for remote data. Can also be any MutableMapping instance, which should be serializable if used in multiple processes.

component: str or None If the location is a zarr group rather than an array, this is the subcomponent that should be created/over-written.

storage_options: dict Any additional parameters for the storage backend (ignored for local paths)

overwrite: bool If given array already exists, overwrite=False will cause an error, where overwrite=True will replace the existing data.

compute, return_stored: see ‘‘store()‘‘

kwargs: passed to the ‘‘zarr.create()‘‘ function, e.g., compression options

Raises

ValueError If `arr` has unknown chunk sizes, which is not supported by Zarr.

See also:

`dask.array.Array.compute_chunk_sizes`

`dask.array.`**`to_npy_stack`**(*dirname*, *x*, *axis=0*)

Write dask array to a stack of .npy files

This partitions the dask.array along one axis and stores each block along that axis as a single .npy file in the specified directory

See also:

`from_npy_stack`

Examples

```
>>> x = da.ones((5, 10, 10), chunks=(2, 4, 4))  # doctest: +SKIP
>>> da.to_npy_stack('data/', x, axis=0)  # doctest: +SKIP
```

$ tree data/ data/ |– 0.npy |– 1.npy |– 2.npy |– info

The `.npy` files store numpy arrays for `x[0:2], x[2:4], and x[4:5]` respectively, as is specified by the chunk size along the zeroth axis. The info file stores the dtype, chunks, and axis information of the array.

You can load these stacks with the `da.from_npy_stack` function.

```
>>> y = da.from_npy_stack('data/')  # doctest: +SKIP
```

`dask.array.`**`to_tiledb`**(*darray*, *uri*, *compute=True*, *return_stored=False*, *storage_options=None*, ***kwargs*)

Save array to the TileDB storage format

Save 'array' using the TileDB storage manager, to any TileDB-supported URI, including local disk, S3, or HDFS.

See https://docs.tiledb.io for more information about TileDB.

Parameters

darray: dask.array A dask array to write.

uri: Any supported TileDB storage location.

storage_options: dict Dict containing any configuration options for the TileDB backend. see https://docs.tiledb.io/en/stable/tutorials/config.html

compute, return_stored: see ‘‘store()‘‘

Returns

None Unless `return_stored` is set to `True` (`False` by default)

Notes

TileDB only supports regularly-chunked arrays. TileDB tile extents correspond to form 2 of the dask chunk specification, and the conversion is done automatically for supported arrays.

Examples

```
>>> import dask.array as da, tempfile  # doctest: +SKIP
>>> uri = tempfile.NamedTemporaryFile().name   # doctest: +SKIP
>>> data = da.random.random(5,5)  # doctest: +SKIP
>>> da.to_tiledb(data, uri)  # doctest: +SKIP
>>> import tiledb  # doctest: +SKIP
>>> tdb_ar = tiledb.open(uri)  # doctest: +SKIP
>>> all(tdb_ar == data)  # doctest: +SKIP
True
```

`dask.array.fft.`**`fft_wrap`**(*fft_func*, *kind=None*, *dtype=None*)

Wrap 1D, 2D, and ND real and complex FFT functions

Takes a function that behaves like `numpy.fft` functions and a specified kind to match it to that are named after the functions in the `numpy.fft` API.

Supported kinds include:

- fft
- fft2
- fftn

- ifft
- ifft2
- ifftn
- rfft
- rfft2
- rfftn
- irfft
- irfft2
- irfftn
- hfft
- ihfft

Examples

```
>>> parallel_fft = fft_wrap(np.fft.fft)
>>> parallel_ifft = fft_wrap(np.fft.ifft)
```

`dask.array.fft.`**`fft`**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.fft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fft docstring follows below:

Compute the one-dimensional discrete Fourier Transform.

This function computes the one-dimensional *n*-point discrete Fourier Transform (DFT) with the efficient Fast Fourier Transform (FFT) algorithm [CT].

Parameters

a [array_like] Input array, can be complex.

n [int, optional] Length of the transformed axis of the output. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified.

Raises

IndexError if *axes* is larger than the last axis of *a*.

See also:

`numpy.fft` for definition of the DFT and conventions used.

ifft The inverse of *fft*.

fft2 The two-dimensional FFT.

fftn The *n*-dimensional FFT.

rfftn The *n*-dimensional FFT of real input.

fftfreq Frequency bins for given FFT parameters.

Notes

FFT (Fast Fourier Transform) refers to a way the discrete Fourier Transform (DFT) can be calculated efficiently, by using symmetries in the calculated terms. The symmetry is highest when *n* is a power of 2, and the transform is therefore most efficient for these sizes.

The DFT is defined, with the conventions used in this implementation, in the documentation for the *numpy.fft* module.

References

[CT]

Examples

```
>>> np.fft.fft(np.exp(2j * np.pi * np.arange(8) / 8))
array([ -3.44505240e-16 +1.14383329e-17j,
         8.00000000e+00 -5.71092652e-15j,
         2.33482938e-16 +1.22460635e-16j,
         1.64863782e-15 +1.77635684e-15j,
         9.95839695e-17 +2.33482938e-16j,
         0.00000000e+00 +1.66837030e-15j,
         1.14383329e-17 +1.22460635e-16j,
         -1.64863782e-15 +1.77635684e-15j])
```

In this example, real input has an FFT which is Hermitian, i.e., symmetric in the real part and anti-symmetric in the imaginary part, as described in the *numpy.fft* documentation:

```
>>> import matplotlib.pyplot as plt
>>> t = np.arange(256)
>>> sp = np.fft.fft(np.sin(t))
>>> freq = np.fft.fftfreq(t.shape[-1])
>>> plt.plot(freq, sp.real, freq, sp.imag)
[<matplotlib.lines.Line2D object at 0x...>, <matplotlib.lines.Line2D object at 0x.
↪..>]
>>> plt.show()
```

`dask.array.fft.`**`fft2`**`(`*a*, *s=None*, *axes=None*`)`

Wrapping of numpy.fft.fft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fft2 docstring follows below:

Compute the 2-dimensional discrete Fourier Transform

This function computes the *n*-dimensional discrete Fourier Transform over any axes in an *M*-dimensional array by means of the Fast Fourier Transform (FFT). By default, the transform is computed over the last two axes of the input array, i.e., a 2-dimensional FFT.

Parameters

a [array_like] Input array, can be complex

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to `n` for `fft(x, n)`. Along each axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last two axes are used. A repeated index in *axes* means the transform over that axis is performed multiple times. A one-element sequence means that a one-dimensional FFT is performed.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or the last two axes if *axes* is not given.

Raises

ValueError If *s* and *axes* have different length, or *axes* not given and `len(s) != 2`.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

`numpy.fft` Overall view of discrete Fourier transforms, with definitions and conventions used.

`ifft2` The inverse two-dimensional FFT.

`fft` The one-dimensional FFT.

`fftn` The *n*-dimensional FFT.

`fftshift` Shifts zero-frequency terms to the center of the array. For two-dimensional input, swaps first and third quadrants, and second and fourth quadrants.

Notes

fft2 is just *fftn* with a different default for *axes*.

The output, analogously to *fft*, contains the term for zero frequency in the low-order corner of the transformed axes, the positive frequency terms in the first half of these axes, the term for the Nyquist frequency in the middle of the axes and the negative frequency terms in the second half of the axes, in order of decreasingly negative frequency.

See *fftn* for details and a plotting example, and *numpy.fft* for definitions and conventions used.

Examples

```
>>> a = np.mgrid[:5, :5][0]
>>> np.fft.fft2(a)
array([[ 50.0 +0.j        ,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5+17.20477401j,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5 +4.0614962j ,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5 -4.0614962j ,   0.0 +0.j        ,   0.0 +0.j        ,
            0.0 +0.j        ,   0.0 +0.j        ],
       [-12.5-17.20477401j,   0.0 +0.j        ,   0.0 +0.j        ,
          0.0 +0.j        ,   0.0 +0.j        ]])
```

dask.array.fft.**fftn**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.fftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.fftn docstring follows below:

Compute the N-dimensional discrete Fourier Transform.

This function computes the *N*-dimensional discrete Fourier Transform over any number of axes in an *M*-dimensional array by means of the Fast Fourier Transform (FFT).

Parameters

a [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to `n` for `fft(x, n)`. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified. Repeated indices in *axes* means that the transform over that axis is performed multiple times.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* and *a*, as explained in the parameters section above.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

numpy.fft Overall view of discrete Fourier transforms, with definitions and conventions used.

ifftn The inverse of *fftn*, the inverse *n*-dimensional FFT.

fft The one-dimensional FFT, with definitions and conventions used.

rfftn The *n*-dimensional FFT of real input.

fft2 The two-dimensional FFT.

fftshift Shifts zero-frequency terms to centre of array

Notes

The output, analogously to *fft*, contains the term for zero frequency in the low-order corner of all axes, the positive frequency terms in the first half of all axes, the term for the Nyquist frequency in the middle of all axes and the negative frequency terms in the second half of all axes, in order of decreasingly negative frequency.

See *numpy.fft* for details, definitions and conventions used.

Examples

```
>>> a = np.mgrid[:3, :3, :3][0]
>>> np.fft.fftn(a, axes=(1, 2))
array([[[  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j]],
       [[  9.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j]],
       [[ 18.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j],
        [  0.+0.j,   0.+0.j,   0.+0.j]]])
>>> np.fft.fftn(a, (2, 2), axes=(0, 1))
array([[[ 2.+0.j,  2.+0.j,  2.+0.j],
        [ 0.+0.j,  0.+0.j,  0.+0.j]],
       [[-2.+0.j, -2.+0.j, -2.+0.j],
        [ 0.+0.j,  0.+0.j,  0.+0.j]]])
```

```
>>> import matplotlib.pyplot as plt
>>> [X, Y] = np.meshgrid(2 * np.pi * np.arange(200) / 12,
...                      2 * np.pi * np.arange(200) / 34)
>>> S = np.sin(X) + np.cos(Y) + np.random.uniform(0, 1, X.shape)
>>> FS = np.fft.fftn(S)
>>> plt.imshow(np.log(np.abs(np.fft.fftshift(FS))**2))
<matplotlib.image.AxesImage object at 0x...>
>>> plt.show()
```

`dask.array.fft.`**`ifft`**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.ifft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.ifft docstring follows below:

Compute the one-dimensional inverse discrete Fourier Transform.

This function computes the inverse of the one-dimensional *n*-point discrete Fourier transform computed by *fft*. In other words, `ifft(fft(a)) == a` to within numerical accuracy. For a general description of the algorithm and definitions, see *numpy.fft*.

The input should be ordered in the same way as is returned by *fft*, i.e.,

- `a[0]` should contain the zero frequency term,

- `a[1:n//2]` should contain the positive-frequency terms,
- `a[n//2 + 1:]` should contain the negative-frequency terms, in increasing order starting from the most negative frequency.

For an even number of input points, `A[n//2]` represents the sum of the values at the positive and negative Nyquist frequencies, as the two are aliased together. See *numpy.fft* for details.

Parameters

a [array_like] Input array, can be complex.

n [int, optional] Length of the transformed axis of the output. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used. See notes about padding issues.

axis [int, optional] Axis over which to compute the inverse DFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified.

Raises

IndexError If *axes* is larger than the last axis of *a*.

See also:

`numpy.fft` An introduction, with definitions and general explanations.

`fft` The one-dimensional (forward) FFT, of which *ifft* is the inverse

`ifft2` The two-dimensional inverse FFT.

`ifftn` The n-dimensional inverse FFT.

Notes

If the input parameter *n* is larger than the size of the input, the input is padded by appending zeros at the end. Even though this is the common approach, it might lead to surprising results. If a different padding is desired, it must be performed before calling *ifft*.

Examples

```
>>> np.fft.ifft([0, 4, 0, 0])
array([ 1.+0.j,  0.+1.j, -1.+0.j,  0.-1.j])
```

Create and plot a band-limited signal with random phases:

```
>>> import matplotlib.pyplot as plt
>>> t = np.arange(400)
>>> n = np.zeros((400,), dtype=complex)
>>> n[40:60] = np.exp(1j*np.random.uniform(0, 2*np.pi, (20,)))
```

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```
>>> s = np.fft.ifft(n)
>>> plt.plot(t, s.real, 'b-', t, s.imag, 'r--')
...
>>> plt.legend(('real', 'imaginary'))
...
>>> plt.show()
```

`dask.array.fft.`**`ifft2`**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.ifft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.ifft2 docstring follows below:

Compute the 2-dimensional inverse discrete Fourier Transform.

This function computes the inverse of the 2-dimensional discrete Fourier Transform over any number of axes in an M-dimensional array by means of the Fast Fourier Transform (FFT). In other words, `ifft2(fft2(a)) == a` to within numerical accuracy. By default, the inverse transform is computed over the last two axes of the input array.

The input, analogously to *ifft*, should be ordered in the same way as is returned by *fft2*, i.e. it should have the term for zero frequency in the low-order corner of the two axes, the positive frequency terms in the first half of these axes, the term for the Nyquist frequency in the middle of the axes and the negative frequency terms in the second half of both axes, in order of decreasingly negative frequency.

Parameters

a [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to *n* for `ifft(x, n)`. Along each axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used. See notes for issue on *ifft* zero padding.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last two axes are used. A repeated index in *axes* means the transform over that axis is performed multiple times. A one-element sequence means that a one-dimensional FFT is performed.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or the last two axes if *axes* is not given.

Raises

ValueError If *s* and *axes* have different length, or *axes* not given and `len(s) != 2`.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

`numpy.fft` Overall view of discrete Fourier transforms, with definitions and conventions used.

`fft2` The forward 2-dimensional FFT, of which *ifft2* is the inverse.

`ifftn` The inverse of the *n*-dimensional FFT.

`fft` The one-dimensional FFT.

`ifft` The one-dimensional inverse FFT.

Notes

ifft2 is just *ifftn* with a different default for *axes*.

See *ifftn* for details and a plotting example, and *numpy.fft* for definition and conventions used.

Zero-padding, analogously with *ifft*, is performed by appending zeros to the input along the specified dimension. Although this is the common approach, it might lead to surprising results. If another form of zero padding is desired, it must be performed before *ifft2* is called.

Examples

```
>>> a = 4 * np.eye(4)
>>> np.fft.ifft2(a)
array([[ 1.+0.j,  0.+0.j,  0.+0.j,  0.+0.j],
       [ 0.+0.j,  0.+0.j,  0.+0.j,  1.+0.j],
       [ 0.+0.j,  0.+0.j,  1.+0.j,  0.+0.j],
       [ 0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j]])
```

`dask.array.fft.`**`ifftn`**(*a*, *s=None*, *axes=None*)

Wrapping of numpy.fft.ifftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.ifftn docstring follows below:

Compute the N-dimensional inverse discrete Fourier Transform.

This function computes the inverse of the N-dimensional discrete Fourier Transform over any number of axes in an M-dimensional array by means of the Fast Fourier Transform (FFT). In other words, `ifftn(fftn(a)) == a` to within numerical accuracy. For a description of the definitions and conventions used, see *numpy.fft*.

The input, analogously to *ifft*, should be ordered in the same way as is returned by *fftn*, i.e. it should have the term for zero frequency in all axes in the low-order corner, the positive frequency terms in the first half of all axes, the term for the Nyquist frequency in the middle of all axes and the negative frequency terms in the second half of all axes, in order of decreasingly negative frequency.

Parameters

a [array_like] Input array, can be complex.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). This corresponds to `n` for `ifft(x, n)`. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used. See notes for issue on *ifft* zero padding.

axes [sequence of ints, optional] Axes over which to compute the IFFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified. Repeated indices in *axes* means that the inverse transform over that axis is performed multiple times.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* or *a*, as explained in the parameters section above.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

`numpy.fft` Overall view of discrete Fourier transforms, with definitions and conventions used.

`fftn` The forward *n*-dimensional FFT, of which *ifftn* is the inverse.

`ifft` The one-dimensional inverse FFT.

`ifft2` The two-dimensional inverse FFT.

`ifftshift` Undoes *fftshift*, shifts zero-frequency terms to beginning of array.

Notes

See *numpy.fft* for definitions and conventions used.

Zero-padding, analogously with *ifft*, is performed by appending zeros to the input along the specified dimension. Although this is the common approach, it might lead to surprising results. If another form of zero padding is desired, it must be performed before *ifftn* is called.

Examples

```
>>> a = np.eye(4)
>>> np.fft.ifftn(np.fft.fftn(a, axes=(0,)), axes=(1,))
array([[ 1.+0.j,  0.+0.j,  0.+0.j,  0.+0.j],
       [ 0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j],
       [ 0.+0.j,  0.+0.j,  1.+0.j,  0.+0.j],
       [ 0.+0.j,  0.+0.j,  0.+0.j,  1.+0.j]])
```

Create and plot an image with band-limited frequency content:

```
>>> import matplotlib.pyplot as plt
>>> n = np.zeros((200,200), dtype=complex)
>>> n[60:80, 20:40] = np.exp(1j*np.random.uniform(0, 2*np.pi, (20, 20)))
>>> im = np.fft.ifftn(n).real
>>> plt.imshow(im)
<matplotlib.image.AxesImage object at 0x...>
>>> plt.show()
```

`dask.array.fft.`**`rfft`**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.rfft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.rfft docstring follows below:

Compute the one-dimensional discrete Fourier Transform for real input.

This function computes the one-dimensional *n*-point discrete Fourier Transform (DFT) of a real-valued array by means of an efficient algorithm called the Fast Fourier Transform (FFT).

Parameters

a [array_like] Input array

n [int, optional] Number of points along transformation axis in the input to use. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. If *n* is even, the length of the transformed axis is `(n/2)+1`. If *n* is odd, the length is `(n+1)/2`.

Raises

IndexError If *axis* is larger than the last axis of *a*.

See also:

`numpy.fft` For definition of the DFT and conventions used.

`irfft` The inverse of *rfft*.

`fft` The one-dimensional FFT of general (complex) input.

`fftn` The *n*-dimensional FFT.

`rfftn` The *n*-dimensional FFT of real input.

Notes

When the DFT is computed for purely real input, the output is Hermitian-symmetric, i.e. the negative frequency terms are just the complex conjugates of the corresponding positive-frequency terms, and the negative-frequency terms are therefore redundant. This function does not compute the negative frequency terms, and the length of the transformed axis of the output is therefore `n//2 + 1`.

When `A = rfft(a)` and fs is the sampling frequency, `A[0]` contains the zero-frequency term 0*fs, which is real due to Hermitian symmetry.

If *n* is even, `A[-1]` contains the term representing both positive and negative Nyquist frequency (+fs/2 and -fs/2), and must also be purely real. If *n* is odd, there is no term at fs/2; `A[-1]` contains the largest positive frequency (fs/2*(n-1)/n), and is complex in the general case.

If the input *a* contains an imaginary part, it is silently discarded.

Examples

```
>>> np.fft.fft([0, 1, 0, 0])
array([ 1.+0.j,  0.-1.j, -1.+0.j,  0.+1.j])
>>> np.fft.rfft([0, 1, 0, 0])
array([ 1.+0.j,  0.-1.j, -1.+0.j])
```

Notice how the final element of the *fft* output is the complex conjugate of the second element, for real input. For *rfft*, this symmetry is exploited to compute only the non-negative frequency terms.

`dask.array.fft.`**`rfft2`**`(`*a*, *s=None*, *axes=None*`)`

Wrapping of numpy.fft.rfft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.rfft2 docstring follows below:

Compute the 2-dimensional FFT of a real array.

Parameters

a [array] Input array, taken to be real.

s [sequence of ints, optional] Shape of the FFT.

axes [sequence of ints, optional] Axes over which to compute the FFT.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The result of the real 2-D FFT.

See also:

`rfftn` Compute the N-dimensional discrete Fourier Transform for real input.

Notes

This is really just *rfftn* with different default behavior. For more details see *rfftn*.

`dask.array.fft.`**`rfftn`**`(`*a*, *s=None*, *axes=None*`)`

Wrapping of numpy.fft.rfftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.rfftn docstring follows below:

Compute the N-dimensional discrete Fourier Transform for real input.

This function computes the N-dimensional discrete Fourier Transform over any number of axes in an M-dimensional real array by means of the Fast Fourier Transform (FFT). By default, all axes are transformed, with the real transform performed over the last axis, while the remaining transforms are complex.

Parameters

a [array_like] Input array, taken to be real.

s [sequence of ints, optional] Shape (length along each transformed axis) to use from the input. (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). The final element of *s* corresponds to *n* for `rfft(x, n)`, while for the remaining axes, it corresponds to *n* for `fft(x, n)`. Along any axis, if the given shape is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. if *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the FFT. If not given, the last `len(s)` axes are used, or all axes if *s* is also not specified.

norm [{None, “ortho”}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* and *a*, as explained in the parameters section above. The length of the last axis transformed will be `s[-1]//2+1`, while the remaining transformed axes will have lengths according to *s*, or unchanged from the input.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

irfftn The inverse of *rfftn*, i.e. the inverse of the n-dimensional FFT of real input.

fft The one-dimensional FFT, with definitions and conventions used.

rfft The one-dimensional FFT of real input.

fftn The n-dimensional FFT.

rfft2 The two-dimensional FFT of real input.

Notes

The transform for real input is performed over the last transformation axis, as by *rfft*, then the transform over the remaining axes is performed as by *fftn*. The order of the output is as for *rfft* for the final transformation axis, and as for *fftn* for the remaining transformation axes.

See *fft* for details, definitions and conventions used.

Examples

```
>>> a = np.ones((2, 2, 2))
>>> np.fft.rfftn(a)
array([[[ 8.+0.j,  0.+0.j],
        [ 0.+0.j,  0.+0.j]],
       [[ 0.+0.j,  0.+0.j],
        [ 0.+0.j,  0.+0.j]]])
```

```
>>> np.fft.rfftn(a, axes=(2, 0))
array([[[ 4.+0.j,  0.+0.j],
        [ 4.+0.j,  0.+0.j]],
       [[ 0.+0.j,  0.+0.j],
        [ 0.+0.j,  0.+0.j]]])
```

`dask.array.fft.`**`irfft`**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.irfft

The axis along which the FFT is applied must have a one chunk. To change the array’s chunking use dask.Array.rechunk.

The numpy.fft.irfft docstring follows below:

Compute the inverse of the n-point DFT for real input.

This function computes the inverse of the one-dimensional *n*-point discrete Fourier Transform of real input computed by *rfft*. In other words, `irfft(rfft(a), len(a)) == a` to within numerical accuracy. (See Notes below for why `len(a)` is necessary here.)

The input is expected to be in the form returned by *rfft*, i.e. the real zero-frequency term followed by the complex positive frequency terms in order of increasing frequency. Since the discrete Fourier Transform of real input is Hermitian-symmetric, the negative frequency terms are taken to be the complex conjugates of the corresponding positive frequency terms.

Parameters

a [array_like] The input array.

n [int, optional] Length of the transformed axis of the output. For *n* output points, `n//2+1` input points are necessary. If the input is longer than this, it is cropped. If it is shorter than this, it is padded with zeros. If *n* is not given, it is determined from the length of the input along the axis specified by *axis*.

axis [int, optional] Axis over which to compute the inverse FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is *n*, or, if *n* is not given, `2*(m-1)` where `m` is the length of the transformed axis of the input. To get an odd number of output points, *n* must be specified.

Raises

IndexError If *axis* is larger than the last axis of *a*.

See also:

`numpy.fft` For definition of the DFT and conventions used.

`rfft` The one-dimensional FFT of real input, of which *irfft* is inverse.

`fft` The one-dimensional FFT.

`irfft2` The inverse of the two-dimensional FFT of real input.

`irfftn` The inverse of the *n*-dimensional FFT of real input.

Notes

Returns the real valued *n*-point inverse discrete Fourier transform of *a*, where *a* contains the non-negative frequency terms of a Hermitian-symmetric sequence. *n* is the length of the result, not the input.

If you specify an *n* such that *a* must be zero-padded or truncated, the extra/removed values will be added/removed at high frequencies. One can thus resample a series to *m* points via Fourier interpolation by: `a_resamp = irfft(rfft(a), m)`.

Examples

```
>>> np.fft.ifft([1, -1j, -1, 1j])
array([ 0.+0.j,  1.+0.j,  0.+0.j,  0.+0.j])
>>> np.fft.irfft([1, -1j, -1])
array([ 0.,  1.,  0.,  0.])
```

Notice how the last term in the input to the ordinary *ifft* is the complex conjugate of the second term, and the output has zero imaginary part everywhere. When calling *irfft*, the negative frequencies are not specified, and the output array is purely real.

`dask.array.fft.`**`irfft2`**`(`*a*, *s=None*, *axes=None*`)`

Wrapping of numpy.fft.irfft2

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.irfft2 docstring follows below:

Compute the 2-dimensional inverse FFT of a real array.

Parameters

a [array_like] The input array

s [sequence of ints, optional] Shape of the inverse FFT.

axes [sequence of ints, optional] The axes over which to compute the inverse fft. Default is the last two axes.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The result of the inverse real 2-D FFT.

See also:

`irfftn` Compute the inverse of the N-dimensional FFT of real input.

Notes

This is really *irfftn* with different defaults. For more details see *irfftn*.

`dask.array.fft.`**`irfftn`**`(`*a*, *s=None*, *axes=None*`)`

Wrapping of numpy.fft.irfftn

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.irfftn docstring follows below:

Compute the inverse of the N-dimensional FFT of real input.

This function computes the inverse of the N-dimensional discrete Fourier Transform for real input over any number of axes in an M-dimensional array by means of the Fast Fourier Transform (FFT). In other words, `irfftn(rfftn(a), a.shape) == a` to within numerical accuracy. (The `a.shape` is necessary like `len(a)` is for *irfft*, and for the same reason.)

The input should be ordered in the same way as is returned by *rfftn*, i.e. as for *irfft* for the final transformation axis, and as for *ifftn* along all the other axes.

Parameters

a [array_like] Input array.

s [sequence of ints, optional] Shape (length of each transformed axis) of the output (`s[0]` refers to axis 0, `s[1]` to axis 1, etc.). *s* is also the number of input points used along this axis, except for the last axis, where `s[-1]//2+1` points of the input are used. Along any axis, if the shape indicated by *s* is smaller than that of the input, the input is cropped. If it is larger, the input is padded with zeros. If *s* is not given, the shape of the input along the axes specified by *axes* is used.

axes [sequence of ints, optional] Axes over which to compute the inverse FFT. If not given, the last *len(s)* axes are used, or all axes if *s* is also not specified. Repeated indices in *axes* means that the inverse transform over that axis is performed multiple times.

norm [{None, "ortho"}, optional] New in version 1.10.0.

Normalization mode (see *numpy.fft*). Default is None.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axes indicated by *axes*, or by a combination of *s* or *a*, as explained in the parameters section above. The length of each transformed axis is as given by the corresponding element of *s*, or the length of the input in every axis except for the last one if *s* is not given. In the final transformed axis the length of the output when *s* is not given is `2*(m-1)` where `m` is the length of the final transformed axis of the input. To get an odd number of output points in the final axis, *s* must be specified.

Raises

ValueError If *s* and *axes* have different length.

IndexError If an element of *axes* is larger than than the number of axes of *a*.

See also:

rfftn The forward n-dimensional FFT of real input, of which *ifftn* is the inverse.

fft The one-dimensional FFT, with definitions and conventions used.

irfft The inverse of the one-dimensional FFT of real input.

irfft2 The inverse of the two-dimensional FFT of real input.

Notes

See *fft* for definitions and conventions used.

See *rfft* for definitions and conventions used for real input.

Examples

```
>>> a = np.zeros((3, 2, 2))
>>> a[0, 0, 0] = 3 * 2 * 2
>>> np.fft.irfftn(a)
array([[[ 1.,  1.],
        [ 1.,  1.]],
       [[ 1.,  1.],
```

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```
         [ 1.,  1.]],
        [[ 1.,  1.],
         [ 1.,  1.]]])
```

dask.array.fft.**hfft**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.hfft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.hfft docstring follows below:

Compute the FFT of a signal that has Hermitian symmetry, i.e., a real spectrum.

Parameters

a [array_like] The input array.

n [int, optional] Length of the transformed axis of the output. For *n* output points, `n//2 + 1` input points are necessary. If the input is longer than this, it is cropped. If it is shorter than this, it is padded with zeros. If *n* is not given, it is determined from the length of the input along the axis specified by *axis*.

axis [int, optional] Axis over which to compute the FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] Normalization mode (see *numpy.fft*). Default is None.

New in version 1.10.0.

Returns

out [ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is *n*, or, if *n* is not given, `2*m - 2` where `m` is the length of the transformed axis of the input. To get an odd number of output points, *n* must be specified, for instance as `2*m - 1` in the typical case,

Raises

IndexError If *axis* is larger than the last axis of *a*.

See also:

rfft Compute the one-dimensional FFT for real input.

ihfft The inverse of *hfft*.

Notes

hfft/*ihfft* are a pair analogous to *rfft*/*irfft*, but for the opposite case: here the signal has Hermitian symmetry in the time domain and is real in the frequency domain. So here it's *hfft* for which you must supply the length of the result if it is to be odd.

- even: `ihfft(hfft(a, 2*len(a) - 2) == a`, within roundoff error,
- odd: `ihfft(hfft(a, 2*len(a) - 1) == a`, within roundoff error.

Examples

```
>>> signal = np.array([1, 2, 3, 4, 3, 2])
>>> np.fft.fft(signal)
array([ 15.+0.j,  -4.+0.j,   0.+0.j,  -1.-0.j,   0.+0.j,  -4.+0.j])
>>> np.fft.hfft(signal[:4]) # Input first half of signal
array([ 15.,  -4.,   0.,  -1.,   0.,  -4.])
>>> np.fft.hfft(signal, 6)  # Input entire signal and truncate
array([ 15.,  -4.,   0.,  -1.,   0.,  -4.])
```

```
>>> signal = np.array([[1, 1.j], [-1.j, 2]])
>>> np.conj(signal.T) - signal   # check Hermitian symmetry
array([[ 0.-0.j,  0.+0.j],
       [ 0.+0.j,  0.-0.j]])
>>> freq_spectrum = np.fft.hfft(signal)
>>> freq_spectrum
array([[ 1.,  1.],
       [ 2., -2.]])
```

`dask.array.fft.`**`ihfft`**(*a*, *n=None*, *axis=None*)

Wrapping of numpy.fft.ihfft

The axis along which the FFT is applied must have a one chunk. To change the array's chunking use dask.Array.rechunk.

The numpy.fft.ihfft docstring follows below:

Compute the inverse FFT of a signal that has Hermitian symmetry.

Parameters

a [array_like] Input array.

n [int, optional] Length of the inverse FFT, the number of points along transformation axis in the input to use. If *n* is smaller than the length of the input, the input is cropped. If it is larger, the input is padded with zeros. If *n* is not given, the length of the input along the axis specified by *axis* is used.

axis [int, optional] Axis over which to compute the inverse FFT. If not given, the last axis is used.

norm [{None, "ortho"}, optional] Normalization mode (see *numpy.fft*). Default is None.

New in version 1.10.0.

Returns

out [complex ndarray] The truncated or zero-padded input, transformed along the axis indicated by *axis*, or the last one if *axis* is not specified. The length of the transformed axis is `n//2 + 1`.

See also:

`hfft`, `irfft`

Notes

hfft/*ihfft* are a pair analogous to *rfft*/*irfft*, but for the opposite case: here the signal has Hermitian symmetry in the time domain and is real in the frequency domain. So here it's *hfft* for which you must supply the length of the result if it is to be odd:

- even: `ihfft(hfft(a, 2*len(a) - 2) == a`, within roundoff error,

- odd: `ihfft(hfft(a, 2*len(a) - 1) == a`, within roundoff error.

Examples

```
>>> spectrum = np.array([ 15, -4, 0, -1, 0, -4])
>>> np.fft.ifft(spectrum)
array([ 1.+0.j,  2.-0.j,  3.+0.j,  4.+0.j,  3.+0.j,  2.-0.j])
>>> np.fft.ihfft(spectrum)
array([ 1.-0.j,  2.-0.j,  3.-0.j,  4.-0.j])
```

`dask.array.fft.`**`fftfreq`**(*n*, *d=1.0*, *chunks='auto'*)

Return the Discrete Fourier Transform sample frequencies.

This docstring was copied from numpy.fft.fftfreq.

Some inconsistencies with the Dask version may exist.

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,   n/2-1,     -n/2, ..., -1] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2, -(n-1)/2, ..., -1] / (d*n)   if n is odd
```

Parameters

n [int] Window length.

d [scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f [ndarray] Array of length *n* containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5], dtype=float)  # doctest: +SKIP
>>> fourier = np.fft.fft(signal)  # doctest: +SKIP
>>> n = signal.size  # doctest: +SKIP
>>> timestep = 0.1  # doctest: +SKIP
>>> freq = np.fft.fftfreq(n, d=timestep)  # doctest: +SKIP
>>> freq  # doctest: +SKIP
array([ 0.  ,  1.25,  2.5 ,  3.75, -5.  , -3.75, -2.5 , -1.25])
```

`dask.array.fft.`**`rfftfreq`**(*n*, *d=1.0*, *chunks='auto'*)

Return the Discrete Fourier Transform sample frequencies (for usage with rfft, irfft).

This docstring was copied from numpy.fft.rfftfreq.

Some inconsistencies with the Dask version may exist.

The returned float array *f* contains the frequency bin centers in cycles per unit of the sample spacing (with zero at the start). For instance, if the sample spacing is in seconds, then the frequency unit is cycles/second.

Given a window length *n* and a sample spacing *d*:

```
f = [0, 1, ...,     n/2-1,     n/2] / (d*n)   if n is even
f = [0, 1, ..., (n-1)/2-1, (n-1)/2] / (d*n)   if n is odd
```

Unlike *fftfreq* (but like *scipy.fftpack.rfftfreq*) the Nyquist frequency component is considered to be positive.

Parameters

n [int] Window length.

d [scalar, optional] Sample spacing (inverse of the sampling rate). Defaults to 1.

Returns

f [ndarray] Array of length `n//2 + 1` containing the sample frequencies.

Examples

```
>>> signal = np.array([-2, 8, 6, 4, 1, 0, 3, 5, -3, 4], dtype=float)  # doctest:␣
↪+SKIP
>>> fourier = np.fft.rfft(signal)  # doctest: +SKIP
>>> n = signal.size  # doctest: +SKIP
>>> sample_rate = 100  # doctest: +SKIP
>>> freq = np.fft.fftfreq(n, d=1./sample_rate)  # doctest: +SKIP
>>> freq  # doctest: +SKIP
array([  0.,  10.,  20.,  30.,  40., -50., -40., -30., -20., -10.])
>>> freq = np.fft.rfftfreq(n, d=1./sample_rate)  # doctest: +SKIP
>>> freq  # doctest: +SKIP
array([  0.,  10.,  20.,  30.,  40.,  50.])
```

`dask.array.fft.`**`fftshift`**`(`*x*, *axes=None*`)`

Shift the zero-frequency component to the center of the spectrum.

This docstring was copied from numpy.fft.fftshift.

Some inconsistencies with the Dask version may exist.

This function swaps half-spaces for all axes listed (defaults to all). Note that `y[0]` is the Nyquist component only if `len(x)` is even.

Parameters

x [array_like] Input array.

axes [int or shape tuple, optional] Axes over which to shift. Default is None, which shifts all axes.

Returns

y [ndarray] The shifted array.

See also:

`ifftshift` The inverse of *fftshift*.

Examples

```
>>> freqs = np.fft.fftfreq(10, 0.1)  # doctest: +SKIP
>>> freqs  # doctest: +SKIP
array([ 0.,  1.,  2.,  3.,  4., -5., -4., -3., -2., -1.])
>>> np.fft.fftshift(freqs)  # doctest: +SKIP
array([-5., -4., -3., -2., -1.,  0.,  1.,  2.,  3.,  4.])
```

Shift the zero-frequency component only along the second axis:

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)  # doctest: +SKIP
>>> freqs  # doctest: +SKIP
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.fftshift(freqs, axes=(1,))  # doctest: +SKIP
array([[ 2.,  0.,  1.],
       [-4.,  3.,  4.],
       [-1., -3., -2.]])
```

`dask.array.fft.`**`ifftshift`**(*x*, *axes=None*)

The inverse of *fftshift*. Although identical for even-length *x*, the functions differ by one sample for odd-length *x*.

This docstring was copied from numpy.fft.ifftshift.

Some inconsistencies with the Dask version may exist.

Parameters

x [array_like] Input array.

axes [int or shape tuple, optional] Axes over which to calculate. Defaults to None, which shifts all axes.

Returns

y [ndarray] The shifted array.

See also:

`fftshift` Shift zero-frequency component to the center of the spectrum.

Examples

```
>>> freqs = np.fft.fftfreq(9, d=1./9).reshape(3, 3)  # doctest: +SKIP
>>> freqs  # doctest: +SKIP
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
>>> np.fft.ifftshift(np.fft.fftshift(freqs))  # doctest: +SKIP
array([[ 0.,  1.,  2.],
       [ 3.,  4., -4.],
       [-3., -2., -1.]])
```

`dask.array.random.`**`beta`**(*a*, *b*, *size=None*)

Draw samples from a Beta distribution.

The Beta distribution is a special case of the Dirichlet distribution, and is related to the Gamma distribution. It has the probability distribution function

$$f(x; a,b) = \frac{1}{B(\alpha, \beta)} x^{\alpha - 1}(1 - x)^{\beta - 1},$$

where the normalisation, B, is the beta function,

$$B(\alpha, \beta) = \int_0^1 t^{\alpha - 1}(1 - t)^{\beta - 1} dt.$$

It is often seen in Bayesian inference and order statistics.

Parameters

a [float or array_like of floats] Alpha, positive (>0).

b [float or array_like of floats] Beta, positive (>0).

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `a` and `b` are both scalars. Otherwise, `np.broadcast(a, b).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized beta distribution.

`dask.array.random.`**`binomial`**`(`*n, p, size=None*`)`

Draw samples from a binomial distribution.

Samples are drawn from a binomial distribution with specified parameters, n trials and p probability of success where n an integer >= 0 and p is in the interval [0,1]. (n may be input as a float, but it is truncated to an integer in use)

Parameters

n [int or array_like of ints] Parameter of the distribution, >= 0. Floats are also accepted, but they will be truncated to integers.

p [float or array_like of floats] Parameter of the distribution, >= 0 and <=1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `n` and `p` are both scalars. Otherwise, `np.broadcast(n, p).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized binomial distribution, where each sample is equal to the number of successes over the n trials.

See also:

`scipy.stats.binom` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the binomial distribution is

$$P(N) = \binom{n}{N}p^N(1-p)^{n-N},$$

where n is the number of trials, p is the probability of success, and N is the number of successes.

When estimating the standard error of a proportion in a population by using a random sample, the normal distribution works well unless the product p*n <=5, where p = population proportion estimate, and n = number of samples, in which case the binomial distribution is used instead. For example, a sample of 15 people shows 4 who are left handed, and 11 who are right handed. Then p = 4/15 = 27%. 0.27*15 = 4, so the binomial distribution should be used in this case.

References

[1], [2], [3], [4], [5]

Examples

Draw samples from the distribution:

```
>>> n, p = 10, .5  # number of trials, probability of each trial  # doctest: +SKIP
>>> s = np.random.binomial(n, p, 1000)  # doctest: +SKIP
# result of flipping a coin 10 times, tested 1000 times.
```

A real world example. A company drills 9 wild-cat oil exploration wells, each with an estimated probability of success of 0.1. All nine wells fail. What is the probability of that happening?

Let's do 20,000 trials of the model, and count the number that generate zero positive results.

```
>>> sum(np.random.binomial(9, 0.1, 20000) == 0)/20000.  # doctest: +SKIP
# answer = 0.38885, or 38%.
```

`dask.array.random.`**`chisquare`**(*df*, *size=None*)

Draw samples from a chi-square distribution.

When *df* independent random variables, each with standard normal distributions (mean 0, variance 1), are squared and summed, the resulting distribution is chi-square (see Notes). This distribution is often used in hypothesis testing.

Parameters

df [float or array_like of floats] Number of degrees of freedom, should be > 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `df` is a scalar. Otherwise, `np.array(df).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized chi-square distribution.

Raises

ValueError When *df* <= 0 or when an inappropriate *size* (e.g. `size=-1`) is given.

Notes

The variable obtained by summing the squares of *df* independent, standard normally distributed random variables:

$$Q = \sum_{i=0}^{\mathtt{df}} X_i^2$$

is chi-square distributed, denoted

$$Q \sim \chi_k^2.$$

The probability density function of the chi-squared distribution is

$$p(x) = \frac{(1/2)^{k/2}}{\Gamma(k/2)} x^{k/2-1} e^{-x/2},$$

where Γ is the gamma function,

$$\Gamma(x) = \int_0^{-\infty} t^{x-1} e^{-t} dt.$$

References

[1]

Examples

```
>>> np.random.chisquare(2,4)  # doctest: +SKIP
array([ 1.89920014,  9.00867716,  3.13710533,  5.62318272])
```

`dask.array.random.`**`choice`**`(`*a*, *size=None*, *replace=True*, *p=None*`)`

Generates a random sample from a given 1-D array

New in version 1.7.0.

Parameters

a [1-D array-like or int] If an ndarray, a random sample is generated from its elements. If an int, the random sample is generated as if a were np.arange(a)

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

replace [boolean, optional] Whether the sample is with or without replacement

p [1-D array-like, optional] The probabilities associated with each entry in a. If not given the sample assumes a uniform distribution over all entries in a.

Returns

samples [single item or ndarray] The generated random samples

Raises

ValueError If a is an int and less than zero, if a or p are not 1-dimensional, if a is an array-like of size 0, if p is not a vector of probabilities, if a and p have different lengths, or if replace=False and the sample size is greater than the population size

See also:

`randint`, `shuffle`, `permutation`

Examples

Generate a uniform random sample from np.arange(5) of size 3:

```
>>> np.random.choice(5, 3)  # doctest: +SKIP
array([0, 3, 4])
>>> #This is equivalent to np.random.randint(0,5,3)
```

Generate a non-uniform random sample from np.arange(5) of size 3:

```
>>> np.random.choice(5, 3, p=[0.1, 0, 0.3, 0.6, 0])  # doctest: +SKIP
array([3, 3, 0])
```

Generate a uniform random sample from np.arange(5) of size 3 without replacement:

```
>>> np.random.choice(5, 3, replace=False)  # doctest: +SKIP
array([3,1,0])
>>> #This is equivalent to np.random.permutation(np.arange(5))[:3]
```

Generate a non-uniform random sample from np.arange(5) of size 3 without replacement:

```
>>> np.random.choice(5, 3, replace=False, p=[0.1, 0, 0.3, 0.6, 0])  # doctest:␣
↪+SKIP
array([2, 3, 0])
```

Any of the above can be repeated with an arbitrary array-like instead of just integers. For instance:

```
>>> aa_milne_arr = ['pooh', 'rabbit', 'piglet', 'Christopher']  # doctest: +SKIP
>>> np.random.choice(aa_milne_arr, 5, p=[0.5, 0.1, 0.1, 0.3])  # doctest: +SKIP
array(['pooh', 'pooh', 'pooh', 'Christopher', 'piglet'],
      dtype='|S11')
```

`dask.array.random.`**`exponential`**`(`*scale=1.0*, *size=None*`)`

Draw samples from an exponential distribution.

Its probability density function is

$$f(x; \frac{1}{\beta}) = \frac{1}{\beta} \exp(-\frac{x}{\beta}),$$

for `x > 0` and 0 elsewhere. β is the scale parameter, which is the inverse of the rate parameter $\lambda = 1/\beta$. The rate parameter is an alternative, widely used parameterization of the exponential distribution [3].

The exponential distribution is a continuous analogue of the geometric distribution. It describes many common situations, such as the size of raindrops measured over many rainstorms [1], or the time between page requests to Wikipedia [2].

Parameters

scale [float or array_like of floats] The scale parameter, $\beta = 1/\lambda$.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `scale` is a scalar. Otherwise, `np.array(scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized exponential distribution.

References

[1], [2], [3]

`dask.array.random.`**`f`**`(`*dfnum*, *dfden*, *size=None*`)`

Draw samples from an F distribution.

Samples are drawn from an F distribution with specified parameters, *dfnum* (degrees of freedom in numerator) and *dfden* (degrees of freedom in denominator), where both parameters should be greater than zero.

The random variate of the F distribution (also known as the Fisher distribution) is a continuous probability distribution that arises in ANOVA tests, and is the ratio of two chi-square variates.

Parameters

dfnum [float or array_like of floats] Degrees of freedom in numerator, should be > 0.

dfden [float or array_like of float] Degrees of freedom in denominator, should be > 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `dfnum` and `dfden` are both scalars. Otherwise, `np.broadcast(dfnum, dfden).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Fisher distribution.

See also:

`scipy.stats.f` probability density function, distribution or cumulative density function, etc.

Notes

The F statistic is used to compare in-group variances to between-group variances. Calculating the distribution depends on the sampling, and so it is a function of the respective degrees of freedom in the problem. The variable *dfnum* is the number of samples minus one, the between-groups degrees of freedom, while *dfden* is the within-groups degrees of freedom, the sum of the number of samples in each group minus the number of groups.

References

[1], [2]

Examples

An example from Glantz[1], pp 47-40:

Two groups, children of diabetics (25 people) and children from people without diabetes (25 controls). Fasting blood glucose was measured, case group had a mean value of 86.1, controls had a mean value of 82.2. Standard deviations were 2.09 and 2.49 respectively. Are these data consistent with the null hypothesis that the parents diabetic status does not affect their children's blood glucose levels? Calculating the F statistic from the data gives a value of 36.01.

Draw samples from the distribution:

```
>>> dfnum = 1. # between group degrees of freedom  # doctest: +SKIP
>>> dfden = 48. # within groups degrees of freedom  # doctest: +SKIP
>>> s = np.random.f(dfnum, dfden, 1000)  # doctest: +SKIP
```

The lower bound for the top 1% of the samples is :

```
>>> sort(s)[-10]  # doctest: +SKIP
7.61988120985
```

So there is about a 1% chance that the F statistic will exceed 7.62, the measured value is 36, so the null hypothesis is rejected at the 1% level.

`dask.array.random.`**`gamma`**(*shape*, *scale=1.0*, *size=None*)

Draw samples from a Gamma distribution.

Samples are drawn from a Gamma distribution with specified parameters, *shape* (sometimes designated "k") and *scale* (sometimes designated "theta"), where both parameters are > 0.

Parameters

shape [float or array_like of floats] The shape of the gamma distribution. Should be greater than zero.

scale [float or array_like of floats, optional] The scale of the gamma distribution. Should be greater than zero. Default is equal to 1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `shape` and `scale` are both scalars. Otherwise, `np.broadcast(shape, scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized gamma distribution.

See also:

`scipy.stats.gamma` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gamma distribution is

$$p(x) = x^{k-1}\frac{e^{-x/\theta}}{\theta^k\Gamma(k)},$$

where k is the shape and θ the scale, and Γ is the Gamma function.

The Gamma distribution is often used to model the times to failure of electronic components, and arises naturally in processes for which the waiting times between Poisson distributed events are relevant.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> shape, scale = 2., 2.  # mean=4, std=2*sqrt(2)  # doctest: +SKIP
>>> s = np.random.gamma(shape, scale, 1000)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> import scipy.special as sps  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 50, density=True)  # doctest: +SKIP
>>> y = bins**(shape-1)*(np.exp(-bins/scale) /  # doctest: +SKIP
...                      (sps.gamma(shape)*scale**shape))
>>> plt.plot(bins, y, linewidth=2, color='r')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`geometric`**(*p*, *size=None*)

Draw samples from the geometric distribution.

Bernoulli trials are experiments with one of two outcomes: success or failure (an example of such an experiment is flipping a coin). The geometric distribution models the number of trials that must be run in order to achieve success. It is therefore supported on the positive integers, `k = 1, 2, ...`.

The probability mass function of the geometric distribution is

$$f(k) = (1 - p)^{k-1} p$$

where p is the probability of success of an individual trial.

Parameters

p [float or array_like of floats] The probability of success of an individual trial.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `p` is a scalar. Otherwise, `np.array(p).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized geometric distribution.

Examples

Draw ten thousand values from the geometric distribution, with the probability of an individual success equal to 0.35:

```
>>> z = np.random.geometric(p=0.35, size=10000)  # doctest: +SKIP
```

How many trials succeeded after a single run?

```
>>> (z == 1).sum() / 10000.  # doctest: +SKIP
0.34889999999999999 #random
```

`dask.array.random.`**`gumbel`**`(`*loc=0.0*, *scale=1.0*, *size=None*`)`

Draw samples from a Gumbel distribution.

Draw samples from a Gumbel distribution with specified location and scale. For more information on the Gumbel distribution, see Notes and References below.

Parameters

loc [float or array_like of floats, optional] The location of the mode of the distribution. Default is 0.

scale [float or array_like of floats, optional] The scale parameter of the distribution. Default is 1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `loc` and `scale` are both scalars. Otherwise, `np.broadcast(loc, scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Gumbel distribution.

See also:

`scipy.stats.gumbel_l`, `scipy.stats.gumbel_r`, `scipy.stats.genextreme`, *`weibull`*

Notes

The Gumbel (or Smallest Extreme Value (SEV) or the Smallest Extreme Value Type I) distribution is one of a class of Generalized Extreme Value (GEV) distributions used in modeling extreme value problems. The Gumbel is a special case of the Extreme Value Type I distribution for maximums from distributions with "exponential-like" tails.

The probability density for the Gumbel distribution is

$$p(x) = \frac{e^{-(x - \mu)/ \beta}}{\beta} e^{ -e^{-(x - \mu)/ \beta}},$$

where μ is the mode, a location parameter, and β is the scale parameter.

The Gumbel (named for German mathematician Emil Julius Gumbel) was used very early in the hydrology literature, for modeling the occurrence of flood events. It is also used for modeling maximum wind speed and rainfall rates. It is a "fat-tailed" distribution - the probability of an event in the tail of the distribution is larger than if one used a Gaussian, hence the surprisingly frequent occurrence of 100-year floods. Floods were initially modeled as a Gaussian process, which underestimated the frequency of extreme events.

It is one of a class of extreme value distributions, the Generalized Extreme Value (GEV) distributions, which also includes the Weibull and Frechet.

The function has a mean of $\mu + 0.57721\beta$ and a variance of $\frac{\pi^2}{6}\beta^2$.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> mu, beta = 0, 0.1 # location and scale  # doctest: +SKIP
>>> s = np.random.gumbel(mu, beta, 1000)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 30, density=True)  # doctest: +SKIP
>>> plt.plot(bins, (1/beta)*np.exp(-(bins - mu)/beta)  # doctest: +SKIP
...          * np.exp( -np.exp( -(bins - mu) /beta) ),
...          linewidth=2, color='r')
>>> plt.show()  # doctest: +SKIP
```

Show how an extreme value distribution can arise from a Gaussian process and compare to a Gaussian:

```
>>> means = []  # doctest: +SKIP
>>> maxima = []  # doctest: +SKIP
>>> for i in range(0,1000) :  # doctest: +SKIP
...    a = np.random.normal(mu, beta, 1000)
...    means.append(a.mean())
...    maxima.append(a.max())
>>> count, bins, ignored = plt.hist(maxima, 30, density=True)  # doctest: +SKIP
>>> beta = np.std(maxima) * np.sqrt(6) / np.pi  # doctest: +SKIP
>>> mu = np.mean(maxima) - 0.57721*beta  # doctest: +SKIP
```

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```
>>> plt.plot(bins, (1/beta)*np.exp(-(bins - mu)/beta)  # doctest: +SKIP
...          * np.exp(-np.exp(-(bins - mu)/beta)),
...          linewidth=2, color='r')
>>> plt.plot(bins, 1/(beta * np.sqrt(2 * np.pi))  # doctest: +SKIP
...          * np.exp(-(bins - mu)**2 / (2 * beta**2)),
...          linewidth=2, color='g')
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`hypergeometric`**`(`*ngood*, *nbad*, *nsample*, *size=None*`)`

Draw samples from a Hypergeometric distribution.

Samples are drawn from a hypergeometric distribution with specified parameters, ngood (ways to make a good selection), nbad (ways to make a bad selection), and nsample = number of items sampled, which is less than or equal to the sum ngood + nbad.

Parameters

ngood [int or array_like of ints] Number of ways to make a good selection. Must be nonnegative.

nbad [int or array_like of ints] Number of ways to make a bad selection. Must be nonnegative.

nsample [int or array_like of ints] Number of items sampled. Must be at least 1 and at most `ngood + nbad`.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `ngood`, `nbad`, and `nsample` are all scalars. Otherwise, `np.broadcast(ngood, nbad, nsample).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized hypergeometric distribution.

See also:

`scipy.stats.hypergeom` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Hypergeometric distribution is

$$P(x) = \frac{\binom{g}{x}\binom{b}{n-x}}{\binom{g+b}{n}},$$

where $0 \le x \le n$ and $n - b \le x \le g$

for P(x) the probability of x successes, g = ngood, b = nbad, and n = number of samples.

Consider an urn with black and white marbles in it, ngood of them black and nbad are white. If you draw nsample balls without replacement, then the hypergeometric distribution describes the distribution of black balls in the drawn sample.

Note that this distribution is very similar to the binomial distribution, except that in this case, samples are drawn without replacement, whereas in the Binomial case samples are drawn with replacement (or the sample space is infinite). As the sample space becomes large, this distribution approaches the binomial.

References

[1], [2], [3]

Examples

Draw samples from the distribution:

```
>>> ngood, nbad, nsamp = 100, 2, 10  # doctest: +SKIP
# number of good, number of bad, and number of samples
>>> s = np.random.hypergeometric(ngood, nbad, nsamp, 1000)  # doctest: +SKIP
>>> from matplotlib.pyplot import hist  # doctest: +SKIP
>>> hist(s)  # doctest: +SKIP
#   note that it is very unlikely to grab both bad items
```

Suppose you have an urn with 15 white and 15 black marbles. If you pull 15 marbles at random, how likely is it that 12 or more of them are one color?

```
>>> s = np.random.hypergeometric(15, 15, 15, 100000)  # doctest: +SKIP
>>> sum(s>=12)/100000. + sum(s<=3)/100000.  # doctest: +SKIP
#   answer = 0.003 ... pretty unlikely!
```

`dask.array.random.`**`laplace`**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw samples from the Laplace or double exponential distribution with specified location (or mean) and scale (decay).

The Laplace distribution is similar to the Gaussian/normal distribution, but is sharper at the peak and has fatter tails. It represents the difference between two independent, identically distributed exponential random variables.

Parameters

loc [float or array_like of floats, optional] The position, μ, of the distribution peak. Default is 0.

scale [float or array_like of floats, optional] λ, the exponential decay. Default is 1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `loc` and `scale` are both scalars. Otherwise, `np.broadcast(loc, scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Laplace distribution.

Notes

It has the probability density function

$$f(x; \mu, \lambda) = \frac{1}{2\lambda} \exp\left(-\frac{|x - \mu|}{\lambda}\right).$$

The first law of Laplace, from 1774, states that the frequency of an error can be expressed as an exponential function of the absolute magnitude of the error, which leads to the Laplace distribution. For many problems in economics and health sciences, this distribution seems to model the data better than the standard Gaussian distribution.

References

[1], [2], [3], [4]

Examples

Draw samples from the distribution

```
>>> loc, scale = 0., 1.  # doctest: +SKIP
>>> s = np.random.laplace(loc, scale, 1000)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 30, density=True)  # doctest: +SKIP
>>> x = np.arange(-8., 8., .01)  # doctest: +SKIP
>>> pdf = np.exp(-abs(x-loc)/scale)/(2.*scale)  # doctest: +SKIP
>>> plt.plot(x, pdf)  # doctest: +SKIP
```

Plot Gaussian for comparison:

```
>>> g = (1/(scale * np.sqrt(2 * np.pi)) *  # doctest: +SKIP
...      np.exp(-(x - loc)**2 / (2 * scale**2)))
>>> plt.plot(x,g)  # doctest: +SKIP
```

dask.array.random.**logistic**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw samples from a logistic distribution.

Samples are drawn from a logistic distribution with specified parameters, loc (location or mean, also median), and scale (>0).

Parameters

loc [float or array_like of floats, optional] Parameter of the distribution. Default is 0.

scale [float or array_like of floats, optional] Parameter of the distribution. Should be greater than zero. Default is 1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `loc` and `scale` are both scalars. Otherwise, `np.broadcast(loc, scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized logistic distribution.

See also:

`scipy.stats.logistic` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Logistic distribution is

$$P(x) = P(x) = \frac{e^{-(x-\mu)/s}}{s(1+e^{-(x-\mu)/s})^2},$$

where μ = location and s = scale.

The Logistic distribution is used in Extreme Value problems where it can act as a mixture of Gumbel distributions, in Epidemiology, and by the World Chess Federation (FIDE) where it is used in the Elo ranking system, assuming the performance of each player is a logistically distributed random variable.

References

[1], [2], [3]

Examples

Draw samples from the distribution:

```
>>> loc, scale = 10, 1  # doctest: +SKIP
>>> s = np.random.logistic(loc, scale, 10000)  # doctest: +SKIP
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, bins=50)  # doctest: +SKIP
```

# plot against distribution

```
>>> def logist(x, loc, scale):  # doctest: +SKIP
...     return exp((loc-x)/scale)/(scale*(1+exp((loc-x)/scale))**2)
>>> plt.plot(bins, logist(bins, loc, scale)*count.max()/\  # doctest: +SKIP
... logist(bins, loc, scale).max())
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`lognormal`**`(`*mean=0.0*, *sigma=1.0*, *size=None*`)`

Draw samples from a log-normal distribution.

Draw samples from a log-normal distribution with specified mean, standard deviation, and array shape. Note that the mean and standard deviation are not the values for the distribution itself, but of the underlying normal distribution it is derived from.

Parameters

mean [float or array_like of floats, optional] Mean value of the underlying normal distribution. Default is 0.

sigma [float or array_like of floats, optional] Standard deviation of the underlying normal distribution. Should be greater than zero. Default is 1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `mean` and `sigma` are both scalars. Otherwise, `np.broadcast(mean, sigma).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized log-normal distribution.

See also:

`scipy.stats.lognorm` probability density function, distribution, cumulative density function, etc.

Notes

A variable *x* has a log-normal distribution if *log(x)* is normally distributed. The probability density function for the log-normal distribution is:

$$p(x) = \frac{1}{\sigma x \sqrt{2\pi}} e^{(-\frac{(ln(x)-\mu)^2}{2\sigma^2})}$$

where μ is the mean and σ is the standard deviation of the normally distributed logarithm of the variable. A log-normal distribution results if a random variable is the *product* of a large number of independent, identically-distributed variables in the same way that a normal distribution results if the variable is the *sum* of a large number of independent, identically-distributed variables.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> mu, sigma = 3., 1. # mean and standard deviation  # doctest: +SKIP
>>> s = np.random.lognormal(mu, sigma, 1000)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 100, density=True, align='mid')  #␣
↪doctest: +SKIP
```

```
>>> x = np.linspace(min(bins), max(bins), 10000)  # doctest: +SKIP
>>> pdf = (np.exp(-(np.log(x) - mu)**2 / (2 * sigma**2))  # doctest: +SKIP
...        / (x * sigma * np.sqrt(2 * np.pi)))
```

```
>>> plt.plot(x, pdf, linewidth=2, color='r')  # doctest: +SKIP
>>> plt.axis('tight')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

Demonstrate that taking the products of random samples from a uniform distribution can be fit well by a log-normal probability density function.

```
>>> # Generate a thousand samples: each is the product of 100 random
>>> # values, drawn from a normal distribution.
>>> b = []  # doctest: +SKIP
>>> for i in range(1000):  # doctest: +SKIP
...    a = 10. + np.random.random(100)
...    b.append(np.product(a))
```

```
>>> b = np.array(b) / np.min(b) # scale values to be positive  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(b, 100, density=True, align='mid')  #␣
↪doctest: +SKIP
>>> sigma = np.std(np.log(b))  # doctest: +SKIP
>>> mu = np.mean(np.log(b))  # doctest: +SKIP
>>> x = np.linspace(min(bins), max(bins), 10000)  # doctest: +SKIP
>>> pdf = (np.exp(-(np.log(x) - mu)**2 / (2 * sigma**2))  # doctest: +SKIP
...        / (x * sigma * np.sqrt(2 * np.pi)))
```

```
>>> plt.plot(x, pdf, color='r', linewidth=2)  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`logseries`**(*p*, *size=None*)

Draw samples from a logarithmic series distribution.

Samples are drawn from a log series distribution with specified shape parameter, 0 < `p` < 1.

Parameters

p [float or array_like of floats] Shape parameter for the distribution. Must be in the range (0, 1).

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `p` is a scalar. Otherwise, `np.array(p).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized logarithmic series distribution.

See also:

`scipy.stats.logser` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Log Series distribution is

$$P(k) = \frac{-p^k}{k \ln(1-p)},$$

where p = probability.

The log series distribution is frequently used to represent species richness and occurrence, first proposed by Fisher, Corbet, and Williams in 1943 [2]. It may also be used to model the numbers of occupants seen in cars [3].

References

[1], [2], [3], [4]

Examples

Draw samples from the distribution:

```
>>> a = .6  # doctest: +SKIP
>>> s = np.random.logseries(a, 10000)  # doctest: +SKIP
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s)  # doctest: +SKIP
```

# plot against distribution

```
>>> def logseries(k, p):  # doctest: +SKIP
...     return -p**k/(k*log(1-p))
>>> plt.plot(bins, logseries(bins, a)*count.max()/  # doctest: +SKIP
         logseries(bins, a).max(), 'r')
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`negative_binomial`**`(`*n, p, size=None*`)`

Draw samples from a negative binomial distribution.

Samples are drawn from a negative binomial distribution with specified parameters, *n* successes and *p* probability of success where *n* is an integer > 0 and *p* is in the interval [0, 1].

Parameters

n [int or array_like of ints] Parameter of the distribution, > 0. Floats are also accepted, but they will be truncated to integers.

p [float or array_like of floats] Parameter of the distribution, >= 0 and <=1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `n` and `p` are both scalars. Otherwise, `np.broadcast(n, p).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized negative binomial distribution, where each sample is equal to N, the number of failures that occurred before a total of n successes was reached.

Notes

The probability density for the negative binomial distribution is

$$P(N; n, p) = \binom{N + n - 1}{N} p^{n}(1 - p)^{N},$$

where n is the number of successes, p is the probability of success, and $N + n$ is the number of trials. The negative binomial distribution gives the probability of N failures given n successes, with a success on the last trial.

If one throws a die repeatedly until the third time a “1” appears, then the probability distribution of the number of non-“1”s that appear before the third “1” is a negative binomial distribution.

References

[1], [2]

Examples

Draw samples from the distribution:

A real world example. A company drills wild-cat oil exploration wells, each with an estimated probability of success of 0.1. What is the probability of having one success for each successive well, that is what is the probability of a single success after drilling 5 wells, after 6 wells, etc.?

```
>>> s = np.random.negative_binomial(1, 0.1, 100000)  # doctest: +SKIP
>>> for i in range(1, 11):  # doctest: +SKIP
...     probability = sum(s<i) / 100000.
...     print i, "wells drilled, probability of one success =", probability
```

`dask.array.random.`**`noncentral_chisquare`**(*df*, *nonc*, *size=None*)

Draw samples from a noncentral chi-square distribution.

The noncentral χ^2 distribution is a generalisation of the χ^2 distribution.

Parameters

df [float or array_like of floats] Degrees of freedom, should be > 0.

Changed in version 1.10.0: Earlier NumPy versions required dfnum > 1.

nonc [float or array_like of floats] Non-centrality, should be non-negative.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `df` and `nonc` are both scalars. Otherwise, `np.broadcast(df, nonc).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized noncentral chi-square distribution.

Notes

The probability density function for the noncentral Chi-square distribution is

$$P(x;df,nonc) = \sum_{i=0}^{\infty} \frac{e^{-nonc/2}(nonc/2)^{i}}{i!} \P_{Y_{df+2i}}(x),$$

where Y_q is the Chi-square with q degrees of freedom.

In Delhi (2007), it is noted that the noncentral chi-square is useful in bombing and coverage problems, the probability of killing the point target given by the noncentral chi-squared distribution.

References

[1], [2]

Examples

Draw values from the distribution and plot the histogram

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> values = plt.hist(np.random.noncentral_chisquare(3, 20, 100000),  # doctest:␣
↪+SKIP
...                   bins=200, density=True)
>>> plt.show()  # doctest: +SKIP
```

Draw values from a noncentral chisquare with very small noncentrality, and compare to a chisquare.

```
>>> plt.figure()   # doctest: +SKIP
>>> values = plt.hist(np.random.noncentral_chisquare(3, .0000001, 100000),   #␣
↪doctest: +SKIP
...                       bins=np.arange(0., 25, .1), density=True)
>>> values2 = plt.hist(np.random.chisquare(3, 100000),   # doctest: +SKIP
...                        bins=np.arange(0., 25, .1), density=True)
>>> plt.plot(values[1][0:-1], values[0]-values2[0], 'ob')   # doctest: +SKIP
>>> plt.show()   # doctest: +SKIP
```

Demonstrate how large values of non-centrality lead to a more symmetric distribution.

```
>>> plt.figure()   # doctest: +SKIP
>>> values = plt.hist(np.random.noncentral_chisquare(3, 20, 100000),   # doctest:␣
↪+SKIP
...                       bins=200, density=True)
>>> plt.show()   # doctest: +SKIP
```

`dask.array.random.`**`noncentral_f`**(*dfnum*, *dfden*, *nonc*, *size=None*)

Draw samples from the noncentral F distribution.

Samples are drawn from an F distribution with specified parameters, *dfnum* (degrees of freedom in numerator) and *dfden* (degrees of freedom in denominator), where both parameters > 1. *nonc* is the non-centrality parameter.

Parameters

dfnum [float or array_like of floats] Numerator degrees of freedom, should be > 0.

Changed in version 1.14.0: Earlier NumPy versions required dfnum > 1.

dfden [float or array_like of floats] Denominator degrees of freedom, should be > 0.

nonc [float or array_like of floats] Non-centrality parameter, the sum of the squares of the numerator means, should be >= 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `dfnum`, `dfden`, and `nonc` are all scalars. Otherwise, `np.broadcast(dfnum, dfden, nonc).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized noncentral Fisher distribution.

Notes

When calculating the power of an experiment (power = probability of rejecting the null hypothesis when a specific alternative is true) the non-central F statistic becomes important. When the null hypothesis is true, the F statistic follows a central F distribution. When the null hypothesis is not true, then it follows a non-central F statistic.

References

[1], [2]

Examples

In a study, testing for a specific alternative to the null hypothesis requires use of the Noncentral F distribution. We need to calculate the area in the tail of the distribution that exceeds the value of the F distribution for the null hypothesis. We'll plot the two probability distributions for comparison.

```
>>> dfnum = 3 # between group deg of freedom  # doctest: +SKIP
>>> dfden = 20 # within groups degrees of freedom  # doctest: +SKIP
>>> nonc = 3.0  # doctest: +SKIP
>>> nc_vals = np.random.noncentral_f(dfnum, dfden, nonc, 1000000)  # doctest:␣
↪+SKIP
>>> NF = np.histogram(nc_vals, bins=50, density=True)  # doctest: +SKIP
>>> c_vals = np.random.f(dfnum, dfden, 1000000)  # doctest: +SKIP
>>> F = np.histogram(c_vals, bins=50, density=True)  # doctest: +SKIP
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> plt.plot(F[1][1:], F[0])  # doctest: +SKIP
>>> plt.plot(NF[1][1:], NF[0])  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`normal`**(*loc=0.0*, *scale=1.0*, *size=None*)

Draw random samples from a normal (Gaussian) distribution.

The probability density function of the normal distribution, first derived by De Moivre and 200 years later by both Gauss and Laplace independently [2], is often called the bell curve because of its characteristic shape (see the example below).

The normal distributions occurs often in nature. For example, it describes the commonly occurring distribution of samples influenced by a large number of tiny, random disturbances, each with its own unique distribution [2].

Parameters

loc [float or array_like of floats] Mean ("centre") of the distribution.

scale [float or array_like of floats] Standard deviation (spread or "width") of the distribution.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `loc` and `scale` are both scalars. Otherwise, `np.broadcast(loc, scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized normal distribution.

See also:

`scipy.stats.norm` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gaussian distribution is

$$p(x) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}},$$

where μ is the mean and σ the standard deviation. The square of the standard deviation, σ^2, is called the variance.

The function has its peak at the mean, and its "spread" increases with the standard deviation (the function reaches 0.607 times its maximum at $x + \sigma$ and $x - \sigma$ [2]). This implies that *numpy.random.normal* is more likely to return samples lying close to the mean, rather than those far away.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> mu, sigma = 0, 0.1 # mean and standard deviation  # doctest: +SKIP
>>> s = np.random.normal(mu, sigma, 1000)  # doctest: +SKIP
```

Verify the mean and the variance:

```
>>> abs(mu - np.mean(s)) < 0.01  # doctest: +SKIP
True
```

```
>>> abs(sigma - np.std(s, ddof=1)) < 0.01  # doctest: +SKIP
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 30, density=True)  # doctest: +SKIP
>>> plt.plot(bins, 1/(sigma * np.sqrt(2 * np.pi)) *  # doctest: +SKIP
...                np.exp( - (bins - mu)**2 / (2 * sigma**2) ),
...          linewidth=2, color='r')
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`pareto`**`(`*a*, *size=None*`)`

Draw samples from a Pareto II or Lomax distribution with specified shape.

The Lomax or Pareto II distribution is a shifted Pareto distribution. The classical Pareto distribution can be obtained from the Lomax distribution by adding 1 and multiplying by the scale parameter `m` (see Notes). The smallest value of the Lomax distribution is zero while for the classical Pareto distribution it is `mu`, where the standard Pareto distribution has location `mu = 1`. Lomax can also be considered as a simplified version of the Generalized Pareto distribution (available in SciPy), with the scale set to one and the location set to zero.

The Pareto distribution must be greater than zero, and is unbounded above. It is also known as the "80-20 rule". In this distribution, 80 percent of the weights are in the lowest 20 percent of the range, while the other 20 percent fill the remaining 80 percent of the range.

Parameters

a [float or array_like of floats] Shape of the distribution. Should be greater than zero.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `a` is a scalar. Otherwise, `np.array(a).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Pareto distribution.

See also:

`scipy.stats.lomax` probability density function, distribution or cumulative density function, etc.

`scipy.stats.genpareto` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Pareto distribution is

$$p(x) = \frac{am^a}{x^{a+1}}$$

where a is the shape and m the scale.

The Pareto distribution, named after the Italian economist Vilfredo Pareto, is a power law probability distribution useful in many real world problems. Outside the field of economics it is generally referred to as the Bradford distribution. Pareto developed the distribution to describe the distribution of wealth in an economy. It has also found use in insurance, web page access statistics, oil field sizes, and many other problems, including the download frequency for projects in Sourceforge [1]. It is one of the so-called "fat-tailed" distributions.

References

[1], [2], [3], [4]

Examples

Draw samples from the distribution:

```
>>> a, m = 3., 2.  # shape and mode  # doctest: +SKIP
>>> s = (np.random.pareto(a, 1000) + 1) * m  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, _ = plt.hist(s, 100, density=True)  # doctest: +SKIP
>>> fit = a*m**a / bins**(a+1)  # doctest: +SKIP
>>> plt.plot(bins, max(count)*fit/max(fit), linewidth=2, color='r')  # doctest:␣
↪+SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`poisson`**(*lam=1.0*, *size=None*)

Draw samples from a Poisson distribution.

The Poisson distribution is the limit of the binomial distribution for large N.

Parameters

lam [float or array_like of floats] Expectation of interval, should be >= 0. A sequence of expectation intervals must be broadcastable over the requested size.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `lam` is a scalar. Otherwise, `np.array(lam).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Poisson distribution.

Notes

The Poisson distribution

$$f(k; \lambda) = \frac{\lambda^k e^{-\lambda}}{k!}$$

For events with an expected separation λ the Poisson distribution $f(k;\lambda)$ describes the probability of k events occurring within the observed interval λ.

Because the output is limited to the range of the C long type, a ValueError is raised when *lam* is within 10 sigma of the maximum representable value.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> import numpy as np  # doctest: +SKIP
>>> s = np.random.poisson(5, 10000)  # doctest: +SKIP
```

Display histogram of the sample:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 14, density=True)  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

Draw each 100 values for lambda 100 and 500:

```
>>> s = np.random.poisson(lam=(100., 500.), size=(100, 2))  # doctest: +SKIP
```

`dask.array.random.`**`power`**(*a*, *size=None*)

Draws samples in [0, 1] from a power distribution with positive exponent a - 1.

Also known as the power function distribution.

Parameters

a [float or array_like of floats] Parameter of the distribution. Should be greater than zero.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `a` is a scalar. Otherwise, `np.array(a).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized power distribution.

Raises

ValueError If a < 1.

Notes

The probability density function is

$$P(x;a) = ax^{a-1}, 0 \le x \le 1, a > 0.$$

The power function distribution is just the inverse of the Pareto distribution. It may also be seen as a special case of the Beta distribution.

It is used, for example, in modeling the over-reporting of insurance claims.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> a = 5. # shape  # doctest: +SKIP
>>> samples = 1000  # doctest: +SKIP
>>> s = np.random.power(a, samples)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, bins=30)  # doctest: +SKIP
>>> x = np.linspace(0, 1, 100)  # doctest: +SKIP
>>> y = a*x**(a-1.)  # doctest: +SKIP
>>> normed_y = samples*np.diff(bins)[0]*y  # doctest: +SKIP
>>> plt.plot(x, normed_y)  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

Compare the power function distribution to the inverse of the Pareto.

```
>>> from scipy import stats  # doctest: +SKIP
>>> rvs = np.random.power(5, 1000000)  # doctest: +SKIP
>>> rvsp = np.random.pareto(5, 1000000)  # doctest: +SKIP
>>> xx = np.linspace(0,1,100)  # doctest: +SKIP
>>> powpdf = stats.powerlaw.pdf(xx,5)  # doctest: +SKIP
```

```
>>> plt.figure()  # doctest: +SKIP
>>> plt.hist(rvs, bins=50, density=True)  # doctest: +SKIP
>>> plt.plot(xx,powpdf,'r-')  # doctest: +SKIP
>>> plt.title('np.random.power(5)')  # doctest: +SKIP
```

```
>>> plt.figure()  # doctest: +SKIP
>>> plt.hist(1./(1.+rvsp), bins=50, density=True)  # doctest: +SKIP
>>> plt.plot(xx,powpdf,'r-')  # doctest: +SKIP
>>> plt.title('inverse of 1 + np.random.pareto(5)')  # doctest: +SKIP
```

```
>>> plt.figure()  # doctest: +SKIP
>>> plt.hist(1./(1.+rvsp), bins=50, density=True)  # doctest: +SKIP
>>> plt.plot(xx,powpdf,'r-')  # doctest: +SKIP
>>> plt.title('inverse of stats.pareto(5)')  # doctest: +SKIP
```

`dask.array.random.`**`randint`**(*low*, *high=None*, *size=None*, *dtype='l'*)

Return random integers from *low* (inclusive) to *high* (exclusive).

Return random integers from the "discrete uniform" distribution of the specified dtype in the "half-open" interval [*low*, *high*). If *high* is None (the default), then results are from [0, *low*).

Parameters

low [int] Lowest (signed) integer to be drawn from the distribution (unless `high=None`, in which case this parameter is one above the *highest* such integer).

high [int, optional] If provided, one above the largest (signed) integer to be drawn from the distribution (see above for behavior if `high=None`).

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

dtype [dtype, optional] Desired dtype of the result. All dtypes are determined by their name, i.e., 'int64', 'int', etc, so byteorder is not available and a specific precision may have different C types depending on the platform. The default value is 'np.int'.

New in version 1.11.0.

Returns

out [int or ndarray of ints] *size*-shaped array of random integers from the appropriate distribution, or a single such random int if *size* not provided.

See also:

`random.random_integers` similar to *randint*, only for the closed interval [*low*, *high*], and 1 is the lowest value if *high* is omitted. In particular, this other one is the one to use to generate uniformly distributed discrete non-integers.

Examples

```
>>> np.random.randint(2, size=10)  # doctest: +SKIP
array([1, 0, 0, 0, 1, 1, 0, 0, 1, 0])
>>> np.random.randint(1, size=10)  # doctest: +SKIP
array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0])
```

Generate a 2 x 4 array of ints between 0 and 4, inclusive:

```
>>> np.random.randint(5, size=(2, 4))  # doctest: +SKIP
array([[4, 0, 2, 1],
       [3, 2, 2, 0]])
```

`dask.array.random.`**`random`**(*size=None*)

Return random floats in the half-open interval [0.0, 1.0).

Results are from the "continuous uniform" distribution over the stated interval. To sample $Unif[a, b), b > a$ multiply the output of *random_sample* by *(b-a)* and add *a*:

```
(b - a) * random_sample() + a
```

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray of floats] Array of random floats of shape *size* (unless `size=None`, in which case a single float is returned).

Examples

```
>>> np.random.random_sample()  # doctest: +SKIP
0.47108547995356098
>>> type(np.random.random_sample())  # doctest: +SKIP
<type 'float'>
>>> np.random.random_sample((5,))  # doctest: +SKIP
array([ 0.30220482,  0.86820401,  0.1654503 ,  0.11659149,  0.54323428])
```

Three-by-two array of random numbers from [-5, 0):

```
>>> 5 * np.random.random_sample((3, 2)) - 5  # doctest: +SKIP
array([[-3.99149989, -0.52338984],
       [-2.99091858, -0.79479508],
       [-1.23204345, -1.75224494]])
```

`dask.array.random.`**`random_sample`**`(`*size=None*`)`

Return random floats in the half-open interval [0.0, 1.0).

Results are from the “continuous uniform” distribution over the stated interval. To sample $Unif[a, b), b > a$ multiply the output of *random_sample* by *(b-a)* and add *a*:

```
(b - a) * random_sample() + a
```

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray of floats] Array of random floats of shape *size* (unless `size=None`, in which case a single float is returned).

Examples

```
>>> np.random.random_sample()  # doctest: +SKIP
0.47108547995356098
>>> type(np.random.random_sample())  # doctest: +SKIP
<type 'float'>
>>> np.random.random_sample((5,))  # doctest: +SKIP
array([ 0.30220482,  0.86820401,  0.1654503 ,  0.11659149,  0.54323428])
```

Three-by-two array of random numbers from [-5, 0):

```
>>> 5 * np.random.random_sample((3, 2)) - 5  # doctest: +SKIP
array([[-3.99149989, -0.52338984],
       [-2.99091858, -0.79479508],
       [-1.23204345, -1.75224494]])
```

`dask.array.random.`**`rayleigh`**`(`*scale=1.0*, *size=None*`)`

Draw samples from a Rayleigh distribution.

The χ and Weibull distributions are generalizations of the Rayleigh.

Parameters

scale [float or array_like of floats, optional] Scale, also equals the mode. Should be >= 0. Default is 1.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `scale` is a scalar. Otherwise, `np.array(scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Rayleigh distribution.

Notes

The probability density function for the Rayleigh distribution is

$$P(x; scale) = \frac{x}{scale^2} e^{\frac{-x^2}{2 \cdot scale^2}}$$

The Rayleigh distribution would arise, for example, if the East and North components of the wind velocity had identical zero-mean Gaussian distributions. Then the wind speed would have a Rayleigh distribution.

References

[1], [2]

Examples

Draw values from the distribution and plot the histogram

```
>>> from matplotlib.pyplot import hist  # doctest: +SKIP
>>> values = hist(np.random.rayleigh(3, 100000), bins=200, density=True)  #␣
↪doctest: +SKIP
```

Wave heights tend to follow a Rayleigh distribution. If the mean wave height is 1 meter, what fraction of waves are likely to be larger than 3 meters?

```
>>> meanvalue = 1  # doctest: +SKIP
>>> modevalue = np.sqrt(2 / np.pi) * meanvalue  # doctest: +SKIP
>>> s = np.random.rayleigh(modevalue, 1000000)  # doctest: +SKIP
```

The percentage of waves larger than 3 meters is:

```
>>> 100.*sum(s>3)/1000000.  # doctest: +SKIP
0.087300000000000003
```

`dask.array.random.`**`standard_cauchy`**`(`*size=None*`)`

Draw samples from a standard Cauchy distribution with mode = 0.

Also known as the Lorentz distribution.

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

samples [ndarray or scalar] The drawn samples.

Notes

The probability density function for the full Cauchy distribution is

$$P(x; x_0, \gamma) = \frac{1}{\pi \gamma \bigl[1+(\frac{x-x_0}{\gamma})^2 \bigr] }$$

and the Standard Cauchy distribution just sets $x_0 = 0$ and $\gamma = 1$

The Cauchy distribution arises in the solution to the driven harmonic oscillator problem, and also describes spectral line broadening. It also describes the distribution of values at which a line tilted at a random angle will cut the x axis.

When studying hypothesis tests that assume normality, seeing how the tests perform on data from a Cauchy distribution is a good indicator of their sensitivity to a heavy-tailed distribution, since the Cauchy looks very much like a Gaussian distribution, but with heavier tails.

References

[1], [2], [3]

Examples

Draw samples and plot the distribution:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> s = np.random.standard_cauchy(1000000)  # doctest: +SKIP
>>> s = s[(s>-25) & (s<25)]  # truncate distribution so it plots well  # doctest:␣
↪+SKIP
>>> plt.hist(s, bins=100)  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`standard_exponential`**`(`*size=None*`)`

Draw samples from the standard exponential distribution.

standard_exponential is identical to the exponential distribution with a scale parameter of 1.

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray] Drawn samples.

Examples

Output a 3x8000 array:

```
>>> n = np.random.standard_exponential((3, 8000))  # doctest: +SKIP
```

`dask.array.random.`**`standard_gamma`**`(`*shape*, *size=None*`)`

Draw samples from a standard Gamma distribution.

Samples are drawn from a Gamma distribution with specified parameters, shape (sometimes designated "k") and scale=1.

Parameters

shape [float or array_like of floats] Parameter, should be > 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `shape` is a scalar. Otherwise, `np.array(shape).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized standard gamma distribution.

See also:

`scipy.stats.gamma` probability density function, distribution or cumulative density function, etc.

Notes

The probability density for the Gamma distribution is

$$p(x) = x^{k-1}\frac{e^{-x/\theta}}{\theta^k\Gamma(k)},$$

where k is the shape and θ the scale, and Γ is the Gamma function.

The Gamma distribution is often used to model the times to failure of electronic components, and arises naturally in processes for which the waiting times between Poisson distributed events are relevant.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> shape, scale = 2., 1. # mean and width  # doctest: +SKIP
>>> s = np.random.standard_gamma(shape, 1000000)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> import scipy.special as sps  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 50, density=True)  # doctest: +SKIP
>>> y = bins**(shape-1) * ((np.exp(-bins/scale))/ \  # doctest: +SKIP
...                       (sps.gamma(shape) * scale**shape))
>>> plt.plot(bins, y, linewidth=2, color='r')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`standard_normal`**`(`*size=None*`)`

Draw samples from a standard Normal distribution (mean=0, stdev=1).

Parameters

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. Default is None, in which case a single value is returned.

Returns

out [float or ndarray] Drawn samples.

Examples

```
>>> s = np.random.standard_normal(8000)  # doctest: +SKIP
>>> s  # doctest: +SKIP
array([ 0.6888893 ,  0.78096262, -0.89086505, ...,  0.49876311, #random
       -0.38672696, -0.4685006 ])                                #random
>>> s.shape  # doctest: +SKIP
(8000,)
>>> s = np.random.standard_normal(size=(3, 4, 2))  # doctest: +SKIP
>>> s.shape  # doctest: +SKIP
(3, 4, 2)
```

`dask.array.random.`**`standard_t`**(*df*, *size=None*)

Draw samples from a standard Student's t distribution with *df* degrees of freedom.

A special case of the hyperbolic distribution. As *df* gets large, the result resembles that of the standard normal distribution (*standard_normal*).

Parameters

df [float or array_like of floats] Degrees of freedom, should be > 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `df` is a scalar. Otherwise, `np.array(df).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized standard Student's t distribution.

Notes

The probability density function for the t distribution is

$$P(x, df) = \frac{\Gamma(\frac{df+1}{2})}{\sqrt{\pi df}\Gamma(\frac{df}{2})}\Big(1 + \frac{x^2}{df}\Big)^{-(df+1)/2}$$

The t test is based on an assumption that the data come from a Normal distribution. The t test provides a way to test whether the sample mean (that is the mean calculated from the data) is a good estimate of the true mean.

The derivation of the t-distribution was first published in 1908 by William Gosset while working for the Guinness Brewery in Dublin. Due to proprietary issues, he had to publish under a pseudonym, and so he used the name Student.

References

[1], [2]

Examples

From Dalgaard page 83 [1], suppose the daily energy intake for 11 women in kilojoules (kJ) is:

```
>>> intake = np.array([5260., 5470, 5640, 6180, 6390, 6515, 6805, 7515, \  #␣
↪doctest: +SKIP
...                    7515, 8230, 8770])
```

Does their energy intake deviate systematically from the recommended value of 7725 kJ?

We have 10 degrees of freedom, so is the sample mean within 95% of the recommended value?

```
>>> s = np.random.standard_t(10, size=100000)  # doctest: +SKIP
>>> np.mean(intake)  # doctest: +SKIP
6753.636363636364
>>> intake.std(ddof=1)  # doctest: +SKIP
1142.1232221373727
```

Calculate the t statistic, setting the ddof parameter to the unbiased value so the divisor in the standard deviation will be degrees of freedom, N-1.

```
>>> t = (np.mean(intake)-7725)/(intake.std(ddof=1)/np.sqrt(len(intake)))  #␣
↪doctest: +SKIP
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> h = plt.hist(s, bins=100, density=True)  # doctest: +SKIP
```

For a one-sided t-test, how far out in the distribution does the t statistic appear?

```
>>> np.sum(s<t) / float(len(s))  # doctest: +SKIP
0.0090699999999999999  #random
```

So the p-value is about 0.009, which says the null hypothesis has a probability of about 99% of being true.

dask.array.random.**triangular**(*left*, *mode*, *right*, *size=None*)

Draw samples from the triangular distribution over the interval `[left, right]`.

The triangular distribution is a continuous probability distribution with lower limit left, peak at mode, and upper limit right. Unlike the other distributions, these parameters directly define the shape of the pdf.

Parameters

left [float or array_like of floats] Lower limit.

mode [float or array_like of floats] The value where the peak of the distribution occurs. The value should fulfill the condition `left <= mode <= right`.

right [float or array_like of floats] Upper limit, should be larger than *left*.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `left`, `mode`, and `right` are all scalars. Otherwise, `np.broadcast(left, mode, right).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized triangular distribution.

Notes

The probability density function for the triangular distribution is

$$P(x;l,m,r) = \begin{cases} \frac{2(x-l)}{(r-l)(m-l)} & \text{for } l \leq x \leq m, \\ \frac{2(r-x)}{(r-l)(r-m)} & \text{for } m \leq x \leq r, \\ 0 & \text{otherwise.} \end{cases}$$

The triangular distribution is often used in ill-defined problems where the underlying distribution is not known, but some knowledge of the limits and mode exists. Often it is used in simulations.

References

[1]

Examples

Draw values from the distribution and plot the histogram:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> h = plt.hist(np.random.triangular(-3, 0, 8, 100000), bins=200,  # doctest:␣
↪+SKIP
...                 density=True)
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`uniform`**`(`*low=0.0*, *high=1.0*, *size=None*`)`

Draw samples from a uniform distribution.

Samples are uniformly distributed over the half-open interval `[low, high)` (includes low, but excludes high). In other words, any value within the given interval is equally likely to be drawn by *uniform*.

Parameters

low [float or array_like of floats, optional] Lower boundary of the output interval. All values generated will be greater than or equal to low. The default value is 0.

high [float or array_like of floats] Upper boundary of the output interval. All values generated will be less than high. The default value is 1.0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `low` and `high` are both scalars. Otherwise, `np.broadcast(low, high).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized uniform distribution.

See also:

`randint` Discrete uniform distribution, yielding integers.

`random_integers` Discrete uniform distribution over the closed interval `[low, high]`.

`random_sample` Floats uniformly distributed over `[0, 1)`.

`random` Alias for *random_sample*.

`rand` Convenience function that accepts dimensions as input, e.g., `rand(2,2)` would generate a 2-by-2 array of floats, uniformly distributed over `[0, 1)`.

Notes

The probability density function of the uniform distribution is

$$p(x) = \frac{1}{b - a}$$

anywhere within the interval `[a, b)`, and zero elsewhere.

When `high` == `low`, values of `low` will be returned. If `high` < `low`, the results are officially undefined and may eventually raise an error, i.e. do not rely on this function to behave when passed arguments satisfying that inequality condition.

Examples

Draw samples from the distribution:

```
>>> s = np.random.uniform(-1,0,1000)  # doctest: +SKIP
```

All values are within the given interval:

```
>>> np.all(s >= -1)  # doctest: +SKIP
True
>>> np.all(s < 0)  # doctest: +SKIP
True
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> count, bins, ignored = plt.hist(s, 15, density=True)  # doctest: +SKIP
>>> plt.plot(bins, np.ones_like(bins), linewidth=2, color='r')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`vonmises`**`(`*mu*, *kappa*, *size=None*`)`

Draw samples from a von Mises distribution.

Samples are drawn from a von Mises distribution with specified mode (mu) and dispersion (kappa), on the interval [-pi, pi].

The von Mises distribution (also known as the circular normal distribution) is a continuous probability distribution on the unit circle. It may be thought of as the circular analogue of the normal distribution.

Parameters

mu [float or array_like of floats] Mode ("center") of the distribution.

kappa [float or array_like of floats] Dispersion of the distribution, has to be >=0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `mu` and `kappa` are both scalars. Otherwise, `np.broadcast(mu, kappa).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized von Mises distribution.

See also:

`scipy.stats.vonmises` probability density function, distribution, or cumulative density function, etc.

Notes

The probability density for the von Mises distribution is

$$p(x) = \frac{e^{\kappa cos(x-\mu)}}{2\pi I_0(\kappa)},$$

where μ is the mode and κ the dispersion, and $I_0(\kappa)$ is the modified Bessel function of order 0.

The von Mises is named for Richard Edler von Mises, who was born in Austria-Hungary, in what is now the Ukraine. He fled to the United States in 1939 and became a professor at Harvard. He worked in probability theory, aerodynamics, fluid mechanics, and philosophy of science.

References

[1], [2]

Examples

Draw samples from the distribution:

```
>>> mu, kappa = 0.0, 4.0 # mean and dispersion  # doctest: +SKIP
>>> s = np.random.vonmises(mu, kappa, 1000)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> from scipy.special import i0  # doctest: +SKIP
>>> plt.hist(s, 50, density=True)  # doctest: +SKIP
>>> x = np.linspace(-np.pi, np.pi, num=51)  # doctest: +SKIP
>>> y = np.exp(kappa*np.cos(x-mu))/(2*np.pi*i0(kappa))  # doctest: +SKIP
>>> plt.plot(x, y, linewidth=2, color='r')  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`wald`**(*mean*, *scale*, *size=None*)

Draw samples from a Wald, or inverse Gaussian, distribution.

As the scale approaches infinity, the distribution becomes more like a Gaussian. Some references claim that the Wald is an inverse Gaussian with mean equal to 1, but this is by no means universal.

The inverse Gaussian distribution was first studied in relationship to Brownian motion. In 1956 M.C.K. Tweedie used the name inverse Gaussian because there is an inverse relationship between the time to cover a unit distance and distance covered in unit time.

Parameters

mean [float or array_like of floats] Distribution mean, should be > 0.

scale [float or array_like of floats] Scale parameter, should be >= 0.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `mean` and `scale` are both scalars. Otherwise, `np.broadcast(mean, scale).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Wald distribution.

Notes

The probability density function for the Wald distribution is

$$P(x; mean, scale) = \sqrt{\frac{scale}{2\pi x^3}}e^{\frac{-scale(x-mean)^2}{2\cdot mean^2 x}}$$

As noted above the inverse Gaussian distribution first arise from attempts to model Brownian motion. It is also a competitor to the Weibull for use in reliability modeling and modeling stock returns and interest rate processes.

References

[1], [2], [3]

Examples

Draw values from the distribution and plot the histogram:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> h = plt.hist(np.random.wald(3, 2, 100000), bins=200, density=True)   #␣
↪doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`weibull`**`(`*a*, *size=None*`)`

Draw samples from a Weibull distribution.

Draw samples from a 1-parameter Weibull distribution with the given shape parameter *a*.

$$X = (-ln(U))^{1/a}$$

Here, U is drawn from the uniform distribution over (0,1].

The more common 2-parameter Weibull, including a scale parameter λ is just $X = \lambda(-ln(U))^{1/a}$.

Parameters

a [float or array_like of floats] Shape parameter of the distribution. Must be nonnegative.

size [int or tuple of ints, optional] Output shape. If the given shape is, e.g., `(m, n, k)`, then `m * n * k` samples are drawn. If size is `None` (default), a single value is returned if `a` is a scalar. Otherwise, `np.array(a).size` samples are drawn.

Returns

out [ndarray or scalar] Drawn samples from the parameterized Weibull distribution.

See also:

`scipy.stats.weibull_max`, `scipy.stats.weibull_min`, `scipy.stats.genextreme`, *`gumbel`*

Notes

The Weibull (or Type III asymptotic extreme value distribution for smallest values, SEV Type III, or Rosin-Rammler distribution) is one of a class of Generalized Extreme Value (GEV) distributions used in modeling extreme value problems. This class includes the Gumbel and Frechet distributions.

The probability density for the Weibull distribution is

$$p(x) = \frac{a}{\lambda}(\frac{x}{\lambda})^{a-1}e^{-(x/\lambda)^a},$$

where a is the shape and λ the scale.

The function has its peak (the mode) at $\lambda(\frac{a-1}{a})^{1/a}$.

When `a = 1`, the Weibull distribution reduces to the exponential distribution.

References

[1], [2], [3]

Examples

Draw samples from the distribution:

```
>>> a = 5. # shape  # doctest: +SKIP
>>> s = np.random.weibull(a, 1000)  # doctest: +SKIP
```

Display the histogram of the samples, along with the probability density function:

```
>>> import matplotlib.pyplot as plt  # doctest: +SKIP
>>> x = np.arange(1,100.)/50.  # doctest: +SKIP
>>> def weib(x,n,a):  # doctest: +SKIP
...     return (a / n) * (x / n)**(a - 1) * np.exp(-(x / n)**a)
```

```
>>> count, bins, ignored = plt.hist(np.random.weibull(5.,1000))  # doctest: +SKIP
>>> x = np.arange(1,100.)/50.  # doctest: +SKIP
>>> scale = count.max()/weib(x, 1., 5.).max()  # doctest: +SKIP
>>> plt.plot(x, weib(x, 1., 5.)*scale)  # doctest: +SKIP
>>> plt.show()  # doctest: +SKIP
```

`dask.array.random.`**`zipf`**`(`*a*, *size=None*`)`

Standard distributions

`dask.array.stats.`**`ttest_ind`**`(`*a*, *b*, *axis=0*, *equal_var=True*`)`

Calculate the T-test for the means of *two independent* samples of scores.

This is a two-sided test for the null hypothesis that 2 independent samples have identical average (expected) values. This test assumes that the populations have identical variances by default.

Parameters

a, b [array_like] The arrays must have the same shape, except in the dimension corresponding to *axis* (the first, by default).

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

equal_var [bool, optional] If True (default), perform a standard independent 2 sample test that assumes equal population variances [1]. If False, perform Welch's t-test, which does not assume equal population variance [2].

New in version 0.11.0.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] The calculated t-statistic.

pvalue [float or array] The two-tailed p-value.

Notes

We can use this test, if we observe two independent samples from the same or different population, e.g. exam scores of boys and girls or of two ethnic groups. The test measures whether the average (expected) value differs significantly across samples. If we observe a large p-value, for example larger than 0.05 or 0.1, then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages.

References

[1], [2]

Examples

```
>>> from scipy import stats  # doctest: +SKIP
>>> np.random.seed(12345678)  # doctest: +SKIP
```

Test with sample with identical means:

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)  # doctest: +SKIP
>>> rvs2 = stats.norm.rvs(loc=5,scale=10,size=500)  # doctest: +SKIP
>>> stats.ttest_ind(rvs1,rvs2)  # doctest: +SKIP
(0.26833823296239279, 0.78849443369564776)
>>> stats.ttest_ind(rvs1,rvs2, equal_var = False)  # doctest: +SKIP
(0.26833823296239279, 0.78849452749500748)
```

ttest_ind underestimates p for unequal variances:

```
>>> rvs3 = stats.norm.rvs(loc=5, scale=20, size=500)  # doctest: +SKIP
>>> stats.ttest_ind(rvs1, rvs3)  # doctest: +SKIP
(-0.46580283298287162, 0.64145827413436174)
>>> stats.ttest_ind(rvs1, rvs3, equal_var = False)  # doctest: +SKIP
(-0.46580283298287162, 0.64149646246569292)
```

When n1 != n2, the equal variance t-statistic is no longer equal to the unequal variance t-statistic:

```
>>> rvs4 = stats.norm.rvs(loc=5, scale=20, size=100)  # doctest: +SKIP
>>> stats.ttest_ind(rvs1, rvs4)  # doctest: +SKIP
(-0.99882539442782481, 0.3182832709103896)
>>> stats.ttest_ind(rvs1, rvs4, equal_var = False)  # doctest: +SKIP
(-0.69712570584654099, 0.48716927725402048)
```

T-test with different means, variance, and n:

```
>>> rvs5 = stats.norm.rvs(loc=8, scale=20, size=100)  # doctest: +SKIP
>>> stats.ttest_ind(rvs1, rvs5)  # doctest: +SKIP
(-1.4679669854490653, 0.14263895620529152)
>>> stats.ttest_ind(rvs1, rvs5, equal_var = False)  # doctest: +SKIP
(-0.94365973617132992, 0.34744170334794122)
```

`dask.array.stats.`**`ttest_1samp`**(*a*, *popmean*, *axis=0*, *nan_policy='propagate'*)

Calculate the T-test for the mean of ONE group of scores.

This is a two-sided test for the null hypothesis that the expected value (mean) of a sample of independent observations *a* is equal to the given population mean, *popmean*.

Parameters

a [array_like] sample observation

popmean [float or array_like] expected value in null hypothesis. If array_like, then it must have the same shape as *a* excluding the axis dimension

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] t-statistic

pvalue [float or array] two-tailed p-value

Examples

```
>>> from scipy import stats  # doctest: +SKIP
```

```
>>> np.random.seed(7654567)  # fix seed to get the same result  # doctest: +SKIP
>>> rvs = stats.norm.rvs(loc=5, scale=10, size=(50,2))  # doctest: +SKIP
```

Test if mean of random sample is equal to true mean, and different mean. We reject the null hypothesis in the second case and don't reject it in the first case.

```
>>> stats.ttest_1samp(rvs,5.0)  # doctest: +SKIP
(array([-0.68014479, -0.04323899]), array([ 0.49961383,  0.96568674]))
>>> stats.ttest_1samp(rvs,0.0)  # doctest: +SKIP
(array([ 2.77025808,  4.11038784]), array([ 0.00789095,  0.00014999]))
```

Examples using axis and non-scalar dimension for population mean.

```
>>> stats.ttest_1samp(rvs,[5.0,0.0])  # doctest: +SKIP
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs.T,[5.0,0.0],axis=1)  # doctest: +SKIP
(array([-0.68014479,  4.11038784]), array([  4.99613833e-01,   1.49986458e-04]))
>>> stats.ttest_1samp(rvs,[[5.0],[0.0]])  # doctest: +SKIP
(array([[-0.68014479, -0.04323899],
       [ 2.77025808,  4.11038784]]), array([[  4.99613833e-01,   9.65686743e-01],
       [  7.89094663e-03,   1.49986458e-04]]))
```

`dask.array.stats.`**`ttest_rel`**(*a*, *b*, *axis=0*, *nan_policy='propagate'*)

Calculate the T-test on TWO RELATED samples of scores, a and b.

This is a two-sided test for the null hypothesis that 2 related or repeated samples have identical average (expected) values.

Parameters

a, b [array_like] The arrays must have the same shape.

axis [int or None, optional] Axis along which to compute test. If None, compute over the whole arrays, *a*, and *b*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] t-statistic

pvalue [float or array] two-tailed p-value

Notes

Examples for the use are scores of the same set of student in different exams, or repeated sampling from the same units. The test measures whether the average score differs significantly across samples (e.g. exams). If we observe a large p-value, for example greater than 0.05 or 0.1 then we cannot reject the null hypothesis of identical average scores. If the p-value is smaller than the threshold, e.g. 1%, 5% or 10%, then we reject the null hypothesis of equal averages. Small p-values are associated with large t-statistics.

References

https://en.wikipedia.org/wiki/T-test#Dependent_t-test_for_paired_samples

Examples

```
>>> from scipy import stats  # doctest: +SKIP
>>> np.random.seed(12345678) # fix random seed to get same numbers  # doctest:␣
↪+SKIP
```

```
>>> rvs1 = stats.norm.rvs(loc=5,scale=10,size=500)  # doctest: +SKIP
>>> rvs2 = (stats.norm.rvs(loc=5,scale=10,size=500) +  # doctest: +SKIP
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs2)  # doctest: +SKIP
(0.24101764965300962, 0.80964043445811562)
>>> rvs3 = (stats.norm.rvs(loc=8,scale=10,size=500) +  # doctest: +SKIP
...         stats.norm.rvs(scale=0.2,size=500))
>>> stats.ttest_rel(rvs1,rvs3)  # doctest: +SKIP
(-3.9995108708727933, 7.3082402191726459e-005)
```

`dask.array.stats.`**`chisquare`**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*)

Calculate a one-way chi square test.

The chi square test tests the null hypothesis that the categorical data has the given frequencies.

Parameters

f_obs [array_like] Observed frequencies in each category.

f_exp [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof [int, optional] "Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis [int or None, optional] The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

Returns

chisq [float or ndarray] The chi-squared test statistic. The value is a float if *axis* is None or *f_obs* and *f_exp* are 1-D.

p [float or ndarray] The p-value of the test. The value is a float if *ddof* and the return value *chisq* are scalars.

See also:

power_divergence, `mstats.chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

References

[1], [2]

Examples

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies.

```
>>> from scipy.stats import chisquare  # doctest: +SKIP
>>> chisquare([16, 18, 16, 14, 12, 12])  # doctest: +SKIP
(2.0, 0.84914503608460956)
```

With *f_exp* the expected frequencies can be given.

```
>>> chisquare([16, 18, 16, 14, 12, 12], f_exp=[16, 16, 16, 16, 16, 8])  #␣
↪doctest: +SKIP
(3.5, 0.62338762774958223)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T  #␣
↪doctest: +SKIP
>>> obs.shape  # doctest: +SKIP
(6, 2)
>>> chisquare(obs)  # doctest: +SKIP
(array([ 2.        ,  6.66666667]), array([ 0.84914504,  0.24663415]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> chisquare(obs, axis=None)  # doctest: +SKIP
(23.31034482758621, 0.015975692534127565)
>>> chisquare(obs.ravel())  # doctest: +SKIP
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=1)  # doctest: +SKIP
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the chi-squared statistic with *ddof*.

```
>>> chisquare([16, 18, 16, 14, 12, 12], ddof=[0,1,2])  # doctest: +SKIP
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we use `axis=1`:

```
>>> chisquare([16, 18, 16, 14, 12, 12],  # doctest: +SKIP
...           f_exp=[[16, 16, 16, 16, 16, 8], [8, 20, 20, 16, 12, 12]],
...           axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`dask.array.stats.`**`power_divergence`**(*f_obs*, *f_exp=None*, *ddof=0*, *axis=0*, *lambda_=None*)

Cressie-Read power divergence statistic and goodness of fit test.

This function tests the null hypothesis that the categorical data has the given frequencies, using the Cressie-Read power divergence statistic.

Parameters

f_obs [array_like] Observed frequencies in each category.

f_exp [array_like, optional] Expected frequencies in each category. By default the categories are assumed to be equally likely.

ddof [int, optional] "Delta degrees of freedom": adjustment to the degrees of freedom for the p-value. The p-value is computed using a chi-squared distribution with `k - 1 - ddof` degrees of freedom, where *k* is the number of observed frequencies. The default value of *ddof* is 0.

axis [int or None, optional] The axis of the broadcast result of *f_obs* and *f_exp* along which to apply the test. If axis is None, all values in *f_obs* are treated as a single data set. Default is 0.

lambda_ [float or str, optional] *lambda_* gives the power in the Cressie-Read power divergence statistic. The default is 1. For convenience, *lambda_* may be assigned one of the following strings, in which case the corresponding numerical value is used:

```
String              Value   Description
"pearson"             1     Pearson's chi-squared statistic.
                            In this case, the function is
                            equivalent to `stats.chisquare`.
"log-likelihood"      0     Log-likelihood ratio. Also known as
                            the G-test [R5ed189a69e5c-3]_.
"freeman-tukey"      -1/2   Freeman-Tukey statistic.
"mod-log-likelihood" -1     Modified log-likelihood ratio.
```

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```
"neyman"              -2     Neyman's statistic.
"cressie-read"         2/3   The power recommended in␣
↪[R5ed189a69e5c-5]_.
```

Returns

statistic [float or ndarray] The Cressie-Read power divergence test statistic. The value is a float if *axis* is None or if‘ *f_obs* and *f_exp* are 1-D.

pvalue [float or ndarray] The p-value of the test. The value is a float if *ddof* and the return value *stat* are scalars.

See also:

`chisquare`

Notes

This test is invalid when the observed or expected frequencies in each category are too small. A typical rule is that all of the observed and expected frequencies should be at least 5.

When *lambda_* is less than zero, the formula for the statistic involves dividing by *f_obs*, so a warning or error may be generated if any value in *f_obs* is 0.

Similarly, a warning or error may be generated if any value in *f_exp* is zero when *lambda_* >= 0.

The default degrees of freedom, k-1, are for the case when no parameters of the distribution are estimated. If p parameters are estimated by efficient maximum likelihood then the correct degrees of freedom are k-1-p. If the parameters are estimated in a different way, then the dof can be between k-1-p and k-1. However, it is also possible that the asymptotic distribution is not a chisquare, in which case this test is not appropriate.

This function handles masked arrays. If an element of *f_obs* or *f_exp* is masked, then data at that position is ignored, and does not count towards the size of the data set.

New in version 0.13.0.

References

[1], [2], [3], [4], [5]

Examples

(See *chisquare* for more examples.)

When just *f_obs* is given, it is assumed that the expected frequencies are uniform and given by the mean of the observed frequencies. Here we perform a G-test (i.e. use the log-likelihood ratio statistic):

```
>>> from scipy.stats import power_divergence  # doctest: +SKIP
>>> power_divergence([16, 18, 16, 14, 12, 12], lambda_='log-likelihood')  #␣
↪doctest: +SKIP
(2.006573162632538, 0.84823476779463769)
```

The expected frequencies can be given with the *f_exp* argument:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],  # doctest: +SKIP
...                  f_exp=[16, 16, 16, 16, 16, 8],
...                  lambda_='log-likelihood')
(3.3281031458963746, 0.6495419288047497)
```

When *f_obs* is 2-D, by default the test is applied to each column.

```
>>> obs = np.array([[16, 18, 16, 14, 12, 12], [32, 24, 16, 28, 20, 24]]).T  #␣
↪doctest: +SKIP
>>> obs.shape  # doctest: +SKIP
(6, 2)
>>> power_divergence(obs, lambda_="log-likelihood")  # doctest: +SKIP
(array([ 2.00657316,  6.77634498]), array([ 0.84823477,  0.23781225]))
```

By setting `axis=None`, the test is applied to all data in the array, which is equivalent to applying the test to the flattened array.

```
>>> power_divergence(obs, axis=None)  # doctest: +SKIP
(23.31034482758621, 0.015975692534127565)
>>> power_divergence(obs.ravel())  # doctest: +SKIP
(23.31034482758621, 0.015975692534127565)
```

ddof is the change to make to the default degrees of freedom.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=1)  # doctest: +SKIP
(2.0, 0.73575888234288467)
```

The calculation of the p-values is done by broadcasting the test statistic with *ddof*.

```
>>> power_divergence([16, 18, 16, 14, 12, 12], ddof=[0,1,2])  # doctest: +SKIP
(2.0, array([ 0.84914504,  0.73575888,  0.5724067 ]))
```

f_obs and *f_exp* are also broadcast. In the following, *f_obs* has shape (6,) and *f_exp* has shape (2, 6), so the result of broadcasting *f_obs* and *f_exp* has shape (2, 6). To compute the desired chi-squared statistics, we must use `axis=1`:

```
>>> power_divergence([16, 18, 16, 14, 12, 12],  # doctest: +SKIP
...                  f_exp=[[16, 16, 16, 16, 16, 8],
...                         [8, 20, 20, 16, 12, 12]],
...                  axis=1)
(array([ 3.5 ,  9.25]), array([ 0.62338763,  0.09949846]))
```

`dask.array.stats.`**`skew`**(*a*, *axis=0*, *bias=True*, *nan_policy='propagate'*)

Compute the skewness of a data set.

For normally distributed data, the skewness should be about 0. For unimodal continuous distributions, a skewness value > 0 means that there is more weight in the right tail of the distribution. The function *skewtest* can be used to determine if the skewness value is close enough to 0, statistically speaking.

Parameters

a [ndarray] data

axis [int or None, optional] Axis along which skewness is calculated. Default is 0. If None, compute over the whole array *a*.

bias [bool, optional] If False, then the calculations are corrected for statistical bias.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

skewness [ndarray] The skewness of values along an axis, returning 0 where all values are equal.

References

[1]

Examples

```
>>> from scipy.stats import skew  # doctest: +SKIP
>>> skew([1, 2, 3, 4, 5])  # doctest: +SKIP
0.0
>>> skew([2, 8, 0, 4, 1, 9, 9, 0])  # doctest: +SKIP
0.2650554122698573
```

`dask.array.stats.skewtest`(*a*, *axis=0*, *nan_policy='propagate'*)

Test whether the skew is different from the normal distribution.

This function tests the null hypothesis that the skewness of the population that the sample was drawn from is the same as that of a corresponding normal distribution.

Parameters

a [array] The data to be tested

axis [int or None, optional] Axis along which statistics are calculated. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float] The computed z-score for this test.

pvalue [float] a 2-sided p-value for the hypothesis test

Notes

The sample size must be at least 8.

References

[1]

Examples

```
>>> from scipy.stats import skewtest  # doctest: +SKIP
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8])  # doctest: +SKIP
SkewtestResult(statistic=1.0108048609177787, pvalue=0.3121098361421897)
>>> skewtest([2, 8, 0, 4, 1, 9, 9, 0])  # doctest: +SKIP
SkewtestResult(statistic=0.44626385374196975, pvalue=0.6554066631275459)
>>> skewtest([1, 2, 3, 4, 5, 6, 7, 8000])  # doctest: +SKIP
SkewtestResult(statistic=3.571773510360407, pvalue=0.0003545719905823133)
>>> skewtest([100, 100, 100, 100, 100, 100, 100, 101])  # doctest: +SKIP
SkewtestResult(statistic=3.5717766638478072, pvalue=0.000354567720281634)
```

`dask.array.stats.`**`kurtosis`**(*a*, *axis=0*, *fisher=True*, *bias=True*, *nan_policy='propagate'*)

Compute the kurtosis (Fisher or Pearson) of a dataset.

Kurtosis is the fourth central moment divided by the square of the variance. If Fisher's definition is used, then 3.0 is subtracted from the result to give 0.0 for a normal distribution.

If bias is False then the kurtosis is calculated using k statistics to eliminate bias coming from biased moment estimators

Use *kurtosistest* to see if result is close enough to normal.

Parameters

a [array] data for which the kurtosis is calculated

axis [int or None, optional] Axis along which the kurtosis is calculated. Default is 0. If None, compute over the whole array *a*.

fisher [bool, optional] If True, Fisher's definition is used (normal ==> 0.0). If False, Pearson's definition is used (normal ==> 3.0).

bias [bool, optional] If False, then the calculations are corrected for statistical bias.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

kurtosis [array] The kurtosis of values along an axis. If all values are equal, return -3 for Fisher's definition and 0 for Pearson's definition.

References

[1]

Examples

```
>>> from scipy.stats import kurtosis  # doctest: +SKIP
>>> kurtosis([1, 2, 3, 4, 5])  # doctest: +SKIP
-1.3
```

`dask.array.stats.`**`kurtosistest`**(*a*, *axis=0*, *nan_policy='propagate'*)

Test whether a dataset has normal kurtosis.

This function tests the null hypothesis that the kurtosis of the population from which the sample was drawn is that of the normal distribution: `kurtosis = 3(n-1)/(n+1)`.

Parameters

a [array] array of the sample data

axis [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float] The computed z-score for this test.

pvalue [float] The 2-sided p-value for the hypothesis test

Notes

Valid only for n>20. This function uses the method described in [1].

References

[1]

Examples

```
>>> from scipy.stats import kurtosistest  # doctest: +SKIP
>>> kurtosistest(list(range(20)))  # doctest: +SKIP
KurtosistestResult(statistic=-1.7058104152122062, pvalue=0.08804338332528348)
```

```
>>> np.random.seed(28041990)  # doctest: +SKIP
>>> s = np.random.normal(0, 1, 1000)  # doctest: +SKIP
>>> kurtosistest(s)  # doctest: +SKIP
KurtosistestResult(statistic=1.2317590987707365, pvalue=0.21803908613450895)
```

`dask.array.stats.`**`normaltest`**(*a*, *axis=0*, *nan_policy='propagate'*)

Test whether a sample differs from a normal distribution.

This function tests the null hypothesis that a sample comes from a normal distribution. It is based on D'Agostino and Pearson's [1], [2] test that combines skew and kurtosis to produce an omnibus test of normality.

Parameters

a [array_like] The array containing the sample to be tested.

axis [int or None, optional] Axis along which to compute test. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

statistic [float or array] `s^2 + k^2`, where `s` is the z-score returned by *skewtest* and `k` is the z-score returned by *kurtosistest*.

pvalue [float or array] A 2-sided chi squared probability for the hypothesis test.

References

[1], [2]

Examples

```
>>> from scipy import stats  # doctest: +SKIP
>>> pts = 1000  # doctest: +SKIP
>>> np.random.seed(28041990)  # doctest: +SKIP
>>> a = np.random.normal(0, 1, size=pts)  # doctest: +SKIP
>>> b = np.random.normal(2, 1, size=pts)  # doctest: +SKIP
>>> x = np.concatenate((a, b))  # doctest: +SKIP
>>> k2, p = stats.normaltest(x)  # doctest: +SKIP
>>> alpha = 1e-3  # doctest: +SKIP
>>> print("p = {:g}".format(p))  # doctest: +SKIP
p = 3.27207e-11
>>> if p < alpha:  # null hypothesis: x comes from a normal distribution  #␣
↪doctest: +SKIP
...     print("The null hypothesis can be rejected")
... else:
...     print("The null hypothesis cannot be rejected")
The null hypothesis can be rejected
```

`dask.array.stats.`**`f_oneway`**`(`*`*args`*`)`

Performs a 1-way ANOVA.

The one-way ANOVA tests the null hypothesis that two or more groups have the same population mean. The test is applied to samples from two or more groups, possibly with differing sizes.

Parameters

sample1, sample2, ... [array_like] The sample measurements for each group.

Returns

statistic [float] The computed F-value of the test.

pvalue [float] The associated p-value from the F-distribution.

Notes

The ANOVA test has important assumptions that must be satisfied in order for the associated p-value to be valid.

1. The samples are independent.
2. Each sample is from a normally distributed population.
3. The population standard deviations of the groups are all equal. This property is known as homoscedasticity.

If these assumptions are not true for a given set of data, it may still be possible to use the Kruskal-Wallis H-test (*scipy.stats.kruskal*) although with some loss of power.

The algorithm is from Heiman[2], pp.394-7.

References

[1], [2], [3]

Examples

```
>>> import scipy.stats as stats  # doctest: +SKIP
```

[3] Here are some data on a shell measurement (the length of the anterior adductor muscle scar, standardized by dividing by length) in the mussel Mytilus trossulus from five locations: Tillamook, Oregon; Newport, Oregon; Petersburg, Alaska; Magadan, Russia; and Tvarminne, Finland, taken from a much larger data set used in McDonald et al. (1991).

```
>>> tillamook = [0.0571, 0.0813, 0.0831, 0.0976, 0.0817, 0.0859, 0.0735,  #␣
↪doctest: +SKIP
...              0.0659, 0.0923, 0.0836]
>>> newport = [0.0873, 0.0662, 0.0672, 0.0819, 0.0749, 0.0649, 0.0835,  #␣
↪doctest: +SKIP
...            0.0725]
>>> petersburg = [0.0974, 0.1352, 0.0817, 0.1016, 0.0968, 0.1064, 0.105]  #␣
↪doctest: +SKIP
>>> magadan = [0.1033, 0.0915, 0.0781, 0.0685, 0.0677, 0.0697, 0.0764,  #␣
↪doctest: +SKIP
...            0.0689]
>>> tvarminne = [0.0703, 0.1026, 0.0956, 0.0973, 0.1039, 0.1045]  # doctest: +SKIP
>>> stats.f_oneway(tillamook, newport, petersburg, magadan, tvarminne)  #␣
↪doctest: +SKIP
(7.1210194716424473, 0.00028122423145345439)
```

`dask.array.stats.moment` (*a*, *moment=1*, *axis=0*, *nan_policy='propagate'*)

Calculate the nth moment about the mean for a sample.

A moment is a specific quantitative measure of the shape of a set of points. It is often used to calculate coefficients of skewness and kurtosis due to its close relationship with them.

Parameters

a [array_like] data

moment [int or array_like of ints, optional] order of central moment that is returned. Default is 1.

axis [int or None, optional] Axis along which the central moment is computed. Default is 0. If None, compute over the whole array *a*.

nan_policy [{'propagate', 'raise', 'omit'}, optional] Defines how to handle when input contains nan. 'propagate' returns nan, 'raise' throws an error, 'omit' performs the calculations ignoring nan values. Default is 'propagate'.

Returns

n-th central moment [ndarray or float] The appropriate moment along the given axis or over all values if axis is None. The denominator for the moment calculation is the number of observations, no degrees of freedom correction is done.

See also:

kurtosis, *skew*, describe

Notes

The k-th central moment of a data sample is:

$$m_k = \frac{1}{n} \sum_{i=1}^{n} (x_i - \bar{x})^k$$

Where n is the number of samples and x-bar is the mean. This function uses exponentiation by squares [1] for efficiency.

References

[1]

Examples

```
>>> from scipy.stats import moment  # doctest: +SKIP
>>> moment([1, 2, 3, 4, 5], moment=1)  # doctest: +SKIP
0.0
>>> moment([1, 2, 3, 4, 5], moment=2)  # doctest: +SKIP
2.0
```

`dask.array.image.`**`imread`**(*filename*, *imread=None*, *preprocess=None*)
Read a stack of images into a dask array

Parameters

filename: string A globstring like 'myfile.*.png'

imread: function (optional) Optionally provide custom imread function. Function should expect a filename and produce a numpy array. Defaults to `skimage.io.imread`.

preprocess: function (optional) Optionally provide custom function to preprocess the image. Function should expect a numpy array for a single image.

Returns

Dask array of all images stacked along the first dimension. All images

will be treated as individual chunks

Examples

```
>>> from dask.array.image import imread
>>> im = imread('2015-*-*.png')  # doctest: +SKIP
>>> im.shape  # doctest: +SKIP
(365, 1000, 1000, 3)
```

`dask.array.gufunc.`**`apply_gufunc`**(*func*, *signature*, **args*, ***kwargs*)
Apply a generalized ufunc or similar python function to arrays.

`signature` determines if the function consumes or produces core dimensions. The remaining dimensions in given input arrays (`*args`) are considered loop dimensions and are required to broadcast naturally against each other.

In other terms, this function is like np.vectorize, but for the blocks of dask arrays. If the function itself shall also be vectorized use `vectorize=True` for convenience.

Parameters

func [callable] Function to call like `func(*args, **kwargs)` on input arrays (`*args`) that returns an array or tuple of arrays. If multiple arguments with non-matching dimensions are supplied, this function is expected to vectorize (broadcast) over axes of positional arguments in the style of NumPy universal functions [1] (if this is not the case, set `vectorize=True`). If this function returns multiple outputs, `output_core_dims` has to be set as well.

signature: string Specifies what core dimensions are consumed and produced by `func`. According to the specification of numpy.gufunc signature [2]

***args** [numeric] Input arrays or scalars to the callable function.

axes: List of tuples, optional, keyword only A list of tuples with indices of axes a generalized ufunc should operate on. For instance, for a signature of `"(i,j),(j,k)->(i,k)"` appropriate for matrix multiplication, the base elements are two-dimensional matrices and these are taken to be stored in the two last axes of each argument. The corresponding axes keyword would be `[(-2, -1), (-2, -1), (-2, -1)]`. For simplicity, for generalized ufuncs that operate on 1-dimensional arrays (vectors), a single integer is accepted instead of a single-element tuple, and for generalized ufuncs for which all outputs are scalars, the output tuples can be omitted.

axis: int, optional, keyword only A single axis over which a generalized ufunc should operate. This is a short-cut for ufuncs that operate over a single, shared core dimension, equivalent to passing in axes with entries of (axis,) for each single-core-dimension argument and `()` for all others. For instance, for a signature `"(i),(i)->()"`, it is equivalent to passing in `axes=[(axis,), (axis,), ()]`.

keepdims: bool, optional, keyword only If this is set to True, axes which are reduced over will be left in the result as a dimension with size one, so that the result will broadcast correctly against the inputs. This option can only be used for generalized ufuncs that operate on inputs that all have the same number of core dimensions and with outputs that have no core dimensions , i.e., with signatures like `"(i),(i)->()"` or `"(m,m)->()"`. If used, the location of the dimensions in the output can be controlled with axes and axis.

output_dtypes [Optional, dtype or list of dtypes, keyword only] Valid numpy dtype specification or list thereof. If not given, a call of `func` with a small set of data is performed in order to try to automatically determine the output dtypes.

output_sizes [dict, optional, keyword only] Optional mapping from dimension names to sizes for outputs. Only used if new core dimensions (not found on inputs) appear on outputs.

vectorize: bool, keyword only If set to `True`, `np.vectorize` is applied to `func` for convenience. Defaults to `False`.

allow_rechunk: Optional, bool, keyword only Allows rechunking, otherwise chunk sizes need to match and core dimensions are to consist only of one chunk. Warning: enabling this can increase memory usage significantly. Defaults to `False`.

****kwargs** [dict] Extra keyword arguments to pass to *func*

Returns

Single dask.array.Array or tuple of dask.array.Array

References

[1], [2]

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> def stats(x):
...     return np.mean(x, axis=-1), np.std(x, axis=-1)
>>> a = da.random.normal(size=(10,20,30), chunks=(5, 10, 30))
>>> mean, std = da.apply_gufunc(stats, "(i)->(),()", a)
>>> mean.compute().shape
(10, 20)
```

```
>>> def outer_product(x, y):
...     return np.einsum("i,j->ij", x, y)
>>> a = da.random.normal(size=(   20,30), chunks=(10, 30))
>>> b = da.random.normal(size=(10, 1,40), chunks=(5, 1, 40))
>>> c = da.apply_gufunc(outer_product, "(i),(j)->(i,j)", a, b, vectorize=True)
>>> c.compute().shape
(10, 20, 30, 40)
```

`dask.array.gufunc.`**`as_gufunc`**(*signature=None*, ***kwargs*)

Decorator for `dask.array.gufunc`.

Parameters

signature [String] Specifies what core dimensions are consumed and produced by `func`. According to the specification of numpy.gufunc signature [2]

axes: List of tuples, optional, keyword only A list of tuples with indices of axes a generalized ufunc should operate on. For instance, for a signature of `"(i,j),(j,k)->(i,k)"` appropriate for matrix multiplication, the base elements are two-dimensional matrices and these are taken to be stored in the two last axes of each argument. The corresponding axes keyword would be `[(-2, -1), (-2, -1), (-2, -1)]`. For simplicity, for generalized ufuncs that operate on 1-dimensional arrays (vectors), a single integer is accepted instead of a single-element tuple, and for generalized ufuncs for which all outputs are scalars, the output tuples can be omitted.

axis: int, optional, keyword only A single axis over which a generalized ufunc should operate. This is a short-cut for ufuncs that operate over a single, shared core dimension, equivalent to passing in axes with entries of (axis,) for each single-core-dimension argument and `()` for all others. For instance, for a signature `"(i),(i)->()"`, it is equivalent to passing in `axes=[(axis,), (axis,), ()]`.

keepdims: bool, optional, keyword only If this is set to True, axes which are reduced over will be left in the result as a dimension with size one, so that the result will broadcast correctly against the inputs. This option can only be used for generalized ufuncs that operate on inputs that all have the same number of core dimensions and with outputs that have no core dimensions , i.e., with signatures like `"(i),(i)->()"` or `"(m,m)->()"`. If used, the location of the dimensions in the output can be controlled with axes and axis.

output_dtypes [Optional, dtype or list of dtypes, keyword only] Valid numpy dtype specification or list thereof. If not given, a call of `func` with a small set of data is performed in order to try to automatically determine the output dtypes.

output_sizes [dict, optional, keyword only] Optional mapping from dimension names to sizes for outputs. Only used if new core dimensions (not found on inputs) appear on outputs.

vectorize: bool, keyword only If set to `True`, `np.vectorize` is applied to `func` for convenience. Defaults to `False`.

allow_rechunk: Optional, bool, keyword only Allows rechunking, otherwise chunk sizes need to match and core dimensions are to consist only of one chunk. Warning: enabling this can increase memory usage significantly. Defaults to `False`.

Returns

Decorator for 'pyfunc' that itself returns a 'gufunc'.

References

[1], [2]

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> a = da.random.normal(size=(10,20,30), chunks=(5, 10, 30))
>>> @da.as_gufunc("(i)->(),()", output_dtypes=(float, float))
... def stats(x):
...     return np.mean(x, axis=-1), np.std(x, axis=-1)
>>> mean, std = stats(a)
>>> mean.compute().shape
(10, 20)
```

```
>>> a = da.random.normal(size=(   20,30), chunks=(10, 30))
>>> b = da.random.normal(size=(10, 1,40), chunks=(5, 1, 40))
>>> @da.as_gufunc("(i),(j)->(i,j)", output_dtypes=float, vectorize=True)
... def outer_product(x, y):
...     return np.einsum("i,j->ij", x, y)
>>> c = outer_product(a, b)
>>> c.compute().shape
(10, 20, 30, 40)
```

`dask.array.gufunc.`**`gufunc`**`(`*pyfunc*, ***kwargs*`)`

Binds *pyfunc* into `dask.array.apply_gufunc` when called.

Parameters

pyfunc [callable] Function to call like `func(*args, **kwargs)` on input arrays (`*args`) that returns an array or tuple of arrays. If multiple arguments with non-matching dimensions are supplied, this function is expected to vectorize (broadcast) over axes of positional arguments in the style of NumPy universal functions [1] (if this is not the case, set `vectorize=True`). If this function returns multiple outputs, `output_core_dims` has to be set as well.

signature [String, keyword only] Specifies what core dimensions are consumed and produced by `func`. According to the specification of numpy.gufunc signature [2]

axes: List of tuples, optional, keyword only A list of tuples with indices of axes a generalized ufunc should operate on. For instance, for a signature of `"(i,j),(j,k)->(i,k)"` appropriate for matrix multiplication, the base elements are two-dimensional matrices and these are taken to be stored in the two last axes of each argument. The corresponding axes keyword would be `[(-2, -1), (-2, -1), (-2, -1)]`. For simplicity, for generalized ufuncs that operate on 1-dimensional arrays (vectors), a single integer is accepted instead of a single-element tuple, and for generalized ufuncs for which all outputs are scalars, the output tuples can be omitted.

axis: int, optional, keyword only A single axis over which a generalized ufunc should operate. This is a short-cut for ufuncs that operate over a single, shared core dimension, equivalent to passing in axes with entries of (axis,) for each single-core-dimension argument and `()` for all others. For instance, for a signature `"(i),(i)->()"`, it is equivalent to passing in `axes=[(axis,), (axis,), ()]`.

keepdims: bool, optional, keyword only If this is set to True, axes which are reduced over will be left in the result as a dimension with size one, so that the result will broadcast correctly against the inputs. This option can only be used for generalized ufuncs that operate on inputs that all have the same number of core dimensions and with outputs that have no core dimensions , i.e., with signatures like `"(i),(i)->()"` or `"(m,m)->()"`. If used, the location of the dimensions in the output can be controlled with axes and axis.

output_dtypes [Optional, dtype or list of dtypes, keyword only] Valid numpy dtype specification or list thereof. If not given, a call of `func` with a small set of data is performed in order to try to automatically determine the output dtypes.

output_sizes [dict, optional, keyword only] Optional mapping from dimension names to sizes for outputs. Only used if new core dimensions (not found on inputs) appear on outputs.

vectorize: bool, keyword only If set to `True`, `np.vectorize` is applied to `func` for convenience. Defaults to `False`.

allow_rechunk: Optional, bool, keyword only Allows rechunking, otherwise chunk sizes need to match and core dimensions are to consist only of one chunk. Warning: enabling this can increase memory usage significantly. Defaults to `False`.

Returns

Wrapped function

References

[1], [2]

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> a = da.random.normal(size=(10,20,30), chunks=(5, 10, 30))
>>> def stats(x):
...     return np.mean(x, axis=-1), np.std(x, axis=-1)
>>> gustats = da.gufunc(stats, signature="(i)->(),()", output_dtypes=(float,␣
↪float))
>>> mean, std = gustats(a)
>>> mean.compute().shape
(10, 20)
```

```
>>> a = da.random.normal(size=(   20,30), chunks=(10, 30))
>>> b = da.random.normal(size=(10, 1,40), chunks=(5, 1, 40))
>>> def outer_product(x, y):
...     return np.einsum("i,j->ij", x, y)
>>> guouter_product = da.gufunc(outer_product, signature="(i),(j)->(i,j)", output_
↪dtypes=float, vectorize=True)
>>> c = guouter_product(a, b)
>>> c.compute().shape
(10, 20, 30, 40)
```

`dask.array.core.`**`map_blocks`**(*func*, **args*, *name=None*, *token=None*, *dtype=None*, *chunks=None*, *drop_axis=[]*, *new_axis=None*, *meta=None*, ***kwargs*)

Map a function across all blocks of a dask array.

Parameters

func [callable] Function to apply to every block in the array.

args [dask arrays or other objects]

dtype [np.dtype, optional] The `dtype` of the output array. It is recommended to provide this. If not provided, will be inferred by applying the function to a small set of fake data.

chunks [tuple, optional] Chunk shape of resulting blocks if the function does not preserve shape. If not provided, the resulting array is assumed to have the same block structure as the first input array.

drop_axis [number or iterable, optional] Dimensions lost by the function.

new_axis [number or iterable, optional] New dimensions created by the function. Note that these are applied after `drop_axis` (if present).

token [string, optional] The key prefix to use for the output array. If not provided, will be determined from the function name.

name [string, optional] The key name to use for the output array. Note that this fully specifies the output key name, and must be unique. If not provided, will be determined by a hash of the arguments.

****kwargs :** Other keyword arguments to pass to function. Values must be constants (not dask.arrays)

Examples

```
>>> import dask.array as da
>>> x = da.arange(6, chunks=3)
```

```
>>> x.map_blocks(lambda x: x * 2).compute()
array([ 0,  2,  4,  6,  8, 10])
```

The `da.map_blocks` function can also accept multiple arrays.

```
>>> d = da.arange(5, chunks=2)
>>> e = da.arange(5, chunks=2)
```

```
>>> f = map_blocks(lambda a, b: a + b**2, d, e)
>>> f.compute()
array([ 0,  2,  6, 12, 20])
```

If the function changes shape of the blocks then you must provide chunks explicitly.

```
>>> y = x.map_blocks(lambda x: x[::2], chunks=((2, 2),))
```

You have a bit of freedom in specifying chunks. If all of the output chunk sizes are the same, you can provide just that chunk size as a single tuple.

```
>>> a = da.arange(18, chunks=(6,))
>>> b = a.map_blocks(lambda x: x[:3], chunks=(3,))
```

If the function changes the dimension of the blocks you must specify the created or destroyed dimensions.

```
>>> b = a.map_blocks(lambda x: x[None, :, None], chunks=(1, 6, 1),
...                  new_axis=[0, 2])
```

If `chunks` is specified but `new_axis` is not, then it is inferred to add the necessary number of axes on the left.

Map_blocks aligns blocks by block positions without regard to shape. In the following example we have two arrays with the same number of blocks but with different shape and chunk sizes.

```
>>> x = da.arange(1000, chunks=(100,))
>>> y = da.arange(100, chunks=(10,))
```

The relevant attribute to match is numblocks.

```
>>> x.numblocks
(10,)
>>> y.numblocks
(10,)
```

If these match (up to broadcasting rules) then we can map arbitrary functions across blocks

```
>>> def func(a, b):
...     return np.array([a.max(), b.max()])
```

```
>>> da.map_blocks(func, x, y, chunks=(2,), dtype='i8')
dask.array<func, shape=(20,), dtype=int64, chunksize=(2,), chunktype=numpy.
↪ndarray>
```

```
>>> _.compute()
array([ 99,   9, 199,  19, 299,  29, 399,  39, 499,  49, 599,  59, 699,
        69, 799,  79, 899,  89, 999,  99])
```

Your block function get information about where it is in the array by accepting a special `block_info` keyword argument.

```
>>> def func(block, block_info=None):
...     pass
```

This will receive the following information:

```
>>> block_info  # doctest: +SKIP
{0: {'shape': (1000,),
     'num-chunks': (10,),
     'chunk-location': (4,),
     'array-location': [(400, 500)]},
 None: {'shape': (1000,),
        'num-chunks': (10,),
        'chunk-location': (4,),
        'array-location': [(400, 500)],
        'chunk-shape': (100,),
        'dtype': dtype('float64')}}
```

For each argument and keyword arguments that are dask arrays (the positions of which are the first index), you will receive the shape of the full array, the number of chunks of the full array in each dimension, the chunk location (for example the fourth chunk over in the first dimension), and the array location (for example the slice corresponding to `40:50`). The same information is provided for the output, with the key `None`, plus the shape and dtype that should be returned.

These features can be combined to synthesize an array from scratch, for example:

```
>>> def func(block_info=None):
...     loc = block_info[None]['array-location'][0]
...     return np.arange(loc[0], loc[1])
```

```
>>> da.map_blocks(func, chunks=((4, 4),), dtype=np.float_)
dask.array<func, shape=(8,), dtype=float64, chunksize=(4,), chunktype=numpy.
↪ndarray>
```

```
>>> _.compute()
array([0, 1, 2, 3, 4, 5, 6, 7])
```

You may specify the key name prefix of the resulting task in the graph with the optional `token` keyword argument.

```
>>> x.map_blocks(lambda x: x + 1, name='increment')  # doctest: +SKIP
dask.array<increment, shape=(100,), dtype=int64, chunksize=(10,), chunktype=numpy.
↪ndarray>
```

`dask.array.core.`**`blockwise`**(*func*, *out_ind*, **args*, *name=None*, *token=None*, *dtype=None*, *adjust_chunks=None*, *new_axes=None*, *align_arrays=True*, *concatenate=None*, *meta=None*, ***kwargs*)

Tensor operation: Generalized inner and outer products

A broad class of blocked algorithms and patterns can be specified with a concise multi-index notation. The `blockwise` function applies an in-memory function across multiple blocks of multiple inputs in a variety of ways. Many dask.array operations are special cases of blockwise including elementwise, broadcasting, reductions, tensordot, and transpose.

Parameters

func [callable] Function to apply to individual tuples of blocks

out_ind [iterable] Block pattern of the output, something like 'ijk' or (1, 2, 3)

***args** [sequence of Array, index pairs] Sequence like (x, 'ij', y, 'jk', z, 'i')

****kwargs** [dict] Extra keyword arguments to pass to function

dtype [np.dtype] Datatype of resulting array.

concatenate [bool, keyword only] If true concatenate arrays along dummy indices, else provide lists

adjust_chunks [dict] Dictionary mapping index to function to be applied to chunk sizes

new_axes [dict, keyword only] New indexes and their dimension lengths

Examples

2D embarrassingly parallel operation from two arrays, x, and y.

```
>>> z = blockwise(operator.add, 'ij', x, 'ij', y, 'ij', dtype='f8')  # z = x + y
↪# doctest: +SKIP
```

Outer product multiplying x by y, two 1-d vectors

```
>>> z = blockwise(operator.mul, 'ij', x, 'i', y, 'j', dtype='f8')  # doctest:␣
↪+SKIP
```

z = x.T

```
>>> z = blockwise(np.transpose, 'ji', x, 'ij', dtype=x.dtype)  # doctest: +SKIP
```

The transpose case above is illustrative because it does same transposition both on each in-memory block by calling `np.transpose` and on the order of the blocks themselves, by switching the order of the index `ij -> ji`.

We can compose these same patterns with more variables and more complex in-memory functions

z = X + Y.T

```
>>> z = blockwise(lambda x, y: x + y.T, 'ij', x, 'ij', y, 'ji', dtype='f8')  #␣
↪doctest: +SKIP
```

Any index, like `i` missing from the output index is interpreted as a contraction (note that this differs from Einstein convention; repeated indices do not imply contraction.) In the case of a contraction the passed function should expect an iterable of blocks on any array that holds that index. To receive arrays concatenated along contracted dimensions instead pass `concatenate=True`.

Inner product multiplying x by y, two 1-d vectors

```
>>> def sequence_dot(x_blocks, y_blocks):
...     result = 0
...     for x, y in zip(x_blocks, y_blocks):
...         result += x.dot(y)
...     return result
```

```
>>> z = blockwise(sequence_dot, '', x, 'i', y, 'i', dtype='f8')  # doctest: +SKIP
```

Add new single-chunk dimensions with the `new_axes=` keyword, including the length of the new dimension. New dimensions will always be in a single chunk.

```
>>> def f(x):
...     return x[:, None] * np.ones((1, 5))
```

```
>>> z = blockwise(f, 'az', x, 'a', new_axes={'z': 5}, dtype=x.dtype)  # doctest:␣
↪+SKIP
```

New dimensions can also be multi-chunk by specifying a tuple of chunk sizes. This has limited utility as is (because the chunks are all the same), but the resulting graph can be modified to achieve more useful results (see `da.map_blocks`).

```
>>> z = blockwise(f, 'az', x, 'a', new_axes={'z': (5, 5)}, dtype=x.dtype)  #␣
↪doctest: +SKIP
```

If the applied function changes the size of each chunk you can specify this with a `adjust_chunks={...}` dictionary holding a function for each index that modifies the dimension size in that index.

```
>>> def double(x):
...     return np.concatenate([x, x])
```

```
>>> y = blockwise(double, 'ij', x, 'ij',
...               adjust_chunks={'i': lambda n: 2 * n}, dtype=x.dtype)  #␣
↪doctest: +SKIP
```

Include literals by indexing with None

```
>>> y = blockwise(add, 'ij', x, 'ij', 1234, None, dtype=x.dtype)  # doctest: +SKIP
```

`dask.array.core.`**`normalize_chunks`**(*chunks*, *shape=None*, *limit=None*, *dtype=None*, *previous_chunks=None*)

Normalize chunks to tuple of tuples

This takes in a variety of input types and information and produces a full tuple-of-tuples result for chunks, suitable to be passed to Array or rechunk or any other operation that creates a Dask array.

Parameters

chunks: tuple, int, dict, or string The chunks to be normalized. See examples below for more details

shape: Tuple[int] The shape of the array

limit: int (optional) The maximum block size to target in bytes, if freedom is given to choose

dtype: np.dtype

previous_chunks: Tuple[Tuple[int]] optional Chunks from a previous array that we should use for inspiration when rechunking auto dimensions. If not provided but auto-chunking exists then auto-dimensions will prefer square-like chunk shapes.

Examples

Specify uniform chunk sizes

```
>>> normalize_chunks((2, 2), shape=(5, 6))
((2, 2, 1), (2, 2, 2))
```

Also passes through fully explicit tuple-of-tuples

```
>>> normalize_chunks(((2, 2, 1), (2, 2, 2)), shape=(5, 6))
((2, 2, 1), (2, 2, 2))
```

Cleans up lists to tuples

```
>>> normalize_chunks([[2, 2], [3, 3]])
((2, 2), (3, 3))
```

Expands integer inputs 10 -> (10, 10)

```
>>> normalize_chunks(10, shape=(30, 5))
((10, 10, 10), (5,))
```

Expands dict inputs

```
>>> normalize_chunks({0: 2, 1: 3}, shape=(6, 6))
((2, 2, 2), (3, 3))
```

The values -1 and None get mapped to full size

```
>>> normalize_chunks((5, -1), shape=(10, 10))
((5, 5), (10,))
```

Use the value "auto" to automatically determine chunk sizes along certain dimensions. This uses the `limit=` and `dtype=` keywords to determine how large to make the chunks. The term "auto" can be used anywhere an integer can be used. See array chunking documentation for more information.

```
>>> normalize_chunks(("auto",), shape=(20,), limit=5, dtype='uint8')
((5, 5, 5, 5),)
```

You can also use byte sizes (see `dask.utils.parse_bytes`) in place of "auto" to ask for a particular size

```
>>> normalize_chunks("1kiB", shape=(2000,), dtype='float32')
((250, 250, 250, 250, 250, 250, 250, 250),)
```

Respects null dimensions

```
>>> normalize_chunks((), shape=(0, 0))
((0,), (0,))
```

Array Methods

class `dask.array.`**`Array`**

Parallel Dask Array

A parallel nd-array comprised of many numpy arrays arranged in a grid.

This constructor is for advanced uses only. For normal use see the `da.from_array` function.

Parameters

dask [dict] Task dependency graph

name [string] Name of array in dask

shape [tuple of ints] Shape of the entire array

chunks: iterable of tuples block sizes along each dimension

dtype [str or dtype] Typecode or data-type for the new Dask Array

meta [empty ndarray] empty ndarray created with same NumPy backend, ndim and dtype as the Dask Array being created (overrides dtype)

See also:

`dask.array.from_array`

`all`(*axis=None*, *out=None*, *keepdims=False*)

This docstring was copied from numpy.ndarray.all.

Some inconsistencies with the Dask version may exist.

Returns True if all elements evaluate to True.

Refer to *numpy.all* for full documentation.

See also:

`numpy.all` equivalent function

`any`(*axis=None*, *out=None*, *keepdims=False*)

This docstring was copied from numpy.ndarray.any.

Some inconsistencies with the Dask version may exist.

Returns True if any of the elements of *a* evaluate to True.

Refer to *numpy.any* for full documentation.

See also:

`numpy.any` equivalent function

argmax(*axis=None*, *out=None*)

This docstring was copied from numpy.ndarray.argmax.

Some inconsistencies with the Dask version may exist.

Return indices of the maximum values along the given axis.

Refer to *numpy.argmax* for full documentation.

See also:

`numpy.argmax` equivalent function

argmin(*axis=None*, *out=None*)

This docstring was copied from numpy.ndarray.argmin.

Some inconsistencies with the Dask version may exist.

Return indices of the minimum values along the given axis of *a*.

Refer to *numpy.argmin* for detailed documentation.

See also:

`numpy.argmin` equivalent function

argtopk(*k*, *axis=-1*, *split_every=None*)

The indices of the top k elements of an array.

See `da.argtopk` for docstring

astype(*dtype*, ***kwargs*)

Copy of the array, cast to a specified type.

Parameters

dtype [str or dtype] Typecode or data-type to which the array is cast.

casting [{'no', 'equiv', 'safe', 'same_kind', 'unsafe'}, optional] Controls what kind of data casting may occur. Defaults to 'unsafe' for backwards compatibility.

- 'no' means the data types should not be cast at all.
- 'equiv' means only byte-order changes are allowed.
- 'safe' means only casts which can preserve values are allowed.
- **'same_kind' means only safe casts or casts within a kind,** like float64 to float32, are allowed.
- 'unsafe' means any data conversions may be done.

copy [bool, optional] By default, astype always returns a newly allocated array. If this is set to False and the *dtype* requirement is satisfied, the input array is returned instead of a copy.

blocks

Slice an array by blocks

This allows blockwise slicing of a Dask array. You can perform normal Numpy-style slicing but now rather than slice elements of the array you slice along blocks so, for example, `x.blocks[0, ::2]` produces a new dask array with every other block in the first row of blocks.

You can index blocks in any way that could index a numpy array of shape equal to the number of blocks in each dimension, (available as array.numblocks). The dimension of the output array will be the same as the dimension of this array, even if integer indices are passed. This does not support slicing with `np.newaxis` or multiple lists.

Returns

A Dask array

Examples

```
>>> import dask.array as da
>>> x = da.arange(10, chunks=2)
>>> x.blocks[0].compute()
array([0, 1])
>>> x.blocks[:3].compute()
array([0, 1, 2, 3, 4, 5])
>>> x.blocks[::2].compute()
array([0, 1, 4, 5, 8, 9])
>>> x.blocks[[-1, 0]].compute()
array([8, 9, 0, 1])
```

choose(*choices*, *out=None*, *mode='raise'*)

This docstring was copied from numpy.ndarray.choose.

Some inconsistencies with the Dask version may exist.

Use an index array to construct a new array from a set of choices.

Refer to *numpy.choose* for full documentation.

See also:

numpy.choose equivalent function

clip(*min=None*, *max=None*, *out=None*)

This docstring was copied from numpy.ndarray.clip.

Some inconsistencies with the Dask version may exist.

Return an array whose values are limited to `[min, max]`. One of max or min must be given.

Refer to *numpy.clip* for full documentation.

See also:

numpy.clip equivalent function

compute_chunk_sizes()

Compute the chunk sizes for a Dask array. This is especially useful when the chunk sizes are unknown (e.g., when indexing one Dask array with another).

Notes

This function modifies the Dask array in-place.

Examples

```
>>> import dask.array as da
>>> import numpy as np
>>> x = da.from_array([-2, -1, 0, 1, 2], chunks=2)
>>> x.chunks
((2, 2, 1),)
>>> y = x[x <= 0]
>>> y.chunks
((nan, nan, nan),)
>>> y.compute_chunk_sizes()  # in-place computation
dask.array<getitem, shape=(3,), dtype=int64, chunksize=(2,), chunktype=numpy.
↪ndarray>
>>> y.chunks
((2, 1, 0),)
```

copy()
Copy array. This is a no-op for dask.arrays, which are immutable

cumprod(*axis*, *dtype=None*, *out=None*)
See da.cumprod for docstring

cumsum(*axis*, *dtype=None*, *out=None*)
See da.cumsum for docstring

dot(*b*, *out=None*)
This docstring was copied from numpy.ndarray.dot.

Some inconsistencies with the Dask version may exist.

Dot product of two arrays.

Refer to *numpy.dot* for full documentation.

See also:

numpy.dot equivalent function

Examples

```
>>> a = np.eye(2)  # doctest: +SKIP
>>> b = np.ones((2, 2)) * 2  # doctest: +SKIP
>>> a.dot(b)  # doctest: +SKIP
array([[ 2.,  2.],
       [ 2.,  2.]])
```

This array method can be conveniently chained:

```
>>> a.dot(b).dot(b)  # doctest: +SKIP
array([[ 8.,  8.],
       [ 8.,  8.]])
```

flatten([*order*])
This docstring was copied from numpy.ndarray.ravel.

Some inconsistencies with the Dask version may exist.

Return a flattened array.

Refer to *numpy.ravel* for full documentation.

See also:

`numpy.ravel` equivalent function

`ndarray.flat` a flat iterator on the array.

`itemsize`
Length of one array element in bytes

`map_blocks`(**args, name=None, token=None, dtype=None, chunks=None, drop_axis=[], new_axis=None, meta=None, **kwargs*)
Map a function across all blocks of a dask array.

Parameters

func [callable] Function to apply to every block in the array.

args [dask arrays or other objects]

dtype [np.dtype, optional] The `dtype` of the output array. It is recommended to provide this. If not provided, will be inferred by applying the function to a small set of fake data.

chunks [tuple, optional] Chunk shape of resulting blocks if the function does not preserve shape. If not provided, the resulting array is assumed to have the same block structure as the first input array.

drop_axis [number or iterable, optional] Dimensions lost by the function.

new_axis [number or iterable, optional] New dimensions created by the function. Note that these are applied after `drop_axis` (if present).

token [string, optional] The key prefix to use for the output array. If not provided, will be determined from the function name.

name [string, optional] The key name to use for the output array. Note that this fully specifies the output key name, and must be unique. If not provided, will be determined by a hash of the arguments.

****kwargs :** Other keyword arguments to pass to function. Values must be constants (not dask.arrays)

Examples

```
>>> import dask.array as da
>>> x = da.arange(6, chunks=3)
```

```
>>> x.map_blocks(lambda x: x * 2).compute()
array([ 0,  2,  4,  6,  8, 10])
```

The `da.map_blocks` function can also accept multiple arrays.

```
>>> d = da.arange(5, chunks=2)
>>> e = da.arange(5, chunks=2)
```

```
>>> f = map_blocks(lambda a, b: a + b**2, d, e)
>>> f.compute()
array([ 0,  2,  6, 12, 20])
```

If the function changes shape of the blocks then you must provide chunks explicitly.

```
>>> y = x.map_blocks(lambda x: x[::2], chunks=((2, 2),))
```

You have a bit of freedom in specifying chunks. If all of the output chunk sizes are the same, you can provide just that chunk size as a single tuple.

```
>>> a = da.arange(18, chunks=(6,))
>>> b = a.map_blocks(lambda x: x[:3], chunks=(3,))
```

If the function changes the dimension of the blocks you must specify the created or destroyed dimensions.

```
>>> b = a.map_blocks(lambda x: x[None, :, None], chunks=(1, 6, 1),
...                  new_axis=[0, 2])
```

If `chunks` is specified but `new_axis` is not, then it is inferred to add the necessary number of axes on the left.

Map_blocks aligns blocks by block positions without regard to shape. In the following example we have two arrays with the same number of blocks but with different shape and chunk sizes.

```
>>> x = da.arange(1000, chunks=(100,))
>>> y = da.arange(100, chunks=(10,))
```

The relevant attribute to match is numblocks.

```
>>> x.numblocks
(10,)
>>> y.numblocks
(10,)
```

If these match (up to broadcasting rules) then we can map arbitrary functions across blocks

```
>>> def func(a, b):
...     return np.array([a.max(), b.max()])
```

```
>>> da.map_blocks(func, x, y, chunks=(2,), dtype='i8')
dask.array<func, shape=(20,), dtype=int64, chunksize=(2,), chunktype=numpy.
↪ndarray>
```

```
>>> _.compute()
array([ 99,   9, 199,  19, 299,  29, 399,  39, 499,  49, 599,  59, 699,
        69, 799,  79, 899,  89, 999,  99])
```

Your block function get information about where it is in the array by accepting a special `block_info` keyword argument.

```
>>> def func(block, block_info=None):
...     pass
```

This will receive the following information:

```
>>> block_info  # doctest: +SKIP
{0: {'shape': (1000,),
     'num-chunks': (10,),
     'chunk-location': (4,),
     'array-location': [(400, 500)]},
```

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```
None: {'shape': (1000,),
       'num-chunks': (10,),
       'chunk-location': (4,),
       'array-location': [(400, 500)],
       'chunk-shape': (100,),
       'dtype': dtype('float64')}}
```

For each argument and keyword arguments that are dask arrays (the positions of which are the first index), you will receive the shape of the full array, the number of chunks of the full array in each dimension, the chunk location (for example the fourth chunk over in the first dimension), and the array location (for example the slice corresponding to `40:50`). The same information is provided for the output, with the key `None`, plus the shape and dtype that should be returned.

These features can be combined to synthesize an array from scratch, for example:

```
>>> def func(block_info=None):
...     loc = block_info[None]['array-location'][0]
...     return np.arange(loc[0], loc[1])
```

```
>>> da.map_blocks(func, chunks=((4, 4),), dtype=np.float_)
dask.array<func, shape=(8,), dtype=float64, chunksize=(4,), chunktype=numpy.
↪ndarray>
```

```
>>> _.compute()
array([0, 1, 2, 3, 4, 5, 6, 7])
```

You may specify the key name prefix of the resulting task in the graph with the optional `token` keyword argument.

```
>>> x.map_blocks(lambda x: x + 1, name='increment')  # doctest: +SKIP
dask.array<increment, shape=(100,), dtype=int64, chunksize=(10,),␣
↪chunktype=numpy.ndarray>
```

map_overlap (*func*, *depth*, *boundary=None*, *trim=True*, ***kwargs*)

Map a function over blocks of the array with some overlap

We share neighboring zones between blocks of the array, then map a function, then trim away the neighboring strips.

Parameters

func: function The function to apply to each extended block

depth: int, tuple, or dict The number of elements that each block should share with its neighbors If a tuple or dict then this can be different per axis

boundary: str, tuple, dict How to handle the boundaries. Values include 'reflect', 'periodic', 'nearest', 'none', or any constant value like 0 or np.nan

trim: bool Whether or not to trim `depth` elements from each block after calling the map function. Set this to False if your mapping function already does this for you

****kwargs:** Other keyword arguments valid in `map_blocks`

Examples

```
>>> x = np.array([1, 1, 2, 3, 3, 3, 2, 1, 1])
>>> x = from_array(x, chunks=5)
>>> def derivative(x):
...     return x - np.roll(x, 1)
```

```
>>> y = x.map_overlap(derivative, depth=1, boundary=0)
>>> y.compute()
array([ 1,  0,  1,  1,  0,  0, -1, -1,  0])
```

```
>>> import dask.array as da
>>> x = np.arange(16).reshape((4, 4))
>>> d = da.from_array(x, chunks=(2, 2))
>>> d.map_overlap(lambda x: x + x.size, depth=1).compute()
array([[16, 17, 18, 19],
       [20, 21, 22, 23],
       [24, 25, 26, 27],
       [28, 29, 30, 31]])
```

```
>>> func = lambda x: x + x.size
>>> depth = {0: 1, 1: 1}
>>> boundary = {0: 'reflect', 1: 'none'}
>>> d.map_overlap(func, depth, boundary).compute()  # doctest: +NORMALIZE_
↪WHITESPACE
array([[12,  13,  14,  15],
       [16,  17,  18,  19],
       [20,  21,  22,  23],
       [24,  25,  26,  27]])
```

max (*axis=None*, *out=None*, *keepdims=False*)

This docstring was copied from numpy.ndarray.max.

Some inconsistencies with the Dask version may exist.

Return the maximum along a given axis.

Refer to *numpy.amax* for full documentation.

See also:

numpy.amax equivalent function

mean (*axis=None*, *dtype=None*, *out=None*, *keepdims=False*)

This docstring was copied from numpy.ndarray.mean.

Some inconsistencies with the Dask version may exist.

Returns the average of the array elements along given axis.

Refer to *numpy.mean* for full documentation.

See also:

numpy.mean equivalent function

min (*axis=None*, *out=None*, *keepdims=False*)

This docstring was copied from numpy.ndarray.min.

Some inconsistencies with the Dask version may exist.

Return the minimum along a given axis.

Refer to *numpy.amin* for full documentation.

See also:

`numpy.amin` equivalent function

`moment`(*order*, *axis=None*, *dtype=None*, *keepdims=False*, *ddof=0*, *split_every=None*, *out=None*)
Calculate the nth centralized moment.

Parameters

order [int] Order of the moment that is returned, must be >= 2.

axis [int, optional] Axis along which the central moment is computed. The default is to compute the moment of the flattened array.

dtype [data-type, optional] Type to use in computing the moment. For arrays of integer type the default is float64; for arrays of float types it is the same as the array type.

keepdims [bool, optional] If this is set to True, the axes which are reduced are left in the result as dimensions with size one. With this option, the result will broadcast correctly against the original array.

ddof [int, optional] "Delta Degrees of Freedom": the divisor used in the calculation is N - ddof, where N represents the number of elements. By default ddof is zero.

Returns

moment [ndarray]

References

Computation of Covariances and Arbitrary-Order Statistical Moments" (PDF), Technical Report SAND2008-6212, Sandia National Laboratories

[1]

`nbytes`
Number of bytes in array

`nonzero`()
This docstring was copied from numpy.ndarray.nonzero.

Some inconsistencies with the Dask version may exist.

Return the indices of the elements that are non-zero.

Refer to *numpy.nonzero* for full documentation.

See also:

`numpy.nonzero` equivalent function

`partitions`
Slice an array by partitions. Alias of dask array .blocks attribute.

This alias allows you to write agnostic code that works with both dask arrays and dask dataframes.

This allows blockwise slicing of a Dask array. You can perform normal Numpy-style slicing but now rather than slice elements of the array you slice along blocks so, for example, `x.blocks[0, ::2]` produces a new dask array with every other block in the first row of blocks.

You can index blocks in any way that could index a numpy array of shape equal to the number of blocks in each dimension, (available as array.numblocks). The dimension of the output array will be the same as the dimension of this array, even if integer indices are passed. This does not support slicing with `np.newaxis` or multiple lists.

Returns

A Dask array

Examples

```
>>> import dask.array as da
>>> x = da.arange(10, chunks=2)
>>> x.partitions[0].compute()
array([0, 1])
>>> x.partitions[:3].compute()
array([0, 1, 2, 3, 4, 5])
>>> x.partitions[::2].compute()
array([0, 1, 4, 5, 8, 9])
>>> x.partitions[[-1, 0]].compute()
array([8, 9, 0, 1])
>>> all(x.partitions[:].compute() == x.blocks[:].compute())
True
```

`prod`(*axis=None*, *dtype=None*, *out=None*, *keepdims=False*)

This docstring was copied from numpy.ndarray.prod.

Some inconsistencies with the Dask version may exist.

Return the product of the array elements over the given axis

Refer to *numpy.prod* for full documentation.

See also:

`numpy.prod` equivalent function

`ravel`([*order*])

This docstring was copied from numpy.ndarray.ravel.

Some inconsistencies with the Dask version may exist.

Return a flattened array.

Refer to *numpy.ravel* for full documentation.

See also:

`numpy.ravel` equivalent function

`ndarray.flat` a flat iterator on the array.

`rechunk`(*chunks*, *threshold=None*, *block_size_limit=None*)

See da.rechunk for docstring

repeat(*repeats*, *axis=None*)

This docstring was copied from numpy.ndarray.repeat.

Some inconsistencies with the Dask version may exist.

Repeat elements of an array.

Refer to *numpy.repeat* for full documentation.

See also:

`numpy.repeat` equivalent function

reshape(*shape*, *order='C'*)

This docstring was copied from numpy.ndarray.reshape.

Some inconsistencies with the Dask version may exist.

Returns an array containing the same data with a new shape.

Refer to *numpy.reshape* for full documentation.

See also:

`numpy.reshape` equivalent function

Notes

Unlike the free function *numpy.reshape*, this method on *ndarray* allows the elements of the shape parameter to be passed in as separate arguments. For example, `a.reshape(10, 11)` is equivalent to `a.reshape((10, 11))`.

round(*decimals=0*, *out=None*)

This docstring was copied from numpy.ndarray.round.

Some inconsistencies with the Dask version may exist.

Return *a* with each element rounded to the given number of decimals.

Refer to *numpy.around* for full documentation.

See also:

`numpy.around` equivalent function

size

Number of elements in array

squeeze(*axis=None*)

This docstring was copied from numpy.ndarray.squeeze.

Some inconsistencies with the Dask version may exist.

Remove single-dimensional entries from the shape of *a*.

Refer to *numpy.squeeze* for full documentation.

See also:

`numpy.squeeze` equivalent function

std(*axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)
This docstring was copied from numpy.ndarray.std.

Some inconsistencies with the Dask version may exist.

Returns the standard deviation of the array elements along given axis.

Refer to *numpy.std* for full documentation.

See also:

`numpy.std` equivalent function

store(*targets*, *lock=True*, *regions=None*, *compute=True*, *return_stored=False*, ***kwargs*)
Store dask arrays in array-like objects, overwrite data in target

This stores dask arrays into object that supports numpy-style setitem indexing. It stores values chunk by chunk so that it does not have to fill up memory. For best performance you can align the block size of the storage target with the block size of your array.

If your data fits in memory then you may prefer calling `np.array(myarray)` instead.

Parameters

sources: Array or iterable of Arrays

targets: array-like or Delayed or iterable of array-likes and/or Delayeds These should support setitem syntax `target[10:20] = ...`

lock: boolean or threading.Lock, optional Whether or not to lock the data stores while storing. Pass True (lock each file individually), False (don't lock) or a particular `threading.Lock` object to be shared among all writes.

regions: tuple of slices or list of tuples of slices Each `region` tuple in `regions` should be such that `target[region].shape = source.shape` for the corresponding source and target in sources and targets, respectively. If this is a tuple, the contents will be assumed to be slices, so do not provide a tuple of tuples.

compute: boolean, optional If true compute immediately, return `dask.delayed.Delayed` otherwise

return_stored: boolean, optional Optionally return the stored result (default False).

Examples

```
>>> x = ...  # doctest: +SKIP
```

```
>>> import h5py  # doctest: +SKIP
>>> f = h5py.File('myfile.hdf5', mode='a')  # doctest: +SKIP
>>> dset = f.create_dataset('/data', shape=x.shape,
...                                  chunks=x.chunks,
...                                  dtype='f8')  # doctest: +SKIP
```

```
>>> store(x, dset)  # doctest: +SKIP
```

Alternatively store many arrays at the same time

```
>>> store([x, y, z], [dset1, dset2, dset3])  # doctest: +SKIP
```

sum(*axis=None*, *dtype=None*, *out=None*, *keepdims=False*)
This docstring was copied from numpy.ndarray.sum.

Some inconsistencies with the Dask version may exist.

Return the sum of the array elements over the given axis.

Refer to *numpy.sum* for full documentation.

See also:

`numpy.sum` equivalent function

swapaxes(*axis1*, *axis2*)
This docstring was copied from numpy.ndarray.swapaxes.

Some inconsistencies with the Dask version may exist.

Return a view of the array with *axis1* and *axis2* interchanged.

Refer to *numpy.swapaxes* for full documentation.

See also:

`numpy.swapaxes` equivalent function

to_dask_dataframe(*columns=None*, *index=None*)
Convert dask Array to dask Dataframe

Parameters

columns: list or string list of column names if DataFrame, single string if Series

index [dask.dataframe.Index, optional] An optional *dask* Index to use for the output Series or DataFrame.

The default output index depends on whether the array has any unknown chunks. If there are any unknown chunks, the output has `None` for all the divisions (one per chunk). If all the chunks are known, a default index with known divsions is created.

Specifying `index` can be useful if you're conforming a Dask Array to an existing dask Series or DataFrame, and you would like the indices to match.

See also:

dask.dataframe.from_dask_array

to_delayed(*optimize_graph=True*)
Convert into an array of `dask.delayed` objects, one per chunk.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

dask.array.from_delayed

to_hdf5(*filename*, *datapath*, ***kwargs*)
Store array in HDF5 file

```
>>> x.to_hdf5('myfile.hdf5', '/x')  # doctest: +SKIP
```

Optionally provide arguments as though to `h5py.File.create_dataset`

```
>>> x.to_hdf5('myfile.hdf5', '/x', compression='lzf', shuffle=True)  #␣
↪doctest: +SKIP
```

See also:

`da.store`, `h5py.File.create_dataset`

`to_svg`(*size=500*)

Convert chunks from Dask Array into an SVG Image

Parameters

chunks: tuple

size: int Rough size of the image

Returns

text: An svg string depicting the array as a grid of chunks

Examples

```
>>> x.to_svg(size=500)  # doctest: +SKIP
```

`to_tiledb`(*uri*, **args*, ***kwargs*)

Save array to the TileDB storage manager

See function `to_tiledb()` for argument documentation.

See https://docs.tiledb.io for details about the format and engine.

`to_zarr`(**args*, ***kwargs*)

Save array to the zarr storage format

See https://zarr.readthedocs.io for details about the format.

See function `to_zarr()` for parameters.

`topk`(*k*, *axis=-1*, *split_every=None*)

The top k elements of an array.

See `da.topk` for docstring

`trace`(*offset=0*, *axis1=0*, *axis2=1*, *dtype=None*, *out=None*)

This docstring was copied from numpy.ndarray.trace.

Some inconsistencies with the Dask version may exist.

Return the sum along diagonals of the array.

Refer to *numpy.trace* for full documentation.

See also:

`numpy.trace` equivalent function

`transpose`(**axes*)

This docstring was copied from numpy.ndarray.transpose.

Some inconsistencies with the Dask version may exist.

Returns a view of the array with axes transposed.

For a 1-D array, this has no effect. (To change between column and row vectors, first cast the 1-D array into a matrix object.) For a 2-D array, this is the usual matrix transpose. For an n-D array, if axes are given, their order indicates how the axes are permuted (see Examples). If axes are not provided and `a.shape = (i[0], i[1], ... i[n-2], i[n-1])`, then `a.transpose().shape = (i[n-1], i[n-2], ... i[1], i[0])`.

Parameters

axes [None, tuple of ints, or *n* ints]

- None or no argument: reverses the order of the axes.
- tuple of ints: *i* in the *j*-th place in the tuple means *a*'s *i*-th axis becomes *a.transpose()*'s *j*-th axis.
- *n* ints: same as an n-tuple of the same ints (this form is intended simply as a "convenience" alternative to the tuple form)

Returns

out [ndarray] View of *a*, with axes suitably permuted.

See also:

`ndarray.T` Array property returning the array transposed.

Examples

```
>>> a = np.array([[1, 2], [3, 4]])  # doctest: +SKIP
>>> a  # doctest: +SKIP
array([[1, 2],
       [3, 4]])
>>> a.transpose()  # doctest: +SKIP
array([[1, 3],
       [2, 4]])
>>> a.transpose((1, 0))  # doctest: +SKIP
array([[1, 3],
       [2, 4]])
>>> a.transpose(1, 0)  # doctest: +SKIP
array([[1, 3],
       [2, 4]])
```

`var`(*axis=None*, *dtype=None*, *out=None*, *ddof=0*, *keepdims=False*)

This docstring was copied from numpy.ndarray.var.

Some inconsistencies with the Dask version may exist.

Returns the variance of the array elements, along given axis.

Refer to *numpy.var* for full documentation.

See also:

`numpy.var` equivalent function

`view`(*dtype*, *order='C'*)

Get a view of the array as a new data type

Parameters

dtype: The dtype by which to view the array

order: string 'C' or 'F' (Fortran) ordering

This reinterprets the bytes of the array under a new dtype. If that dtype does not have the same size as the original array then the shape will change.

Beware that both numpy and dask.array can behave oddly when taking shape-changing views of arrays under Fortran ordering. Under some versions of NumPy this function will fail when taking shape-changing views of Fortran ordered arrays if the first dimension has chunks of size one.

vindex

Vectorized indexing with broadcasting.

This is equivalent to numpy's advanced indexing, using arrays that are broadcast against each other. This allows for pointwise indexing:

```
>>> x = np.array([[1, 2, 3], [4, 5, 6], [7, 8, 9]])
>>> x = from_array(x, chunks=2)
>>> x.vindex[[0, 1, 2], [0, 1, 2]].compute()
array([1, 5, 9])
```

Mixed basic/advanced indexing with slices/arrays is also supported. The order of dimensions in the result follows those proposed for ndarray.vindex [1]_: the subspace spanned by arrays is followed by all slices.

Note: `vindex` provides more general functionality than standard indexing, but it also has fewer optimizations and can be significantly slower.

_[1]: https://github.com/numpy/numpy/pull/6256

3.7.2 Best Practices

It is easy to get started with Dask arrays, but using them *well* does require some experience. This page contains suggestions for best practices, and includes solutions to common problems.

Use NumPy

If your data fits comfortably in RAM and you are not performance bound, then using NumPy might be the right choice. Dask adds another layer of complexity which may get in the way.

If you are just looking for speedups rather than scalability then you may want to consider a project like Numba

Select a good chunk size

A common performance problem among Dask Array users is that they have chosen a chunk size that is either too small (leading to lots of overhead) or poorly aligned with their data (leading to inefficient reading).

While optimal sizes and shapes are highly problem specific, it is rare to see chunk sizes below 100 MB in size. If you are dealing with float64 data then this is around `(4000, 4000)` in size for a 2D array or `(100, 400, 400)` for a 3D array.

You want to choose a chunk size that is large in order to reduce the number of chunks that Dask has to think about (which affects overhead) but also small enough so that many of them can fit in memory at once. Dask will often have as many chunks in memory as twice the number of active threads.

Orient your chunks

When reading data you should align your chunks with your storage format. Most array storage formats store data in chunks themselves. If your Dask array chunks aren't multiples of these chunk shapes then you will have to read the same data repeatedly, which can be expensive. Note though that often storage formats choose chunk sizes that are much smaller than is ideal for Dask, closer to 1MB than 100MB. In these cases you should choose a Dask chunk size that aligns with the storage chunk size and that every Dask chunk dimension is a multiple of the storage chunk dimension.

So for example if we have an HDF file that has chunks of size `(128, 64)`, we might choose a chunk shape of `(1280, 6400)`.

```
>>> import h5py
>>> storage = h5py.File('myfile.hdf5')['x']
>>> storage.chunks
(128, 64)

>>> import dask.array as da
>>> x = da.from_array(storage, chunks=(1280, 6400))
```

Note that if you provide `chunks='auto'` then Dask Array will look for a `.chunks` attribute and use that to provide a good chunking.

Avoid Oversubscribing Threads

By default Dask will run as many concurrent tasks as you have logical cores. It assumes that each task will consume about one core. However, many array-computing libraries are themselves multi-threaded, which can cause contention and low performance. In particular the BLAS/LAPACK libraries that back most of NumPy's linear algebra routines are often multi-threaded, and need to be told to use only one thread explicitly. You can do this with the following environment variables (using bash `export` command below, but this may vary depending on your operating system).

```
export OMP_NUM_THREADS=1
export MKL_NUM_THREADS=1
export OPENBLAS_NUM_THREADS=1
```

You need to run this before you start your Python process for it to take effect.

Consider Xarray

The Xarray package wraps around Dask Array, and so offers the same scalability, but also adds convenience when dealing with complex datasets. In particular Xarray can help with the following:

1. Manage multiple arrays together as a consistent dataset
2. Read from a stack of HDF or NetCDF files at once
3. Switch between Dask Array and NumPy with a consistent API

Xarray is used in wide range of fields, including physics, astronomy, geoscience, microscopy, bioinformatics, engineering, finance, and deep learning. Xarray also has a thriving user community that is good at providing support.

Build your own Operations

Often we want to perform computations for which there is no exact function in Dask Array. In these cases we may be able to use some of the more generic functions to build our own. These include:

`blockwise`(func, out_ind, *args[, name, . . .])	Tensor operation: Generalized inner and outer products
`map_blocks`(func, *args[, name, token, . . .])	Map a function across all blocks of a dask array.
`map_overlap`(x, func, depth[, boundary, trim])	Map a function over blocks of the array with some overlap
`reduction`(x, chunk, aggregate[, axis, . . .])	General version of reductions

These functions may help you to apply a function that you write for NumPy functions onto larger Dask arrays.

3.7.3 Chunks

Dask arrays are composed of many NumPy arrays. How these arrays are arranged can significantly affect performance. For example, for a square array you might arrange your chunks along rows, along columns, or in a more square-like fashion. Different arrangements of NumPy arrays will be faster or slower for different algorithms.

Thinking about and controlling chunking is important to optimize advanced algorithms.

Specifying Chunk shapes

We always specify a `chunks` argument to tell dask.array how to break up the underlying array into chunks. We can specify `chunks` in a variety of ways:

1. A uniform dimension size like `1000`, meaning chunks of size `1000` in each dimension
2. A uniform chunk shape like `(1000, 2000, 3000)`, meaning chunks of size `1000` in the first axis, `2000` in the second axis, and `3000` in the third
3. Fully explicit sizes of all blocks along all dimensions, like `((1000, 1000, 500), (400, 400), (5, 5, 5, 5, 5))`
4. A dictionary specifying chunk size per dimension like `{0: 1000, 1: 2000, 2: 3000}`. This is just another way of writing the forms 2 and 3 above

Your chunks input will be normalized and stored in the third and most explicit form. Note that `chunks` stands for "chunk shape" rather than "number of chunks", so specifying `chunks=1` means that you will have many chunks, each with exactly one element.

For performance, a good choice of `chunks` follows the following rules:

1. A chunk should be small enough to fit comfortably in memory. We'll have many chunks in memory at once
2. A chunk must be large enough so that computations on that chunk take significantly longer than the 1ms overhead per task that Dask scheduling incurs. A task should take longer than 100ms
3. Chunk sizes between 10MB-1GB are common, depending on the availability of RAM and the duration of computations
4. Chunks should align with the computation that you want to do.

   For example, if you plan to frequently slice along a particular dimension, then it's more efficient if your chunks are aligned so that you have to touch fewer chunks. If you want to add two arrays, then its convenient if those arrays have matching chunks patterns

5. Chunks should align with your storage, if applicable.

   Array data formats are often chunked as well. When loading or saving data, if is useful to have Dask array chunks that are aligned with the chunking of your storage, often an even multiple times larger in each direction

Unknown Chunks

Some arrays have unknown chunk sizes. This arises whenever the size of an array depends on lazy computations that we haven't yet performed like the following:

```
>>> x = da.from_array(np.random.randn(100), chunks=20)
>>> x += 0.1
>>> y = x[x > 0]  # don't know how many values are greater than 0 ahead of time
```

Operations like the above result in arrays with unknown shapes and unknown chunk sizes. Unknown values within shape or chunks are designated using `np.nan` rather than an integer. These arrays support many (but not all) operations. In particular, operations like slicing are not possible and will result in an error.

```
>>> y.shape
(np.nan,)
>>> y[4]
...
ValueError: Array chunk sizes unknown

A possible solution: https://docs.dask.org/en/latest/array-chunks.html#unknown-chunks.
Summary: to compute chunks sizes, use

    x.compute_chunk_sizes()  # for Dask Array
    ddf.to_dask_array(lengths=True)  # for Dask DataFrame ddf
```

Using *`compute_chunk_sizes()`* allows this example run:

```
>>> y.compute_chunk_sizes()
dask.array<..., chunksize=(19,), ...>
>>> y.shape
(44,)
>>> y[4].compute()
0.78621774046566
```

Note that *`compute_chunk_sizes()`* immediately performs computation and modifies the array in-place.

Unknown chunksizes also occur when using a Dask DataFrame to create a Dask array:

```
>>> ddf = dask.dataframe.from_pandas(...)
>>> ddf.to_dask_array()
dask.array<..., shape=(nan, 2), ..., chunksize=(nan, 2)>
```

Using *`to_dask_array()`* resolves this issue:

```
>>> ddf.to_dask_array(lengths=True)
dask.array<..., shape=(100, 2), ..., chunksize=(20, 2)>
```

More details on *`to_dask_array()`* are in mentioned in how to create a Dask array from a Dask DataFrame in the *documentation on Dask array creation*.

Chunks Examples

In this example we show how different inputs for `chunks=` cut up the following array:

```
1 2 3 4 5 6
7 8 9 0 1 2
3 4 5 6 7 8
9 0 1 2 3 4
5 6 7 8 9 0
1 2 3 4 5 6
```

Here, we show how different `chunks=` arguments split the array into different blocks

chunks=3: Symmetric blocks of size 3:

```
1 2 3  4 5 6
7 8 9  0 1 2
3 4 5  6 7 8

9 0 1  2 3 4
5 6 7  8 9 0
1 2 3  4 5 6
```

chunks=2: Symmetric blocks of size 2:

```
1 2  3 4  5 6
7 8  9 0  1 2

3 4  5 6  7 8
9 0  1 2  3 4

5 6  7 8  9 0
1 2  3 4  5 6
```

chunks=(3, 2): Asymmetric but repeated blocks of size `(3, 2)`:

```
1 2  3 4  5 6
7 8  9 0  1 2
3 4  5 6  7 8

9 0  1 2  3 4
5 6  7 8  9 0
1 2  3 4  5 6
```

chunks=(1, 6): Asymmetric but repeated blocks of size `(1, 6)`:

```
1 2 3 4 5 6

7 8 9 0 1 2

3 4 5 6 7 8

9 0 1 2 3 4

5 6 7 8 9 0

1 2 3 4 5 6
```

chunks=((2, 4), (3, 3)): Asymmetric and non-repeated blocks:

```
1 2 3  4 5 6
7 8 9  0 1 2

3 4 5  6 7 8
9 0 1  2 3 4
5 6 7  8 9 0
1 2 3  4 5 6
```

chunks=((2, 2, 1, 1), (3, 2, 1)): Asymmetric and non-repeated blocks:

```
1 2 3  4 5  6
7 8 9  0 1  2

3 4 5  6 7  8
9 0 1  2 3  4

5 6 7  8 9  0

1 2 3  4 5  6
```

Discussion

The latter examples are rarely provided by users on original data but arise from complex slicing and broadcasting operations. Generally people use the simplest form until they need more complex forms. The choice of chunks should align with the computations you want to do.

For example, if you plan to take out thin slices along the first dimension, then you might want to make that dimension skinnier than the others. If you plan to do linear algebra, then you might want more symmetric blocks.

Loading Chunked Data

Modern NDArray storage formats like HDF5, NetCDF, TIFF, and Zarr, allow arrays to be stored in chunks or tiles so that blocks of data can be pulled out efficiently without having to seek through a linear data stream. It is best to align the chunks of your Dask array with the chunks of your underlying data store.

However, data stores often chunk more finely than is ideal for Dask array, so it is common to choose a chunking that is a multiple of your storage chunk size, otherwise you might incur high overhead.

For example, if you are loading a data store that is chunked in blocks of `(100, 100)`, then you might choose a chunking more like `(1000, 2000)` that is larger, but still evenly divisible by `(100, 100)`. Data storage technologies will be able to tell you how their data is chunked.

Rechunking

`rechunk`(x, chunks[, threshold, block_size_limit])	Convert blocks in dask array x for new chunks.

Sometimes you need to change the chunking layout of your data. For example, perhaps it comes to you chunked row-wise, but you need to do an operation that is much faster if done across columns. You can change the chunking with the `rechunk` method.

```
x = x.rechunk((50, 1000))
```

Rechunking across axes can be expensive and incur a lot of communication, but Dask array has fairly efficient algorithms to accomplish this.

You can pass rechunk any valid chunking form:

```
x = x.rechunk(1000)
x = x.rechunk((50, 1000))
x = x.rechunk({0: 50, 1: 1000})
```

Automatic Chunking

Chunks also includes three special values:

1. `-1`: no chunking along this dimension
2. `None`: no change to the chunking along this dimension (useful for rechunk)
3. `"auto"`: allow the chunking in this dimension to accommodate ideal chunk sizes

So, for example, one could rechunk a 3D array to have no chunking along the zeroth dimension, but still have sensible chunk sizes as follows:

```
x = x.rechunk({0: -1, 1: 'auto', 2: 'auto'})
```

Or one can allow *all* dimensions to be auto-scaled to get to a good chunk size:

```
x = x.rechunk('auto')
```

Automatic chunking expands or contracts all dimensions marked with `"auto"` to try to reach chunk sizes with a number of bytes equal to the config value `array.chunk-size`, which is set to 128MiB by default, but which you can change in your *configuration*.

```
>>> dask.config.get('array.chunk-size')
'128MiB'
```

Automatic rechunking tries to respect the median chunk shape of the auto-rescaled dimensions, but will modify this to accommodate the shape of the full array (can't have larger chunks than the array itself) and to find chunk shapes that nicely divide the shape.

These values can also be used when creating arrays with operations like `dask.array.ones` or `dask.array.from_array`

```
>>> dask.array.ones((10000, 10000), chunks=(-1, 'auto'))
dask.array<wrapped, shape=(10000, 10000), dtype=float64, chunksize=(10000, 1250),␣
↪chunktype=numpy.ndarray>
```

3.7.4 Create Dask Arrays

You can load or store Dask arrays from a variety of common sources like HDF5, NetCDF, Zarr, or any format that supports NumPy-style slicing.

`from_array`(x[, chunks, name, lock, asarray, ...])	Create dask array from something that looks like an array
`from_delayed`(value, shape[, dtype, meta, name])	Create a dask array from a dask delayed value
`from_npy_stack`(dirname[, mmap_mode])	Load dask array from stack of npy files
`from_zarr`(url[, component, storage_options, ...])	Load array from the zarr storage format
`stack`(seq[, axis])	Stack arrays along a new axis
`concatenate`(seq[, axis, ...])	Concatenate arrays along an existing axis

NumPy Slicing

from_array(x[, chunks, name, lock, asarray, . . .])	Create dask array from something that looks like an array

Many storage formats have Python projects that expose storage using NumPy slicing syntax. These include HDF5, NetCDF, BColz, Zarr, GRIB, etc. For example, we can load a Dask array from an HDF5 file using h5py:

```
>>> import h5py
>>> f = h5py.File('myfile.hdf5') # HDF5 file
>>> d = f['/data/path']          # Pointer on on-disk array
>>> d.shape                      # d can be very large
(1000000, 1000000)

>>> x = d[:5, :5]                # We slice to get numpy arrays
```

Given an object like `d` above that has `dtype` and `shape` properties and that supports NumPy style slicing, we can construct a lazy Dask array:

```
>>> import dask.array as da
>>> x = da.from_array(d, chunks=(1000, 1000))
```

This process is entirely lazy. Neither creating the h5py object nor wrapping it with `da.from_array` have loaded any data.

Random Data

For experimentation or benchmarking it is common to create arrays of random data. The `dask.array.random` module implements most of the functions in the `numpy.random` module. We list some common functions below but for a full list see the *Array API*:

random.binomial(n, p[, size])	Draw samples from a binomial distribution.
random.normal([loc, scale, size])	Draw random samples from a normal (Gaussian) distribution.
random.poisson([lam, size])	Draw samples from a Poisson distribution.
random.random([size])	Return random floats in the half-open interval [0.0, 1.0).

```
>>> import dask.array as da
>>> x = da.random.random((10000, 10000), chunks=(1000, 1000))
```

Concatenation and Stacking

stack(seq[, axis])	Stack arrays along a new axis
concatenate(seq[, axis, . . .])	Concatenate arrays along an existing axis

Often we store data in several different locations and want to stitch them together:

```
dask_arrays = []
for fn in filenames:
    f = h5py.File(fn)
```

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```
    d = f['/data']
    array = da.from_array(d, chunks=(1000, 1000))
    dask_arrays.append(array)

x = da.concatenate(dask_arrays, axis=0)  # concatenate arrays along first axis
```

For more information, see *concatenation and stacking* docs.

Using `dask.delayed`

`from_delayed`(value, shape[, dtype, meta, name])	Create a dask array from a dask delayed value
`stack`(seq[, axis])	Stack arrays along a new axis
`concatenate`(seq[, axis, . . .])	Concatenate arrays along an existing axis

Sometimes NumPy-style data resides in formats that do not support NumPy-style slicing. We can still construct Dask arrays around this data if we have a Python function that can generate pieces of the full array if we use *dask.delayed*. Dask delayed lets us delay a single function call that would create a NumPy array. We can then wrap this delayed object with `da.from_delayed`, providing a dtype and shape to produce a single-chunked Dask array. Furthermore, we can use `stack` or `concatenate` from before to construct a larger lazy array.

As an example, consider loading a stack of images using `skimage.io.imread`:

```
import skimage.io
import dask.array as da
import dask

imread = dask.delayed(skimage.io.imread, pure=True)  # Lazy version of imread

filenames = sorted(glob.glob('*.jpg'))

lazy_images = [imread(path) for path in filenames]   # Lazily evaluate imread on each␣
↪path
sample = lazy_images[0].compute()  # load the first image (assume rest are same shape/
↪dtype)

arrays = [da.from_delayed(lazy_image,           # Construct a small Dask array
                          dtype=sample.dtype,   # for every lazy value
                          shape=sample.shape)
          for lazy_image in lazy_images]

stack = da.stack(arrays, axis=0)                # Stack all small Dask arrays into one
```

See *documentation on using dask.delayed with collections*.

From Dask DataFrame

There are several ways to create a Dask array from a Dask DataFrame. Dask DataFrames have a `to_dask_array` method:

```
>>> df = dask.dataframes.from_pandas(...)
>>> df.to_dask_array()
dask.array<values, shape=(nan, 3), dtype=float64, chunksize=(nan, 3), chunktype=numpy.
↪ndarray>
```

This mirrors the to_numpy function in Pandas. The `values` attribute is also supported:

```
>>> df.values
dask.array<values, shape=(nan, 3), dtype=float64, chunksize=(nan, 3), chunktype=numpy.
↪ndarray>
```

However, these arrays do not have known chunk sizes because dask.dataframe does not track the number of rows in each partition. This means that some operations like slicing will not operate correctly.

The chunk sizes can be computed:

```
>>> df.to_dask_array(lengths=True)
dask.array<array, shape=(100, 3), dtype=float64, chunksize=(50, 3), chunktype=numpy.
↪ndarray>
```

Specifying `lengths=True` triggers immediate computation of the chunk sizes. This enables downstream computations that rely on having known chunk sizes (e.g., slicing).

The Dask DataFrame `to_records` method also returns a Dask Array, but does not compute the shape information:

```
>>> df.to_records()
dask.array<to_records, shape=(nan,), dtype=(numpy.record, [('index', '<i8'), ('x', '
↪<f8'), ('y', '<f8'), ('z', '<f8')]), chunksize=(nan,), chunktype=numpy.ndarray>
```

If you have a function that converts a Pandas DataFrame into a NumPy array, then calling `map_partitions` with that function on a Dask DataFrame will produce a Dask array:

```
>>> df.map_partitions(np.asarray)
dask.array<asarray, shape=(nan, 3), dtype=float64, chunksize=(nan, 3),␣
↪chunktype=numpy.ndarray>
```

Interactions with NumPy arrays

Dask array operations will automatically convert NumPy arrays into single-chunk dask arrays:

```
>>> x = da.sum(np.ones(5))
>>> x.compute()
5
```

When NumPy and Dask arrays interact, the result will be a Dask array. Automatic rechunking rules will generally slice the NumPy array into the appropriate Dask chunk shape:

```
>>> x = da.ones(10, chunks=(5,))
>>> y = np.ones(10)
>>> z = x + y
>>> z
dask.array<add, shape=(10,), dtype=float64, chunksize=(5,), chunktype=numpy.ndarray>
```

These interactions work not just for NumPy arrays but for any object that has shape and dtype attributes and implements NumPy slicing syntax.

Chunks

See *documentation on Array Chunks* for more information.

3.7.5 Store Dask Arrays

store(sources, targets[, lock, regions, . . .])	Store dask arrays in array-like objects, overwrite data in target
to_hdf5(filename, *args, **kwargs)	Store arrays in HDF5 file
to_npy_stack(dirname, x[, axis])	Write dask array to a stack of .npy files
to_zarr(arr, url[, component, . . .])	Save array to the zarr storage format
compute(*args, **kwargs)	Compute several dask collections at once.

In Memory

compute(*args, **kwargs)	Compute several dask collections at once.

If you have a small amount of data, you can call `np.array` or `.compute()` on your Dask array to turn in to a normal NumPy array:

```
>>> x = da.arange(6, chunks=3)
>>> y = x**2
>>> np.array(y)
array([0, 1, 4, 9, 16, 25])

>>> y.compute()
array([0, 1, 4, 9, 16, 25])
```

NumPy style slicing

store(sources, targets[, lock, regions, . . .])	Store dask arrays in array-like objects, overwrite data in target

You can store Dask arrays in any object that supports NumPy-style slice assignment like `h5py.Dataset`:

```
>>> import h5py
>>> f = h5py.File('myfile.hdf5')
>>> d = f.require_dataset('/data', shape=x.shape, dtype=x.dtype)
>>> da.store(x, d)
```

Also, you can store several arrays in one computation by passing lists of sources and destinations:

```
>>> da.store([array1, array2], [output1, output2])  # doctest: +SKIP
```

HDF5

to_hdf5(filename, *args, **kwargs)	Store arrays in HDF5 file

HDF5 is sufficiently common that there is a special function `to_hdf5` to store data into HDF5 files using `h5py`:

```
>>> da.to_hdf5('myfile.hdf5', '/y', y)  # doctest: +SKIP
```

You can store several arrays in one computation with the function `da.to_hdf5` by passing in a dictionary:

```
>>> da.to_hdf5('myfile.hdf5', {'/x': x, '/y': y})  # doctest: +SKIP
```

Zarr

The Zarr format is a chunk-wise binary array storage file format with a good selection of encoding and compression options. Due to each chunk being stored in a separate file, it is ideal for parallel access in both reading and writing (for the latter, if the Dask array chunks are aligned with the target). Furthermore, storage in *remote data services* such as S3 and GCS is supported.

For example, to save data to a local zarr dataset you would do:

```
>>> arr.to_zarr('output.zarr')
```

or to save to a particular bucket on S3:

```
>>> arr.to_zarr('s3://mybucket/output.zarr', storage_option={'key': 'mykey',
                'secret': 'mysecret'})
```

or your own custom zarr Array:

```
>>> z = zarr.create((10,), dtype=float, store=zarr.ZipStore("output.zarr"))
>>> arr.to_zarr(z)
```

To retrieve those data, you would do `da.from_zarr` with exactly the same arguments. The chunking of the resultant Dask array is defined by how the files were saved, unless otherwise specified.

TileDB

TileDB is a binary array format and storage manager with tunable chunking, layout, and compression options. The TileDB storage manager library includes support for scalable storage backends such as S3 API compatible object stores and HDFS, with automatic scaling, and supports multi-threaded and multi-process reads (consistent) and writes (eventually-consistent).

To save data to a local TileDB array:

```
>>> arr.to_tiledb('output.tdb')
```

or to save to a bucket on S3:

```
>>> arr.to_tiledb('s3://mybucket/output.tdb',
                  storage_options={'vfs.s3.aws_access_key_id': 'mykey',
                                   'vfs.s3.aws_secret_access_key': 'mysecret'})
```

Files may be retrieved by running *da.from_tiledb* with the same URI, and any necessary arguments.

Intermediate storage

`store`(sources, targets[, lock, regions, . . .])	Store dask arrays in array-like objects, overwrite data in target

In some cases, one may wish to store an intermediate result in long term storage. This differs from `persist`, which is mainly used to manage intermediate results within Dask that don't necessarily have longevity. Also it differs from storing final results as these mark the end of the Dask graph. Thus intermediate results are easier to reuse without reloading data. Intermediate storage is mainly useful in cases where the data is needed outside of Dask (e.g. on disk, in a database, in the cloud, etc.). It can be useful as a checkpoint for long running or error-prone computations.

The intermediate storage use case differs from the typical storage use case as a Dask Array is returned to the user that represents the result of that storage operation. This is typically done by setting the `store` function's `return_stored` flag to `True`.

```
x.store()  # stores data, returns nothing
x = x.store(return_stored=True)  # stores data, returns new dask array backed by that␣
↪data
```

The user can then decide whether the storage operation happens immediately (by setting the `compute` flag to `True`) or later (by setting the `compute` flag to `False`). In all other ways, this behaves the same as a normal call to `store`. Some examples are shown below.

```
>>> import dask.array as da
>>> import zarr as zr
>>> c = (2, 2)
>>> d = da.ones((10, 11), chunks=c)
>>> z1 = zr.open_array('lazy.zarr', shape=d.shape, dtype=d.dtype, chunks=c)
>>> z2 = zr.open_array('eager.zarr', shape=d.shape, dtype=d.dtype, chunks=c)
>>> d1 = d.store(z1, compute=False, return_stored=True)
>>> d2 = d.store(z2, compute=True, return_stored=True)
```

This can be combined with any other storage strategies either noted above, in the docs or for any specialized storage types.

3.7.6 Plugins

We can run arbitrary user-defined functions on Dask arrays whenever they are constructed. This allows us to build a variety of custom behaviors that improve debugging, user warning, etc. You can register a list of functions to run on all Dask arrays to the global `array_plugins=` value:

```
>>> def f(x):
...     print(x.nbytes)

>>> with dask.config.set(array_plugins=[f]):
...     x = da.ones((10, 1), chunks=(5, 1))
...     y = x.dot(x.T)
80
80
800
800
```

If the plugin function returns None, then the input Dask array will be returned without change. If the plugin function returns something else, then that value will be the result of the constructor.

Examples

Automatically compute

We may wish to turn some Dask array code into normal NumPy code. This is useful, for example, to track down errors immediately that would otherwise be hidden by Dask's lazy semantics:

```
>>> with dask.config.set(array_plugins=[lambda x: x.compute()]):
...     x = da.arange(5, chunks=2)

>>> x  # this was automatically converted into a numpy array
array([0, 1, 2, 3, 4])
```

Warn on large chunks

We may wish to warn users if they are creating chunks that are too large:

```
def warn_on_large_chunks(x):
    shapes = list(itertools.product(*x.chunks))
    nbytes = [x.dtype.itemsize * np.prod(shape) for shape in shapes]
    if any(nb > 1e9 for nb in nbytes):
        warnings.warn("Array contains very large chunks")

with dask.config.set(array_plugins=[warn_on_large_chunks]):
    ...
```

Combine

You can also combine these plugins into a list. They will run one after the other, chaining results through them:

```
with dask.config.set(array_plugins=[warn_on_large_chunks, lambda x: x.compute()]):
    ...
```

3.7.7 Overlapping Computations

Some array operations require communication of borders between neighboring blocks. Example operations include the following:

- Convolve a filter across an image
- Sliding sum/mean/max, ...
- Search for image motifs like a Gaussian blob that might span the border of a block
- Evaluate a partial derivative
- Play the game of Life

Dask Array supports these operations by creating a new array where each block is slightly expanded by the borders of its neighbors. This costs an excess copy and the communication of many small chunks, but allows localized functions to evaluate in an embarrassingly parallel manner.

The main API for these computations is the `map_overlap` method defined below:

map_overlap(x, func, depth[, boundary, trim])	Map a function over blocks of the array with some overlap

`dask.array.`**`map_overlap`**(*x*, *func*, *depth*, *boundary=None*, *trim=True*, ***kwargs*)

Map a function over blocks of the array with some overlap

We share neighboring zones between blocks of the array, then map a function, then trim away the neighboring strips.

Parameters

func: function The function to apply to each extended block

depth: int, tuple, or dict The number of elements that each block should share with its neighbors If a tuple or dict then this can be different per axis. Asymmetric depths may be specified using a dict value of (-/+) tuples. Note that asymmetric depths are currently only supported when `boundary` is 'none'.

boundary: str, tuple, dict How to handle the boundaries. Values include 'reflect', 'periodic', 'nearest', 'none', or any constant value like 0 or np.nan

trim: bool Whether or not to trim `depth` elements from each block after calling the map function. Set this to False if your mapping function already does this for you

****kwargs:** Other keyword arguments valid in `map_blocks`

Examples

```
>>> import numpy as np
>>> import dask.array as da
```

```
>>> x = np.array([1, 1, 2, 3, 3, 3, 2, 1, 1])
>>> x = da.from_array(x, chunks=5)
>>> def derivative(x):
...     return x - np.roll(x, 1)
```

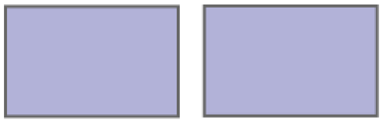
```
>>> y = x.map_overlap(derivative, depth=1, boundary=0)
>>> y.compute()
array([ 1,  0,  1,  1,  0,  0, -1, -1,  0])
```

```
>>> x = np.arange(16).reshape((4, 4))
>>> d = da.from_array(x, chunks=(2, 2))
>>> d.map_overlap(lambda x: x + x.size, depth=1).compute()
array([[16, 17, 18, 19],
       [20, 21, 22, 23],
       [24, 25, 26, 27],
       [28, 29, 30, 31]])
```

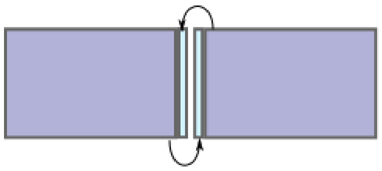
```
>>> func = lambda x: x + x.size
>>> depth = {0: 1, 1: 1}
>>> boundary = {0: 'reflect', 1: 'none'}
>>> d.map_overlap(func, depth, boundary).compute()  # doctest: +NORMALIZE_
↪WHITESPACE
array([[12,  13,  14,  15],
       [16,  17,  18,  19],
       [20,  21,  22,  23],
       [24,  25,  26,  27]])
```

Explanation

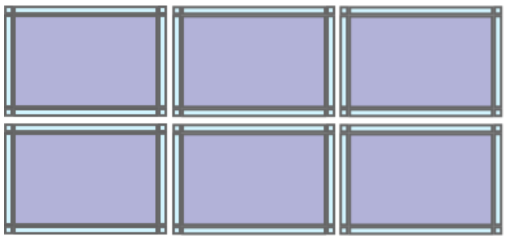
Consider two neighboring blocks in a Dask array:



We extend each block by trading thin nearby slices between arrays:



We do this in all directions, including also diagonal interactions with the overlap function:



```
>>> import dask.array as da
>>> import numpy as np

>>> x = np.arange(64).reshape((8, 8))
>>> d = da.from_array(x, chunks=(4, 4))
>>> d.chunks
((4, 4), (4, 4))

>>> g = da.overlap.overlap(d, depth={0: 2, 1: 1},
...                        boundary={0: 100, 1: 'reflect'})
>>> g.chunks
((8, 8), (6, 6))

>>> np.array(g)
array([[100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [  0,   0,   1,   2,   3,   4,   3,   4,   5,   6,   7,   7],
       [  8,   8,   9,  10,  11,  12,  11,  12,  13,  14,  15,  15],
       [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
       [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
       [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
       [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
       [ 16,  16,  17,  18,  19,  20,  19,  20,  21,  22,  23,  23],
       [ 24,  24,  25,  26,  27,  28,  27,  28,  29,  30,  31,  31],
       [ 32,  32,  33,  34,  35,  36,  35,  36,  37,  38,  39,  39],
       [ 40,  40,  41,  42,  43,  44,  43,  44,  45,  46,  47,  47],
       [ 48,  48,  49,  50,  51,  52,  51,  52,  53,  54,  55,  55],
       [ 56,  56,  57,  58,  59,  60,  59,  60,  61,  62,  63,  63],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100],
       [100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100]])
```

Boundaries

With respect to overlaping, you can specify how to handle the boundaries. Current policies include the following:

- `periodic` - wrap borders around to the other side
- `reflect` - reflect each border outwards
- `any-constant` - pad the border with this value

An example boundary kind argument might look like the following:

```
{0: 'periodic',
 1: 'reflect',
 2: np.nan}
```

Alternatively, you can use *`dask.array.pad()`* for other types of paddings.

Map a function across blocks

Overlapping goes hand-in-hand with mapping a function across blocks. This function can now use the additional information copied over from the neighbors that is not stored locally in each block:

```
>>> from scipy.ndimage.filters import gaussian_filter
>>> def func(block):
...    return gaussian_filter(block, sigma=1)

>>> filt = g.map_blocks(func)
```

While in this case we used a SciPy function, any arbitrary function could have been used instead. This is a good interaction point with Numba.

If your function does not preserve the shape of the block, then you will need to provide a `chunks` keyword argument. If your block size is regular, then this argument can take a block shape of, for example, `(1000, 1000)`. In case of irregular block sizes, it must be a tuple with the full chunks shape like `((1000, 700, 1000), (200, 300))`.

```
>>> g.map_blocks(myfunc, chunks=(5, 5))
```

If your function needs to know the location of the block on which it operates, you can give your function a keyword argument `block_id`:

```
def func(block, block_id=None):
    ...
```

This extra keyword argument will be given a tuple that provides the block location like `(0, 0)` for the upper-left block or `(0, 1)` for the block just to the right of that block.

Trim Excess

After mapping a blocked function, you may want to trim off the borders from each block by the same amount by which they were expanded. The function `trim_internal` is useful here and takes the same `depth` argument given to `overlap`:

```
>>> x.chunks
((10, 10, 10, 10), (10, 10, 10, 10))

>>> y = da.overlap.trim_internal(x, {0: 2, 1: 1})
>>> y.chunks
((6, 6, 6, 6), (8, 8, 8, 8))
```

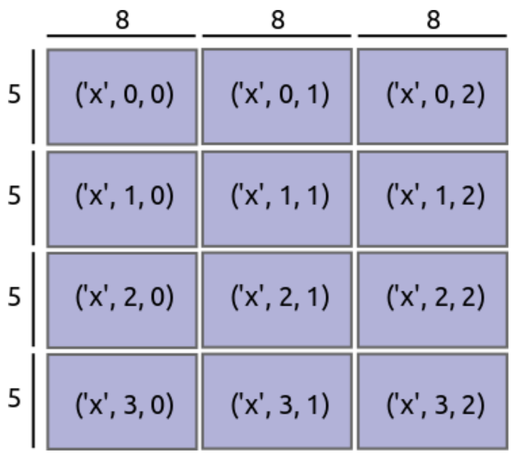
Full Workflow

And so, a pretty typical overlaping workflow includes `overlap`, `map_blocks` and `trim_internal`:

```
>>> x = ...
>>> g = da.overlap.overlap(x, depth={0: 2, 1: 2},
...                       boundary={0: 'periodic', 1: 'periodic'})
>>> g2 = g.map_blocks(myfunc)
>>> result = da.overlap.trim_internal(g2, {0: 2, 1: 2})
```

3.7.8 Internal Design

Overview



Dask arrays define a large array with a grid of blocks of smaller arrays. These arrays may be actual arrays or functions that produce arrays. We define a Dask array with the following components:

- A Dask graph with a special set of keys designating blocks such as `('x', 0, 0), ('x', 0, 1), ...` (See *Dask graph documentation* for more details)
- A sequence of chunk sizes along each dimension called `chunks`, for example `((5, 5, 5, 5), (8, 8, 8))`
- A name to identify which keys in the Dask graph refer to this array, like `'x'`
- A NumPy dtype

Example

```
>>> import dask.array as da
>>> x = da.arange(0, 15, chunks=(5,))

>>> x.name
'arange-539766a'

>>> x.dask  # somewhat simplified
{('arange-539766a', 0): (np.arange, 0, 5),
 ('arange-539766a', 1): (np.arange, 5, 10),
 ('arange-539766a', 2): (np.arange, 10, 15)}
```

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```
>>> x.chunks
((5, 5, 5),)

>>> x.dtype
dtype('int64')
```

Keys of the Dask graph

By special convention, we refer to each block of the array with a tuple of the form `(name, i, j, k)`, with `i, j, k` being the indices of the block ranging from `0` to the number of blocks in that dimension. The Dask graph must hold key-value pairs referring to these keys. Moreover, it likely also holds other key-value pairs required to eventually compute the desired values:

```
{
 ('x', 0, 0): (add, 1, ('y', 0, 0)),
 ('x', 0, 1): (add, 1, ('y', 0, 1)),
 ...
 ('y', 0, 0): (getitem, dataset, (slice(0, 1000), slice(0, 1000))),
 ('y', 0, 1): (getitem, dataset, (slice(0, 1000), slice(1000, 2000)))
 ...
}
```

The name of an `Array` object can be found in the `name` attribute. One can get a nested list of keys with the `.__dask_keys__()` method. Additionally, one can flatten down this list with `dask.array.core.flatten()`. This is sometimes useful when building new dictionaries.

Chunks

We also store the size of each block along each axis. This is composed of a tuple of tuples such that the length of the outer tuple is equal to the number of dimensions of the array, and the lengths of the inner tuples are equal to the number of blocks along each dimension. In the example illustrated above this value is as follows:

```
chunks = ((5, 5, 5, 5), (8, 8, 8))
```

Note that these numbers do not necessarily need to be regular. We often create regularly sized grids but blocks change shape after complex slicing. Beware that some operations do expect certain symmetries in the block-shapes. For example, matrix multiplication requires that blocks on each side have anti-symmetric shapes.

Some ways in which `chunks` reflects properties of our array:

1. `len(x.chunks) == x.ndim`: the length of chunks is the number of dimensions
2. `tuple(map(sum, x.chunks)) == x.shape`: the sum of each internal chunk is the length of that dimension
3. The length of each internal chunk is the number of keys in that dimension. For instance, for `chunks == ((a, b), (d, e, f))` and name == `'x'` our array has tasks with the following keys:

   ```
   ('x', 0, 0), ('x', 0, 1), ('x', 0, 2)
   ('x', 1, 0), ('x', 1, 1), ('x', 1, 2)
   ```

Create an Array Object

In order to create an `da.Array` object we need a dictionary with these special keys:

```
dsk = {('x', 0, 0): ...}
```

a name specifying which keys this array refers to:

```
name = 'x'
```

and a chunks tuple:

```
chunks = ((5, 5, 5, 5), (8, 8, 8))
```

Then, using these elements, one can construct an array:

```
x = da.Array(dsk, name, chunks)
```

In short, `dask.array` operations update Dask graphs, update dtypes, and track chunk shapes.

Example - `eye` function

As an example, lets build the `np.eye` function for `dask.array` to make the identity matrix:

```
def eye(n, blocksize):
    chunks = ((blocksize,) * (n // blocksize),
              (blocksize,) * (n // blocksize))

    name = 'eye' + next(tokens)  # unique identifier

    dsk = {(name, i, j): (np.eye, blocksize)
                         if i == j else
                         (np.zeros, (blocksize, blocksize))
             for i in range(n // blocksize)
             for j in range(n // blocksize)}

    dtype = np.eye(0).dtype  # take dtype default from numpy

    return dask.array.Array(dsk, name, chunks, dtype)
```

3.7.9 Sparse Arrays

By swapping out in-memory NumPy arrays with in-memory sparse arrays, we can reuse the blocked algorithms of Dask's Array to achieve parallel and distributed sparse arrays.

The blocked algorithms in Dask Array normally parallelize around in-memory NumPy arrays. However, if another in-memory array library supports the NumPy interface, then it too can take advantage of Dask Array's parallel algorithms. In particular the sparse array library satisfies a subset of the NumPy API and works well with (and is tested against) Dask Array.

Example

Say we have a Dask array with mostly zeros:

```
x = da.random.random((100000, 100000), chunks=(1000, 1000))
x[x < 0.95] = 0
```

We can convert each of these chunks of NumPy arrays into a **sparse.COO** array:

```
import sparse
s = x.map_blocks(sparse.COO)
```

Now, our array is not composed of many NumPy arrays, but rather of many sparse arrays. Semantically, this does not change anything. Operations that work will continue to work identically (assuming that the behavior of `numpy` and `sparse` are identical), but performance characteristics and storage costs may change significantly:

```
>>> s.sum(axis=0)[:100].compute()
<COO: shape=(100,), dtype=float64, nnz=100>

>>> _.todense()
array([ 4803.06859272,  4913.94964525,  4877.13266438,  4860.7470773 ,
        4938.94446802,  4849.51326473,  4858.83977856,  4847.81468485,
        ... ])
```

Requirements

Any in-memory library that copies the NumPy ndarray interface should work here. The sparse library is a minimal example. In particular, an in-memory library should implement at least the following operations:

1. Simple slicing with slices, lists, and elements (for slicing, rechunking, reshaping, etc)
2. A `concatenate` function matching the interface of `np.concatenate`. This must be registered in `dask.array.core.concatenate_lookup`
3. All ufuncs must support the full ufunc interface, including `dtype=` and `out=` parameters (even if they don't function properly)
4. All reductions must support the full `axis=` and `keepdims=` keywords and behave like NumPy in this respect
5. The array class should follow the `__array_priority__` protocol and be prepared to respond to other arrays of lower priority
6. If `dot` support is desired, a `tensordot` function matching the interface of `np.tensordot` should be registered in `dask.array.core.tensordot_lookup`

The implementation of other operations like reshape, transpose, etc., should follow standard NumPy conventions regarding shape and dtype. Not implementing these is fine; the parallel `dask.array` will err at runtime if these operations are attempted.

Mixed Arrays

Dask's Array supports mixing different kinds of in-memory arrays. This relies on the in-memory arrays knowing how to interact with each other when necessary. When two arrays interact, the functions from the array with the highest `__array_priority__` will take precedence (for example, for concatenate, tensordot, etc.).

3.7.10 Stats

Dask Array implements a subset of the scipy.stats package.

Statistical Functions

You can calculate various measures of an array including skewness, kurtosis, and arbitrary moments.

```
>>> from dask.array import stats
>>> x = da.random.beta(1, 1, size=(1000,), chunks=10)
>>> k, s, m = [stats.kurtosis(x), stats.skew(x), stats.moment(x, 5)]
>>> dask.compute(k, s, m)
(1.7612340817172787, -0.064073498030693302, -0.00054523780628304799)
```

Statistical Tests

You can perform basic statistical tests on Dask arrays. Each of these tests return a `dask.delayed` wrapping one of the scipy `namedtuple` results.

```
>>> a = da.random.uniform(size=(50,), chunks=(25,))
>>> b = a + da.random.uniform(low=-0.15, high=0.15, size=(50,), chunks=(25,))
>>> result = stats.ttest_rel(a, b)
>>> result.compute()
Ttest_relResult(statistic=-1.5102104380013242, pvalue=0.13741197274874514)
```

3.7.11 LinearOperator

Dask Array implements the SciPy LinearOperator interface and it can be used with any SciPy algorithm depending on that interface.

Example

```
import dask.array as da
x = da.random.random(size=(10000, 10000), chunks=(1000, 1000))

from scipy.sparse.linalg.interface import MatrixLinearOperator
A = MatrixLinearOperator(x)

import numpy as np
b = np.random.random(10000)

from scipy.sparse.linalg import gmres
x = gmres(A, b)
```

Disclaimer: This is just a toy example and not necessarily the best way to solve this problem for this data.

3.7.12 Slicing

Dask Array supports most of the NumPy slicing syntax. In particular, it supports the following:

- Slicing by integers and slices: `x[0, :5]`
- Slicing by lists/arrays of integers: `x[[1, 2, 4]]`
- Slicing by lists/arrays of booleans: `x[[False, True, True, False, True]]`
- Slicing one *`Array`* with an *`Array`* of bools: `x[x > 0]`

- Slicing one *Array* with a zero or one-dimensional *Array* of ints: `a[b.argtopk(5)]`

However, it does not currently support the following:

- Slicing with lists in multiple axes: `x[[1, 2, 3], [3, 2, 1]]`

  This is straightforward to add though. If you have a use case then raise an issue. Also, users interested in this should take a look at *vindex*.
- Slicing one *Array* with a multi-dimensional *Array* of ints

Efficiency

The normal Dask schedulers are smart enough to compute only those blocks that are necessary to achieve the desired slicing. Hence, large operations may be cheap if only a small output is desired.

In the example below, we create a Dask array with a trillion elements with million element sized blocks. We then operate on the entire array and finally slice out only a portion of the output:

```
>>> # Trillion element array of ones, in 1000 by 1000 blocks
>>> x = da.ones((1000000, 1000000), chunks=(1000, 1000))

>>> da.exp(x)[:1500, :1500]
...
```

This only needs to compute the top-left four blocks to achieve the result. We are slightly wasteful on those blocks where we need only partial results. Moreover, we are also a bit wasteful in that we still need to manipulate the Dask graph with a million or so tasks in it. This can cause an interactive overhead of a second or two.

But generally, slicing works well.

3.7.13 Stack, Concatenate, and Block

Often we have many arrays stored on disk that we want to stack together and think of as one large array. This is common with geospatial data in which we might have many HDF5/NetCDF files on disk, one for every day, but we want to do operations that span multiple days.

To solve this problem, we use the functions `da.stack`, `da.concatenate`, and `da.block`.

Stack

We stack many existing Dask arrays into a new array, creating a new dimension as we go.

```
>>> import dask.array as da

>>> arr0 = da.from_array(np.zeros((3, 4)), chunks=(1, 2))
>>> arr1 = da.from_array(np.ones((3, 4)), chunks=(1, 2))

>>> data = [arr0, arr1]

>>> x = da.stack(data, axis=0)
>>> x.shape
(2, 3, 4)

>>> da.stack(data, axis=1).shape
(3, 2, 4)
```

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```
>>> da.stack(data, axis=-1).shape
(3, 4, 2)
```

This creates a new dimension with length equal to the number of slices

Concatenate

We concatenate existing arrays into a new array, extending them along an existing dimension

```
>>> import dask.array as da
>>> import numpy as np

>>> arr0 = da.from_array(np.zeros((3, 4)), chunks=(1, 2))
>>> arr1 = da.from_array(np.ones((3, 4)), chunks=(1, 2))

>>> data = [arr0, arr1]

>>> x = da.concatenate(data, axis=0)
>>> x.shape
(6, 4)

>>> da.concatenate(data, axis=1).shape
(3, 8)
```

Block

We can handle a larger variety of cases with `da.block` as it allows concatenation to be applied over multiple dimensions at once. This is useful if your chunks tile a space, for example if small squares tile a larger 2-D plane.

```
>>> import dask.array as da
>>> import numpy as np

>>> arr0 = da.from_array(np.zeros((3, 4)), chunks=(1, 2))
>>> arr1 = da.from_array(np.ones((3, 4)), chunks=(1, 2))

>>> data = [
...     [arr0, arr1],
...     [arr1, arr0]
... ]

>>> x = da.block(data)
>>> x.shape
(6, 8)
```

3.7.14 Generalized Ufuncs

NumPy provides the concept of generalized ufuncs. Generalized ufuncs are functions that distinguish the various dimensions of passed arrays in the two classes loop dimensions and core dimensions. To accomplish this, a signature is specified for NumPy generalized ufuncs.

Dask integrates interoperability with NumPy's generalized ufuncs by adhering to respective ufunc protocol, and provides a wrapper to make a Python function a generalized ufunc.

Usage

NumPy Generalized UFuncs

Note: NumPy generalized ufuncs are currently (v1.14.3 and below) stored in inside `np.linalg._umath_linalg` and might change in the future.

```
import dask.array as da
import numpy as np

x = da.random.normal(size=(3, 10, 10), chunks=(2, 10, 10))

w, v = np.linalg._umath_linalg.eig(x, output_dtypes=(float, float))
```

Create Generalized UFuncs

It can be difficult to create your own GUFuncs without going into the CPython API. However, the Numba project does provide a nice implementation with their `numba.guvectorize` decorator. See Numba's documentation for more information.

Wrap your own Python function

`gufunc` can be used to make a Python function behave like a generalized ufunc:

```
x = da.random.normal(size=(10, 5), chunks=(2, 5))

def foo(x):
    return np.mean(x, axis=-1)

gufoo = da.gufunc(foo, signature="(i)->()", output_dtypes=float, vectorize=True)

y = gufoo(x)
```

Instead of `gufunc`, also the `as_gufunc` decorator can be used for convenience:

```
x = da.random.normal(size=(10, 5), chunks=(2, 5))

@da.as_gufunc(signature="(i)->()", output_dtypes=float, vectorize=True)
def gufoo(x):
    return np.mean(x, axis=-1)

y = gufoo(x)
```

Disclaimer

This experimental generalized ufunc integration is not complete:

- `gufunc` does not create a true generalized ufunc to be used with other input arrays besides Dask. I.e., at the moment, `gufunc` casts all input arguments to `dask.array.Array`
- Inferring `output_dtypes` automatically is not implemented yet

API

`apply_gufunc`(func, signature, *args, **kwargs)	Apply a generalized ufunc or similar python function to arrays.
`as_gufunc`([signature])	Decorator for `dask.array.gufunc`.
`gufunc`(pyfunc, **kwargs)	Binds *pyfunc* into `dask.array.apply_gufunc` when called.

Dask Array implements a subset of the NumPy ndarray interface using blocked algorithms, cutting up the large array into many small arrays. This lets us compute on arrays larger than memory using all of our cores. We coordinate these blocked algorithms using Dask graphs.

3.7.15 Design

Dask arrays coordinate many NumPy arrays arranged into a grid. These NumPy arrays may live on disk or on other machines.

3.7.16 Common Uses

Dask Array is used in fields like atmospheric and oceanographic science, large scale imaging, genomics, numerical algorithms for optimization or statistics, and more.

3.7.17 Scope

Dask arrays support most of the NumPy interface like the following:

- Arithmetic and scalar mathematics: `+, *, exp, log, ...`
- Reductions along axes: `sum(), mean(), std(), sum(axis=0), ...`
- Tensor contractions / dot products / matrix multiply: `tensordot`
- Axis reordering / transpose: `transpose`
- Slicing: `x[:100, 500:100:-2]`
- Fancy indexing along single axes with lists or NumPy arrays: `x[:, [10, 1, 5]]`
- Array protocols like `__array__` and `__array_ufunc__`
- Some linear algebra: `svd, qr, solve, solve_triangular, lstsq`
- ...

However, Dask Array does not implement the entire NumPy interface. Users expecting this will be disappointed. Notably, Dask Array lacks the following features:

- Much of `np.linalg` has not been implemented. This has been done by a number of excellent BLAS/LAPACK implementations, and is the focus of numerous ongoing academic research projects
- Arrays with unknown shapes do not support all operations
- Operations like `sort` which are notoriously difficult to do in parallel, and are of somewhat diminished value on very large data (you rarely actually need a full sort). Often we include parallel-friendly alternatives like `topk`

- Dask Array doesn't implement operations like `tolist` that would be very inefficient for larger datasets. Likewise, it is very inefficient to iterate over a Dask array with for loops
- Dask development is driven by immediate need, hence many lesser used functions have not been implemented. Community contributions are encouraged

See *the dask.array API* for a more extensive list of functionality.

3.7.18 Execution

By default, Dask Array uses the threaded scheduler in order to avoid data transfer costs, and because NumPy releases the GIL well. It is also quite effective on a cluster using the dask.distributed scheduler.

3.8 Bag

3.8.1 Create Dask Bags

There are several ways to create Dask bags around your data:

`db.from_sequence`

You can create a bag from an existing Python iterable:

```
>>> import dask.bag as db
>>> b = db.from_sequence([1, 2, 3, 4, 5, 6])
```

You can control the number of partitions into which this data is binned:

```
>>> b = db.from_sequence([1, 2, 3, 4, 5, 6], npartitions=2)
```

This controls the granularity of the parallelism that you expose. By default, Dask will try to partition your data into about 100 partitions.

IMPORTANT: do not load your data into Python and then load that data into a Dask bag. Instead, use Dask Bag to load your data. This parallelizes the loading step and reduces inter-worker communication:

```
>>> b = db.from_sequence(['1.dat', '2.dat', ...]).map(load_from_filename)
```

`db.read_text`

Dask Bag can load data directly from text files. You can pass either a single file name, a list of file names, or a globstring. The resulting bag will have one item per line and one file per partition:

```
>>> b = db.read_text('myfile.txt')
>>> b = db.read_text(['myfile.1.txt', 'myfile.2.txt', ...])
>>> b = db.read_text('myfile.*.txt')
```

This handles standard compression libraries like `gzip`, `bz2`, `xz`, or any easily installed compression library that has a file-like object. Compression will be inferred by the file name extension, or by using the `compression='gzip'` keyword:

```
>>> b = db.read_text('myfile.*.txt.gz')
```

The resulting items in the bag are strings. If you have encoded data like line-delimited JSON, then you may want to map a decoding or load function across the bag:

```
>>> import json
>>> b = db.read_text('myfile.*.json').map(json.loads)
```

Or do string munging tasks. For convenience, there is a string namespace attached directly to bags with `.str.methodname`:

```
>>> b = db.read_text('myfile.*.csv').str.strip().str.split(',')
```

db.read_avro

Dask Bag can read binary files in the Avro format if fastavro is installed. A bag can be made from one or more files, with optional chunking within files. The resulting bag will have one item per Avro record, which will be a dictionary of the form given by the Avro schema. There will be at least one partition per input file:

```
>>> b = db.read_avro('datafile.avro')
>>> b = db.read_avro('data.*.avro')
```

By default, Dask will split data files into chunks of approximately `blocksize` bytes in size. The actual blocks you would get depend on the internal blocking of the file.

For files that are compressed after creation (this is not the same as the internal "codec" used by Avro), no chunking should be used, and there will be exactly one partition per file:

```
> b = bd.read_avro('compressed.*.avro.gz', blocksize=None, compression='gzip')
```

db.from_delayed

You can construct a Dask bag from *dask.delayed* values using the `db.from_delayed` function. For more information, see *documentation on using dask.delayed with collections*.

3.8.2 Store Dask Bags

In Memory

You can convert a Dask bag to a list or Python iterable by calling `compute()` or by converting the object into a list:

```
>>> result = b.compute()
or
>>> result = list(b)
```

To Text Files

You can convert a Dask bag into a sequence of files on disk by calling the `.to_textfiles()` method:

`dask.bag.core.`**`to_textfiles`**`(`*b, path, name_function=None, compression='infer', encoding='utf-8', compute=True, storage_options=None, last_endline=False, **kwargs*`)`

Write dask Bag to disk, one filename per partition, one line per element.

Paths: This will create one file for each partition in your bag. You can specify the filenames in a variety of ways.

Use a globstring

```
>>> b.to_textfiles('/path/to/data/*.json.gz')  # doctest: +SKIP
```

The * will be replaced by the increasing sequence 1, 2, …

```
/path/to/data/0.json.gz
/path/to/data/1.json.gz
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> b.to_textfiles('/path/to/data/*.json.gz', name_function=name)  # doctest:␣
↪+SKIP
```

```
/path/to/data/2015-01-01.json.gz
/path/to/data/2015-01-02.json.gz
...
```

You can also provide an explicit list of paths.

```
>>> paths = ['/path/to/data/alice.json.gz', '/path/to/data/bob.json.gz', ...]  #␣
↪doctest: +SKIP
>>> b.to_textfiles(paths) # doctest: +SKIP
```

Compression: Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly.

Bag Contents: The bag calling `to_textfiles` must be a bag of text strings. For example, a bag of dictionaries could be written to JSON text files by mapping `json.dumps` on to the bag first, and then calling `to_textfiles`:

```
>>> b_dict.map(json.dumps).to_textfiles("/path/to/data/*.json")  # doctest: +SKIP
```

Last endline: By default the last line does not end with a newline character. Pass `last_endline=True` to invert the default.

To Avro

Dask bags can be written directly to Avro binary format using fastavro. One file will be written per bag partition. This requires the user to provide a fully-specified schema dictionary (see the docstring of the `.to_avro()` method).

`dask.bag.avro.`**`to_avro`**`(`*b, filename, schema, name_function=None, storage_options=None, codec='null', sync_interval=16000, metadata=None, compute=True, **kwargs*`)`

Write bag to set of avro files

The schema is a complex dictionary describing the data, see https://avro.apache.org/docs/1.8.2/gettingstartedpython.html#Defining+a+schema and https://fastavro.readthedocs.io/en/latest/writer.html . It's structure is as follows:

```
{'name': 'Test',
 'namespace': 'Test',
 'doc': 'Descriptive text',
 'type': 'record',
 'fields': [
    {'name': 'a', 'type': 'int'},
 ]}
```

where the "name" field is required, but "namespace" and "doc" are optional descriptors; "type" must always be "record". The list of fields should have an entry for every key of the input records, and the types are like the primitive, complex or logical types of the Avro spec (https://avro.apache.org/docs/1.8.2/spec.html).

Results in one avro file per input partition.

Parameters

b: dask.bag.Bag

filename: list of str or str Filenames to write to. If a list, number must match the number of partitions. If a string, must include a glob character "*", which will be expanded using name_function

schema: dict Avro schema dictionary, see above

name_function: None or callable Expands integers into strings, see `dask.bytes.utils.build_name_function`

storage_options: None or dict Extra key/value options to pass to the backend file-system

codec: 'null', 'deflate', or 'snappy' Compression algorithm

sync_interval: int Number of records to include in each block within a file

metadata: None or dict Included in the file header

compute: bool If True, files are written immediately, and function blocks. If False, returns delayed objects, which can be computed by the user where convenient.

kwargs: passed to compute(), if compute=True

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence([{'name': 'Alice', 'value': 100},
...                       {'name': 'Bob', 'value': 200}])
>>> schema = {'name': 'People', 'doc': "Set of people's scores",
```

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```
...             'type': 'record',
...             'fields': [
...                 {'name': 'name', 'type': 'string'},
...                 {'name': 'value', 'type': 'int'}]}
>>> b.to_avro('my-data.*.avro', schema)  # doctest: +SKIP
['my-data.0.avro', 'my-data.1.avro']
```

To DataFrames

You can convert a Dask bag into a *Dask DataFrame* and use those storage solutions.

`Bag.to_dataframe`(*meta=None*, *columns=None*)
Create Dask Dataframe from a Dask Bag.

Bag should contain tuples, dict records, or scalars.

Index will not be particularly meaningful. Use `reindex` afterwards if necessary.

Parameters

meta [pd.DataFrame, dict, iterable, optional] An empty `pd.DataFrame` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. If not provided or a list, a single element from the first partition will be computed, triggering a potentially expensive call to `compute`. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

columns [sequence, optional] Column names to use. If the passed data do not have names associated with them, this argument provides names for the columns. Otherwise this argument indicates the order of the columns in the result (any names not found in the data will become all-NA columns). Note that if `meta` is provided, column names will be taken from there and this parameter is invalid.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence([{'name': 'Alice',   'balance': 100},
...                       {'name': 'Bob',     'balance': 200},
...                       {'name': 'Charlie', 'balance': 300}],
...                      npartitions=2)
>>> df = b.to_dataframe()
```

```
>>> df.compute()
   balance     name
0      100    Alice
1      200      Bob
0      300  Charlie
```

To Delayed Values

You can convert a Dask bag into a list of *Dask delayed values* and custom storage solutions from there.

Bag.**to_delayed**(*optimize_graph=True*)
Convert into a list of `dask.delayed` objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

dask.bag.from_delayed

3.8.3 API

Top level user functions:

Bag(dsk, name, npartitions)	Parallel collection of Python objects
Bag.all([split_every])	Are all elements truthy?
Bag.any([split_every])	Are any of the elements truthy?
Bag.compute(**kwargs)	Compute this dask collection
Bag.count([split_every])	Count the number of elements.
Bag.distinct([key])	Distinct elements of collection
Bag.filter(predicate)	Filter elements in collection by a predicate function.
Bag.flatten()	Concatenate nested lists into one long list.
Bag.fold(binop[, combine, initial, . . .])	Parallelizable reduction
Bag.foldby(key, binop[, initial, combine, . . .])	Combined reduction and groupby.
Bag.frequencies([split_every, sort])	Count number of occurrences of each distinct element.
Bag.groupby(grouper[, method, npartitions, . . .])	Group collection by key function
Bag.join(other, on_self[, on_other])	Joins collection with another collection.
Bag.map(func, *args, **kwargs)	Apply a function elementwise across one or more bags.
Bag.map_partitions(func, *args, **kwargs)	Apply a function to every partition across one or more bags.
Bag.max([split_every])	Maximum element
Bag.mean()	Arithmetic mean
Bag.min([split_every])	Minimum element
Bag.pluck(key[, default])	Select item from all tuples/dicts in collection.
Bag.product(other)	Cartesian product between two bags.
Bag.reduction(perpartition, aggregate[, . . .])	Reduce collection with reduction operators.
Bag.random_sample(prob[, random_state])	Return elements from bag with probability of `prob`.
Bag.remove(predicate)	Remove elements in collection that match predicate.
Bag.repartition(npartitions)	Coalesce bag into fewer partitions.
Bag.starmap(func, **kwargs)	Apply a function using argument tuples from the given bag.
Bag.std([ddof])	Standard deviation
Bag.sum([split_every])	Sum all elements
Bag.take(k[, npartitions, compute, warn])	Take the first k elements.
Bag.to_dataframe([meta, columns])	Create Dask Dataframe from a Dask Bag.
Bag.to_delayed([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
Bag.to_textfiles(path[, name_function, . . .])	Write dask Bag to disk, one filename per partition, one line per element.
Bag.to_avro(filename, schema[, . . .])	Write bag to set of avro files
Bag.topk(k[, key, split_every])	K largest elements in collection

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`Bag.var`([ddof])	Variance
`Bag.visualize`([filename, format, optimize_graph])	Render the computation of this object's task graph using graphviz.

Create Bags

`from_sequence`(seq[, partition_size, npartitions])	Create a dask Bag from Python sequence.
`from_delayed`(values)	Create bag from many dask Delayed objects.
`read_text`(urlpath[, blocksize, compression, ...])	Read lines from text files
`from_url`(urls)	Create a dask Bag from a url.
`read_avro`(urlpath[, blocksize, ...])	Read set of avro files
`range`(n, npartitions)	Numbers from zero to n

Top-level functions

`concat`(bags)	Concatenate many bags together, unioning all elements.
`map`(func, *args, **kwargs)	Apply a function elementwise across one or more bags.
`map_partitions`(func, *args, **kwargs)	Apply a function to every partition across one or more bags.
`zip`(*bags)	Partition-wise bag zip

Turn Bags into other things

`Bag.to_textfiles`(path[, name_function, ...])	Write dask Bag to disk, one filename per partition, one line per element.
`Bag.to_dataframe`([meta, columns])	Create Dask Dataframe from a Dask Bag.
`Bag.to_delayed`([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
`Bag.to_avro`(filename, schema[, ...])	Write bag to set of avro files

Bag methods

class `dask.bag.`**`Bag`**(*dsk*, *name*, *npartitions*)

Parallel collection of Python objects

Examples

Create Bag from sequence

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.filter(lambda x: x % 2 == 0).map(lambda x: x * 10))   # doctest: +SKIP
[0, 20, 40]
```

Create Bag from filename or globstring of filenames

```
>>> b = db.read_text('/path/to/mydata.*.json.gz').map(json.loads)   # doctest:␣
↪+SKIP
```

Create manually (expert use)

```
>>> dsk = {('x', 0): (range, 5),
...        ('x', 1): (range, 5),
...        ('x', 2): (range, 5)}
>>> b = Bag(dsk, 'x', npartitions=3)
```

```
>>> sorted(b.map(lambda x: x * 10))  # doctest: +SKIP
[0, 0, 0, 10, 10, 10, 20, 20, 20, 30, 30, 30, 40, 40, 40]
```

```
>>> int(b.fold(lambda x, y: x + y))  # doctest: +SKIP
30
```

accumulate(*binop, initial='__no__default__'*)
Repeatedly apply binary function to a sequence, accumulating results.

This assumes that the bag is ordered. While this is typically the case not all Dask.bag functions preserve this property.

Examples

```
>>> from operator import add
>>> b = from_sequence([1, 2, 3, 4, 5], npartitions=2)
>>> b.accumulate(add).compute()  # doctest: +SKIP
[1, 3, 6, 10, 15]
```

Accumulate also takes an optional argument that will be used as the first value.

```
>>> b.accumulate(add, initial=-1)  # doctest: +SKIP
[-1, 0, 2, 5, 9, 14]
```

all(*split_every=None*)
Are all elements truthy?

any(*split_every=None*)
Are any of the elements truthy?

count(*split_every=None*)
Count the number of elements.

distinct(*key=None*)
Distinct elements of collection

Unordered without repeats.

Parameters

key: {callable,str} Defines uniqueness of items in bag by calling `key` on each item. If a string is passed `key` is considered to be `lambda x: x[key]`.

Examples

```
>>> b = from_sequence(['Alice', 'Bob', 'Alice'])
>>> sorted(b.distinct())
['Alice', 'Bob']
>>> b = from_sequence([{'name': 'Alice'}, {'name': 'Bob'}, {'name': 'Alice'}
↪])
```

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```
>>> b.distinct(key=lambda x: x['name']).compute()
[{'name': 'Alice'}, {'name': 'Bob'}]
>>> b.distinct(key='name').compute()
[{'name': 'Alice'}, {'name': 'Bob'}]
```

filter(*predicate*)
Filter elements in collection by a predicate function.

```
>>> def iseven(x):
...     return x % 2 == 0
```

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.filter(iseven))  # doctest: +SKIP
[0, 2, 4]
```

flatten()
Concatenate nested lists into one long list.

```
>>> b = from_sequence([[1], [2, 3]])
>>> list(b)
[[1], [2, 3]]
```

```
>>> list(b.flatten())
[1, 2, 3]
```

fold(*binop, combine=None, initial='__no__default__', split_every=None, out_type=<class 'dask.bag.core.Item'>*)
Parallelizable reduction

Fold is like the builtin function `reduce` except that it works in parallel. Fold takes two binary operator functions, one to reduce each partition of our dataset and another to combine results between partitions

1. `binop`: Binary operator to reduce within each partition
2. `combine`: Binary operator to combine results from binop

Sequentially this would look like the following:

```
>>> intermediates = [reduce(binop, part) for part in partitions]  # doctest:␣
↪+SKIP
>>> final = reduce(combine, intermediates)  # doctest: +SKIP
```

If only one function is given then it is used for both functions `binop` and `combine` as in the following example to compute the sum:

```
>>> def add(x, y):
...     return x + y
```

```
>>> b = from_sequence(range(5))
>>> b.fold(add).compute()  # doctest: +SKIP
10
```

In full form we provide both binary operators as well as their default arguments

```
>>> b.fold(binop=add, combine=add, initial=0).compute()  # doctest: +SKIP
10
```

More complex binary operators are also doable

```
>>> def add_to_set(acc, x):
...     ''' Add new element x to set acc '''
...     return acc | set([x])
>>> b.fold(add_to_set, set.union, initial=set()).compute()  # doctest: +SKIP
{1, 2, 3, 4, 5}
```

See also:

Bag.foldby

foldby(*key*, *binop*, *initial='__no__default__'*, *combine=None*, *combine_initial='__no__default__'*, *split_every=None*)

Combined reduction and groupby.

Foldby provides a combined groupby and reduce for efficient parallel split-apply-combine tasks.

The computation

```
>>> b.foldby(key, binop, init)                        # doctest: +SKIP
```

is equivalent to the following:

```
>>> def reduction(group):                               # doctest: +SKIP
...     return reduce(binop, group, init)               # doctest: +SKIP
```

```
>>> b.groupby(key).map(lambda (k, v): (k, reduction(v)))# doctest: +SKIP
```

But uses minimal communication and so is *much* faster.

```
>>> b = from_sequence(range(10))
>>> iseven = lambda x: x % 2 == 0
>>> add = lambda x, y: x + y
>>> dict(b.foldby(iseven, add))                         # doctest: +SKIP
{True: 20, False: 25}
```

Key Function

The key function determines how to group the elements in your bag. In the common case where your bag holds dictionaries then the key function often gets out one of those elements.

```
>>> def key(x):
...     return x['name']
```

This case is so common that it is special cased, and if you provide a key that is not a callable function then dask.bag will turn it into one automatically. The following are equivalent:

```
>>> b.foldby(lambda x: x['name'], ...)  # doctest: +SKIP
>>> b.foldby('name', ...)  # doctest: +SKIP
```

Binops

It can be tricky to construct the right binary operators to perform analytic queries. The `foldby` method accepts two binary operators, `binop` and `combine`. Binary operators two inputs and output must have the same type.

Binop takes a running total and a new element and produces a new total:

```
>>> def binop(total, x):
...     return total + x['amount']
```

Combine takes two totals and combines them:

```
>>> def combine(total1, total2):
...     return total1 + total2
```

Each of these binary operators may have a default first value for total, before any other value is seen. For addition binary operators like above this is often `0` or the identity element for your operation.

split_every

Group partitions into groups of this size while performing reduction. Defaults to 8.

```
>>> b.foldby('name', binop, 0, combine, 0)  # doctest: +SKIP
```

See also:

`toolz.reduceby`, `pyspark.combineByKey`

Examples

We can compute the maximum of some `(key, value)` pairs, grouped by the `key`. (You might be better off converting the `Bag` to a `dask.dataframe` and using its groupby).

```
>>> import random
>>> import dask.bag as db
```

```
>>> tokens = list('abcdefg')
>>> values = range(10000)
>>> a = [(random.choice(tokens), random.choice(values))
...       for _ in range(100)]
>>> a[:2]  # doctest: +SKIP
[('g', 676), ('a', 871)]
```

```
>>> a = db.from_sequence(a)
```

```
>>> def binop(t, x):
...     return max((t, x), key=lambda x: x[1])
```

```
>>> a.foldby(lambda x: x[0], binop).compute()  # doctest: +SKIP
[('g', ('g', 984)),
 ('a', ('a', 871)),
 ('b', ('b', 999)),
 ('c', ('c', 765)),
 ('f', ('f', 955)),
 ('e', ('e', 991)),
 ('d', ('d', 854))]
```

frequencies(*split_every=None, sort=False*)
Count number of occurrences of each distinct element.

```
>>> b = from_sequence(['Alice', 'Bob', 'Alice'])
>>> dict(b.frequencies())  # doctest: +SKIP
{'Alice': 2, 'Bob', 1}
```

groupby(*grouper*, *method=None*, *npartitions=None*, *blocksize=1048576*, *max_branch=None*, *shuffle=None*)

Group collection by key function

This requires a full dataset read, serialization and shuffle. This is expensive. If possible you should use `foldby`.

Parameters

grouper: function Function on which to group elements

shuffle: str Either 'disk' for an on-disk shuffle or 'tasks' to use the task scheduling framework. Use 'disk' if you are on a single machine and 'tasks' if you are on a distributed cluster.

npartitions: int If using the disk-based shuffle, the number of output partitions

blocksize: int If using the disk-based shuffle, the size of shuffle blocks (bytes)

max_branch: int If using the task-based shuffle, the amount of splitting each partition undergoes. Increase this for fewer copies but more scheduler overhead.

See also:

`Bag.foldby`

Examples

```
>>> b = from_sequence(range(10))
>>> iseven = lambda x: x % 2 == 0
>>> dict(b.groupby(iseven))   # doctest: +SKIP
{True: [0, 2, 4, 6, 8], False: [1, 3, 5, 7, 9]}
```

join(*other*, *on_self*, *on_other=None*)

Joins collection with another collection.

Other collection must be one of the following:

1. An iterable. We recommend tuples over lists for internal performance reasons.
2. A delayed object, pointing to a tuple. This is recommended if the other collection is sizable and you're using the distributed scheduler. Dask is able to pass around data wrapped in delayed objects with greater sophistication.
3. A Bag with a single partition

You might also consider Dask Dataframe, whose join operations are much more heavily optimized.

Parameters

other: Iterable, Delayed, Bag Other collection on which to join

on_self: callable Function to call on elements in this collection to determine a match

on_other: callable (defaults to on_self) Function to call on elements in the other collection to determine a match

Examples

```
>>> people = from_sequence(['Alice', 'Bob', 'Charlie'])
>>> fruit = ['Apple', 'Apricot', 'Banana']
>>> list(people.join(fruit, lambda x: x[0]))  # doctest: +SKIP
[('Apple', 'Alice'), ('Apricot', 'Alice'), ('Banana', 'Bob')]
```

map (*func*, **args*, ***kwargs*)
Apply a function elementwise across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable]

***args, **kwargs** [Bag, Item, or object] Extra arguments and keyword arguments to pass to `func` *after* the calling bag instance. Non-Bag args/kwargs are broadcasted across all calls to `func`.

Notes

For calls with multiple *Bag* arguments, corresponding partitions should have the same length; if they do not, the call will error at compute time.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5), npartitions=2)
>>> b2 = db.from_sequence(range(5, 10), npartitions=2)
```

Apply a function to all elements in a bag:

```
>>> b.map(lambda x: x + 1).compute()
[1, 2, 3, 4, 5]
```

Apply a function with arguments from multiple bags:

```
>>> from operator import add
>>> b.map(add, b2).compute()
[5, 7, 9, 11, 13]
```

Non-bag arguments are broadcast across all calls to the mapped function:

```
>>> b.map(add, 1).compute()
[1, 2, 3, 4, 5]
```

Keyword arguments are also supported, and have the same semantics as regular arguments:

```
>>> def myadd(x, y=0):
...     return x + y
>>> b.map(myadd, y=b2).compute()
[5, 7, 9, 11, 13]
>>> b.map(myadd, y=1).compute()
[1, 2, 3, 4, 5]
```

Both arguments and keyword arguments can also be instances of `dask.bag.Item`. Here we'll add the max value in the bag to each element:

```
>>> b.map(myadd, b.max()).compute()
[4, 5, 6, 7, 8]
```

map_partitions (*func*, **args*, ***kwargs*)

Apply a function to every partition across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable] The function to be called on every partition. This function should expect an `Iterator` or `Iterable` for every partition and should return an `Iterator` or `Iterable` in return.

***args, **kwargs** [Bag, Item, Delayed, or object] Arguments and keyword arguments to pass to `func`. Partitions from this bag will be the first argument, and these will be passed *after*.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(1, 101), npartitions=10)
>>> def div(nums, den=1):
...     return [num / den for num in nums]
```

Using a python object:

```
>>> hi = b.max().compute()
>>> hi
100
>>> b.map_partitions(div, den=hi).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Using an `Item`:

```
>>> b.map_partitions(div, den=b.max()).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Note that while both versions give the same output, the second forms a single graph, and then computes everything at once, and in some cases may be more efficient.

max (*split_every=None*)

Maximum element

mean ()

Arithmetic mean

min (*split_every=None*)

Minimum element

pluck (*key*, *default='__no__default__'*)

Select item from all tuples/dicts in collection.

```
>>> b = from_sequence([{'name': 'Alice', 'credits': [1, 2, 3]},
...                    {'name': 'Bob',   'credits': [10, 20]}])
>>> list(b.pluck('name'))  # doctest: +SKIP
['Alice', 'Bob']
```

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```
>>> list(b.pluck('credits').pluck(0))  # doctest: +SKIP
[1, 10]
```

product (*other*)
Cartesian product between two bags.

random_sample (*prob*, *random_state=None*)
Return elements from bag with probability of `prob`.

Parameters

prob [float] A float between 0 and 1, representing the probability that each element will be returned.

random_state [int or random.Random, optional] If an integer, will be used to seed a new `random.Random` object. If provided, results in deterministic sampling.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.random_sample(0.5, 42))
[1, 3]
>>> list(b.random_sample(0.5, 42))
[1, 3]
```

reduction (*perpartition*, *aggregate*, *split_every=None*, *out_type=<class 'dask.bag.core.Item'>*, *name=None*)
Reduce collection with reduction operators.

Parameters

perpartition: function reduction to apply to each partition

aggregate: function reduction to apply to the results of all partitions

split_every: int (optional) Group partitions into groups of this size while performing reduction Defaults to 8

out_type: {Bag, Item} The out type of the result, Item if a single element, Bag if a list of elements. Defaults to Item.

Examples

```
>>> b = from_sequence(range(10))
>>> b.reduction(sum, sum).compute()
45
```

remove (*predicate*)
Remove elements in collection that match predicate.

```
>>> def iseven(x):
...     return x % 2 == 0
```

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5))
>>> list(b.remove(iseven))  # doctest: +SKIP
[1, 3]
```

repartition(*npartitions*)
Coalesce bag into fewer partitions.

Examples

```
>>> b.repartition(5)  # set to have 5 partitions  # doctest: +SKIP
```

starmap(*func*, ***kwargs*)
Apply a function using argument tuples from the given bag.

This is similar to `itertools.starmap`, except it also accepts keyword arguments. In pseudocode, this is could be written as:

```
>>> def starmap(func, bag, **kwargs):
...     return (func(*args, **kwargs) for args in bag)
```

Parameters

func [callable]

****kwargs** [Item, Delayed, or object, optional] Extra keyword arguments to pass to `func`. These can either be normal objects, `dask.bag.Item`, or `dask.delayed.Delayed`.

Examples

```
>>> import dask.bag as db
>>> data = [(1, 2), (3, 4), (5, 6), (7, 8), (9, 10)]
>>> b = db.from_sequence(data, npartitions=2)
```

Apply a function to each argument tuple:

```
>>> from operator import add
>>> b.starmap(add).compute()
[3, 7, 11, 15, 19]
```

Apply a function to each argument tuple, with additional keyword arguments:

```
>>> def myadd(x, y, z=0):
...     return x + y + z
>>> b.starmap(myadd, z=10).compute()
[13, 17, 21, 25, 29]
```

Keyword arguments can also be instances of `dask.bag.Item` or `dask.delayed.Delayed`:

```
>>> max_second = b.pluck(1).max()
>>> max_second.compute()
10
>>> b.starmap(myadd, z=max_second).compute()
[13, 17, 21, 25, 29]
```

std(*ddof=0*)
Standard deviation

str
String processing functions

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(['Alice Smith', 'Bob Jones', 'Charlie Smith'])
>>> list(b.str.lower())
['alice smith', 'bob jones', 'charlie smith']
```

```
>>> list(b.str.match('*Smith'))
['Alice Smith', 'Charlie Smith']
```

```
>>> list(b.str.split(' '))
[['Alice', 'Smith'], ['Bob', 'Jones'], ['Charlie', 'Smith']]
```

sum(*split_every=None*)
Sum all elements

take(*k*, *npartitions=1*, *compute=True*, *warn=True*)
Take the first k elements.

Parameters

k [int] The number of elements to return

npartitions [int, optional] Elements are only taken from the first `npartitions`, with a default of 1. If there are fewer than `k` rows in the first `npartitions` a warning will be raised and any found rows returned. Pass -1 to use all partitions.

compute [bool, optional] Whether to compute the result, default is True.

warn [bool, optional] Whether to warn if the number of elements returned is less than requested, default is True.

>>> b = from_sequence(range(10))

>>> b.take(3) # doctest: +SKIP

(0, 1, 2)

to_avro(*filename*, *schema*, *name_function=None*, *storage_options=None*, *codec='null'*, *sync_interval=16000*, *metadata=None*, *compute=True*, ***kwargs*)
Write bag to set of avro files

The schema is a complex dictionary describing the data, see https://avro.apache.org/docs/1.8.2/gettingstartedpython.html#Defining+a+schema and https://fastavro.readthedocs.io/en/latest/writer.html . It's structure is as follows:

```
{'name': 'Test',
 'namespace': 'Test',
 'doc': 'Descriptive text',
 'type': 'record',
 'fields': [
    {'name': 'a', 'type': 'int'},
 ]}
```

where the "name" field is required, but "namespace" and "doc" are optional descriptors; "type" must always be "record". The list of fields should have an entry for every key of the input records, and the types are like the primitive, complex or logical types of the Avro spec (https://avro.apache.org/docs/1.8.2/spec.html).

Results in one avro file per input partition.

Parameters

b: dask.bag.Bag

filename: list of str or str Filenames to write to. If a list, number must match the number of partitions. If a string, must include a glob character "*", which will be expanded using name_function

schema: dict Avro schema dictionary, see above

name_function: None or callable Expands integers into strings, see `dask.bytes.utils.build_name_function`

storage_options: None or dict Extra key/value options to pass to the backend file-system

codec: 'null', 'deflate', or 'snappy' Compression algorithm

sync_interval: int Number of records to include in each block within a file

metadata: None or dict Included in the file header

compute: bool If True, files are written immediately, and function blocks. If False, returns delayed objects, which can be computed by the user where convenient.

kwargs: passed to compute(), if compute=True

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence([{'name': 'Alice', 'value': 100},
...                       {'name': 'Bob', 'value': 200}])
>>> schema = {'name': 'People', 'doc': "Set of people's scores",
...           'type': 'record',
...           'fields': [
...               {'name': 'name', 'type': 'string'},
...               {'name': 'value', 'type': 'int'}]}
>>> b.to_avro('my-data.*.avro', schema)  # doctest: +SKIP
['my-data.0.avro', 'my-data.1.avro']
```

`to_dataframe`(*meta=None*, *columns=None*)
Create Dask Dataframe from a Dask Bag.

Bag should contain tuples, dict records, or scalars.

Index will not be particularly meaningful. Use `reindex` afterwards if necessary.

Parameters

meta [pd.DataFrame, dict, iterable, optional] An empty `pd.DataFrame` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided. If not provided or a list, a single element from the first partition will be computed, triggering a potentially expensive call to compute. This may lead to unexpected results, so providing meta is recommended. For more information, see dask.dataframe.utils.make_meta.

columns [sequence, optional] Column names to use. If the passed data do not have names associated with them, this argument provides names for the columns. Otherwise this argument indicates the order of the columns in the result (any names not found in the data will become all-NA columns). Note that if meta is provided, column names will be taken from there and this parameter is invalid.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence([{'name': 'Alice',   'balance': 100},
...                       {'name': 'Bob',     'balance': 200},
...                       {'name': 'Charlie', 'balance': 300}],
...                      npartitions=2)
>>> df = b.to_dataframe()
```

```
>>> df.compute()
   balance     name
0      100    Alice
1      200      Bob
0      300  Charlie
```

to_delayed(*optimize_graph=True*)

Convert into a list of dask.delayed objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into dask.delayed objects.

See also:

dask.bag.from_delayed

to_textfiles(*path*, *name_function=None*, *compression='infer'*, *encoding='utf-8'*, *compute=True*, *storage_options=None*, *last_endline=False*, ***kwargs*)

Write dask Bag to disk, one filename per partition, one line per element.

Paths: This will create one file for each partition in your bag. You can specify the filenames in a variety of ways.

Use a globstring

```
>>> b.to_textfiles('/path/to/data/*.json.gz')  # doctest: +SKIP
```

The * will be replaced by the increasing sequence 1, 2, …

```
/path/to/data/0.json.gz
/path/to/data/1.json.gz
```

Use a globstring and a name_function= keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> b.to_textfiles('/path/to/data/*.json.gz', name_function=name)  #␣
↪doctest: +SKIP
```

```
/path/to/data/2015-01-01.json.gz
/path/to/data/2015-01-02.json.gz
...
```

You can also provide an explicit list of paths.

```
>>> paths = ['/path/to/data/alice.json.gz', '/path/to/data/bob.json.gz', ...
↪]  # doctest: +SKIP
>>> b.to_textfiles(paths) # doctest: +SKIP
```

Compression: Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly.

Bag Contents: The bag calling `to_textfiles` must be a bag of text strings. For example, a bag of dictionaries could be written to JSON text files by mapping `json.dumps` on to the bag first, and then calling `to_textfiles` :

```
>>> b_dict.map(json.dumps).to_textfiles("/path/to/data/*.json")  # doctest:␣
↪+SKIP
```

Last endline: By default the last line does not end with a newline character. Pass `last_endline=True` to invert the default.

topk (*k*, *key=None*, *split_every=None*)
K largest elements in collection

Optionally ordered by some key function

```
>>> b = from_sequence([10, 3, 5, 7, 11, 4])
>>> list(b.topk(2))  # doctest: +SKIP
[11, 10]
```

```
>>> list(b.topk(2, lambda x: -x))  # doctest: +SKIP
[3, 4]
```

unzip (*n*)
Transform a bag of tuples to `n` bags of their elements.

Examples

```
>>> b = from_sequence([(i, i + 1, i + 2) for i in range(10)])
>>> first, second, third = b.unzip(3)
>>> isinstance(first, Bag)
True
>>> first.compute()
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9]
```

Note that this is equivalent to:

```
>>> first, second, third = (b.pluck(i) for i in range(3))
```

var (*ddof=0*)
Variance

Other functions

dask.bag.**from_sequence** (*seq*, *partition_size=None*, *npartitions=None*)
Create a dask Bag from Python sequence.

This sequence should be relatively small in memory. Dask Bag works best when it handles loading your data itself. Commonly we load a sequence of filenames into a Bag and then use `.map` to open them.

Parameters

seq: Iterable A sequence of elements to put into the dask

partition_size: int (optional) The length of each partition

npartitions: int (optional) The number of desired partitions

It is best to provide either ‘‘partition_size‘‘ or ‘‘npartitions‘‘

(though not both.)

See also:

read_text Create bag from text files

Examples

```
>>> b = from_sequence(['Alice', 'Bob', 'Chuck'], partition_size=2)
```

dask.bag.**from_delayed** (*values*)
Create bag from many dask Delayed objects.

These objects will become the partitions of the resulting Bag. They should evaluate to a `list` or some other concrete sequence.

Parameters

values: list of delayed values An iterable of dask Delayed objects. Each evaluating to a list.

Returns

Bag

See also:

`dask.delayed`

Examples

```
>>> x, y, z = [delayed(load_sequence_from_file)(fn)
...             for fn in filenames] # doctest: +SKIP
>>> b = from_delayed([x, y, z])  # doctest: +SKIP
```

`dask.bag.`**`read_text`**`(`*urlpath, blocksize=None, compression='infer', encoding='utf-8', errors='strict', linedelimiter='\n', collection=True, storage_options=None, files_per_partition=None*`)`

Read lines from text files

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

blocksize: None, int, or str Size (in bytes) to cut up larger files. Streams by default. Can be `None` for streaming, an integer number of bytes, or a string like "128MiB"

compression: string Compression format like 'gzip' or 'xz'. Defaults to 'infer'

encoding: string

errors: string

linedelimiter: string

collection: bool, optional Return dask.bag if True, or list of delayed values if false

storage_options: dict Extra options that make sense to a particular storage connection, e.g. host, port, username, password, etc.

files_per_partition: None or int If set, group input files into partitions of the requested size, instead of one partition per file. Mutually exclusive with blocksize.

Returns

dask.bag.Bag if collection is True or list of Delayed lists otherwise

See also:

`from_sequence` Build bag from Python sequence

Examples

```
>>> b = read_text('myfiles.1.txt')  # doctest: +SKIP
>>> b = read_text('myfiles.*.txt')  # doctest: +SKIP
>>> b = read_text('myfiles.*.txt.gz')  # doctest: +SKIP
>>> b = read_text('s3://bucket/myfiles.*.txt')  # doctest: +SKIP
>>> b = read_text('s3://key:secret@bucket/myfiles.*.txt')  # doctest: +SKIP
>>> b = read_text('hdfs://namenode.example.com/myfiles.*.txt')  # doctest: +SKIP
```

Parallelize a large file by providing the number of uncompressed bytes to load into each partition.

```
>>> b = read_text('largefile.txt', blocksize='10MB')  # doctest: +SKIP
```

`dask.bag.`**`from_url`**`(`*urls*`)`

Create a dask Bag from a url.

Examples

```
>>> a = from_url('http://raw.githubusercontent.com/dask/dask/master/README.rst')
↪# doctest: +SKIP
>>> a.npartitions  # doctest: +SKIP
1
```

```
>>> a.take(8)  # doctest: +SKIP
(b'Dask\n',
 b'====\n',
 b'\n',
 b'|Build Status| |Coverage| |Doc Status| |Gitter| |Version Status|\n',
 b'\n',
 b'Dask is a flexible parallel computing library for analytics.  See\n',
 b'documentation_ for more information.\n',
 b'\n')
```

```
>>> b = from_url(['http://github.com', 'http://google.com'])  # doctest: +SKIP
>>> b.npartitions  # doctest: +SKIP
2
```

`dask.bag.`**`read_avro`**(*urlpath*, *blocksize=100000000*, *storage_options=None*, *compression=None*)

Read set of avro files

Use this with arbitrary nested avro schemas. Please refer to the fastavro documentation for its capabilities: https://github.com/fastavro/fastavro

Parameters

urlpath: string or list Absolute or relative filepath, URL (may include protocols like `s3://`), or globstring pointing to data.

blocksize: int or None Size of chunks in bytes. If None, there will be no chunking and each file will become one partition.

storage_options: dict or None passed to backend file-system

compression: str or None Compression format of the targe(s), like 'gzip'. Should only be used with blocksize=None.

`dask.bag.`**`range`**(*n*, *npartitions*)

Numbers from zero to n

Examples

```
>>> import dask.bag as db
>>> b = db.range(5, npartitions=2)
>>> list(b)
[0, 1, 2, 3, 4]
```

`dask.bag.`**`concat`**(*bags*)

Concatenate many bags together, unioning all elements.

```
>>> import dask.bag as db
>>> a = db.from_sequence([1, 2, 3])
>>> b = db.from_sequence([4, 5, 6])
>>> c = db.concat([a, b])
>>> list(c)
[1, 2, 3, 4, 5, 6]
```

`dask.bag.map_partitions`(*func*, **args*, ***kwargs*)

Apply a function to every partition across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable]

***args, **kwargs** [Bag, Item, Delayed, or object] Arguments and keyword arguments to pass to `func`.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(1, 101), npartitions=10)
>>> def div(nums, den=1):
...     return [num / den for num in nums]
```

Using a python object:

```
>>> hi = b.max().compute()
>>> hi
100
>>> b.map_partitions(div, den=hi).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Using an `Item`:

```
>>> b.map_partitions(div, den=b.max()).take(5)
(0.01, 0.02, 0.03, 0.04, 0.05)
```

Note that while both versions give the same output, the second forms a single graph, and then computes everything at once, and in some cases may be more efficient.

`dask.bag.map`(*func*, **args*, ***kwargs*)

Apply a function elementwise across one or more bags.

Note that all `Bag` arguments must be partitioned identically.

Parameters

func [callable]

***args, **kwargs** [Bag, Item, Delayed, or object] Arguments and keyword arguments to pass to `func`. Non-Bag args/kwargs are broadcasted across all calls to `func`.

Notes

For calls with multiple *Bag* arguments, corresponding partitions should have the same length; if they do not, the call will error at compute time.

Examples

```
>>> import dask.bag as db
>>> b = db.from_sequence(range(5), npartitions=2)
>>> b2 = db.from_sequence(range(5, 10), npartitions=2)
```

Apply a function to all elements in a bag:

```
>>> db.map(lambda x: x + 1, b).compute()
[1, 2, 3, 4, 5]
```

Apply a function with arguments from multiple bags:

```
>>> from operator import add
>>> db.map(add, b, b2).compute()
[5, 7, 9, 11, 13]
```

Non-bag arguments are broadcast across all calls to the mapped function:

```
>>> db.map(add, b, 1).compute()
[1, 2, 3, 4, 5]
```

Keyword arguments are also supported, and have the same semantics as regular arguments:

```
>>> def myadd(x, y=0):
...     return x + y
>>> db.map(myadd, b, y=b2).compute()
[5, 7, 9, 11, 13]
>>> db.map(myadd, b, y=1).compute()
[1, 2, 3, 4, 5]
```

Both arguments and keyword arguments can also be instances of `dask.bag.Item` or `dask.delayed.Delayed`. Here we'll add the max value in the bag to each element:

```
>>> db.map(myadd, b, b.max()).compute()
[4, 5, 6, 7, 8]
```

`dask.bag.`**`zip`**`(`*`*bags`*`)`

Partition-wise bag zip

All passed bags must have the same number of partitions.

NOTE: corresponding partitions should have the same length; if they do not, the "extra" elements from the longer partition(s) will be dropped. If you have this case chances are that what you really need is a data alignment mechanism like pandas's, and not a missing value filler like zip_longest.

Examples

Correct usage:

```
>>> import dask.bag as db
>>> evens = db.from_sequence(range(0, 10, 2), partition_size=4)
>>> odds = db.from_sequence(range(1, 10, 2), partition_size=4)
>>> pairs = db.zip(evens, odds)
>>> list(pairs)
[(0, 1), (2, 3), (4, 5), (6, 7), (8, 9)]
```

Incorrect usage:

```
>>> numbers = db.range(20) # doctest: +SKIP
>>> fizz = numbers.filter(lambda n: n % 3 == 0) # doctest: +SKIP
>>> buzz = numbers.filter(lambda n: n % 5 == 0) # doctest: +SKIP
>>> fizzbuzz = db.zip(fizz, buzz) # doctest: +SKIP
>>> list(fizzbuzzz) # doctest: +SKIP
[(0, 0), (3, 5), (6, 10), (9, 15), (12, 20), (15, 25), (18, 30)]
```

When what you really wanted was more along the lines of the following:

```
>>> list(fizzbuzzz) # doctest: +SKIP
[(0, 0), (3, None), (None, 5), (6, None), (None 10), (9, None),
(12, None), (15, 15), (18, None), (None, 20), (None, 25), (None, 30)]
```

Dask Bag implements operations like `map`, `filter`, `fold`, and `groupby` on collections of generic Python objects. It does this in parallel with a small memory footprint using Python iterators. It is similar to a parallel version of PyToolz or a Pythonic version of the PySpark RDD.

3.8.4 Design

Dask bags coordinate many Python lists or Iterators, each of which forms a partition of a larger collection.

3.8.5 Common Uses

Dask bags are often used to parallelize simple computations on unstructured or semi-structured data like text data, log files, JSON records, or user defined Python objects.

3.8.6 Execution

Execution on bags provide two benefits:

1. Parallel: data is split up, allowing multiple cores or machines to execute in parallel
2. Iterating: data processes lazily, allowing smooth execution of larger-than-memory data, even on a single machine within a single partition

Default scheduler

By default, `dask.bag` uses `dask.multiprocessing` for computation. As a benefit, Dask bypasses the GIL and uses multiple cores on pure Python objects. As a drawback, Dask Bag doesn't perform well on computations that include a great deal of inter-worker communication. For common operations this is rarely an issue as most Dask Bag workflows are embarrassingly parallel or result in reductions with little data moving between workers.

Shuffle

Some operations, like `groupby`, require substantial inter-worker communication. On a single machine, Dask uses partd to perform efficient, parallel, spill-to-disk shuffles. When working in a cluster, Dask uses a task based shuffle.

These shuffle operations are expensive and better handled by projects like `dask.dataframe`. It is best to use `dask.bag` to clean and process data, then transform it into an array or DataFrame before embarking on the more complex operations that require shuffle steps.

3.8.7 Known Limitations

Bags provide very general computation (any Python function). This generality comes at cost. Bags have the following known limitations:

1. By default, they rely on the multiprocessing scheduler, which has its own set of known limitations (see shared)
2. Bags are immutable and so you can not change individual elements
3. Bag operations tend to be slower than array/DataFrame computations in the same way that standard Python containers tend to be slower than NumPy arrays and Pandas DataFrames
4. Bag's `groupby` is slow. You should try to use Bag's `foldby` if possible. Using `foldby` requires more thought tough

3.8.8 Name

Bag is the mathematical name for an unordered collection allowing repeats. It is a friendly synonym to multiset. A bag, or a multiset, is a generalization of the concept of a set that, unlike a set, allows multiple instances of the multiset's elements:

- `list`: *ordered* collection *with repeats*, `[1, 2, 3, 2]`
- `set`: *unordered* collection *without repeats*, `{1, 2, 3}`
- `bag`: *unordered* collection *with repeats*, `{1, 2, 2, 3}`

So, a bag is like a list, but it doesn't guarantee an ordering among elements. There can be repeated elements but you can't ask for the ith element.

3.9 DataFrame

3.9.1 API

Dataframe

`DataFrame`(dsk, name, meta, divisions)	Parallel Pandas DataFrame
`DataFrame.add`(other[, axis, level, fill_value])	Addition of dataframe and other, element-wise (binary operator *add*).
`DataFrame.append`(other[, interleave_partitions])	Append rows of *other* to the end of caller, returning a new object.
`DataFrame.apply`(func[, axis, broadcast, . . .])	Parallel version of pandas.DataFrame.apply
`DataFrame.assign`(**kwargs)	Assign new columns to a DataFrame.
`DataFrame.astype`(dtype)	Cast a pandas object to a specified dtype `dtype`.
`DataFrame.categorize`([columns, index, . . .])	Convert columns of the DataFrame to category dtype.
`DataFrame.columns`	
`DataFrame.compute`(**kwargs)	Compute this dask collection
`DataFrame.corr`([method, min_periods, . . .])	Compute pairwise correlation of columns, excluding NA/null values.
`DataFrame.count`([axis, split_every])	Count non-NA cells for each column or row.
`DataFrame.cov`([min_periods, split_every])	Compute pairwise covariance of columns, excluding NA/null values.

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DataFrame.cummax([axis, skipna, out])	Return cumulative maximum over a DataFrame or Series axis.
DataFrame.cummin([axis, skipna, out])	Return cumulative minimum over a DataFrame or Series axis.
DataFrame.cumprod([axis, skipna, dtype, out])	Return cumulative product over a DataFrame or Series axis.
DataFrame.cumsum([axis, skipna, dtype, out])	Return cumulative sum over a DataFrame or Series axis.
DataFrame.describe([split_every, . . .])	Generate descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding `NaN` values.
DataFrame.div(other[, axis, level, fill_value])	Floating division of dataframe and other, element-wise (binary operator *truediv*).
DataFrame.drop([labels, axis, columns, errors])	Drop specified labels from rows or columns.
DataFrame.drop_duplicates([subset, . . .])	Return DataFrame with duplicate rows removed, optionally only considering certain columns.
DataFrame.dropna([how, subset, thresh])	Remove missing values.
DataFrame.dtypes	Return data types
DataFrame.explode(column)	
DataFrame.fillna([value, method, limit, axis])	Fill NA/NaN values using the specified method.
DataFrame.floordiv(other[, axis, level, . . .])	Integer division of dataframe and other, element-wise (binary operator *floordiv*).
DataFrame.get_partition(n)	Get a dask DataFrame/Series representing the *nth* partition.
DataFrame.groupby([by])	Group DataFrame or Series using a mapper or by a Series of columns.
DataFrame.head([n, npartitions, compute])	First n rows of the dataset
DataFrame.iloc	Purely integer-location based indexing for selection by position.
DataFrame.index	Return dask Index instance
DataFrame.isna()	Detect missing values.
DataFrame.isnull()	Detect missing values.
DataFrame.iterrows()	Iterate over DataFrame rows as (index, Series) pairs.
DataFrame.itertuples([index, name])	Iterate over DataFrame rows as namedtuples.
DataFrame.join(other[, on, how, lsuffix, . . .])	Join columns of another DataFrame.
DataFrame.known_divisions	Whether divisions are already known
DataFrame.loc	Purely label-location based indexer for selection by label.
DataFrame.map_partitions(func, *args, **kwargs)	Apply Python function on each DataFrame partition.
DataFrame.mask(cond[, other])	Replace values where the condition is True.
DataFrame.max([axis, skipna, split_every, out])	Return the maximum of the values for the requested axis.
DataFrame.mean([axis, skipna, split_every, . . .])	Return the mean of the values for the requested axis.
DataFrame.merge(right[, how, on, left_on, . . .])	Merge the DataFrame with another DataFrame
DataFrame.min([axis, skipna, split_every, out])	Return the minimum of the values for the requested axis.
DataFrame.mod(other[, axis, level, fill_value])	Modulo of dataframe and other, element-wise (binary operator *mod*).
DataFrame.mul(other[, axis, level, fill_value])	Multiplication of dataframe and other, element-wise (binary operator *mul*).
DataFrame.ndim	Return dimensionality

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DataFrame.nlargest([n, columns, split_every])	Return the first *n* rows ordered by *columns* in descending order.
DataFrame.npartitions	Return number of partitions
DataFrame.partitions	Slice dataframe by partitions
DataFrame.pop(item)	Return item and drop from frame.
DataFrame.pow(other[, axis, level, fill_value])	Exponential power of dataframe and other, element-wise (binary operator *pow*).
DataFrame.prod([axis, skipna, split_every, ...])	Return the product of the values for the requested axis.
DataFrame.quantile([q, axis, method])	Approximate row-wise and precise column-wise quantiles of DataFrame
DataFrame.query(expr, **kwargs)	Filter dataframe with complex expression
DataFrame.radd(other[, axis, level, fill_value])	Addition of dataframe and other, element-wise (binary operator *radd*).
DataFrame.random_split(frac[, random_state])	Pseudorandomly split dataframe into different pieces row-wise
DataFrame.rdiv(other[, axis, level, fill_value])	Floating division of dataframe and other, element-wise (binary operator *rtruediv*).
DataFrame.rename([index, columns])	Alter axes labels.
DataFrame.repartition([divisions, ...])	Repartition dataframe along new divisions
DataFrame.replace([to_replace, value, regex])	Replace values given in *to_replace* with *value*.
DataFrame.reset_index([drop])	Reset the index to the default index.
DataFrame.rfloordiv(other[, axis, level, ...])	Integer division of dataframe and other, element-wise (binary operator *rfloordiv*).
DataFrame.rmod(other[, axis, level, fill_value])	Modulo of dataframe and other, element-wise (binary operator *rmod*).
DataFrame.rmul(other[, axis, level, fill_value])	Multiplication of dataframe and other, element-wise (binary operator *rmul*).
DataFrame.rpow(other[, axis, level, fill_value])	Exponential power of dataframe and other, element-wise (binary operator *rpow*).
DataFrame.rsub(other[, axis, level, fill_value])	Subtraction of dataframe and other, element-wise (binary operator *rsub*).
DataFrame.rtruediv(other[, axis, level, ...])	Floating division of dataframe and other, element-wise (binary operator *rtruediv*).
DataFrame.sample([n, frac, replace, ...])	Random sample of items
DataFrame.set_index(other[, drop, sorted, ...])	Set the DataFrame index (row labels) using an existing column.
DataFrame.shape	Return a tuple representing the dimensionality of the DataFrame.
DataFrame.std([axis, skipna, ddof, ...])	Return sample standard deviation over requested axis.
DataFrame.sub(other[, axis, level, fill_value])	Subtraction of dataframe and other, element-wise (binary operator *sub*).
DataFrame.sum([axis, skipna, split_every, ...])	Return the sum of the values for the requested axis.
DataFrame.tail([n, compute])	Last n rows of the dataset
DataFrame.to_bag([index])	Create Dask Bag from a Dask DataFrame
DataFrame.to_csv(filename, **kwargs)	Store Dask DataFrame to CSV files
DataFrame.to_dask_array([lengths])	Convert a dask DataFrame to a dask array.
DataFrame.to_delayed([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
DataFrame.to_hdf(path_or_buf, key[, mode, ...])	Store Dask Dataframe to Hierarchical Data Format (HDF) files
DataFrame.to_json(filename, *args, **kwargs)	See dd.to_json docstring for more information

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DataFrame.to_parquet(path, *args, **kwargs)	Store Dask.dataframe to Parquet files
DataFrame.to_records([index, lengths])	Create Dask Array from a Dask Dataframe
DataFrame.truediv(other[, axis, level, . . .])	Floating division of dataframe and other, element-wise (binary operator *truediv*).
DataFrame.values	Return a dask.array of the values of this dataframe
DataFrame.var([axis, skipna, ddof, . . .])	Return unbiased variance over requested axis.
DataFrame.visualize([filename, format, . . .])	Render the computation of this object's task graph using graphviz.
DataFrame.where(cond[, other])	Replace values where the condition is False.

Series

Series(dsk, name, meta, divisions)	Parallel Pandas Series
Series.add(other[, level, fill_value, axis])	Addition of series and other, element-wise (binary operator *add*).
Series.align(other[, join, axis, fill_value])	Align two objects on their axes with the specified join method for each axis Index.
Series.all([axis, skipna, split_every, out])	Return whether all elements are True, potentially over an axis.
Series.any([axis, skipna, split_every, out])	Return whether any element is True, potentially over an axis.
Series.append(other[, interleave_partitions])	Concatenate two or more Series.
Series.apply(func[, convert_dtype, meta, args])	Parallel version of pandas.Series.apply
Series.astype(dtype)	Cast a pandas object to a specified dtype `dtype`.
Series.autocorr([lag, split_every])	Compute the lag-N autocorrelation.
Series.between(left, right[, inclusive])	Return boolean Series equivalent to left <= series <= right.
Series.bfill([axis, limit])	Synonym for DataFrame.fillna() with `method='bfill'`.
Series.cat	
Series.clear_divisions()	Forget division information
Series.clip([lower, upper, out])	Trim values at input threshold(s).
Series.clip_lower(threshold)	Trim values below a given threshold.
Series.clip_upper(threshold)	Trim values above a given threshold.
Series.compute(**kwargs)	Compute this dask collection
Series.copy()	Make a copy of the dataframe
Series.corr(other[, method, min_periods, . . .])	Compute correlation with *other* Series, excluding missing values.
Series.count([split_every])	Return number of non-NA/null observations in the Series.
Series.cov(other[, min_periods, split_every])	Compute covariance with Series, excluding missing values.
Series.cummax([axis, skipna, out])	Return cumulative maximum over a DataFrame or Series axis.
Series.cummin([axis, skipna, out])	Return cumulative minimum over a DataFrame or Series axis.
Series.cumprod([axis, skipna, dtype, out])	Return cumulative product over a DataFrame or Series axis.
Series.cumsum([axis, skipna, dtype, out])	Return cumulative sum over a DataFrame or Series axis.

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`Series.describe`([split_every, percentiles, . . .])	Generate descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding `NaN` values.
`Series.diff`([periods, axis])	First discrete difference of element.
`Series.div`(other[, level, fill_value, axis])	Floating division of series and other, element-wise (binary operator *truediv*).
`Series.drop_duplicates`([subset, . . .])	Return DataFrame with duplicate rows removed, optionally only considering certain columns.
`Series.dropna`()	Return a new Series with missing values removed.
`Series.dt`	Namespace of datetime methods
`Series.dtype`	Return data type
`Series.eq`(other[, level, fill_value, axis])	Equal to of series and other, element-wise (binary operator *eq*).
`Series.explode`()	
`Series.ffill`([axis, limit])	Synonym for `DataFrame.fillna()` with `method='ffill'`.
`Series.fillna`([value, method, limit, axis])	Fill NA/NaN values using the specified method.
`Series.first`(offset)	Convenience method for subsetting initial periods of time series data based on a date offset.
`Series.floordiv`(other[, level, fill_value, axis])	Integer division of series and other, element-wise (binary operator *floordiv*).
`Series.ge`(other[, level, fill_value, axis])	Greater than or equal to of series and other, element-wise (binary operator *ge*).
`Series.get_partition`(n)	Get a dask DataFrame/Series representing the *nth* partition.
`Series.groupby`([by])	Group DataFrame or Series using a mapper or by a Series of columns.
`Series.gt`(other[, level, fill_value, axis])	Greater than of series and other, element-wise (binary operator *gt*).
`Series.head`([n, npartitions, compute])	First n rows of the dataset
`Series.idxmax`([axis, skipna, split_every])	Return index of first occurrence of maximum over requested axis.
`Series.idxmin`([axis, skipna, split_every])	Return index of first occurrence of minimum over requested axis.
`Series.isin`(values)	Check whether *values* are contained in Series.
`Series.isna`()	Detect missing values.
`Series.isnull`()	Detect missing values.
`Series.iteritems`()	Lazily iterate over (index, value) tuples.
`Series.known_divisions`	Whether divisions are already known
`Series.last`(offset)	Convenience method for subsetting final periods of time series data based on a date offset.
`Series.le`(other[, level, fill_value, axis])	Less than or equal to of series and other, element-wise (binary operator *le*).
`Series.loc`	Purely label-location based indexer for selection by label.
`Series.lt`(other[, level, fill_value, axis])	Less than of series and other, element-wise (binary operator *lt*).
`Series.map`(arg[, na_action, meta])	Map values of Series according to input correspondence.
`Series.map_overlap`(func, before, after, . . .)	Apply a function to each partition, sharing rows with adjacent partitions.

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Series.map_partitions(func, *args, **kwargs)	Apply Python function on each DataFrame partition.
Series.mask(cond[, other])	Replace values where the condition is True.
Series.max([axis, skipna, split_every, out])	Return the maximum of the values for the requested axis.
Series.mean([axis, skipna, split_every, . . .])	Return the mean of the values for the requested axis.
Series.memory_usage([index, deep])	Return the memory usage of the Series.
Series.min([axis, skipna, split_every, out])	Return the minimum of the values for the requested axis.
Series.mod(other[, level, fill_value, axis])	Modulo of series and other, element-wise (binary operator *mod*).
Series.mul(other[, level, fill_value, axis])	Multiplication of series and other, element-wise (binary operator *mul*).
Series.nbytes	Number of bytes
Series.ndim	Return dimensionality
Series.ne(other[, level, fill_value, axis])	Not equal to of series and other, element-wise (binary operator *ne*).
Series.nlargest([n, split_every])	Return the largest *n* elements.
Series.notnull()	Detect existing (non-missing) values.
Series.nsmallest([n, split_every])	Return the smallest *n* elements.
Series.nunique([split_every])	Return number of unique elements in the object.
Series.nunique_approx([split_every])	Approximate number of unique rows.
Series.persist(**kwargs)	Persist this dask collection into memory
Series.pipe(func, *args, **kwargs)	Apply func(self, *args, **kwargs).
Series.pow(other[, level, fill_value, axis])	Exponential power of series and other, element-wise (binary operator *pow*).
Series.prod([axis, skipna, split_every, . . .])	Return the product of the values for the requested axis.
Series.quantile([q, method])	Approximate quantiles of Series
Series.radd(other[, level, fill_value, axis])	Addition of series and other, element-wise (binary operator *radd*).
Series.random_split(frac[, random_state])	Pseudorandomly split dataframe into different pieces row-wise
Series.rdiv(other[, level, fill_value, axis])	Floating division of series and other, element-wise (binary operator *rtruediv*).
Series.reduction(chunk[, aggregate, . . .])	Generic row-wise reductions.
Series.repartition([divisions, npartitions, . . .])	Repartition dataframe along new divisions
Series.replace([to_replace, value, regex])	Replace values given in *to_replace* with *value*.
Series.rename([index, inplace, sorted_index])	Alter Series index labels or name
Series.resample(rule[, closed, label])	Resample time-series data.
Series.reset_index([drop])	Reset the index to the default index.
Series.rolling(window[, min_periods, . . .])	Provides rolling transformations.
Series.round([decimals])	Round each value in a Series to the given number of decimals.
Series.sample([n, frac, replace, random_state])	Random sample of items
Series.sem([axis, skipna, ddof, split_every])	Return unbiased standard error of the mean over requested axis.
Series.shape	Return a tuple representing the dimensionality of a Series.
Series.shift([periods, freq, axis])	Shift index by desired number of periods with an optional time *freq*.
Series.size	Size of the Series or DataFrame as a Delayed object.
Series.std([axis, skipna, ddof, . . .])	Return sample standard deviation over requested axis.
Series.str	Namespace for string methods

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Series.sub(other[, level, fill_value, axis])	Subtraction of series and other, element-wise (binary operator *sub*).
Series.sum([axis, skipna, split_every, . . .])	Return the sum of the values for the requested axis.
Series.to_bag([index])	Create a Dask Bag from a Series
Series.to_csv(filename, **kwargs)	Store Dask DataFrame to CSV files
Series.to_dask_array([lengths])	Convert a dask DataFrame to a dask array.
Series.to_delayed([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
Series.to_frame([name])	Convert Series to DataFrame.
Series.to_hdf(path_or_buf, key[, mode, append])	Store Dask Dataframe to Hierarchical Data Format (HDF) files
Series.to_string([max_rows])	Render a string representation of the Series.
Series.to_timestamp([freq, how, axis])	Cast to DatetimeIndex of timestamps, at *beginning* of period.
Series.truediv(other[, level, fill_value, axis])	Floating division of series and other, element-wise (binary operator *truediv*).
Series.unique([split_every, split_out])	Return Series of unique values in the object.
Series.value_counts([split_every, split_out])	Return a Series containing counts of unique values.
Series.values	Return a dask.array of the values of this dataframe
Series.var([axis, skipna, ddof, . . .])	Return unbiased variance over requested axis.
Series.visualize([filename, format, . . .])	Render the computation of this object's task graph using graphviz.
Series.where(cond[, other])	Replace values where the condition is False.

Groupby Operations

DataFrameGroupBy.aggregate(arg[, . . .])	Aggregate using one or more operations over the specified axis.
DataFrameGroupBy.apply(func, *args, **kwargs)	Parallel version of pandas GroupBy.apply
DataFrameGroupBy.count([split_every, split_out])	Compute count of group, excluding missing values.
DataFrameGroupBy.cumcount([axis])	Number each item in each group from 0 to the length of that group - 1.
DataFrameGroupBy.cumprod([axis])	Cumulative product for each group.
DataFrameGroupBy.cumsum([axis])	Cumulative sum for each group.
DataFrameGroupBy.get_group(key)	Constructs NDFrame from group with provided name.
DataFrameGroupBy.max([split_every, split_out])	Compute max of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
DataFrameGroupBy.mean([split_every, split_out])	Compute mean of groups, excluding missing values.
DataFrameGroupBy.min([split_every, split_out])	Compute min of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
DataFrameGroupBy.size([split_every, split_out])	Compute group sizes.
DataFrameGroupBy.std([ddof, split_every, . . .])	Compute standard deviation of groups, excluding missing values.
DataFrameGroupBy.sum([split_every, . . .])	Compute sum of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

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DataFrameGroupBy.var([ddof, split_every, ...])	Compute variance of groups, excluding missing values.
DataFrameGroupBy.cov([ddof, split_every, ...])	Compute pairwise covariance of columns, excluding NA/null values.
DataFrameGroupBy.corr([ddof, split_every, ...])	Compute pairwise correlation of columns, excluding NA/null values.
DataFrameGroupBy.first([split_every, split_out])	Compute first of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
DataFrameGroupBy.last([split_every, split_out])	Compute last of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
DataFrameGroupBy.idxmin([split_every, ...])	Return index of first occurrence of minimum over requested axis.
DataFrameGroupBy.idxmax([split_every, ...])	Return index of first occurrence of maximum over requested axis.

SeriesGroupBy.aggregate(arg[, split_every, ...])	Aggregate using one or more operations over the specified axis.
SeriesGroupBy.apply(func, *args, **kwargs)	Parallel version of pandas GroupBy.apply
SeriesGroupBy.count([split_every, split_out])	Compute count of group, excluding missing values.
SeriesGroupBy.cumcount([axis])	Number each item in each group from 0 to the length of that group - 1.
SeriesGroupBy.cumprod([axis])	Cumulative product for each group.
SeriesGroupBy.cumsum([axis])	Cumulative sum for each group.
SeriesGroupBy.get_group(key)	Constructs NDFrame from group with provided name.
SeriesGroupBy.max([split_every, split_out])	Compute max of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
SeriesGroupBy.mean([split_every, split_out])	Compute mean of groups, excluding missing values.
SeriesGroupBy.min([split_every, split_out])	Compute min of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
SeriesGroupBy.nunique([split_every, split_out])	
SeriesGroupBy.size([split_every, split_out])	Compute group sizes.
SeriesGroupBy.std([ddof, split_every, split_out])	Compute standard deviation of groups, excluding missing values.
SeriesGroupBy.sum([split_every, split_out, ...])	Compute sum of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
SeriesGroupBy.var([ddof, split_every, split_out])	Compute variance of groups, excluding missing values.
SeriesGroupBy.first([split_every, split_out])	Compute first of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
SeriesGroupBy.last([split_every, split_out])	Compute last of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby
SeriesGroupBy.idxmin([split_every, ...])	Return index of first occurrence of minimum over requested axis.
SeriesGroupBy.idxmax([split_every, ...])	Return index of first occurrence of maximum over requested axis.

Aggregation(name, chunk, agg[, finalize])	User defined groupby-aggregation.

Rolling Operations

rolling.map_overlap(func, df, before, after, . . .)	Apply a function to each partition, sharing rows with adjacent partitions.
Series.rolling(window[, min_periods, . . .])	Provides rolling transformations.
DataFrame.rolling(window[, min_periods, . . .])	Provides rolling transformations.

Rolling.apply(func[, args, kwargs])	The rolling function's apply function.
Rolling.count()	The rolling count of any non-NaN observations inside the window.
Rolling.kurt()	Calculate unbiased rolling kurtosis.
Rolling.max()	Calculate the rolling maximum.
Rolling.mean()	Calculate the rolling mean of the values.
Rolling.median()	Calculate the rolling median.
Rolling.min()	Calculate the rolling minimum.
Rolling.quantile(quantile)	Calculate the rolling quantile.
Rolling.skew()	Unbiased rolling skewness.
Rolling.std([ddof])	Calculate rolling standard deviation.
Rolling.sum()	Calculate rolling sum of given DataFrame or Series.
Rolling.var([ddof])	Calculate unbiased rolling variance.

Create DataFrames

read_csv(urlpath[, blocksize, collection, . . .])	Read CSV files into a Dask.DataFrame
read_table(urlpath[, blocksize, collection, . . .])	Read delimited files into a Dask.DataFrame
read_fwf(urlpath[, blocksize, collection, . . .])	Read fixed-width files into a Dask.DataFrame
read_parquet(path[, columns, filters, . . .])	Read a Parquet file into a Dask DataFrame
read_hdf(pattern, key[, start, stop, . . .])	Read HDF files into a Dask DataFrame
read_json(url_path[, orient, lines, . . .])	Create a dataframe from a set of JSON files
read_orc(path[, columns, storage_options])	Read dataframe from ORC file(s)
read_sql_table(table, uri, index_col[, . . .])	Create dataframe from an SQL table.
from_array(x[, chunksize, columns])	Read any slicable array into a Dask Dataframe
from_bcolz(x[, chunksize, categorize, . . .])	Read BColz CTable into a Dask Dataframe
from_dask_array(x[, columns, index])	Create a Dask DataFrame from a Dask Array.
from_delayed(dfs[, meta, divisions, prefix, . . .])	Create Dask DataFrame from many Dask Delayed objects
from_pandas(data[, npartitions, chunksize, . . .])	Construct a Dask DataFrame from a Pandas DataFrame
dask.bag.core.Bag.to_dataframe([meta, columns])	Create Dask Dataframe from a Dask Bag.

Store DataFrames

to_csv(df, filename[, single_file, . . .])	Store Dask DataFrame to CSV files
to_parquet(df, path[, engine, compression, . . .])	Store Dask.dataframe to Parquet files

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to_hdf(df, path, key[, mode, append, ...])	Store Dask Dataframe to Hierarchical Data Format (HDF) files
to_records(df)	Create Dask Array from a Dask Dataframe
to_bag(df[, index])	Create Dask Bag from a Dask DataFrame
to_json(df, url_path[, orient, lines, ...])	Write dataframe into JSON text files

Convert DataFrames

`to_dask_array`
`to_delayed`

Reshape DataFrames

get_dummies(data[, prefix, prefix_sep, ...])	Convert categorical variable into dummy/indicator variables.
pivot_table(df[, index, columns, values, ...])	Create a spreadsheet-style pivot table as a DataFrame.
melt(frame[, id_vars, value_vars, var_name, ...])	Unpivots a DataFrame from wide format to long format, optionally leaving identifier variables set.

DataFrame Methods

class `dask.dataframe.`**`DataFrame`**(*dsk*, *name*, *meta*, *divisions*)

Parallel Pandas DataFrame

Do not use this class directly. Instead use functions like `dd.read_csv`, `dd.read_parquet`, or `dd.from_pandas`.

Parameters

dsk: dict The dask graph to compute this DataFrame

name: str The key prefix that specifies which keys in the dask comprise this particular DataFrame

meta: pandas.DataFrame An empty `pandas.DataFrame` with names, dtypes, and index matching the expected output.

divisions: tuple of index values Values along which we partition our blocks on the index

abs()

Return a Series/DataFrame with absolute numeric value of each element.

This docstring was copied from pandas.core.frame.DataFrame.abs.

Some inconsistencies with the Dask version may exist.

This function only applies to elements that are all numeric.

Returns

abs Series/DataFrame containing the absolute value of each element.

See also:

`numpy.absolute` Calculate the absolute value element-wise.

Notes

For `complex` inputs, `1.2 + 1j`, the absolute value is $\sqrt{a^2 + b^2}$.

Examples

Absolute numeric values in a Series.

```
>>> s = pd.Series([-1.10, 2, -3.33, 4])  # doctest: +SKIP
>>> s.abs()  # doctest: +SKIP
0    1.10
1    2.00
2    3.33
3    4.00
dtype: float64
```

Absolute numeric values in a Series with complex numbers.

```
>>> s = pd.Series([1.2 + 1j])  # doctest: +SKIP
>>> s.abs()  # doctest: +SKIP
0    1.56205
dtype: float64
```

Absolute numeric values in a Series with a Timedelta element.

```
>>> s = pd.Series([pd.Timedelta('1 days')])  # doctest: +SKIP
>>> s.abs()  # doctest: +SKIP
0   1 days
dtype: timedelta64[ns]
```

Select rows with data closest to certain value using argsort (from StackOverflow).

```
>>> df = pd.DataFrame({  # doctest: +SKIP
...     'a': [4, 5, 6, 7],
...     'b': [10, 20, 30, 40],
...     'c': [100, 50, -30, -50]
... })
>>> df  # doctest: +SKIP
     a    b    c
0    4   10  100
1    5   20   50
2    6   30  -30
3    7   40  -50
>>> df.loc[(df.c - 43).abs().argsort()]  # doctest: +SKIP
     a    b    c
1    5   20   50
0    4   10  100
2    6   30  -30
3    7   40  -50
```

add(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Addition of dataframe and other, element-wise (binary operator *add*).

Equivalent to `dataframe + other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *radd*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
```

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```
triangle         9       NaN
rectangle       16       NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                                 'degrees': [360, 180, 360, 360, 540, 720]},
...                                index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                       ['circle', 'triangle', 'rectangle',
...                                        'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

align(*other*, *join='outer'*, *axis=None*, *fill_value=None*)

Align two objects on their axes with the specified join method for each axis Index.

This docstring was copied from pandas.core.frame.DataFrame.align.

Some inconsistencies with the Dask version may exist.

Parameters

other [DataFrame or Series]

join [{'outer', 'inner', 'left', 'right'}, default 'outer']

axis [allowed axis of the other object, default None] Align on index (0), columns (1), or both (None)

level [int or level name, default None (Not supported in Dask)] Broadcast across a level, matching Index values on the passed MultiIndex level

copy [boolean, default True (Not supported in Dask)] Always returns new objects. If copy=False and no reindexing is required then original objects are returned.

fill_value [scalar, default np.NaN] Value to use for missing values. Defaults to NaN, but can be any "compatible" value

method [{'backfill', 'bfill', 'pad', 'ffill', None}, default None (Not supported in Dask)] Method to use for filling holes in reindexed Series pad / ffill: propagate last valid observation forward to next valid backfill / bfill: use NEXT valid observation to fill gap

limit [int, default None (Not supported in Dask)] If method is specified, this is the maximum number of consecutive NaN values to forward/backward fill. In other words, if there is a gap with more than this number of consecutive NaNs, it will only be partially filled. If method is not specified, this is the maximum number of entries along the entire axis where NaNs will be filled. Must be greater than 0 if not None.

fill_axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Filling axis, method and limit

broadcast_axis [{0 or 'index', 1 or 'columns'}, default None (Not supported in Dask)] Broadcast values along this axis, if aligning two objects of different dimensions

Returns

(left, right) [(DataFrame, type of other)] Aligned objects

all(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

Return whether all elements are True, potentially over an axis.

This docstring was copied from pandas.core.frame.DataFrame.all.

Some inconsistencies with the Dask version may exist.

Returns True unless there at least one element within a series or along a Dataframe axis that is False or equivalent (e.g. zero or empty).

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.
- None : reduce all axes, return a scalar.

bool_only [bool, default None (Not supported in Dask)] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

skipna [bool, default True] Exclude NA/null values. If the entire row/column is NA and skipna is True, then the result will be True, as for an empty row/column. If skipna is False, then NA are treated as True, because these are not equal to zero.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

Series or DataFrame If level is specified, then, DataFrame is returned; otherwise, Series is returned.

See also:

Series.all Return True if all elements are True.

DataFrame.any Return True if one (or more) elements are True.

Examples

Series

```
>>> pd.Series([True, True]).all()  # doctest: +SKIP
True
>>> pd.Series([True, False]).all()  # doctest: +SKIP
False
>>> pd.Series([]).all()  # doctest: +SKIP
True
>>> pd.Series([np.nan]).all()  # doctest: +SKIP
True
>>> pd.Series([np.nan]).all(skipna=False)  # doctest: +SKIP
True
```

DataFrames

Create a dataframe from a dictionary.

```
>>> df = pd.DataFrame({'col1': [True, True], 'col2': [True, False]})  #␣
↪doctest: +SKIP
>>> df  # doctest: +SKIP
   col1   col2
0  True   True
1  True  False
```

Default behaviour checks if column-wise values all return True.

```
>>> df.all()  # doctest: +SKIP
col1     True
col2    False
dtype: bool
```

Specify `axis='columns'` to check if row-wise values all return True.

```
>>> df.all(axis='columns')  # doctest: +SKIP
0     True
1    False
dtype: bool
```

Or `axis=None` for whether every value is True.

```
>>> df.all(axis=None)  # doctest: +SKIP
False
```

any (*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

Return whether any element is True, potentially over an axis.

This docstring was copied from pandas.core.frame.DataFrame.any.

Some inconsistencies with the Dask version may exist.

Returns False unless there at least one element within a series or along a Dataframe axis that is True or equivalent (e.g. non-zero or non-empty).

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.
- None : reduce all axes, return a scalar.

bool_only [bool, default None (Not supported in Dask)] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

skipna [bool, default True] Exclude NA/null values. If the entire row/column is NA and skipna is True, then the result will be False, as for an empty row/column. If skipna is False, then NA are treated as True, because these are not equal to zero.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

Series or DataFrame If level is specified, then, DataFrame is returned; otherwise, Series is returned.

See also:

`numpy.any` Numpy version of this method.

`Series.any` Return whether any element is True.

`Series.all` Return whether all elements are True.

`DataFrame.any` Return whether any element is True over requested axis.

`DataFrame.all` Return whether all elements are True over requested axis.

Examples

Series

For Series input, the output is a scalar indicating whether any element is True.

```
>>> pd.Series([False, False]).any()  # doctest: +SKIP
False
>>> pd.Series([True, False]).any()  # doctest: +SKIP
True
>>> pd.Series([]).any()  # doctest: +SKIP
False
>>> pd.Series([np.nan]).any()  # doctest: +SKIP
False
>>> pd.Series([np.nan]).any(skipna=False)  # doctest: +SKIP
True
```

DataFrame

Whether each column contains at least one True element (the default).

```
>>> df = pd.DataFrame({"A": [1, 2], "B": [0, 2], "C": [0, 0]})  # doctest:␣
↪+SKIP
>>> df  # doctest: +SKIP
   A  B  C
0  1  0  0
1  2  2  0
```

```
>>> df.any()  # doctest: +SKIP
A     True
B     True
C    False
dtype: bool
```

Aggregating over the columns.

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 2]})  # doctest: +SKIP
>>> df  # doctest: +SKIP
       A  B
0   True  1
1  False  2
```

```
>>> df.any(axis='columns')  # doctest: +SKIP
0    True
1    True
dtype: bool
```

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 0]})  # doctest: +SKIP
>>> df  # doctest: +SKIP
       A  B
0   True  1
1  False  0
```

```
>>> df.any(axis='columns')  # doctest: +SKIP
0    True
1    False
dtype: bool
```

Aggregating over the entire DataFrame with `axis=None`.

```
>>> df.any(axis=None)  # doctest: +SKIP
True
```

any for an empty DataFrame is an empty Series.

```
>>> pd.DataFrame([]).any()  # doctest: +SKIP
Series([], dtype: bool)
```

append(*other*, *interleave_partitions=False*)

Append rows of *other* to the end of caller, returning a new object.

This docstring was copied from pandas.core.frame.DataFrame.append.

Some inconsistencies with the Dask version may exist.

Columns in *other* that are not in the caller are added as new columns.

Parameters

other [DataFrame or Series/dict-like object, or list of these] The data to append.

ignore_index [boolean, default False (Not supported in Dask)] If True, do not use the index labels.

verify_integrity [boolean, default False (Not supported in Dask)] If True, raise ValueError on creating index with duplicates.

sort [boolean, default None (Not supported in Dask)] Sort columns if the columns of *self* and *other* are not aligned. The default sorting is deprecated and will change to not-sorting in a future version of pandas. Explicitly pass `sort=True` to silence the warning and sort. Explicitly pass `sort=False` to silence the warning and not sort.

New in version 0.23.0.

Returns

appended [DataFrame]

See also:

`pandas.concat` General function to concatenate DataFrame, Series or Panel objects.

Notes

If a list of dict/series is passed and the keys are all contained in the DataFrame's index, the order of the columns in the resulting DataFrame will be unchanged.

Iteratively appending rows to a DataFrame can be more computationally intensive than a single concatenate. A better solution is to append those rows to a list and then concatenate the list with the original DataFrame all at once.

Examples

```
>>> df = pd.DataFrame([[1, 2], [3, 4]], columns=list('AB'))  # doctest: +SKIP
>>> df  # doctest: +SKIP
   A  B
0  1  2
1  3  4
>>> df2 = pd.DataFrame([[5, 6], [7, 8]], columns=list('AB'))  # doctest:␣
↪+SKIP
>>> df.append(df2)  # doctest: +SKIP
   A  B
0  1  2
1  3  4
0  5  6
1  7  8
```

With *ignore_index* set to True:

```
>>> df.append(df2, ignore_index=True)  # doctest: +SKIP
   A  B
0  1  2
1  3  4
2  5  6
3  7  8
```

The following, while not recommended methods for generating DataFrames, show two ways to generate a DataFrame from multiple data sources.

Less efficient:

```
>>> df = pd.DataFrame(columns=['A'])  # doctest: +SKIP
>>> for i in range(5):  # doctest: +SKIP
...     df = df.append({'A': i}, ignore_index=True)
>>> df  # doctest: +SKIP
   A
0  0
1  1
2  2
3  3
4  4
```

More efficient:

```
>>> pd.concat([pd.DataFrame([i], columns=['A']) for i in range(5)],  #␣
↪doctest: +SKIP
...           ignore_index=True)
   A
0  0
1  1
2  2
3  3
4  4
```

apply(*func*, *axis=0*, *broadcast=None*, *raw=False*, *reduce=None*, *args=()*, *meta='__no_default__'*, ***kwds*)

Parallel version of pandas.DataFrame.apply

This mimics the pandas version except for the following:

1. Only `axis=1` is supported (and must be specified explicitly).
2. The user should provide output metadata via the *meta* keyword.

Parameters

func [function] Function to apply to each column/row

axis [{0 or 'index', 1 or 'columns'}, default 0]

- 0 or 'index': apply function to each column (NOT SUPPORTED)
- 1 or 'columns': apply function to each row

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

args [tuple] Positional arguments to pass to function in addition to the array/series

Additional keyword arguments will be passed as keywords to the function

Returns

applied [Series or DataFrame]

See also:

`dask.DataFrame.map_partitions`

Examples

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 3, 4, 5],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

Apply a function to row-wise passing in extra arguments in `args` and `kwargs`:

```
>>> def myadd(row, a, b=1):
...     return row.sum() + a + b
>>> res = ddf.apply(myadd, axis=1, args=(2,), b=1.5)  # doctest: +SKIP
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with name `'x'`, and dtype `float64`:

```
>>> res = ddf.apply(myadd, axis=1, args=(2,), b=1.5, meta=('x', 'f8'))
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ddf.apply(lambda row: row + 1, axis=1, meta=ddf)
```

applymap (*func*, *meta='__no_default__'*)

Apply a function to a Dataframe elementwise.

This docstring was copied from pandas.core.frame.DataFrame.applymap.

Some inconsistencies with the Dask version may exist.

This method applies a function that accepts and returns a scalar to every element of a DataFrame.

Parameters

func [callable] Python function, returns a single value from a single value.

Returns

DataFrame Transformed DataFrame.

See also:

DataFrame.apply Apply a function along input axis of DataFrame.

Notes

In the current implementation applymap calls *func* twice on the first column/row to decide whether it can take a fast or slow code path. This can lead to unexpected behavior if *func* has side-effects, as they will take effect twice for the first column/row.

Examples

```
>>> df = pd.DataFrame([[1, 2.12], [3.356, 4.567]])  # doctest: +SKIP
>>> df  # doctest: +SKIP
       0      1
0  1.000  2.120
1  3.356  4.567
```

```
>>> df.applymap(lambda x: len(str(x)))  # doctest: +SKIP
   0  1
0  3  4
1  5  5
```

Note that a vectorized version of *func* often exists, which will be much faster. You could square each number elementwise.

```
>>> df.applymap(lambda x: x**2)  # doctest: +SKIP
           0          1
0   1.000000   4.494400
1  11.262736  20.857489
```

But it's better to avoid applymap in that case.

```
>>> df ** 2  # doctest: +SKIP
           0          1
0   1.000000   4.494400
1  11.262736  20.857489
```

assign(***kwargs*)

Assign new columns to a DataFrame.

This docstring was copied from pandas.core.frame.DataFrame.assign.

Some inconsistencies with the Dask version may exist.

Returns a new object with all original columns in addition to new ones. Existing columns that are re-assigned will be overwritten.

Parameters

****kwargs** [dict of {str: callable or Series}] The column names are keywords. If the values are callable, they are computed on the DataFrame and assigned to the new columns. The callable must not change input DataFrame (though pandas doesn't check it). If the values are not callable, (e.g. a Series, scalar, or array), they are simply assigned.

Returns

DataFrame A new DataFrame with the new columns in addition to all the existing columns.

Notes

Assigning multiple columns within the same `assign` is possible. For Python 3.6 and above, later items in '**kwargs' may refer to newly created or modified columns in 'df'; items are computed and assigned into 'df' in order. For Python 3.5 and below, the order of keyword arguments is not specified, you cannot refer to newly created or modified columns. All items are computed first, and then assigned in alphabetical order.

Changed in version 0.23.0: Keyword argument order is maintained for Python 3.6 and later.

Examples

```
>>> df = pd.DataFrame({'temp_c': [17.0, 25.0]},  # doctest: +SKIP
...                   index=['Portland', 'Berkeley'])
>>> df  # doctest: +SKIP
          temp_c
Portland    17.0
Berkeley    25.0
```

Where the value is a callable, evaluated on *df*:

```
>>> df.assign(temp_f=lambda x: x.temp_c * 9 / 5 + 32)  # doctest: +SKIP
          temp_c  temp_f
Portland    17.0    62.6
Berkeley    25.0    77.0
```

Alternatively, the same behavior can be achieved by directly referencing an existing Series or sequence:

```
>>> df.assign(temp_f=df['temp_c'] * 9 / 5 + 32)  # doctest: +SKIP
          temp_c  temp_f
Portland    17.0    62.6
Berkeley    25.0    77.0
```

In Python 3.6+, you can create multiple columns within the same assign where one of the columns depends on another one defined within the same assign:

```
>>> df.assign(temp_f=lambda x: x['temp_c'] * 9 / 5 + 32,  # doctest: +SKIP
...           temp_k=lambda x: (x['temp_f'] +  459.67) * 5 / 9)
          temp_c  temp_f  temp_k
Portland    17.0    62.6  290.15
Berkeley    25.0    77.0  298.15
```

astype(*dtype*)

Cast a pandas object to a specified dtype `dtype`.

This docstring was copied from pandas.core.frame.DataFrame.astype.

Some inconsistencies with the Dask version may exist.

Parameters

dtype [data type, or dict of column name -> data type] Use a numpy.dtype or Python type to cast entire pandas object to the same type. Alternatively, use {col: dtype, …}, where col is a column label and dtype is a numpy.dtype or Python type to cast one or more of the DataFrame's columns to column-specific types.

copy [bool, default True (Not supported in Dask)] Return a copy when `copy=True` (be very careful setting `copy=False` as changes to values then may propagate to other pandas objects).

errors [{'raise', 'ignore'}, default 'raise' (Not supported in Dask)] Control raising of exceptions on invalid data for provided dtype.

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

New in version 0.20.0.

kwargs [keyword arguments to pass on to the constructor]

Returns

casted [same type as caller]

See also:

to_datetime Convert argument to datetime.

to_timedelta Convert argument to timedelta.

to_numeric Convert argument to a numeric type.

numpy.ndarray.astype Cast a numpy array to a specified type.

Examples

```
>>> ser = pd.Series([1, 2], dtype='int32')  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    1
1    2
dtype: int32
>>> ser.astype('int64')  # doctest: +SKIP
0    1
1    2
dtype: int64
```

Convert to categorical type:

```
>>> ser.astype('category')  # doctest: +SKIP
0    1
1    2
dtype: category
Categories (2, int64): [1, 2]
```

Convert to ordered categorical type with custom ordering:

```
>>> cat_dtype = pd.api.types.CategoricalDtype(  # doctest: +SKIP
...                     categories=[2, 1], ordered=True)
>>> ser.astype(cat_dtype)  # doctest: +SKIP
0    1
1    2
dtype: category
Categories (2, int64): [2 < 1]
```

Note that using `copy=False` and changing data on a new pandas object may propagate changes:

```
>>> s1 = pd.Series([1,2])  # doctest: +SKIP
>>> s2 = s1.astype('int64', copy=False)  # doctest: +SKIP
>>> s2[0] = 10  # doctest: +SKIP
>>> s1  # note that s1[0] has changed too  # doctest: +SKIP
0    10
1     2
dtype: int64
```

bfill(*axis=None*, *limit=None*)
Synonym for `DataFrame.fillna()` with `method='bfill'`.

categorize(*columns=None*, *index=None*, *split_every=None*, ***kwargs*)
Convert columns of the DataFrame to category dtype.

Parameters

columns [list, optional] A list of column names to convert to categoricals. By default any column with an object dtype is converted to a categorical, and any unknown categoricals are made known.

index [bool, optional] Whether to categorize the index. By default, object indices are converted to categorical, and unknown categorical indices are made known. Set True to always categorize the index, False to never.

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used. Default is 16.

kwargs Keyword arguments are passed on to compute.

clear_divisions()
Forget division information

clip(*lower=None*, *upper=None*, *out=None*)
Trim values at input threshold(s).

This docstring was copied from pandas.core.frame.DataFrame.clip.

Some inconsistencies with the Dask version may exist.

Assigns values outside boundary to boundary values. Thresholds can be singular values or array like, and in the latter case the clipping is performed element-wise in the specified axis.

Parameters

lower [float or array_like, default None] Minimum threshold value. All values below this threshold will be set to it.

upper [float or array_like, default None] Maximum threshold value. All values above this threshold will be set to it.

axis [int or string axis name, optional (Not supported in Dask)] Align object with lower and upper along the given axis.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

New in version 0.21.0.

***args, **kwargs** Additional keywords have no effect but might be accepted for compatibility with numpy.

Returns

Series or DataFrame Same type as calling object with the values outside the clip boundaries replaced

Examples

```
>>> data = {'col_0': [9, -3, 0, -1, 5], 'col_1': [-2, -7, 6, 8, -5]}  #␣
↪doctest: +SKIP
>>> df = pd.DataFrame(data)  # doctest: +SKIP
>>> df  # doctest: +SKIP
   col_0  col_1
0      9     -2
1     -3     -7
2      0      6
3     -1      8
4      5     -5
```

Clips per column using lower and upper thresholds:

```
>>> df.clip(-4, 6)  # doctest: +SKIP
   col_0  col_1
0      6     -2
1     -3     -4
2      0      6
3     -1      6
4      5     -4
```

Clips using specific lower and upper thresholds per column element:

```
>>> t = pd.Series([2, -4, -1, 6, 3])  # doctest: +SKIP
>>> t  # doctest: +SKIP
0    2
1   -4
2   -1
3    6
4    3
dtype: int64
```

```
>>> df.clip(t, t + 4, axis=0)  # doctest: +SKIP
   col_0  col_1
0      6      2
1     -3     -4
2      0      3
3      6      8
4      5      3
```

clip_lower(*threshold*)

Trim values below a given threshold.

This docstring was copied from pandas.core.frame.DataFrame.clip_lower.

Some inconsistencies with the Dask version may exist.

Deprecated since version 0.24.0: Use clip(lower=threshold) instead.

Elements below the *threshold* will be changed to match the *threshold* value(s). Threshold can be a single value or an array, in the latter case it performs the truncation element-wise.

Parameters

threshold [numeric or array-like] Minimum value allowed. All values below threshold will be set to this value.

- float : every value is compared to *threshold*.
- array-like : The shape of *threshold* should match the object it's compared to. When *self* is a Series, *threshold* should be the length. When *self* is a DataFrame, *threshold* should 2-D and the same shape as *self* for `axis=None`, or 1-D and the same length as the axis being compared.

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Align *self* with *threshold* along the given axis.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

New in version 0.21.0.

Returns

Series or DataFrame Original data with values trimmed.

See also:

`Series.clip` General purpose method to trim Series values to given threshold(s).

`DataFrame.clip` General purpose method to trim DataFrame values to given threshold(s).

Examples

Series single threshold clipping:

```
>>> s = pd.Series([5, 6, 7, 8, 9])  # doctest: +SKIP
>>> s.clip(lower=8)  # doctest: +SKIP
0    8
1    8
2    8
3    8
4    9
dtype: int64
```

Series clipping element-wise using an array of thresholds. *threshold* should be the same length as the Series.

```
>>> elemwise_thresholds = [4, 8, 7, 2, 5]  # doctest: +SKIP
>>> s.clip(lower=elemwise_thresholds)  # doctest: +SKIP
0    5
1    8
2    7
3    8
4    9
dtype: int64
```

DataFrames can be compared to a scalar.

```
>>> df = pd.DataFrame({"A": [1, 3, 5], "B": [2, 4, 6]})  # doctest: +SKIP
>>> df  # doctest: +SKIP
   A  B
0  1  2
```

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```
1  3  4
2  5  6
```

```
>>> df.clip(lower=3)  # doctest: +SKIP
   A  B
0  3  3
1  3  4
2  5  6
```

Or to an array of values. By default, *threshold* should be the same shape as the DataFrame.

```
>>> df.clip(lower=np.array([[3, 4], [2, 2], [6, 2]]))  # doctest: +SKIP
   A  B
0  3  4
1  3  4
2  6  6
```

Control how *threshold* is broadcast with *axis*. In this case *threshold* should be the same length as the axis specified by *axis*.

```
>>> df.clip(lower=[3, 3, 5], axis='index')  # doctest: +SKIP
   A  B
0  3  3
1  3  4
2  5  6
```

```
>>> df.clip(lower=[4, 5], axis='columns')  # doctest: +SKIP
   A  B
0  4  5
1  4  5
2  5  6
```

clip_upper(*threshold*)

Trim values above a given threshold.

This docstring was copied from pandas.core.frame.DataFrame.clip_upper.

Some inconsistencies with the Dask version may exist.

Deprecated since version 0.24.0: Use clip(upper=threshold) instead.

Elements above the *threshold* will be changed to match the *threshold* value(s). Threshold can be a single value or an array, in the latter case it performs the truncation element-wise.

Parameters

threshold [numeric or array-like] Maximum value allowed. All values above threshold will be set to this value.

- float : every value is compared to *threshold*.
- array-like : The shape of *threshold* should match the object it's compared to. When *self* is a Series, *threshold* should be the length. When *self* is a DataFrame, *threshold* should 2-D and the same shape as *self* for `axis=None`, or 1-D and the same length as the axis being compared.

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Align object with *threshold* along the given axis.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

New in version 0.21.0.

Returns

Series or DataFrame Original data with values trimmed.

See also:

`Series.clip` General purpose method to trim Series values to given threshold(s).

`DataFrame.clip` General purpose method to trim DataFrame values to given threshold(s).

Examples

```
>>> s = pd.Series([1, 2, 3, 4, 5])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    1
1    2
2    3
3    4
4    5
dtype: int64
```

```
>>> s.clip(upper=3)  # doctest: +SKIP
0    1
1    2
2    3
3    3
4    3
dtype: int64
```

```
>>> elemwise_thresholds = [5, 4, 3, 2, 1]  # doctest: +SKIP
>>> elemwise_thresholds  # doctest: +SKIP
[5, 4, 3, 2, 1]
```

```
>>> s.clip(upper=elemwise_thresholds)  # doctest: +SKIP
0    1
1    2
2    3
3    2
4    1
dtype: int64
```

`combine`(*other*, *func*, *fill_value=None*, *overwrite=True*)

Perform column-wise combine with another DataFrame based on a passed function.

This docstring was copied from pandas.core.frame.DataFrame.combine.

Some inconsistencies with the Dask version may exist.

Combines a DataFrame with *other* DataFrame using *func* to element-wise combine columns. The row and column indexes of the resulting DataFrame will be the union of the two.

Parameters

other [DataFrame] The DataFrame to merge column-wise.

func [function] Function that takes two series as inputs and return a Series or a scalar. Used to merge the two dataframes column by columns.

fill_value [scalar value, default None] The value to fill NaNs with prior to passing any column to the merge func.

overwrite [boolean, default True] If True, columns in *self* that do not exist in *other* will be overwritten with NaNs.

Returns

result [DataFrame]

See also:

DataFrame.combine_first Combine two DataFrame objects and default to non-null values in frame calling the method.

Examples

Combine using a simple function that chooses the smaller column.

```
>>> df1 = pd.DataFrame({'A': [0, 0], 'B': [4, 4]})  # doctest: +SKIP
>>> df2 = pd.DataFrame({'A': [1, 1], 'B': [3, 3]})  # doctest: +SKIP
>>> take_smaller = lambda s1, s2: s1 if s1.sum() < s2.sum() else s2  #␣
↪doctest: +SKIP
>>> df1.combine(df2, take_smaller)  # doctest: +SKIP
   A  B
0  0  3
1  0  3
```

Example using a true element-wise combine function.

```
>>> df1 = pd.DataFrame({'A': [5, 0], 'B': [2, 4]})  # doctest: +SKIP
>>> df2 = pd.DataFrame({'A': [1, 1], 'B': [3, 3]})  # doctest: +SKIP
>>> df1.combine(df2, np.minimum)  # doctest: +SKIP
   A  B
0  1  2
1  0  3
```

Using *fill_value* fills Nones prior to passing the column to the merge function.

```
>>> df1 = pd.DataFrame({'A': [0, 0], 'B': [None, 4]})  # doctest: +SKIP
>>> df2 = pd.DataFrame({'A': [1, 1], 'B': [3, 3]})  # doctest: +SKIP
>>> df1.combine(df2, take_smaller, fill_value=-5)  # doctest: +SKIP
   A    B
0  0 -5.0
1  0  4.0
```

However, if the same element in both dataframes is None, that None is preserved

```
>>> df1 = pd.DataFrame({'A': [0, 0], 'B': [None, 4]})  # doctest: +SKIP
>>> df2 = pd.DataFrame({'A': [1, 1], 'B': [None, 3]})  # doctest: +SKIP
>>> df1.combine(df2, take_smaller, fill_value=-5)  # doctest: +SKIP
   A    B
0  0  NaN
1  0  3.0
```

Example that demonstrates the use of *overwrite* and behavior when the axis differ between the dataframes.

```
>>> df1 = pd.DataFrame({'A': [0, 0], 'B': [4, 4]})  # doctest: +SKIP
>>> df2 = pd.DataFrame({'B': [3, 3], 'C': [-10, 1],}, index=[1, 2])  #␣
↪doctest: +SKIP
>>> df1.combine(df2, take_smaller)  # doctest: +SKIP
     A    B     C
0  NaN  NaN   NaN
1  NaN  3.0 -10.0
2  NaN  3.0   1.0
```

```
>>> df1.combine(df2, take_smaller, overwrite=False)  # doctest: +SKIP
     A    B     C
0  0.0  NaN   NaN
1  0.0  3.0 -10.0
2  NaN  3.0   1.0
```

Demonstrating the preference of the passed in dataframe.

```
>>> df2 = pd.DataFrame({'B': [3, 3], 'C': [1, 1],}, index=[1, 2])  #␣
↪doctest: +SKIP
>>> df2.combine(df1, take_smaller)  # doctest: +SKIP
   A    B   C
0  0.0  NaN NaN
1  0.0  3.0 NaN
2  NaN  3.0 NaN
```

```
>>> df2.combine(df1, take_smaller, overwrite=False)  # doctest: +SKIP
     A    B   C
0  0.0  NaN NaN
1  0.0  3.0 1.0
2  NaN  3.0 1.0
```

combine_first(*other*)

Update null elements with value in the same location in *other*.

This docstring was copied from pandas.core.frame.DataFrame.combine_first.

Some inconsistencies with the Dask version may exist.

Combine two DataFrame objects by filling null values in one DataFrame with non-null values from other DataFrame. The row and column indexes of the resulting DataFrame will be the union of the two.

Parameters

other [DataFrame] Provided DataFrame to use to fill null values.

Returns

combined [DataFrame]

See also:

DataFrame.combine Perform series-wise operation on two DataFrames using a given function.

Examples

```
>>> df1 = pd.DataFrame({'A': [None, 0], 'B': [None, 4]})  # doctest: +SKIP
>>> df2 = pd.DataFrame({'A': [1, 1], 'B': [3, 3]})  # doctest: +SKIP
```

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```
>>> df1.combine_first(df2)  # doctest: +SKIP
     A    B
0  1.0  3.0
1  0.0  4.0
```

Null values still persist if the location of that null value does not exist in *other*

```
>>> df1 = pd.DataFrame({'A': [None, 0], 'B': [4, None]})  # doctest: +SKIP
>>> df2 = pd.DataFrame({'B': [3, 3], 'C': [1, 1]}, index=[1, 2])  # doctest:␣
↪+SKIP
>>> df1.combine_first(df2)  # doctest: +SKIP
     A    B    C
0  NaN  4.0  NaN
1  0.0  3.0  1.0
2  NaN  3.0  1.0
```

compute(***kwargs*)
Compute this dask collection

This turns a lazy Dask collection into its in-memory equivalent. For example a Dask.array turns into a `numpy.array()` and a Dask.dataframe turns into a Pandas dataframe. The entire dataset must fit into memory before calling this operation.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

See also:

`dask.base.compute`

copy()
Make a copy of the dataframe

This is strictly a shallow copy of the underlying computational graph. It does not affect the underlying data

corr(*method='pearson'*, *min_periods=None*, *split_every=False*)
Compute pairwise correlation of columns, excluding NA/null values.

This docstring was copied from pandas.core.frame.DataFrame.corr.

Some inconsistencies with the Dask version may exist.

Parameters

method [{'pearson', 'kendall', 'spearman'} or callable]

- pearson : standard correlation coefficient
- kendall : Kendall Tau correlation coefficient
- spearman : Spearman rank correlation
- **callable: callable with input two 1d ndarrays** and returning a float .. versionadded:: 0.24.0

min_periods [int, optional] Minimum number of observations required per pair of columns to have a valid result. Currently only available for pearson and spearman correlation

Returns

y [DataFrame]

See also:

DataFrame.corrwith, *Series.corr*

Examples

```
>>> histogram_intersection = lambda a, b: np.minimum(a, b  # doctest: +SKIP
... ).sum().round(decimals=1)
>>> df = pd.DataFrame([(.2, .3), (.0, .6), (.6, .0), (.2, .1)],  # doctest:␣
↪+SKIP
...                   columns=['dogs', 'cats'])
>>> df.corr(method=histogram_intersection)  # doctest: +SKIP
      dogs cats
dogs   1.0  0.3
cats   0.3  1.0
```

count (*axis=None*, *split_every=False*)

Count non-NA cells for each column or row.

This docstring was copied from pandas.core.frame.DataFrame.count.

Some inconsistencies with the Dask version may exist.

The values *None*, *NaN*, *NaT*, and optionally *numpy.inf* (depending on *pandas.options.mode.use_inf_as_na*) are considered NA.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] If 0 or 'index' counts are generated for each column. If 1 or 'columns' counts are generated for each **row**.

level [int or str, optional (Not supported in Dask)] If the axis is a *MultiIndex* (hierarchical), count along a particular *level*, collapsing into a *DataFrame*. A *str* specifies the level name.

numeric_only [boolean, default False (Not supported in Dask)] Include only *float*, *int* or *boolean* data.

Returns

Series or DataFrame For each column/row the number of non-NA/null entries. If *level* is specified returns a *DataFrame*.

See also:

Series.count Number of non-NA elements in a Series.

DataFrame.shape Number of DataFrame rows and columns (including NA elements).

DataFrame.isna Boolean same-sized DataFrame showing places of NA elements.

Examples

Constructing DataFrame from a dictionary:

```
>>> df = pd.DataFrame({"Person":  # doctest: +SKIP
...                    ["John", "Myla", "Lewis", "John", "Myla"],
...                    "Age": [24., np.nan, 21., 33, 26],
...                    "Single": [False, True, True, True, False]})
>>> df  # doctest: +SKIP
   Person   Age  Single
0    John  24.0   False
1    Myla   NaN    True
2   Lewis  21.0    True
3    John  33.0    True
4    Myla  26.0   False
```

Notice the uncounted NA values:

```
>>> df.count()  # doctest: +SKIP
Person    5
Age       4
Single    5
dtype: int64
```

Counts for each **row**:

```
>>> df.count(axis='columns')  # doctest: +SKIP
0    3
1    2
2    3
3    3
4    3
dtype: int64
```

Counts for one level of a *MultiIndex*:

```
>>> df.set_index(["Person", "Single"]).count(level="Person")  # doctest:␣
↪+SKIP
        Age
Person
John      2
Lewis     1
Myla      1
```

cov (*min_periods=None*, *split_every=False*)

Compute pairwise covariance of columns, excluding NA/null values.

This docstring was copied from pandas.core.frame.DataFrame.cov.

Some inconsistencies with the Dask version may exist.

Compute the pairwise covariance among the series of a DataFrame. The returned data frame is the covariance matrix of the columns of the DataFrame.

Both NA and null values are automatically excluded from the calculation. (See the note below about bias from missing values.) A threshold can be set for the minimum number of observations for each value created. Comparisons with observations below this threshold will be returned as `NaN`.

This method is generally used for the analysis of time series data to understand the relationship between different measures across time.

Parameters

min_periods [int, optional] Minimum number of observations required per pair of columns to have a valid result.

Returns

DataFrame The covariance matrix of the series of the DataFrame.

See also:

pandas.Series.cov Compute covariance with another Series.

pandas.core.window.EWM.cov Exponential weighted sample covariance.

pandas.core.window.Expanding.cov Expanding sample covariance.

pandas.core.window.Rolling.cov Rolling sample covariance.

Notes

Returns the covariance matrix of the DataFrame's time series. The covariance is normalized by N-1.

For DataFrames that have Series that are missing data (assuming that data is missing at random) the returned covariance matrix will be an unbiased estimate of the variance and covariance between the member Series.

However, for many applications this estimate may not be acceptable because the estimate covariance matrix is not guaranteed to be positive semi-definite. This could lead to estimate correlations having absolute values which are greater than one, and/or a non-invertible covariance matrix. See Estimation of covariance matrices for more details.

Examples

```
>>> df = pd.DataFrame([(1, 2), (0, 3), (2, 0), (1, 1)],  # doctest: +SKIP
...                   columns=['dogs', 'cats'])
>>> df.cov()  # doctest: +SKIP
          dogs      cats
dogs  0.666667 -1.000000
cats -1.000000  1.666667
```

```
>>> np.random.seed(42)  # doctest: +SKIP
>>> df = pd.DataFrame(np.random.randn(1000, 5),  # doctest: +SKIP
...                   columns=['a', 'b', 'c', 'd', 'e'])
>>> df.cov()  # doctest: +SKIP
          a         b         c         d         e
a  0.998438 -0.020161  0.059277 -0.008943  0.014144
b -0.020161  1.059352 -0.008543 -0.024738  0.009826
c  0.059277 -0.008543  1.010670 -0.001486 -0.000271
d -0.008943 -0.024738 -0.001486  0.921297 -0.013692
e  0.014144  0.009826 -0.000271 -0.013692  0.977795
```

Minimum number of periods

This method also supports an optional `min_periods` keyword that specifies the required minimum number of non-NA observations for each column pair in order to have a valid result:

```
>>> np.random.seed(42)  # doctest: +SKIP
>>> df = pd.DataFrame(np.random.randn(20, 3),  # doctest: +SKIP
...                   columns=['a', 'b', 'c'])
>>> df.loc[df.index[:5], 'a'] = np.nan  # doctest: +SKIP
>>> df.loc[df.index[5:10], 'b'] = np.nan  # doctest: +SKIP
>>> df.cov(min_periods=12)  # doctest: +SKIP
          a         b         c
a  0.316741       NaN -0.150812
b       NaN  1.248003  0.191417
c -0.150812  0.191417  0.895202
```

cummax(*axis=None*, *skipna=True*, *out=None*)

Return cumulative maximum over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cummax.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative maximum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummax [Series or DataFrame]

See also:

core.window.Expanding.max Similar functionality but ignores `NaN` values.

DataFrame.max Return the maximum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummax()  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3    5.0
4    5.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummax(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the maximum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummax()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  3.0  1.0
```

To iterate over columns and find the maximum in each row, use `axis=1`

```
>>> df.cummax(axis=1)  # doctest: +SKIP
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  1.0
```

cummin(*axis=None*, *skipna=True*, *out=None*)

Return cumulative minimum over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cummin.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative minimum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummin [Series or DataFrame]

See also:

`core.window.Expanding.min` Similar functionality but ignores `NaN` values.

`DataFrame.min` Return the minimum over DataFrame axis.

`DataFrame.cummax` Return cumulative maximum over DataFrame axis.

`DataFrame.cummin` Return cumulative minimum over DataFrame axis.

`DataFrame.cumsum` Return cumulative sum over DataFrame axis.

`DataFrame.cumprod` Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummin()  # doctest: +SKIP
0    2.0
1    NaN
2    2.0
3   -1.0
4   -1.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummin(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the minimum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummin()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  2.0  NaN
2  1.0  0.0
```

To iterate over columns and find the minimum in each row, use `axis=1`

```
>>> df.cummin(axis=1)  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

cumprod(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative product over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cumprod.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative product.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumprod [Series or DataFrame]

See also:

`core.window.Expanding.prod` Similar functionality but ignores `NaN` values.

`DataFrame.prod` Return the product over DataFrame axis.

`DataFrame.cummax` Return cumulative maximum over DataFrame axis.

`DataFrame.cummin` Return cumulative minimum over DataFrame axis.

`DataFrame.cumsum` Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumprod()  # doctest: +SKIP
0     2.0
1     NaN
2    10.0
3   -10.0
4    -0.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumprod(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the product in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumprod()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  6.0  NaN
2  6.0  0.0
```

To iterate over columns and find the product in each row, use `axis=1`

```
>>> df.cumprod(axis=1)  # doctest: +SKIP
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  0.0
```

cumsum(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative sum over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cumsum.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative sum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumsum [Series or DataFrame]

See also:

core.window.Expanding.sum Similar functionality but ignores `NaN` values.

DataFrame.sum Return the sum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumsum()  # doctest: +SKIP
0    2.0
1    NaN
2    7.0
3    6.0
4    6.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumsum(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the sum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumsum()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  5.0  NaN
2  6.0  1.0
```

To iterate over columns and find the sum in each row, use `axis=1`

```
>>> df.cumsum(axis=1)  # doctest: +SKIP
     A    B
0  2.0  3.0
1  3.0  NaN
2  1.0  1.0
```

describe(*split_every=False*, *percentiles=None*, *percentiles_method='default'*, *include=None*, *exclude=None*)

Generate descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding `NaN` values.

This docstring was copied from pandas.core.frame.DataFrame.describe.

Some inconsistencies with the Dask version may exist.

Analyzes both numeric and object series, as well as `DataFrame` column sets of mixed data types. The output will vary depending on what is provided. Refer to the notes below for more detail.

Parameters

percentiles [list-like of numbers, optional] The percentiles to include in the output. All should fall between 0 and 1. The default is `[.25, .5, .75]`, which returns the 25th, 50th, and 75th percentiles.

include ['all', list-like of dtypes or None (default), optional] A white list of data types to include in the result. Ignored for `Series`. Here are the options:

- 'all' : All columns of the input will be included in the output.
- A list-like of dtypes : Limits the results to the provided data types. To limit the result to numeric types submit `numpy.number`. To limit it instead to object columns submit the `numpy.object` data type. Strings can also be used in the style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To select pandas categorical columns, use `'category'`
- None (default) : The result will include all numeric columns.

exclude [list-like of dtypes or None (default), optional,] A black list of data types to omit from the result. Ignored for `Series`. Here are the options:

- A list-like of dtypes : Excludes the provided data types from the result. To exclude numeric types submit `numpy.number`. To exclude object columns submit the data type `numpy.object`. Strings can also be used in the style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To exclude pandas categorical columns, use `'category'`
- None (default) : The result will exclude nothing.

Returns

Series or DataFrame Summary statistics of the Series or Dataframe provided.

See also:

`DataFrame.count` Count number of non-NA/null observations.

`DataFrame.max` Maximum of the values in the object.

`DataFrame.min` Minimum of the values in the object.

`DataFrame.mean` Mean of the values.

`DataFrame.std` Standard deviation of the obersvations.

`DataFrame.select_dtypes` Subset of a DataFrame including/excluding columns based on their dtype.

Notes

For numeric data, the result's index will include `count`, `mean`, `std`, `min`, `max` as well as lower, `50` and upper percentiles. By default the lower percentile is `25` and the upper percentile is `75`. The `50` percentile is the same as the median.

For object data (e.g. strings or timestamps), the result's index will include `count`, `unique`, `top`, and `freq`. The `top` is the most common value. The `freq` is the most common value's frequency. Timestamps also include the `first` and `last` items.

If multiple object values have the highest count, then the `count` and `top` results will be arbitrarily chosen from among those with the highest count.

For mixed data types provided via a DataFrame, the default is to return only an analysis of numeric columns. If the dataframe consists only of object and categorical data without any numeric columns, the default is to return an analysis of both the object and categorical columns. If include='all' is provided as an option, the result will include a union of attributes of each type.

The *include* and *exclude* parameters can be used to limit which columns in a DataFrame are analyzed for the output. The parameters are ignored when analyzing a Series.

Examples

Describing a numeric Series.

```
>>> s = pd.Series([1, 2, 3])  # doctest: +SKIP
>>> s.describe()  # doctest: +SKIP
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
75%      2.5
max      3.0
dtype: float64
```

Describing a categorical Series.

```
>>> s = pd.Series(['a', 'a', 'b', 'c'])  # doctest: +SKIP
>>> s.describe()  # doctest: +SKIP
count     4
unique    3
top       a
freq      2
dtype: object
```

Describing a timestamp Series.

```
>>> s = pd.Series([  # doctest: +SKIP
...   np.datetime64("2000-01-01"),
...   np.datetime64("2010-01-01"),
...   np.datetime64("2010-01-01")
... ])
>>> s.describe()  # doctest: +SKIP
count                       3
unique                      2
top       2010-01-01 00:00:00
freq                        2
first     2000-01-01 00:00:00
last      2010-01-01 00:00:00
dtype: object
```

Describing a DataFrame. By default only numeric fields are returned.

```
>>> df = pd.DataFrame({'categorical': pd.Categorical(['d','e','f']),  #␣
↪doctest: +SKIP
...                    'numeric': [1, 2, 3],
...                    'object': ['a', 'b', 'c']
...                   })
```

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```
>>> df.describe()  # doctest: +SKIP
       numeric
count      3.0
mean       2.0
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Describing all columns of a `DataFrame` regardless of data type.

```
>>> df.describe(include='all')  # doctest: +SKIP
        categorical  numeric object
count            3      3.0      3
unique           3      NaN      3
top              f      NaN      c
freq             1      NaN      1
mean           NaN      2.0    NaN
std            NaN      1.0    NaN
min            NaN      1.0    NaN
25%            NaN      1.5    NaN
50%            NaN      2.0    NaN
75%            NaN      2.5    NaN
max            NaN      3.0    NaN
```

Describing a column from a `DataFrame` by accessing it as an attribute.

```
>>> df.numeric.describe()  # doctest: +SKIP
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
75%      2.5
max      3.0
Name: numeric, dtype: float64
```

Including only numeric columns in a `DataFrame` description.

```
>>> df.describe(include=[np.number])  # doctest: +SKIP
       numeric
count      3.0
mean       2.0
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Including only string columns in a `DataFrame` description.

```
>>> df.describe(include=[np.object])  # doctest: +SKIP
       object
```

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```
count       3
unique      3
top         c
freq        1
```

Including only categorical columns from a `DataFrame` description.

```
>>> df.describe(include=['category'])  # doctest: +SKIP
       categorical
count            3
unique           3
top              f
freq             1
```

Excluding numeric columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.number])  # doctest: +SKIP
       categorical object
count            3      3
unique           3      3
top              f      c
freq             1      1
```

Excluding object columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.object])  # doctest: +SKIP
       categorical  numeric
count            3      3.0
unique           3      NaN
top              f      NaN
freq             1      NaN
mean           NaN      2.0
std            NaN      1.0
min            NaN      1.0
25%            NaN      1.5
50%            NaN      2.0
75%            NaN      2.5
max            NaN      3.0
```

diff(*periods=1*, *axis=0*)

First discrete difference of element.

This docstring was copied from pandas.core.frame.DataFrame.diff.

Some inconsistencies with the Dask version may exist.

Note: Pandas currently uses an `object`-dtype column to represent boolean data with missing values. This can cause issues for boolean-specific operations, like `|`. To enable boolean- specific operations, at the cost of metadata that doesn't match pandas, use `.astype(bool)` after the `shift`.

Calculates the difference of a DataFrame element compared with another element in the DataFrame (default is the element in the same column of the previous row).

Parameters

periods [int, default 1] Periods to shift for calculating difference, accepts negative values.

axis [{0 or 'index', 1 or 'columns'}, default 0] Take difference over rows (0) or columns (1).

New in version 0.16.1..

Returns

diffed [DataFrame]

See also:

`Series.diff` First discrete difference for a Series.

`DataFrame.pct_change` Percent change over given number of periods.

`DataFrame.shift` Shift index by desired number of periods with an optional time freq.

Examples

Difference with previous row

```
>>> df = pd.DataFrame({'a': [1, 2, 3, 4, 5, 6],  # doctest: +SKIP
...                    'b': [1, 1, 2, 3, 5, 8],
...                    'c': [1, 4, 9, 16, 25, 36]})
>>> df  # doctest: +SKIP
   a  b   c
0  1  1   1
1  2  1   4
2  3  2   9
3  4  3  16
4  5  5  25
5  6  8  36
```

```
>>> df.diff()  # doctest: +SKIP
     a    b     c
0  NaN  NaN   NaN
1  1.0  0.0   3.0
2  1.0  1.0   5.0
3  1.0  1.0   7.0
4  1.0  2.0   9.0
5  1.0  3.0  11.0
```

Difference with previous column

```
>>> df.diff(axis=1)  # doctest: +SKIP
    a    b     c
0 NaN  0.0   0.0
1 NaN -1.0   3.0
2 NaN -1.0   7.0
3 NaN -1.0  13.0
4 NaN  0.0  20.0
5 NaN  2.0  28.0
```

Difference with 3rd previous row

```
>>> df.diff(periods=3)  # doctest: +SKIP
     a    b     c
0  NaN  NaN   NaN
```

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```
1  NaN  NaN   NaN
2  NaN  NaN   NaN
3  3.0  2.0  15.0
4  3.0  4.0  21.0
5  3.0  6.0  27.0
```

Difference with following row

```
>>> df.diff(periods=-1)  # doctest: +SKIP
     a    b     c
0 -1.0  0.0  -3.0
1 -1.0 -1.0  -5.0
2 -1.0 -1.0  -7.0
3 -1.0 -2.0  -9.0
4 -1.0 -3.0 -11.0
5  NaN  NaN   NaN
```

div(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Floating division of dataframe and other, element-wise (binary operator *truediv*).

Equivalent to `dataframe / other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rtruediv*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...         axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

divide(*other, axis='columns', level=None, fill_value=None*)

Floating division of dataframe and other, element-wise (binary operator *truediv*).

Equivalent to `dataframe / other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rtruediv*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
```

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```
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                                 'degrees': [360, 180, 360, 360, 540, 720]},
...                                index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                       ['circle', 'triangle', 'rectangle',
...                                        'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

drop(*labels=None*, *axis=0*, *columns=None*, *errors='raise'*)
Drop specified labels from rows or columns.

This docstring was copied from pandas.core.frame.DataFrame.drop.

Some inconsistencies with the Dask version may exist.

Remove rows or columns by specifying label names and corresponding axis, or by specifying directly index or column names. When using a multi-index, labels on different levels can be removed by specifying the level.

Parameters

labels [single label or list-like] Index or column labels to drop.

axis [{0 or 'index', 1 or 'columns'}, default 0] Whether to drop labels from the index (0 or 'index') or columns (1 or 'columns').

index, columns [single label or list-like] Alternative to specifying axis (`labels, axis=1` is equivalent to `columns=labels`).

New in version 0.21.0.

level [int or level name, optional (Not supported in Dask)] For MultiIndex, level from which the labels will be removed.

inplace [bool, default False (Not supported in Dask)] If True, do operation inplace and return None.

errors [{'ignore', 'raise'}, default 'raise'] If 'ignore', suppress error and only existing labels are dropped.

Returns

dropped [pandas.DataFrame]

Raises

KeyError If none of the labels are found in the selected axis

See also:

`DataFrame.loc` Label-location based indexer for selection by label.

`DataFrame.dropna` Return DataFrame with labels on given axis omitted where (all or any) data are missing.

`DataFrame.drop_duplicates` Return DataFrame with duplicate rows removed, optionally only considering certain columns.

`Series.drop` Return Series with specified index labels removed.

Examples

```
>>> df = pd.DataFrame(np.arange(12).reshape(3,4),  # doctest: +SKIP
...                   columns=['A', 'B', 'C', 'D'])
>>> df  # doctest: +SKIP
   A  B   C   D
0  0  1   2   3
1  4  5   6   7
2  8  9  10  11
```

Drop columns

```
>>> df.drop(['B', 'C'], axis=1)  # doctest: +SKIP
   A   D
0  0   3
1  4   7
2  8  11
```

```
>>> df.drop(columns=['B', 'C'])  # doctest: +SKIP
   A   D
0  0   3
1  4   7
2  8  11
```

Drop a row by index

```
>>> df.drop([0, 1])  # doctest: +SKIP
   A  B   C   D
2  8  9  10  11
```

Drop columns and/or rows of MultiIndex DataFrame

```
>>> midx = pd.MultiIndex(levels=[['lama', 'cow', 'falcon'],  # doctest: +SKIP
...                              ['speed', 'weight', 'length']],
...                      codes=[[0, 0, 0, 1, 1, 1, 2, 2, 2],
...                             [0, 1, 2, 0, 1, 2, 0, 1, 2]])
>>> df = pd.DataFrame(index=midx, columns=['big', 'small'],  # doctest: +SKIP
...                   data=[[45, 30], [200, 100], [1.5, 1], [30, 20],
...                         [250, 150], [1.5, 0.8], [320, 250],
...                         [1, 0.8], [0.3,0.2]])
>>> df  # doctest: +SKIP
                big     small
lama    speed   45.0    30.0
        weight  200.0   100.0
        length  1.5     1.0
cow     speed   30.0    20.0
        weight  250.0   150.0
        length  1.5     0.8
falcon  speed   320.0   250.0
        weight  1.0     0.8
        length  0.3     0.2
```

```
>>> df.drop(index='cow', columns='small')  # doctest: +SKIP
                big
lama    speed   45.0
        weight  200.0
        length  1.5
falcon  speed   320.0
        weight  1.0
        length  0.3
```

```
>>> df.drop(index='length', level=1)  # doctest: +SKIP
                big     small
lama    speed   45.0    30.0
        weight  200.0   100.0
cow     speed   30.0    20.0
        weight  250.0   150.0
falcon  speed   320.0   250.0
        weight  1.0     0.8
```

drop_duplicates(*subset=None*, *split_every=None*, *split_out=1*, ***kwargs*)

Return DataFrame with duplicate rows removed, optionally only considering certain columns.

This docstring was copied from pandas.core.frame.DataFrame.drop_duplicates.

Some inconsistencies with the Dask version may exist.

Parameters

subset [column label or sequence of labels, optional] Only consider certain columns for identifying duplicates, by default use all of the columns

keep [{‘first’, ‘last’, False}, default ‘first’ (Not supported in Dask)]

- `first` : Drop duplicates except for the first occurrence.

- `last` : Drop duplicates except for the last occurrence.
- False : Drop all duplicates.

inplace [boolean, default False (Not supported in Dask)] Whether to drop duplicates in place or to return a copy

Returns

deduplicated [DataFrame]

`dropna`(*how='any'*, *subset=None*, *thresh=None*)

Remove missing values.

This docstring was copied from pandas.core.frame.DataFrame.dropna.

Some inconsistencies with the Dask version may exist.

See the User Guide for more on which values are considered missing, and how to work with missing data.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Determine if rows or columns which contain missing values are removed.

- 0, or 'index' : Drop rows which contain missing values.
- 1, or 'columns' : Drop columns which contain missing value.

Deprecated since version 0.23.0: Pass tuple or list to drop on multiple axes. Only a single axis is allowed.

how [{'any', 'all'}, default 'any'] Determine if row or column is removed from DataFrame, when we have at least one NA or all NA.

- 'any' : If any NA values are present, drop that row or column.
- 'all' : If all values are NA, drop that row or column.

thresh [int, optional] Require that many non-NA values.

subset [array-like, optional] Labels along other axis to consider, e.g. if you are dropping rows these would be a list of columns to include.

inplace [bool, default False (Not supported in Dask)] If True, do operation inplace and return None.

Returns

DataFrame DataFrame with NA entries dropped from it.

See also:

`DataFrame.isna` Indicate missing values.

`DataFrame.notna` Indicate existing (non-missing) values.

`DataFrame.fillna` Replace missing values.

`Series.dropna` Drop missing values.

`Index.dropna` Drop missing indices.

Examples

```
>>> df = pd.DataFrame({"name": ['Alfred', 'Batman', 'Catwoman'],  # doctest:␣
↪+SKIP
...                    "toy": [np.nan, 'Batmobile', 'Bullwhip'],
...                    "born": [pd.NaT, pd.Timestamp("1940-04-25"),
...                             pd.NaT]})
>>> df  # doctest: +SKIP
       name        toy       born
0    Alfred        NaN        NaT
1    Batman  Batmobile 1940-04-25
2  Catwoman   Bullwhip        NaT
```

Drop the rows where at least one element is missing.

```
>>> df.dropna()  # doctest: +SKIP
     name        toy       born
1  Batman  Batmobile 1940-04-25
```

Drop the columns where at least one element is missing.

```
>>> df.dropna(axis='columns')  # doctest: +SKIP
       name
0    Alfred
1    Batman
2  Catwoman
```

Drop the rows where all elements are missing.

```
>>> df.dropna(how='all')  # doctest: +SKIP
       name        toy       born
0    Alfred        NaN        NaT
1    Batman  Batmobile 1940-04-25
2  Catwoman   Bullwhip        NaT
```

Keep only the rows with at least 2 non-NA values.

```
>>> df.dropna(thresh=2)  # doctest: +SKIP
       name        toy       born
1    Batman  Batmobile 1940-04-25
2  Catwoman   Bullwhip        NaT
```

Define in which columns to look for missing values.

```
>>> df.dropna(subset=['name', 'born'])  # doctest: +SKIP
       name        toy       born
1    Batman  Batmobile 1940-04-25
```

Keep the DataFrame with valid entries in the same variable.

```
>>> df.dropna(inplace=True)  # doctest: +SKIP
>>> df  # doctest: +SKIP
     name        toy       born
1  Batman  Batmobile 1940-04-25
```

`dtypes`
Return data types

eq(*other*, *axis='columns'*, *level=None*)

Equal to of dataframe and other, element-wise (binary operator *eq*).

Among flexible wrappers (*eq*, *ne*, *le*, *lt*, *ge*, *gt*) to comparison operators.

Equivalent to ==, =!, <=, <, >=, > with support to choose axis (rows or columns) and level for comparison.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}, default 'columns'] Whether to compare by the index (0 or 'index') or columns (1 or 'columns').

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

Returns

DataFrame of bool Result of the comparison.

See also:

`DataFrame.eq`	Compare DataFrames for equality elementwise.
`DataFrame.ne`	Compare DataFrames for inequality elementwise.
`DataFrame.le`	Compare DataFrames for less than inequality or equality elementwise.
`DataFrame.lt`	Compare DataFrames for strictly less than inequality elementwise.
`DataFrame.ge`	Compare DataFrames for greater than inequality or equality elementwise.
`DataFrame.gt`	Compare DataFrames for strictly greater than inequality elementwise.

Notes

Mismatched indices will be unioned together. *NaN* values are considered different (i.e. *NaN* != *NaN*).

Examples

```
>>> df = pd.DataFrame({'cost': [250, 150, 100],  # doctest: +SKIP
...                    'revenue': [100, 250, 300]},
...                   index=['A', 'B', 'C'])
>>> df  # doctest: +SKIP
   cost  revenue
A   250      100
B   150      250
C   100      300
```

Comparison with a scalar, using either the operator or method:

```
>>> df == 100  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

```
>>> df.eq(100)  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

When *other* is a `Series`, the columns of a DataFrame are aligned with the index of *other* and broadcast:

```
>>> df != pd.Series([100, 250], index=["cost", "revenue"])  # doctest: +SKIP
    cost  revenue
A   True     True
B   True    False
C  False     True
```

Use the method to control the broadcast axis:

```
>>> df.ne(pd.Series([100, 300], index=["A", "D"]), axis='index')  # doctest:␣
↪+SKIP
   cost  revenue
A  True    False
B  True     True
C  True     True
D  True     True
```

When comparing to an arbitrary sequence, the number of columns must match the number elements in *other*:

```
>>> df == [250, 100]  # doctest: +SKIP
    cost  revenue
A   True     True
B  False    False
C  False    False
```

Use the method to control the axis:

```
>>> df.eq([250, 250, 100], axis='index')  # doctest: +SKIP
    cost  revenue
A   True    False
B  False     True
C   True    False
```

Compare to a DataFrame of different shape.

```
>>> other = pd.DataFrame({'revenue': [300, 250, 100, 150]},  # doctest: +SKIP
...                      index=['A', 'B', 'C', 'D'])
>>> other  # doctest: +SKIP
   revenue
A      300
B      250
C      100
D      150
```

```
>>> df.gt(other)  # doctest: +SKIP
    cost  revenue
A  False    False
B  False    False
```

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```
C  False     True
D  False    False
```

Compare to a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'cost': [250, 150, 100, 150, 300, 220],  #␣
↪doctest: +SKIP
...                              'revenue': [100, 250, 300, 200, 175, 225]},
...                             index=[['Q1', 'Q1', 'Q1', 'Q2', 'Q2', 'Q2'],
...                                    ['A', 'B', 'C', 'A', 'B', 'C']])
>>> df_multindex  # doctest: +SKIP
      cost  revenue
Q1 A   250      100
   B   150      250
   C   100      300
Q2 A   150      200
   B   300      175
   C   220      225
```

```
>>> df.le(df_multindex, level=1)  # doctest: +SKIP
       cost  revenue
Q1 A   True     True
   B   True     True
   C   True     True
Q2 A  False     True
   B   True    False
   C   True    False
```

eval(*expr*, *inplace=None*, ***kwargs*)

Evaluate a string describing operations on DataFrame columns.

This docstring was copied from pandas.core.frame.DataFrame.eval.

Some inconsistencies with the Dask version may exist.

Operates on columns only, not specific rows or elements. This allows *eval* to run arbitrary code, which can make you vulnerable to code injection if you pass user input to this function.

Parameters

expr [str] The expression string to evaluate.

inplace [bool, default False] If the expression contains an assignment, whether to perform the operation inplace and mutate the existing DataFrame. Otherwise, a new DataFrame is returned.

New in version 0.18.0..

kwargs [dict] See the documentation for `eval()` for complete details on the keyword arguments accepted by `query()`.

Returns

ndarray, scalar, or pandas object The result of the evaluation.

See also:

DataFrame.query Evaluates a boolean expression to query the columns of a frame.

DataFrame.assign Can evaluate an expression or function to create new values for a column.

`pandas.eval` Evaluate a Python expression as a string using various backends.

Notes

For more details see the API documentation for `eval()`. For detailed examples see enhancing performance with eval.

Examples

```
>>> df = pd.DataFrame({'A': range(1, 6), 'B': range(10, 0, -2)})  # doctest:␣
↪+SKIP
>>> df  # doctest: +SKIP
   A   B
0  1  10
1  2   8
2  3   6
3  4   4
4  5   2
>>> df.eval('A + B')  # doctest: +SKIP
0    11
1    10
2     9
3     8
4     7
dtype: int64
```

Assignment is allowed though by default the original DataFrame is not modified.

```
>>> df.eval('C = A + B')  # doctest: +SKIP
   A   B   C
0  1  10  11
1  2   8  10
2  3   6   9
3  4   4   8
4  5   2   7
>>> df  # doctest: +SKIP
   A   B
0  1  10
1  2   8
2  3   6
3  4   4
4  5   2
```

Use `inplace=True` to modify the original DataFrame.

```
>>> df.eval('C = A + B', inplace=True)  # doctest: +SKIP
>>> df  # doctest: +SKIP
   A   B   C
0  1  10  11
1  2   8  10
2  3   6   9
3  4   4   8
4  5   2   7
```

ffill(*axis=None*, *limit=None*)
Synonym for `DataFrame.fillna()` with `method='ffill'`.

fillna(*value=None*, *method=None*, *limit=None*, *axis=None*)
Fill NA/NaN values using the specified method.

This docstring was copied from pandas.core.frame.DataFrame.fillna.

Some inconsistencies with the Dask version may exist.

Parameters

value [scalar, dict, Series, or DataFrame] Value to use to fill holes (e.g. 0), alternately a dict/Series/DataFrame of values specifying which value to use for each index (for a Series) or column (for a DataFrame). (values not in the dict/Series/DataFrame will not be filled). This value cannot be a list.

method [{'backfill', 'bfill', 'pad', 'ffill', None}, default None] Method to use for filling holes in reindexed Series pad / ffill: propagate last valid observation forward to next valid backfill / bfill: use NEXT valid observation to fill gap

axis [{0 or 'index', 1 or 'columns'}]

inplace [boolean, default False (Not supported in Dask)] If True, fill in place. Note: this will modify any other views on this object, (e.g. a no-copy slice for a column in a DataFrame).

limit [int, default None] If method is specified, this is the maximum number of consecutive NaN values to forward/backward fill. In other words, if there is a gap with more than this number of consecutive NaNs, it will only be partially filled. If method is not specified, this is the maximum number of entries along the entire axis where NaNs will be filled. Must be greater than 0 if not None.

downcast [dict, default is None (Not supported in Dask)] a dict of item->dtype of what to downcast if possible, or the string 'infer' which will try to downcast to an appropriate equal type (e.g. float64 to int64 if possible)

Returns

filled [DataFrame]

See also:

interpolate Fill NaN values using interpolation.

reindex, asfreq

Examples

```
>>> df = pd.DataFrame([[np.nan, 2, np.nan, 0],  # doctest: +SKIP
...                    [3, 4, np.nan, 1],
...                    [np.nan, np.nan, np.nan, 5],
...                    [np.nan, 3, np.nan, 4]],
...                    columns=list('ABCD'))
>>> df  # doctest: +SKIP
     A    B   C  D
0  NaN  2.0 NaN  0
1  3.0  4.0 NaN  1
2  NaN  NaN NaN  5
3  NaN  3.0 NaN  4
```

Replace all NaN elements with 0s.

```
>>> df.fillna(0)  # doctest: +SKIP
    A    B    C    D
0   0.0  2.0  0.0  0
1   3.0  4.0  0.0  1
2   0.0  0.0  0.0  5
3   0.0  3.0  0.0  4
```

We can also propagate non-null values forward or backward.

```
>>> df.fillna(method='ffill')  # doctest: +SKIP
    A    B    C    D
0   NaN  2.0  NaN  0
1   3.0  4.0  NaN  1
2   3.0  4.0  NaN  5
3   3.0  3.0  NaN  4
```

Replace all NaN elements in column 'A', 'B', 'C', and 'D', with 0, 1, 2, and 3 respectively.

```
>>> values = {'A': 0, 'B': 1, 'C': 2, 'D': 3}  # doctest: +SKIP
>>> df.fillna(value=values)  # doctest: +SKIP
    A    B    C    D
0   0.0  2.0  2.0  0
1   3.0  4.0  2.0  1
2   0.0  1.0  2.0  5
3   0.0  3.0  2.0  4
```

Only replace the first NaN element.

```
>>> df.fillna(value=values, limit=1)  # doctest: +SKIP
    A    B    C    D
0   0.0  2.0  2.0  0
1   3.0  4.0  NaN  1
2   NaN  1.0  NaN  5
3   NaN  3.0  NaN  4
```

first(*offset*)

Convenience method for subsetting initial periods of time series data based on a date offset.

This docstring was copied from pandas.core.frame.DataFrame.first.

Some inconsistencies with the Dask version may exist.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [same type as caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

last Select final periods of time series based on a date offset.

at_time Select values at a particular time of the day.

between_time Select values between particular times of the day.

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')  # doctest: +SKIP
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)  # doctest: +SKIP
>>> ts  # doctest: +SKIP
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the first 3 days:

```
>>> ts.first('3D')  # doctest: +SKIP
            A
2018-04-09  1
2018-04-11  2
```

Notice the data for 3 first calender days were returned, not the first 3 days observed in the dataset, and therefore data for 2018-04-13 was not returned.

floordiv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Integer division of dataframe and other, element-wise (binary operator *floordiv*).

Equivalent to `dataframe // other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rfloordiv*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod`	Calculate modulo (remainder after division).
`DataFrame.pow`	Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multiindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multiindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multiindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
```

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```
  triangle       1.0       1.0
  rectangle      1.0       1.0
B square         0.0       0.0
  pentagon       0.0       0.0
  hexagon        0.0       0.0
```

ge (*other*, *axis='columns'*, *level=None*)

Greater than or equal to of dataframe and other, element-wise (binary operator *ge*).

Among flexible wrappers (*eq*, *ne*, *le*, *lt*, *ge*, *gt*) to comparison operators.

Equivalent to ==, =!, <=, <, >=, > with support to choose axis (rows or columns) and level for comparison.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}, default 'columns'] Whether to compare by the index (0 or 'index') or columns (1 or 'columns').

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

Returns

DataFrame of bool Result of the comparison.

See also:

`DataFrame.eq` Compare DataFrames for equality elementwise.

`DataFrame.ne` Compare DataFrames for inequality elementwise.

`DataFrame.le` Compare DataFrames for less than inequality or equality elementwise.

`DataFrame.lt` Compare DataFrames for strictly less than inequality elementwise.

`DataFrame.ge` Compare DataFrames for greater than inequality or equality elementwise.

`DataFrame.gt` Compare DataFrames for strictly greater than inequality elementwise.

Notes

Mismatched indices will be unioned together. *NaN* values are considered different (i.e. *NaN* != *NaN*).

Examples

```
>>> df = pd.DataFrame({'cost': [250, 150, 100],  # doctest: +SKIP
...                    'revenue': [100, 250, 300]},
...                   index=['A', 'B', 'C'])
>>> df  # doctest: +SKIP
   cost  revenue
A   250      100
B   150      250
C   100      300
```

Comparison with a scalar, using either the operator or method:

```
>>> df == 100  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

```
>>> df.eq(100)  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

When *other* is a `Series`, the columns of a DataFrame are aligned with the index of *other* and broadcast:

```
>>> df != pd.Series([100, 250], index=["cost", "revenue"])  # doctest: +SKIP
    cost  revenue
A   True     True
B   True    False
C  False     True
```

Use the method to control the broadcast axis:

```
>>> df.ne(pd.Series([100, 300], index=["A", "D"]), axis='index')  # doctest:␣
↪+SKIP
   cost  revenue
A  True    False
B  True     True
C  True     True
D  True     True
```

When comparing to an arbitrary sequence, the number of columns must match the number elements in *other*:

```
>>> df == [250, 100]  # doctest: +SKIP
    cost  revenue
A   True     True
B  False    False
C  False    False
```

Use the method to control the axis:

```
>>> df.eq([250, 250, 100], axis='index')  # doctest: +SKIP
    cost  revenue
A   True    False
B  False     True
C   True    False
```

Compare to a DataFrame of different shape.

```
>>> other = pd.DataFrame({'revenue': [300, 250, 100, 150]},  # doctest: +SKIP
...                      index=['A', 'B', 'C', 'D'])
>>> other  # doctest: +SKIP
   revenue
A      300
B      250
C      100
D      150
```

```
>>> df.gt(other)  # doctest: +SKIP
     cost  revenue
A  False     False
B  False     False
C  False      True
D  False     False
```

Compare to a MultiIndex by level.

```
>>> df_multiindex = pd.DataFrame({'cost': [250, 150, 100, 150, 300, 220],   #␣
↪doctest: +SKIP
...                                'revenue': [100, 250, 300, 200, 175, 225]},
...                               index=[['Q1', 'Q1', 'Q1', 'Q2', 'Q2', 'Q2'],
...                                      ['A', 'B', 'C', 'A', 'B', 'C']])
>>> df_multiindex  # doctest: +SKIP
      cost  revenue
Q1 A   250      100
   B   150      250
   C   100      300
Q2 A   150      200
   B   300      175
   C   220      225
```

```
>>> df.le(df_multiindex, level=1)  # doctest: +SKIP
       cost  revenue
Q1 A   True     True
   B   True     True
   C   True     True
Q2 A  False     True
   B   True    False
   C   True    False
```

get_dtype_counts()

Return counts of unique dtypes in this object.

This docstring was copied from pandas.core.frame.DataFrame.get_dtype_counts.

Some inconsistencies with the Dask version may exist.

Returns

dtype [Series] Series with the count of columns with each dtype.

See also:

dtypes Return the dtypes in this object.

Examples

```
>>> a = [['a', 1, 1.0], ['b', 2, 2.0], ['c', 3, 3.0]]  # doctest: +SKIP
>>> df = pd.DataFrame(a, columns=['str', 'int', 'float'])  # doctest: +SKIP
>>> df  # doctest: +SKIP
  str  int  float
0   a    1    1.0
1   b    2    2.0
2   c    3    3.0
```

```
>>> df.get_dtype_counts()  # doctest: +SKIP
float64    1
int64      1
object     1
dtype: int64
```

get_ftype_counts()

Return counts of unique ftypes in this object.

This docstring was copied from pandas.core.frame.DataFrame.get_ftype_counts.

Some inconsistencies with the Dask version may exist.

Deprecated since version 0.23.0.

This is useful for SparseDataFrame or for DataFrames containing sparse arrays.

Returns

dtype [Series] Series with the count of columns with each type and sparsity (dense/sparse)

See also:

ftypes Return ftypes (indication of sparse/dense and dtype) in this object.

Examples

```
>>> a = [['a', 1, 1.0], ['b', 2, 2.0], ['c', 3, 3.0]]  # doctest: +SKIP
>>> df = pd.DataFrame(a, columns=['str', 'int', 'float'])  # doctest: +SKIP
>>> df  # doctest: +SKIP
  str  int  float
0   a    1    1.0
1   b    2    2.0
2   c    3    3.0
```

```
>>> df.get_ftype_counts()  # doctest: +SKIP
float64:dense    1
int64:dense      1
object:dense     1
dtype: int64
```

get_partition(*n*)

Get a dask DataFrame/Series representing the *nth* partition.

groupby(*by=None*, ***kwargs*)

Group DataFrame or Series using a mapper or by a Series of columns.

This docstring was copied from pandas.core.frame.DataFrame.groupby.

Some inconsistencies with the Dask version may exist.

A groupby operation involves some combination of splitting the object, applying a function, and combining the results. This can be used to group large amounts of data and compute operations on these groups.

Parameters

by [mapping, function, label, or list of labels] Used to determine the groups for the groupby. If `by` is a function, it's called on each value of the object's index. If a dict or Series is passed, the Series or dict VALUES will be used to determine the groups (the Series' values are first aligned; see `.align()` method). If an ndarray is passed, the values are used as-is determine the groups. A label or list of labels may be passed to group by the columns in `self`. Notice that a tuple is interpreted a (single) key.

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Split along rows (0) or columns (1).

level [int, level name, or sequence of such, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), group by a particular level or levels.

as_index [bool, default True (Not supported in Dask)] For aggregated output, return object with group labels as the index. Only relevant for DataFrame input. as_index=False is effectively "SQL-style" grouped output.

sort [bool, default True (Not supported in Dask)] Sort group keys. Get better performance by turning this off. Note this does not influence the order of observations within each group. Groupby preserves the order of rows within each group.

group_keys [bool, default True (Not supported in Dask)] When calling apply, add group keys to index to identify pieces.

squeeze [bool, default False (Not supported in Dask)] Reduce the dimensionality of the return type if possible, otherwise return a consistent type.

observed [bool, default False (Not supported in Dask)] This only applies if any of the groupers are Categoricals. If True: only show observed values for categorical groupers. If False: show all values for categorical groupers.

New in version 0.23.0.

****kwargs** Optional, only accepts keyword argument 'mutated' and is passed to groupby.

Returns

DataFrameGroupBy or SeriesGroupBy Depends on the calling object and returns groupby object that contains information about the groups.

See also:

`resample` Convenience method for frequency conversion and resampling of time series.

Notes

See the user guide for more.

Examples

```
>>> df = pd.DataFrame({'Animal' : ['Falcon', 'Falcon',  # doctest: +SKIP
...                               'Parrot', 'Parrot'],
...                     'Max Speed' : [380., 370., 24., 26.]})
>>> df  # doctest: +SKIP
   Animal  Max Speed
0  Falcon      380.0
1  Falcon      370.0
2  Parrot       24.0
3  Parrot       26.0
```

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```
>>> df.groupby(['Animal']).mean()  # doctest: +SKIP
        Max Speed
Animal
Falcon      375.0
Parrot       25.0
```

Hierarchical Indexes

We can groupby different levels of a hierarchical index using the *level* parameter:

```
>>> arrays = [['Falcon', 'Falcon', 'Parrot', 'Parrot'],  # doctest: +SKIP
...           ['Capitve', 'Wild', 'Capitve', 'Wild']]
>>> index = pd.MultiIndex.from_arrays(arrays, names=('Animal', 'Type'))  #␣
↪doctest: +SKIP
>>> df = pd.DataFrame({'Max Speed' : [390., 350., 30., 20.]},  # doctest:␣
↪+SKIP
...                   index=index)
>>> df  # doctest: +SKIP
                Max Speed
Animal Type
Falcon Capitve      390.0
       Wild         350.0
Parrot Capitve       30.0
       Wild          20.0
>>> df.groupby(level=0).mean()  # doctest: +SKIP
        Max Speed
Animal
Falcon      370.0
Parrot       25.0
>>> df.groupby(level=1).mean()  # doctest: +SKIP
         Max Speed
Type
Capitve      210.0
Wild         185.0
```

gt (*other*, *axis='columns'*, *level=None*)

Greater than of dataframe and other, element-wise (binary operator *gt*).

Among flexible wrappers (*eq*, *ne*, *le*, *lt*, *ge*, *gt*) to comparison operators.

Equivalent to ==, =!, <=, <, >=, > with support to choose axis (rows or columns) and level for comparison.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}, default 'columns'] Whether to compare by the index (0 or 'index') or columns (1 or 'columns').

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

Returns

DataFrame of bool Result of the comparison.

See also:

`DataFrame.eq`	Compare DataFrames for equality elementwise.
`DataFrame.ne`	Compare DataFrames for inequality elementwise.
`DataFrame.le`	Compare DataFrames for less than inequality or equality elementwise.
`DataFrame.lt`	Compare DataFrames for strictly less than inequality elementwise.
`DataFrame.ge`	Compare DataFrames for greater than inequality or equality elementwise.
`DataFrame.gt`	Compare DataFrames for strictly greater than inequality elementwise.

Notes

Mismatched indices will be unioned together. *NaN* values are considered different (i.e. *NaN* != *NaN*).

Examples

```
>>> df = pd.DataFrame({'cost': [250, 150, 100],  # doctest: +SKIP
...                    'revenue': [100, 250, 300]},
...                   index=['A', 'B', 'C'])
>>> df  # doctest: +SKIP
   cost  revenue
A   250      100
B   150      250
C   100      300
```

Comparison with a scalar, using either the operator or method:

```
>>> df == 100  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

```
>>> df.eq(100)  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

When *other* is a `Series`, the columns of a DataFrame are aligned with the index of *other* and broadcast:

```
>>> df != pd.Series([100, 250], index=["cost", "revenue"])  # doctest: +SKIP
    cost  revenue
A   True     True
B   True    False
C  False     True
```

Use the method to control the broadcast axis:

```
>>> df.ne(pd.Series([100, 300], index=["A", "D"]), axis='index')  # doctest:␣
↪+SKIP
   cost  revenue
A  True    False
B  True     True
```

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```
C   True      True
D   True      True
```

When comparing to an arbitrary sequence, the number of columns must match the number elements in *other*:

```
>>> df == [250, 100]  # doctest: +SKIP
    cost  revenue
A   True     True
B  False    False
C  False    False
```

Use the method to control the axis:

```
>>> df.eq([250, 250, 100], axis='index')  # doctest: +SKIP
    cost  revenue
A   True    False
B  False     True
C   True    False
```

Compare to a DataFrame of different shape.

```
>>> other = pd.DataFrame({'revenue': [300, 250, 100, 150]},  # doctest: +SKIP
...                      index=['A', 'B', 'C', 'D'])
>>> other  # doctest: +SKIP
   revenue
A      300
B      250
C      100
D      150
```

```
>>> df.gt(other)  # doctest: +SKIP
    cost  revenue
A  False    False
B  False    False
C  False     True
D  False    False
```

Compare to a MultiIndex by level.

```
>>> df_multiindex = pd.DataFrame({'cost': [250, 150, 100, 150, 300, 220],  #␣
↪doctest: +SKIP
...                              'revenue': [100, 250, 300, 200, 175, 225]},
...                             index=[['Q1', 'Q1', 'Q1', 'Q2', 'Q2', 'Q2'],
...                                    ['A', 'B', 'C', 'A', 'B', 'C']])
>>> df_multiindex  # doctest: +SKIP
      cost  revenue
Q1 A   250      100
   B   150      250
   C   100      300
Q2 A   150      200
   B   300      175
   C   220      225
```

```
>>> df.le(df_multiindex, level=1)  # doctest: +SKIP
       cost  revenue
```

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```
Q1 A   True     True
   B   True     True
   C   True     True
Q2 A  False     True
   B   True    False
   C   True    False
```

head(*n=5*, *npartitions=1*, *compute=True*)

First n rows of the dataset

Parameters

n [int, optional] The number of rows to return. Default is 5.

npartitions [int, optional] Elements are only taken from the first `npartitions`, with a default of 1. If there are fewer than `n` rows in the first `npartitions` a warning will be raised and any found rows returned. Pass -1 to use all partitions.

compute [bool, optional] Whether to compute the result, default is True.

idxmax(*axis=None*, *skipna=True*, *split_every=False*)

Return index of first occurrence of maximum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmax.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmax [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmax

Notes

This method is the DataFrame version of `ndarray.argmax`.

idxmin(*axis=None*, *skipna=True*, *split_every=False*)

Return index of first occurrence of minimum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmin.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmin [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmin

Notes

This method is the DataFrame version of `ndarray.argmin`.

iloc

Purely integer-location based indexing for selection by position.

Only indexing the column positions is supported. Trying to select row positions will raise a ValueError.

See *Indexing into Dask DataFrames* for more.

Examples

```
>>> df.iloc[:, [2, 0, 1]]  # doctest: +SKIP
```

index

Return dask Index instance

info(*buf=None*, *verbose=False*, *memory_usage=False*)

Concise summary of a Dask DataFrame.

isin(*values*)

Whether each element in the DataFrame is contained in values.

This docstring was copied from pandas.core.frame.DataFrame.isin.

Some inconsistencies with the Dask version may exist.

Parameters

values [iterable, Series, DataFrame or dict] The result will only be true at a location if all the labels match. If *values* is a Series, that's the index. If *values* is a dict, the keys must be the column names, which must match. If *values* is a DataFrame, then both the index and column labels must match.

Returns

DataFrame DataFrame of booleans showing whether each element in the DataFrame is contained in values.

See also:

DataFrame.eq Equality test for DataFrame.

Series.isin Equivalent method on Series.

Series.str.contains Test if pattern or regex is contained within a string of a Series or Index.

Examples

```
>>> df = pd.DataFrame({'num_legs': [2, 4], 'num_wings': [2, 0]},  # doctest:␣
↪+SKIP
...                   index=['falcon', 'dog'])
>>> df  # doctest: +SKIP
        num_legs  num_wings
falcon         2          2
dog            4          0
```

When `values` is a list check whether every value in the DataFrame is present in the list (which animals have 0 or 2 legs or wings)

```
>>> df.isin([0, 2])  # doctest: +SKIP
        num_legs  num_wings
falcon      True       True
dog        False       True
```

When `values` is a dict, we can pass values to check for each column separately:

```
>>> df.isin({'num_wings': [0, 3]})  # doctest: +SKIP
        num_legs  num_wings
falcon     False      False
dog        False       True
```

When `values` is a Series or DataFrame the index and column must match. Note that 'falcon' does not match based on the number of legs in df2.

```
>>> other = pd.DataFrame({'num_legs': [8, 2],'num_wings': [0, 2]},  #␣
↪doctest: +SKIP
...                      index=['spider', 'falcon'])
>>> df.isin(other)  # doctest: +SKIP
        num_legs  num_wings
falcon      True       True
dog        False      False
```

isna()

Detect missing values.

This docstring was copied from pandas.core.frame.DataFrame.isna.

Some inconsistencies with the Dask version may exist.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.isnull Alias of isna.

DataFrame.notna Boolean inverse of isna.

DataFrame.dropna Omit axes labels with missing values.

isna Top-level isna.

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],  # doctest: +SKIP
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df  # doctest: +SKIP
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.isna()  # doctest: +SKIP
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()  # doctest: +SKIP
0    False
1    False
2     True
dtype: bool
```

isnull()

Detect missing values.

This docstring was copied from pandas.core.frame.DataFrame.isnull.

Some inconsistencies with the Dask version may exist.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

`DataFrame.isnull` Alias of isna.

`DataFrame.notna` Boolean inverse of isna.

`DataFrame.dropna` Omit axes labels with missing values.

`isna` Top-level isna.

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],  # doctest: +SKIP
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df  # doctest: +SKIP
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.isna()  # doctest: +SKIP
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()  # doctest: +SKIP
0    False
1    False
2     True
dtype: bool
```

`iterrows``()`

Iterate over DataFrame rows as (index, Series) pairs.

This docstring was copied from pandas.core.frame.DataFrame.iterrows.

Some inconsistencies with the Dask version may exist.

Yields

index [label or tuple of label] The index of the row. A tuple for a *MultiIndex*.

data [Series] The data of the row as a Series.

it [generator] A generator that iterates over the rows of the frame.

See also:

itertuples Iterate over DataFrame rows as namedtuples of the values.

iteritems Iterate over (column name, Series) pairs.

Notes

1. Because `iterrows` returns a Series for each row, it does **not** preserve dtypes across the rows (dtypes are preserved across columns for DataFrames). For example,

```
>>> df = pd.DataFrame([[1, 1.5]], columns=['int', 'float'])  # doctest:␣
↪+SKIP
>>> row = next(df.iterrows())[1]  # doctest: +SKIP
>>> row  # doctest: +SKIP
int      1.0
float    1.5
Name: 0, dtype: float64
>>> print(row['int'].dtype)  # doctest: +SKIP
float64
>>> print(df['int'].dtype)  # doctest: +SKIP
int64
```

   To preserve dtypes while iterating over the rows, it is better to use *itertuples()* which returns namedtuples of the values and which is generally faster than `iterrows`.

2. You should **never modify** something you are iterating over. This is not guaranteed to work in all cases. Depending on the data types, the iterator returns a copy and not a view, and writing to it will have no effect.

itertuples(*index=True*, *name='Pandas'*)

Iterate over DataFrame rows as namedtuples.

This docstring was copied from pandas.core.frame.DataFrame.itertuples.

Some inconsistencies with the Dask version may exist.

Parameters

index [bool, default True] If True, return the index as the first element of the tuple.

name [str or None, default "Pandas"] The name of the returned namedtuples or None to return regular tuples.

Yields

collections.namedtuple Yields a namedtuple for each row in the DataFrame with the first field possibly being the index and following fields being the column values.

See also:

DataFrame.iterrows Iterate over DataFrame rows as (index, Series) pairs.

DataFrame.iteritems Iterate over (column name, Series) pairs.

Notes

The column names will be renamed to positional names if they are invalid Python identifiers, repeated, or start with an underscore. With a large number of columns (>255), regular tuples are returned.

Examples

```
>>> df = pd.DataFrame({'num_legs': [4, 2], 'num_wings': [0, 2]},  # doctest:␣
↪+SKIP
...                   index=['dog', 'hawk'])
>>> df  # doctest: +SKIP
      num_legs  num_wings
dog          4          0
hawk         2          2
>>> for row in df.itertuples():  # doctest: +SKIP
...     print(row)
...
Pandas(Index='dog', num_legs=4, num_wings=0)
Pandas(Index='hawk', num_legs=2, num_wings=2)
```

By setting the *index* parameter to False we can remove the index as the first element of the tuple:

```
>>> for row in df.itertuples(index=False):  # doctest: +SKIP
...     print(row)
...
Pandas(num_legs=4, num_wings=0)
Pandas(num_legs=2, num_wings=2)
```

With the *name* parameter set we set a custom name for the yielded namedtuples:

```
>>> for row in df.itertuples(name='Animal'):  # doctest: +SKIP
...     print(row)
...
Animal(Index='dog', num_legs=4, num_wings=0)
Animal(Index='hawk', num_legs=2, num_wings=2)
```

join(*other*, *on=None*, *how='left'*, *lsuffix=''*, *rsuffix=''*, *npartitions=None*, *shuffle=None*)
Join columns of another DataFrame.

This docstring was copied from pandas.core.frame.DataFrame.join.

Some inconsistencies with the Dask version may exist.

Join columns with *other* DataFrame either on index or on a key column. Efficiently join multiple DataFrame objects by index at once by passing a list.

Parameters

other [DataFrame, Series, or list of DataFrame] Index should be similar to one of the columns in this one. If a Series is passed, its name attribute must be set, and that will be used as the column name in the resulting joined DataFrame.

on [str, list of str, or array-like, optional] Column or index level name(s) in the caller to join on the index in *other*, otherwise joins index-on-index. If multiple values given, the *other* DataFrame must have a MultiIndex. Can pass an array as the join key if it is not already contained in the calling DataFrame. Like an Excel VLOOKUP operation.

how [{'left', 'right', 'outer', 'inner'}, default 'left'] How to handle the operation of the two objects.

- left: use calling frame's index (or column if on is specified)
- right: use *other*'s index.
- outer: form union of calling frame's index (or column if on is specified) with *other*'s index, and sort it. lexicographically.
- inner: form intersection of calling frame's index (or column if on is specified) with *other*'s index, preserving the order of the calling's one.

lsuffix [str, default ''] Suffix to use from left frame's overlapping columns.

rsuffix [str, default ''] Suffix to use from right frame's overlapping columns.

sort [bool, default False (Not supported in Dask)] Order result DataFrame lexicographically by the join key. If False, the order of the join key depends on the join type (how keyword).

Returns

DataFrame A dataframe containing columns from both the caller and *other*.

See also:

`DataFrame.merge` For column(s)-on-columns(s) operations.

Notes

Parameters *on*, *lsuffix*, and *rsuffix* are not supported when passing a list of *DataFrame* objects.

Support for specifying index levels as the *on* parameter was added in version 0.23.0.

Examples

```
>>> df = pd.DataFrame({'key': ['K0', 'K1', 'K2', 'K3', 'K4', 'K5'],  #␣
↪doctest: +SKIP
...                    'A': ['A0', 'A1', 'A2', 'A3', 'A4', 'A5']})
```

```
>>> df  # doctest: +SKIP
  key   A
0  K0  A0
1  K1  A1
2  K2  A2
3  K3  A3
4  K4  A4
5  K5  A5
```

```
>>> other = pd.DataFrame({'key': ['K0', 'K1', 'K2'],  # doctest: +SKIP
...                       'B': ['B0', 'B1', 'B2']})
```

```
>>> other  # doctest: +SKIP
  key   B
0  K0  B0
1  K1  B1
2  K2  B2
```

Join DataFrames using their indexes.

```
>>> df.join(other, lsuffix='_caller', rsuffix='_other')  # doctest: +SKIP
  key_caller   A key_other    B
0         K0  A0        K0   B0
1         K1  A1        K1   B1
2         K2  A2        K2   B2
3         K3  A3       NaN  NaN
4         K4  A4       NaN  NaN
5         K5  A5       NaN  NaN
```

If we want to join using the key columns, we need to set key to be the index in both *df* and *other*. The joined DataFrame will have key as its index.

```
>>> df.set_index('key').join(other.set_index('key'))  # doctest: +SKIP
      A    B
key
K0   A0   B0
K1   A1   B1
K2   A2   B2
K3   A3  NaN
K4   A4  NaN
K5   A5  NaN
```

Another option to join using the key columns is to use the *on* parameter. DataFrame.join always uses *other*'s index but we can use any column in *df*. This method preserves the original DataFrame's index in the result.

```
>>> df.join(other.set_index('key'), on='key')  # doctest: +SKIP
  key   A    B
0  K0  A0   B0
1  K1  A1   B1
2  K2  A2   B2
3  K3  A3  NaN
4  K4  A4  NaN
5  K5  A5  NaN
```

known_divisions
Whether divisions are already known

last (*offset*)
Convenience method for subsetting final periods of time series data based on a date offset.

This docstring was copied from pandas.core.frame.DataFrame.last.

Some inconsistencies with the Dask version may exist.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [same type as caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

first Select initial periods of time series based on a date offset.

at_time Select values at a particular time of the day.

between_time Select values between particular times of the day.

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')  # doctest: +SKIP
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)  # doctest: +SKIP
>>> ts  # doctest: +SKIP
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the last 3 days:

```
>>> ts.last('3D')  # doctest: +SKIP
            A
2018-04-13  3
2018-04-15  4
```

Notice the data for 3 last calender days were returned, not the last 3 observed days in the dataset, and therefore data for 2018-04-11 was not returned.

le(*other*, *axis='columns'*, *level=None*)

Less than or equal to of dataframe and other, element-wise (binary operator *le*).

Among flexible wrappers (*eq*, *ne*, *le*, *lt*, *ge*, *gt*) to comparison operators.

Equivalent to ==, =!, <=, <, >=, > with support to choose axis (rows or columns) and level for comparison.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}, default 'columns'] Whether to compare by the index (0 or 'index') or columns (1 or 'columns').

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

Returns

DataFrame of bool Result of the comparison.

See also:

DataFrame.eq Compare DataFrames for equality elementwise.

DataFrame.ne Compare DataFrames for inequality elementwise.

DataFrame.le Compare DataFrames for less than inequality or equality elementwise.

DataFrame.lt Compare DataFrames for strictly less than inequality elementwise.

DataFrame.ge Compare DataFrames for greater than inequality or equality elementwise.

DataFrame.gt Compare DataFrames for strictly greater than inequality elementwise.

Notes

Mismatched indices will be unioned together. *NaN* values are considered different (i.e. *NaN* != *NaN*).

Examples

```
>>> df = pd.DataFrame({'cost': [250, 150, 100],   # doctest: +SKIP
...                    'revenue': [100, 250, 300]},
...                   index=['A', 'B', 'C'])
>>> df  # doctest: +SKIP
   cost  revenue
A   250      100
B   150      250
C   100      300
```

Comparison with a scalar, using either the operator or method:

```
>>> df == 100  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

```
>>> df.eq(100)  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

When *other* is a `Series`, the columns of a DataFrame are aligned with the index of *other* and broadcast:

```
>>> df != pd.Series([100, 250], index=["cost", "revenue"])  # doctest: +SKIP
    cost  revenue
A   True     True
B   True    False
C  False     True
```

Use the method to control the broadcast axis:

```
>>> df.ne(pd.Series([100, 300], index=["A", "D"]), axis='index')  # doctest:␣
↪+SKIP
   cost  revenue
A  True    False
B  True     True
C  True     True
D  True     True
```

When comparing to an arbitrary sequence, the number of columns must match the number elements in *other*:

```
>>> df == [250, 100]  # doctest: +SKIP
    cost  revenue
A   True     True
B  False    False
C  False    False
```

Use the method to control the axis:

```
>>> df.eq([250, 250, 100], axis='index')  # doctest: +SKIP
    cost  revenue
A   True    False
B  False     True
C   True    False
```

Compare to a DataFrame of different shape.

```
>>> other = pd.DataFrame({'revenue': [300, 250, 100, 150]},  # doctest: +SKIP
...                      index=['A', 'B', 'C', 'D'])
>>> other  # doctest: +SKIP
   revenue
A      300
B      250
C      100
D      150
```

```
>>> df.gt(other)  # doctest: +SKIP
    cost  revenue
A  False    False
B  False    False
C  False     True
D  False    False
```

Compare to a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'cost': [250, 150, 100, 150, 300, 220],  #␣
↪doctest: +SKIP
...                              'revenue': [100, 250, 300, 200, 175, 225]},
...                             index=[['Q1', 'Q1', 'Q1', 'Q2', 'Q2', 'Q2'],
...                                    ['A', 'B', 'C', 'A', 'B', 'C']])
>>> df_multindex  # doctest: +SKIP
      cost  revenue
Q1 A   250      100
   B   150      250
   C   100      300
Q2 A   150      200
   B   300      175
   C   220      225
```

```
>>> df.le(df_multindex, level=1)  # doctest: +SKIP
       cost  revenue
Q1 A   True     True
   B   True     True
   C   True     True
Q2 A  False     True
   B   True    False
   C   True    False
```

loc

Purely label-location based indexer for selection by label.

```
>>> df.loc["b"]  # doctest: +SKIP
>>> df.loc["b":"d"]  # doctest: +SKIP
```

lt(*other*, *axis='columns'*, *level=None*)

Less than of dataframe and other, element-wise (binary operator *lt*).

Among flexible wrappers (*eq*, *ne*, *le*, *lt*, *ge*, *gt*) to comparison operators.

Equivalent to ==, =!, <=, <, >=, > with support to choose axis (rows or columns) and level for comparison.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}, default 'columns'] Whether to compare by the index (0 or 'index') or columns (1 or 'columns').

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

Returns

DataFrame of bool Result of the comparison.

See also:

`DataFrame.eq`	Compare DataFrames for equality elementwise.
`DataFrame.ne`	Compare DataFrames for inequality elementwise.
`DataFrame.le`	Compare DataFrames for less than inequality or equality elementwise.
`DataFrame.lt`	Compare DataFrames for strictly less than inequality elementwise.
`DataFrame.ge`	Compare DataFrames for greater than inequality or equality elementwise.
`DataFrame.gt`	Compare DataFrames for strictly greater than inequality elementwise.

Notes

Mismatched indices will be unioned together. *NaN* values are considered different (i.e. *NaN* != *NaN*).

Examples

```
>>> df = pd.DataFrame({'cost': [250, 150, 100],   # doctest: +SKIP
...                    'revenue': [100, 250, 300]},
...                   index=['A', 'B', 'C'])
>>> df  # doctest: +SKIP
   cost  revenue
A   250      100
B   150      250
C   100      300
```

Comparison with a scalar, using either the operator or method:

```
>>> df == 100  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

```
>>> df.eq(100)  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

When *other* is a `Series`, the columns of a DataFrame are aligned with the index of *other* and broadcast:

```
>>> df != pd.Series([100, 250], index=["cost", "revenue"])  # doctest: +SKIP
    cost  revenue
A   True     True
B   True    False
C  False     True
```

Use the method to control the broadcast axis:

```
>>> df.ne(pd.Series([100, 300], index=["A", "D"]), axis='index')  # doctest:␣
↪+SKIP
   cost  revenue
A  True    False
B  True     True
C  True     True
D  True     True
```

When comparing to an arbitrary sequence, the number of columns must match the number elements in *other*:

```
>>> df == [250, 100]  # doctest: +SKIP
    cost  revenue
A   True     True
B  False    False
C  False    False
```

Use the method to control the axis:

```
>>> df.eq([250, 250, 100], axis='index')  # doctest: +SKIP
    cost  revenue
A   True    False
B  False     True
C   True    False
```

Compare to a DataFrame of different shape.

```
>>> other = pd.DataFrame({'revenue': [300, 250, 100, 150]},  # doctest: +SKIP
...                      index=['A', 'B', 'C', 'D'])
>>> other  # doctest: +SKIP
   revenue
A      300
B      250
C      100
D      150
```

```
>>> df.gt(other)  # doctest: +SKIP
    cost  revenue
A  False    False
B  False    False
```

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```
C  False     True
D  False    False
```

Compare to a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'cost': [250, 150, 100, 150, 300, 220],  #␣
↪doctest: +SKIP
...                              'revenue': [100, 250, 300, 200, 175, 225]},
...                             index=[['Q1', 'Q1', 'Q1', 'Q2', 'Q2', 'Q2'],
...                                    ['A', 'B', 'C', 'A', 'B', 'C']])
>>> df_multindex  # doctest: +SKIP
      cost  revenue
Q1 A   250      100
   B   150      250
   C   100      300
Q2 A   150      200
   B   300      175
   C   220      225
```

```
>>> df.le(df_multindex, level=1)  # doctest: +SKIP
       cost  revenue
Q1 A   True     True
   B   True     True
   C   True     True
Q2 A  False     True
   B   True    False
   C   True    False
```

map_overlap (*func*, *before*, *after*, **args*, ***kwargs*)

Apply a function to each partition, sharing rows with adjacent partitions.

This can be useful for implementing windowing functions such as `df.rolling(...).mean()` or `df.diff()`.

Parameters

func [function] Function applied to each partition.

before [int] The number of rows to prepend to partition `i` from the end of partition `i - 1`.

after [int] The number of rows to append to partition `i` from the beginning of partition `i + 1`.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Notes

Given positive integers before and after, and a function func, map_overlap does the following:

1. Prepend before rows to each partition i from the end of partition i - 1. The first partition has no rows prepended.
2. Append after rows to each partition i from the beginning of partition i + 1. The last partition has no rows appended.
3. Apply func to each partition, passing in any extra args and kwargs if provided.
4. Trim before rows from the beginning of all but the first partition.
5. Trim after rows from the end of all but the last partition.

Note that the index and divisions are assumed to remain unchanged.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 4, 7, 11],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

A rolling sum with a trailing moving window of size 2 can be computed by overlapping 2 rows before each partition, and then mapping calls to df.rolling(2).sum():

```
>>> ddf.compute()
    x    y
0   1  1.0
1   2  2.0
2   4  3.0
3   7  4.0
4  11  5.0
>>> ddf.map_overlap(lambda df: df.rolling(2).sum(), 2, 0).compute()
      x    y
0   NaN  NaN
1   3.0  3.0
2   6.0  5.0
3  11.0  7.0
4  18.0  9.0
```

The pandas diff method computes a discrete difference shifted by a number of periods (can be positive or negative). This can be implemented by mapping calls to df.diff to each partition after prepending/appending that many rows, depending on sign:

```
>>> def diff(df, periods=1):
...     before, after = (periods, 0) if periods > 0 else (0, -periods)
...     return df.map_overlap(lambda df, periods=1: df.diff(periods),
...                           periods, 0, periods=periods)
>>> diff(ddf, 1).compute()
     x    y
0  NaN  NaN
1  1.0  1.0
2  2.0  1.0
```

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```
3  3.0  1.0
4  4.0  1.0
```

If you have a `DatetimeIndex`, you can use a `pd.Timedelta` for time- based windows.

```
>>> ts = pd.Series(range(10), index=pd.date_range('2017', periods=10))
>>> dts = dd.from_pandas(ts, npartitions=2)
>>> dts.map_overlap(lambda df: df.rolling('2D').sum(),
...                 pd.Timedelta('2D'), 0).compute()
2017-01-01     0.0
2017-01-02     1.0
2017-01-03     3.0
2017-01-04     5.0
2017-01-05     7.0
2017-01-06     9.0
2017-01-07    11.0
2017-01-08    13.0
2017-01-09    15.0
2017-01-10    17.0
dtype: float64
```

map_partitions (*func*, **args*, ***kwargs*)

Apply Python function on each DataFrame partition.

Note that the index and divisions are assumed to remain unchanged.

Parameters

func [function] Function applied to each partition.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*. Arguments and keywords may contain `Scalar`, `Delayed` or regular python objects. DataFrame-like args (both dask and pandas) will be repartitioned to align (if necessary) before applying the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 3, 4, 5],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

One can use `map_partitions` to apply a function on each partition. Extra arguments and keywords can optionally be provided, and will be passed to the function after the partition.

Here we apply a function with arguments and keywords to a DataFrame, resulting in a Series:

```
>>> def myadd(df, a, b=1):
...     return df.x + df.y + a + b
>>> res = ddf.map_partitions(myadd, 1, b=2)
>>> res.dtype
dtype('float64')
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with no name, and dtype `float64`:

```
>>> res = ddf.map_partitions(myadd, 1, b=2, meta=(None, 'f8'))
```

Here we map a function that takes in a DataFrame, and returns a DataFrame with a new column:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y))
>>> res.dtypes
x      int64
y    float64
z    float64
dtype: object
```

As before, the output metadata can also be specified manually. This time we pass in a `dict`, as the output is a DataFrame:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y),
...                          meta={'x': 'i8', 'y': 'f8', 'z': 'f8'})
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ddf.map_partitions(lambda df: df.head(), meta=df)
```

Also note that the index and divisions are assumed to remain unchanged. If the function you're mapping changes the index/divisions, you'll need to clear them afterwards:

```
>>> ddf.map_partitions(func).clear_divisions()  # doctest: +SKIP
```

mask(*cond*, *other=nan*)
Replace values where the condition is True.

This docstring was copied from pandas.core.frame.DataFrame.mask.

Some inconsistencies with the Dask version may exist.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is False, keep the original value. Where True, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is True are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

axis [int, default None (Not supported in Dask)] Alignment axis if needed.

level [int, default None (Not supported in Dask)] Alignment level if needed.

errors [str, {'raise', 'ignore'}, default *raise* (Not supported in Dask)] Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

- *raise* : allow exceptions to be raised.
- *ignore* : suppress exceptions. On error return original object.

try_cast [boolean, default False (Not supported in Dask)] Try to cast the result back to the input type (if possible).

raise_on_error [boolean, default True (Not supported in Dask)] Whether to raise on invalid data types (e.g. trying to where on strings).

Deprecated since version 0.21.0: Use *errors*.

Returns

wh [same type as caller]

See also:

`DataFrame.where()` Return an object of same shape as self.

Notes

The mask method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `False` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for `DataFrame.where()` differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `mask` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))  # doctest: +SKIP
>>> s.where(s > 0)  # doctest: +SKIP
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
dtype: float64
```

```
>>> s.mask(s > 0)  # doctest: +SKIP
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

```
>>> s.where(s > 1, 10)  # doctest: +SKIP
0    10
1    10
2    2
3    3
4    4
dtype: int64
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])  #␣
↪doctest: +SKIP
>>> m = df % 3 == 0  # doctest: +SKIP
>>> df.where(m, -df)  # doctest: +SKIP
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)  # doctest: +SKIP
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)  # doctest: +SKIP
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
```

max(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return the maximum of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.max.

Some inconsistencies with the Dask version may exist.

If you want the *index* of the maximum, use `idxmax`. This is the equivalent of the `numpy.ndarray` method `argmax`.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

max [Series or DataFrame (if level specified)]

See also:

`Series.sum` Return the sum.

`Series.min` Return the minimum.

`Series.max` Return the maximum.

`Series.idxmin` Return the index of the minimum.

`Series.idxmax` Return the index of the maximum.

`DataFrame.min` Return the sum over the requested axis.

`DataFrame.min` Return the minimum over the requested axis.

`DataFrame.max` Return the maximum over the requested axis.

`DataFrame.idxmin` Return the index of the minimum over the requested axis.

`DataFrame.idxmax` Return the index of the maximum over the requested axis.

Examples

```
>>> idx = pd.MultiIndex.from_arrays([  # doctest: +SKIP
...     ['warm', 'warm', 'cold', 'cold'],
...     ['dog', 'falcon', 'fish', 'spider']],
...     names=['blooded', 'animal'])
>>> s = pd.Series([4, 2, 0, 8], name='legs', index=idx)  # doctest: +SKIP
>>> s  # doctest: +SKIP
blooded  animal
warm     dog       4
         falcon    2
cold     fish      0
         spider    8
Name: legs, dtype: int64
```

```
>>> s.max()  # doctest: +SKIP
8
```

Max using level names, as well as indices.

```
>>> s.max(level='blooded')  # doctest: +SKIP
blooded
warm    4
cold    8
Name: legs, dtype: int64
```

```
>>> s.max(level=0)  # doctest: +SKIP
blooded
warm    4
cold    8
Name: legs, dtype: int64
```

mean(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)
Return the mean of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.mean.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

mean [Series or DataFrame (if level specified)]

melt(*id_vars=None*, *value_vars=None*, *var_name=None*, *value_name='value'*, *col_level=None*)
Unpivots a DataFrame from wide format to long format, optionally leaving identifier variables set.

This function is useful to massage a DataFrame into a format where one or more columns are identifier variables (`id_vars`), while all other columns, considered measured variables (`value_vars`), are "unpivoted" to the row axis, leaving just two non-identifier columns, 'variable' and 'value'.

Parameters

frame [DataFrame]

id_vars [tuple, list, or ndarray, optional] Column(s) to use as identifier variables.

value_vars [tuple, list, or ndarray, optional] Column(s) to unpivot. If not specified, uses all columns that are not set as *id_vars*.

var_name [scalar] Name to use for the 'variable' column. If None it uses `frame.columns.name` or 'variable'.

value_name [scalar, default 'value'] Name to use for the 'value' column.

col_level [int or string, optional] If columns are a MultiIndex then use this level to melt.

Returns

DataFrame Unpivoted DataFrame.

See also:

`pandas.DataFrame.melt`

memory_usage(*index=True*, *deep=False*)
Return the memory usage of each column in bytes.

This docstring was copied from pandas.core.frame.DataFrame.memory_usage.

Some inconsistencies with the Dask version may exist.

The memory usage can optionally include the contribution of the index and elements of *object* dtype.

This value is displayed in *DataFrame.info* by default. This can be suppressed by setting `pandas.options.display.memory_usage` to False.

Parameters

index [bool, default True] Specifies whether to include the memory usage of the DataFrame's index in returned Series. If `index=True` the memory usage of the index the first item in the output.

deep [bool, default False] If True, introspect the data deeply by interrogating *object* dtypes for system-level memory consumption, and include it in the returned values.

Returns

sizes [Series] A Series whose index is the original column names and whose values is the memory usage of each column in bytes.

See also:

`numpy.ndarray.nbytes` Total bytes consumed by the elements of an ndarray.

`Series.memory_usage` Bytes consumed by a Series.

`pandas.Categorical` Memory-efficient array for string values with many repeated values.

`DataFrame.info` Concise summary of a DataFrame.

Examples

```
>>> dtypes = ['int64', 'float64', 'complex128', 'object', 'bool']  #␣
↪doctest: +SKIP
>>> data = dict([(t, np.ones(shape=5000).astype(t))  # doctest: +SKIP
...              for t in dtypes])
>>> df = pd.DataFrame(data)  # doctest: +SKIP
>>> df.head()  # doctest: +SKIP
   int64  float64  complex128 object  bool
0      1      1.0      (1+0j)      1  True
1      1      1.0      (1+0j)      1  True
2      1      1.0      (1+0j)      1  True
3      1      1.0      (1+0j)      1  True
4      1      1.0      (1+0j)      1  True
```

```
>>> df.memory_usage()  # doctest: +SKIP
Index            80
int64         40000
float64       40000
complex128    80000
object        40000
bool           5000
dtype: int64
```

```
>>> df.memory_usage(index=False)  # doctest: +SKIP
int64         40000
```

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```
float64        40000
complex128     80000
object         40000
bool            5000
dtype: int64
```

The memory footprint of *object* dtype columns is ignored by default:

```
>>> df.memory_usage(deep=True)  # doctest: +SKIP
Index              80
int64           40000
float64         40000
complex128      80000
object         160000
bool             5000
dtype: int64
```

Use a Categorical for efficient storage of an object-dtype column with many repeated values.

```
>>> df['object'].astype('category').memory_usage(deep=True)  # doctest: +SKIP
5168
```

merge(*right*, *how='inner'*, *on=None*, *left_on=None*, *right_on=None*, *left_index=False*, *right_index=False*, *suffixes=('_x', '_y')*, *indicator=False*, *npartitions=None*, *shuffle=None*)

Merge the DataFrame with another DataFrame

This will merge the two datasets, either on the indices, a certain column in each dataset or the index in one dataset and the column in another.

Parameters

right: dask.dataframe.DataFrame

how [{'left', 'right', 'outer', 'inner'}, default: 'inner'] How to handle the operation of the two objects: - left: use calling frame's index (or column if on is specified) - right: use other frame's index - outer: form union of calling frame's index (or column if on is

specified) with other frame's index, and sort it lexicographically

- inner: form intersection of calling frame's index (or column if on is specified) with other frame's index, preserving the order of the calling's one

on [label or list] Column or index level names to join on. These must be found in both DataFrames. If on is None and not merging on indexes then this defaults to the intersection of the columns in both DataFrames.

left_on [label or list, or array-like] Column to join on in the left DataFrame. Other than in pandas arrays and lists are only support if their length is 1.

right_on [label or list, or array-like] Column to join on in the right DataFrame. Other than in pandas arrays and lists are only support if their length is 1.

left_index [boolean, default False] Use the index from the left DataFrame as the join key.

right_index [boolean, default False] Use the index from the right DataFrame as the join key.

suffixes [2-length sequence (tuple, list, ...)] Suffix to apply to overlapping column names in the left and right side, respectively

indicator [boolean or string, default False] If True, adds a column to output DataFrame called "_merge" with information on the source of each row. If string, column with information on source of each row will be added to output DataFrame, and column will be named value of string. Information column is Categorical-type and takes on a value of "left_only" for observations whose merge key only appears in *left* DataFrame, "right_only" for observations whose merge key only appears in *right* DataFrame, and "both" if the observation's merge key is found in both.

npartitions: int, None, or 'auto' The ideal number of output partitions. This is only utilised when performing a hash_join (merging on columns only). If *None* npartitions = max(lhs.npartitions, rhs.npartitions)

shuffle: {'disk', 'tasks'}, optional Either `'disk'` for single-node operation or `'tasks'` for distributed operation. Will be inferred by your current scheduler.

Notes

There are three ways to join dataframes:

1. Joining on indices. In this case the divisions are aligned using the function `dask.dataframe.multi.align_partitions`. Afterwards, each partition is merged with the pandas merge function.
2. Joining one on index and one on column. In this case the divisions of dataframe merged by index (d_i) are used to divide the column merged dataframe (d_c) one using `dask.dataframe.multi.rearrange_by_divisions`. In this case the merged dataframe (d_m) has the exact same divisions as (d_i). This can lead to issues if you merge multiple rows from (d_c) to one row in (d_i).
3. Joining both on columns. In this case a hash join is performed using `dask.dataframe.multi.hash_join`.

min(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return the minimum of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.min.

Some inconsistencies with the Dask version may exist.

If you want the *index* of the minimum, use `idxmin`. This is the equivalent of the `numpy.ndarray` method `argmin`.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

min [Series or DataFrame (if level specified)]

See also:

`Series.sum`	Return the sum.
`Series.min`	Return the minimum.
`Series.max`	Return the maximum.
`Series.idxmin`	Return the index of the minimum.
`Series.idxmax`	Return the index of the maximum.
`DataFrame.min`	Return the sum over the requested axis.
`DataFrame.min`	Return the minimum over the requested axis.
`DataFrame.max`	Return the maximum over the requested axis.
`DataFrame.idxmin`	Return the index of the minimum over the requested axis.
`DataFrame.idxmax`	Return the index of the maximum over the requested axis.

Examples

```
>>> idx = pd.MultiIndex.from_arrays([  # doctest: +SKIP
...     ['warm', 'warm', 'cold', 'cold'],
...     ['dog', 'falcon', 'fish', 'spider']],
...     names=['blooded', 'animal'])
>>> s = pd.Series([4, 2, 0, 8], name='legs', index=idx)  # doctest: +SKIP
>>> s  # doctest: +SKIP
blooded  animal
warm     dog       4
         falcon    2
cold     fish      0
         spider    8
Name: legs, dtype: int64
```

```
>>> s.min()  # doctest: +SKIP
0
```

Min using level names, as well as indices.

```
>>> s.min(level='blooded')  # doctest: +SKIP
blooded
warm    2
cold    0
Name: legs, dtype: int64
```

```
>>> s.min(level=0)  # doctest: +SKIP
blooded
warm    2
cold    0
Name: legs, dtype: int64
```

mod(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Modulo of dataframe and other, element-wise (binary operator *mod*).

Equivalent to `dataframe % other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rmod*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

DataFrame.add Add DataFrames.

DataFrame.sub Subtract DataFrames.

DataFrame.mul Multiply DataFrames.

DataFrame.div Divide DataFrames (float division).

DataFrame.truediv Divide DataFrames (float division).

DataFrame.floordiv Divide DataFrames (integer division).

DataFrame.mod Calculate modulo (remainder after division).

DataFrame.pow Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
```

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```
triangle         9       NaN
rectangle       16       NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                                 'degrees': [360, 180, 360, 360, 540, 720]},
...                                index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                       ['circle', 'triangle', 'rectangle',
...                                        'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

mul(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Multiplication of dataframe and other, element-wise (binary operator *mul*).

Equivalent to `dataframe * other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rmul*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
```

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```
...                                        ['circle', 'triangle', 'rectangle',
...                                         'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

ndim
Return dimensionality

ne (*other*, *axis='columns'*, *level=None*)
Not equal to of dataframe and other, element-wise (binary operator *ne*).

Among flexible wrappers (*eq*, *ne*, *le*, *lt*, *ge*, *gt*) to comparison operators.

Equivalent to ==, =!, <=, <, >=, > with support to choose axis (rows or columns) and level for comparison.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}, default 'columns'] Whether to compare by the index (0 or 'index') or columns (1 or 'columns').

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

Returns

DataFrame of bool Result of the comparison.

See also:

`DataFrame.eq` Compare DataFrames for equality elementwise.

`DataFrame.ne` Compare DataFrames for inequality elementwise.

`DataFrame.le` Compare DataFrames for less than inequality or equality elementwise.

`DataFrame.lt` Compare DataFrames for strictly less than inequality elementwise.

`DataFrame.ge` Compare DataFrames for greater than inequality or equality elementwise.

`DataFrame.gt` Compare DataFrames for strictly greater than inequality elementwise.

Notes

Mismatched indices will be unioned together. *NaN* values are considered different (i.e. *NaN* != *NaN*).

Examples

```
>>> df = pd.DataFrame({'cost': [250, 150, 100],  # doctest: +SKIP
...                    'revenue': [100, 250, 300]},
...                   index=['A', 'B', 'C'])
>>> df  # doctest: +SKIP
   cost  revenue
A   250      100
B   150      250
C   100      300
```

Comparison with a scalar, using either the operator or method:

```
>>> df == 100  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

```
>>> df.eq(100)  # doctest: +SKIP
    cost  revenue
A  False     True
B  False    False
C   True    False
```

When *other* is a `Series`, the columns of a DataFrame are aligned with the index of *other* and broadcast:

```
>>> df != pd.Series([100, 250], index=["cost", "revenue"])  # doctest: +SKIP
    cost  revenue
A   True     True
B   True    False
C  False     True
```

Use the method to control the broadcast axis:

```
>>> df.ne(pd.Series([100, 300], index=["A", "D"]), axis='index')  # doctest:␣
↪+SKIP
   cost  revenue
A  True    False
B  True     True
C  True     True
D  True     True
```

When comparing to an arbitrary sequence, the number of columns must match the number elements in *other*:

```
>>> df == [250, 100]  # doctest: +SKIP
    cost  revenue
A   True     True
B  False    False
C  False    False
```

Use the method to control the axis:

```
>>> df.eq([250, 250, 100], axis='index')  # doctest: +SKIP
    cost  revenue
A   True    False
B  False     True
C   True    False
```

Compare to a DataFrame of different shape.

```
>>> other = pd.DataFrame({'revenue': [300, 250, 100, 150]},  # doctest: +SKIP
...                      index=['A', 'B', 'C', 'D'])
>>> other  # doctest: +SKIP
   revenue
A      300
B      250
C      100
D      150
```

```
>>> df.gt(other)  # doctest: +SKIP
    cost  revenue
A  False    False
B  False    False
C  False     True
D  False    False
```

Compare to a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'cost': [250, 150, 100, 150, 300, 220],  #␣
↪doctest: +SKIP
...                              'revenue': [100, 250, 300, 200, 175, 225]},
...                             index=[['Q1', 'Q1', 'Q1', 'Q2', 'Q2', 'Q2'],
...                                    ['A', 'B', 'C', 'A', 'B', 'C']])
>>> df_multindex  # doctest: +SKIP
      cost  revenue
Q1 A   250      100
   B   150      250
   C   100      300
Q2 A   150      200
   B   300      175
   C   220      225
```

```
>>> df.le(df_multindex, level=1)  # doctest: +SKIP
       cost  revenue
Q1 A   True     True
   B   True     True
   C   True     True
Q2 A  False     True
   B   True    False
   C   True    False
```

nlargest (*n=5*, *columns=None*, *split_every=None*)

Return the first *n* rows ordered by *columns* in descending order.

This docstring was copied from pandas.core.frame.DataFrame.nlargest.

Some inconsistencies with the Dask version may exist.

Return the first *n* rows with the largest values in *columns*, in descending order. The columns that are not specified are returned as well, but not used for ordering.

This method is equivalent to `df.sort_values(columns, ascending=False).head(n)`, but more performant.

Parameters

n [int] Number of rows to return.

columns [label or list of labels] Column label(s) to order by.

keep [{'first', 'last', 'all'}, default 'first' (Not supported in Dask)] Where there are duplicate values:

- *first* : prioritize the first occurrence(s)
- *last* : prioritize the last occurrence(s)
- **`all`** [do not drop any duplicates, even it means] selecting more than *n* items.

New in version 0.24.0.

Returns

DataFrame The first *n* rows ordered by the given columns in descending order.

See also:

`DataFrame.nsmallest` Return the first *n* rows ordered by *columns* in ascending order.

`DataFrame.sort_values` Sort DataFrame by the values.

`DataFrame.head` Return the first *n* rows without re-ordering.

Notes

This function cannot be used with all column types. For example, when specifying columns with *object* or *category* dtypes, `TypeError` is raised.

Examples

```
>>> df = pd.DataFrame({'population': [59000000, 65000000, 434000,  #␣
↪doctest: +SKIP
...                                   434000, 434000, 337000, 11300,
...                                   11300, 11300],
...                    'GDP': [1937894, 2583560 , 12011, 4520, 12128,
...                            17036, 182, 38, 311],
...                    'alpha-2': ["IT", "FR", "MT", "MV", "BN",
...                                "IS", "NR", "TV", "AI"]},
...                   index=["Italy", "France", "Malta",
...                          "Maldives", "Brunei", "Iceland",
...                          "Nauru", "Tuvalu", "Anguilla"])
>>> df  # doctest: +SKIP
          population      GDP alpha-2
Italy       59000000  1937894      IT
France      65000000  2583560      FR
Malta         434000    12011      MT
Maldives      434000     4520      MV
Brunei        434000    12128      BN
```

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```
Iceland        337000    17036      IS
Nauru           11300      182      NR
Tuvalu          11300       38      TV
Anguilla        11300      311      AI
```

In the following example, we will use `nlargest` to select the three rows having the largest values in column "population".

```
>>> df.nlargest(3, 'population')  # doctest: +SKIP
        population      GDP alpha-2
France    65000000  2583560      FR
Italy     59000000  1937894      IT
Malta       434000    12011      MT
```

When using `keep='last'`, ties are resolved in reverse order:

```
>>> df.nlargest(3, 'population', keep='last')  # doctest: +SKIP
        population      GDP alpha-2
France    65000000  2583560      FR
Italy     59000000  1937894      IT
Brunei      434000    12128      BN
```

When using `keep='all'`, all duplicate items are maintained:

```
>>> df.nlargest(3, 'population', keep='all')  # doctest: +SKIP
          population      GDP alpha-2
France      65000000  2583560      FR
Italy       59000000  1937894      IT
Malta         434000    12011      MT
Maldives      434000     4520      MV
Brunei        434000    12128      BN
```

To order by the largest values in column "population" and then "GDP", we can specify multiple columns like in the next example.

```
>>> df.nlargest(3, ['population', 'GDP'])  # doctest: +SKIP
        population      GDP alpha-2
France    65000000  2583560      FR
Italy     59000000  1937894      IT
Brunei      434000    12128      BN
```

notnull()

Detect existing (non-missing) values.

This docstring was copied from pandas.core.frame.DataFrame.notnull.

Some inconsistencies with the Dask version may exist.

Return a boolean same-sized object indicating if the values are not NA. Non-missing values get mapped to True. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`). NA values, such as None or `numpy.NaN`, get mapped to False values.

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.notnull Alias of notna.

DataFrame.isna Boolean inverse of notna.

DataFrame.dropna Omit axes labels with missing values.

notna Top-level notna.

Examples

Show which entries in a DataFrame are not NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],  # doctest: +SKIP
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df  # doctest: +SKIP
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.notna()  # doctest: +SKIP
     age   born  name    toy
0   True  False  True  False
1   True   True  True   True
2  False   True  True   True
```

Show which entries in a Series are not NA.

```
>>> ser = pd.Series([5, 6, np.NaN])  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.notna()  # doctest: +SKIP
0     True
1     True
2    False
dtype: bool
```

npartitions

Return number of partitions

nsmallest (*n=5*, *columns=None*, *split_every=None*)

Return the first *n* rows ordered by *columns* in ascending order.

This docstring was copied from pandas.core.frame.DataFrame.nsmallest.

Some inconsistencies with the Dask version may exist.

Return the first *n* rows with the smallest values in *columns*, in ascending order. The columns that are not specified are returned as well, but not used for ordering.

This method is equivalent to `df.sort_values(columns, ascending=True).head(n)`, but more performant.

Parameters

n [int] Number of items to retrieve.

columns [list or str] Column name or names to order by.

keep [{'first', 'last', 'all'}, default 'first' (Not supported in Dask)] Where there are duplicate values:

- `first` : take the first occurrence.
- `last` : take the last occurrence.
- `all` : do not drop any duplicates, even it means selecting more than *n* items.

New in version 0.24.0.

Returns

DataFrame

See also:

`DataFrame.nlargest` Return the first *n* rows ordered by *columns* in descending order.

`DataFrame.sort_values` Sort DataFrame by the values.

`DataFrame.head` Return the first *n* rows without re-ordering.

Examples

```
>>> df = pd.DataFrame({'population': [59000000, 65000000, 434000,  #␣
↪doctest: +SKIP
...                                   434000, 434000, 337000, 11300,
...                                   11300, 11300],
...                    'GDP': [1937894, 2583560 , 12011, 4520, 12128,
...                            17036, 182, 38, 311],
...                    'alpha-2': ["IT", "FR", "MT", "MV", "BN",
...                                "IS", "NR", "TV", "AI"]},
...                   index=["Italy", "France", "Malta",
...                          "Maldives", "Brunei", "Iceland",
...                          "Nauru", "Tuvalu", "Anguilla"])
>>> df  # doctest: +SKIP
          population      GDP alpha-2
Italy       59000000  1937894      IT
France      65000000  2583560      FR
Malta         434000    12011      MT
Maldives      434000     4520      MV
Brunei        434000    12128      BN
Iceland       337000    17036      IS
Nauru          11300      182      NR
Tuvalu         11300       38      TV
Anguilla       11300      311      AI
```

In the following example, we will use `nsmallest` to select the three rows having the smallest values in column "a".

```
>>> df.nsmallest(3, 'population')  # doctest: +SKIP
          population  GDP alpha-2
Nauru          11300  182      NR
```

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```
Tuvalu          11300   38       TV
Anguilla        11300  311       AI
```

When using `keep='last'`, ties are resolved in reverse order:

```
>>> df.nsmallest(3, 'population', keep='last')  # doctest: +SKIP
          population  GDP alpha-2
Anguilla        11300  311       AI
Tuvalu          11300   38       TV
Nauru           11300  182       NR
```

When using `keep='all'`, all duplicate items are maintained:

```
>>> df.nsmallest(3, 'population', keep='all')  # doctest: +SKIP
          population  GDP alpha-2
Nauru           11300  182       NR
Tuvalu          11300   38       TV
Anguilla        11300  311       AI
```

To order by the largest values in column "a" and then "c", we can specify multiple columns like in the next example.

```
>>> df.nsmallest(3, ['population', 'GDP'])  # doctest: +SKIP
          population  GDP alpha-2
Tuvalu          11300   38       TV
Nauru           11300  182       NR
Anguilla        11300  311       AI
```

`nunique_approx`(*split_every=None*)

Approximate number of unique rows.

This method uses the HyperLogLog algorithm for cardinality estimation to compute the approximate number of unique rows. The approximate error is 0.406%.

Parameters

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used. Default is 8.

Returns

a float representing the approximate number of elements

`partitions`

Slice dataframe by partitions

This allows partitionwise slicing of a Dask Dataframe. You can perform normal Numpy-style slicing but now rather than slice elements of the array you slice along partitions so, for example, `df.partitions[:5]` produces a new Dask Dataframe of the first five partitions.

Returns

A Dask DataFrame

Examples

```
>>> df.partitions[0]  # doctest: +SKIP
>>> df.partitions[:3]  # doctest: +SKIP
>>> df.partitions[::10]  # doctest: +SKIP
```

persist(***kwargs*)

Persist this dask collection into memory

This turns a lazy Dask collection into a Dask collection with the same metadata, but now with the results fully computed or actively computing in the background.

The action of function differs significantly depending on the active task scheduler. If the task scheduler supports asynchronous computing, such as is the case of the dask.distributed scheduler, then persist will return *immediately* and the return value's task graph will contain Dask Future objects. However if the task scheduler only supports blocking computation then the call to persist will *block* and the return value's task graph will contain concrete Python results.

This function is particularly useful when using distributed systems, because the results will be kept in distributed memory, rather than returned to the local process as with compute.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

****kwargs** Extra keywords to forward to the scheduler function.

Returns

New dask collections backed by in-memory data

See also:

`dask.base.persist`

pipe(*func*, **args*, ***kwargs*)

Apply func(self, *args, **kwargs).

This docstring was copied from pandas.core.frame.DataFrame.pipe.

Some inconsistencies with the Dask version may exist.

Parameters

func [function] function to apply to the NDFrame. `args`, and `kwargs` are passed into `func`. Alternatively a `(callable, data_keyword)` tuple where `data_keyword` is a string indicating the keyword of `callable` that expects the NDFrame.

args [iterable, optional] positional arguments passed into `func`.

kwargs [mapping, optional] a dictionary of keyword arguments passed into `func`.

Returns

object [the return type of `func`.]

See also:

`DataFrame.apply`, *`DataFrame.applymap`*, *`Series.map`*

Notes

Use `.pipe` when chaining together functions that expect Series, DataFrames or GroupBy objects. Instead of writing

```
>>> f(g(h(df), arg1=a), arg2=b, arg3=c)  # doctest: +SKIP
```

You can write

```
>>> (df.pipe(h)  # doctest: +SKIP
...     .pipe(g, arg1=a)
...     .pipe(f, arg2=b, arg3=c)
... )
```

If you have a function that takes the data as (say) the second argument, pass a tuple indicating which keyword expects the data. For example, suppose `f` takes its data as `arg2`:

```
>>> (df.pipe(h)  # doctest: +SKIP
...     .pipe(g, arg1=a)
...     .pipe((f, 'arg2'), arg1=a, arg3=c)
...  )
```

pivot_table(*index=None*, *columns=None*, *values=None*, *aggfunc='mean'*)

Create a spreadsheet-style pivot table as a DataFrame. Target `columns` must have category dtype to infer result's `columns`. `index`, `columns`, `values` and `aggfunc` must be all scalar.

Parameters

values [scalar] column to aggregate

index [scalar] column to be index

columns [scalar] column to be columns

aggfunc [{'mean', 'sum', 'count'}, default 'mean']

Returns

table [DataFrame]

pop(*item*)

Return item and drop from frame. Raise KeyError if not found.

This docstring was copied from pandas.core.frame.DataFrame.pop.

Some inconsistencies with the Dask version may exist.

Parameters

item [str] Column label to be popped

Returns

popped [Series]

Examples

```
>>> df = pd.DataFrame([('falcon', 'bird',    389.0),   # doctest: +SKIP
...                    ('parrot', 'bird',     24.0),
...                    ('lion',   'mammal',   80.5),
...                    ('monkey', 'mammal', np.nan)],
```

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```
...                    columns=('name', 'class', 'max_speed'))
>>> df  # doctest: +SKIP
     name   class  max_speed
0  falcon    bird      389.0
1  parrot    bird       24.0
2    lion  mammal       80.5
3  monkey  mammal        NaN
```

```
>>> df.pop('class')  # doctest: +SKIP
0      bird
1      bird
2    mammal
3    mammal
Name: class, dtype: object
```

```
>>> df  # doctest: +SKIP
     name  max_speed
0  falcon      389.0
1  parrot       24.0
2    lion       80.5
3  monkey        NaN
```

pow(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Exponential power of dataframe and other, element-wise (binary operator *pow*).

Equivalent to `dataframe ** other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rpow*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

DataFrame.floordiv	Divide DataFrames (integer division).
DataFrame.mod	Calculate modulo (remainder after division).
DataFrame.pow	Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
```

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```
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

prod(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*, *min_count=None*)

Return the product of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.prod.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

prod [Series or DataFrame (if level specified)]

Examples

By default, the product of an empty or all-NA Series is `1`

```
>>> pd.Series([]).prod()  # doctest: +SKIP
1.0
```

This can be controlled with the `min_count` parameter

```
>>> pd.Series([]).prod(min_count=1)  # doctest: +SKIP
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).prod()  # doctest: +SKIP
1.0
```

```
>>> pd.Series([np.nan]).prod(min_count=1)  # doctest: +SKIP
nan
```

quantile(*q=0.5*, *axis=0*, *method='default'*)
Approximate row-wise and precise column-wise quantiles of DataFrame

Parameters

q [list/array of floats, default 0.5 (50%)] Iterable of numbers ranging from 0 to 1 for the desired quantiles

axis [{0, 1, 'index', 'columns'} (default 0)] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

method [{'default', 'tdigest', 'dask'}, optional] What method to use. By default will use dask's internal custom algorithm (`'dask'`). If set to `'tdigest'` will use tdigest for floats and ints and fallback to the `'dask'` otherwise.

query(*expr*, ***kwargs*)
Filter dataframe with complex expression

Blocked version of pd.DataFrame.query

This is like the sequential version except that this will also happen in many threads. This may conflict with `numexpr` which will use multiple threads itself. We recommend that you set numexpr to use a single thread

import numexpr numexpr.set_num_threads(1)

See also:

`pandas.DataFrame.query`

radd(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Addition of dataframe and other, element-wise (binary operator *radd*).

Equivalent to `other + dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *add*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div`	Divide DataFrames (float division).
`DataFrame.truediv`	Divide DataFrames (float division).
`DataFrame.floordiv`	Divide DataFrames (integer division).
`DataFrame.mod`	Calculate modulo (remainder after division).
`DataFrame.pow`	Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],  # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                             'degrees': [360, 180, 360, 360, 540, 720]},
...                            index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                   ['circle', 'triangle', 'rectangle',
...                                    'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
```

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```
  pentagon         5      540
  hexagon          6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

random_split (*frac*, *random_state=None*)
Pseudorandomly split dataframe into different pieces row-wise

Parameters

frac [list] List of floats that should sum to one.

random_state: int or np.random.RandomState If int create a new RandomState with this as the seed

Otherwise draw from the passed RandomState

See also:

`dask.DataFrame.sample`

Examples

50/50 split

```
>>> a, b = df.random_split([0.5, 0.5])  # doctest: +SKIP
```

80/10/10 split, consistent random_state

```
>>> a, b, c = df.random_split([0.8, 0.1, 0.1], random_state=123)  # doctest:␣
↪+SKIP
```

rdiv (*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Floating division of dataframe and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *truediv*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

DataFrame.add Add DataFrames.

DataFrame.sub Subtract DataFrames.

DataFrame.mul Multiply DataFrames.

DataFrame.div Divide DataFrames (float division).

DataFrame.truediv Divide DataFrames (float division).

DataFrame.floordiv Divide DataFrames (integer division).

DataFrame.mod Calculate modulo (remainder after division).

DataFrame.pow Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

reduction(*chunk*, *aggregate=None*, *combine=None*, *meta='__no_default__'*, *token=None*, *split_every=None*, *chunk_kwargs=None*, *aggregate_kwargs=None*, *combine_kwargs=None*, ***kwargs*)

Generic row-wise reductions.

Parameters

chunk [callable] Function to operate on each partition. Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

aggregate [callable, optional] Function to operate on the concatenated result of `chunk`. If not specified, defaults to `chunk`. Used to do the final aggregation in a tree reduction.

The input to `aggregate` depends on the output of `chunk`. If the output of `chunk` is a:

- scalar: Input is a Series, with one row per partition.
- Series: Input is a DataFrame, with one row per partition. Columns are the rows in the output series.
- DataFrame: Input is a DataFrame, with one row per partition. Columns are the columns in the output dataframes.

Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

combine [callable, optional] Function to operate on intermediate concatenated results of `chunk` in a tree-reduction. If not provided, defaults to `aggregate`. The input/output requirements should match that of `aggregate` described above.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a dict of {name: dtype} or iterable of (name, dtype) can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of (name, dtype) can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing meta is recommended. For more information, see dask.dataframe.utils.make_meta.

token [str, optional] The name to use for the output keys.

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used, and all intermediates will be concatenated and passed to aggregate. Default is 8.

chunk_kwargs [dict, optional] Keyword arguments to pass on to chunk only.

aggregate_kwargs [dict, optional] Keyword arguments to pass on to aggregate only.

combine_kwargs [dict, optional] Keyword arguments to pass on to combine only.

kwargs : All remaining keywords will be passed to chunk, combine, and aggregate.

Examples

```
>>> import pandas as pd
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': range(50), 'y': range(50, 100)})
>>> ddf = dd.from_pandas(df, npartitions=4)
```

Count the number of rows in a DataFrame. To do this, count the number of rows in each partition, then sum the results:

```
>>> res = ddf.reduction(lambda x: x.count(),
...                     aggregate=lambda x: x.sum())
>>> res.compute()
x    50
y    50
dtype: int64
```

Count the number of rows in a Series with elements greater than or equal to a value (provided via a keyword).

```
>>> def count_greater(x, value=0):
...     return (x >= value).sum()
>>> res = ddf.x.reduction(count_greater, aggregate=lambda x: x.sum(),
...                       chunk_kwargs={'value': 25})
>>> res.compute()
25
```

Aggregate both the sum and count of a Series at the same time:

```
>>> def sum_and_count(x):
...     return pd.Series({'count': x.count(), 'sum': x.sum()},
...                      index=['count', 'sum'])
>>> res = ddf.x.reduction(sum_and_count, aggregate=lambda x: x.sum())
>>> res.compute()
count      50
sum      1225
dtype: int64
```

Doing the same, but for a DataFrame. Here `chunk` returns a DataFrame, meaning the input to `aggregate` is a DataFrame with an index with non-unique entries for both 'x' and 'y'. We groupby the index, and sum each group to get the final result.

```
>>> def sum_and_count(x):
...     return pd.DataFrame({'count': x.count(), 'sum': x.sum()},
...                         columns=['count', 'sum'])
>>> res = ddf.reduction(sum_and_count,
...                     aggregate=lambda x: x.groupby(level=0).sum())
>>> res.compute()
   count   sum
x     50  1225
y     50  3725
```

rename(*index=None*, *columns=None*)

Alter axes labels.

This docstring was copied from pandas.core.frame.DataFrame.rename.

Some inconsistencies with the Dask version may exist.

Function / dict values must be unique (1-to-1). Labels not contained in a dict / Series will be left as-is. Extra labels listed don't throw an error.

See the user guide for more.

Parameters

mapper, index, columns [dict-like or function, optional] dict-like or functions transformations to apply to that axis' values. Use either `mapper` and `axis` to specify the axis to target with `mapper`, or `index` and `columns`.

axis [int or str, optional (Not supported in Dask)] Axis to target with `mapper`. Can be either the axis name ('index', 'columns') or number (0, 1). The default is 'index'.

copy [boolean, default True (Not supported in Dask)] Also copy underlying data

inplace [boolean, default False (Not supported in Dask)] Whether to return a new DataFrame. If True then value of copy is ignored.

level [int or level name, default None (Not supported in Dask)] In case of a MultiIndex, only rename labels in the specified level.

Returns

renamed [DataFrame]

See also:

`pandas.DataFrame.rename_axis`

Examples

`DataFrame.rename` supports two calling conventions

- `(index=index_mapper, columns=columns_mapper, ...)`
- `(mapper, axis={'index', 'columns'}, ...)`

We *highly* recommend using keyword arguments to clarify your intent.

```
>>> df = pd.DataFrame({"A": [1, 2, 3], "B": [4, 5, 6]})  # doctest: +SKIP
>>> df.rename(index=str, columns={"A": "a", "B": "c"})  # doctest: +SKIP
   a  c
0  1  4
1  2  5
2  3  6
```

```
>>> df.rename(index=str, columns={"A": "a", "C": "c"})  # doctest: +SKIP
   a  B
0  1  4
1  2  5
2  3  6
```

Using axis-style parameters

```
>>> df.rename(str.lower, axis='columns')  # doctest: +SKIP
   a  b
0  1  4
1  2  5
2  3  6
```

```
>>> df.rename({1: 2, 2: 4}, axis='index')  # doctest: +SKIP
   A  B
0  1  4
2  2  5
4  3  6
```

repartition(*divisions=None*, *npartitions=None*, *partition_size=None*, *freq=None*, *force=False*)
Repartition dataframe along new divisions

Parameters

divisions [list, optional] List of partitions to be used. Only used if npartitions and partition_size isn't specified.

npartitions [int, optional] Number of partitions of output. Only used if partition_size isn't specified.

partition_size: int or string, optional Max number of bytes of memory for each partition. Use numbers or strings like 5MB. If specified npartitions and divisions will be ignored.

> **Warning:** This keyword argument triggers computation to determine the memory size of each partition, which may be expensive.

freq [str, pd.Timedelta] A period on which to partition timeseries data like `'7D'` or `'12h'` or `pd.Timedelta(hours=12)`. Assumes a datetime index.

force [bool, default False] Allows the expansion of the existing divisions. If False then the new divisions lower and upper bounds must be the same as the old divisions.

Notes

Exactly one of *divisions*, *npartitions*, *partition_size*, or *freq* should be specified. A `ValueError` will be raised when that is not the case.

Examples

```
>>> df = df.repartition(npartitions=10)  # doctest: +SKIP
>>> df = df.repartition(divisions=[0, 5, 10, 20])  # doctest: +SKIP
>>> df = df.repartition(freq='7d')  # doctest: +SKIP
```

replace(*to_replace=None*, *value=None*, *regex=False*)

Replace values given in *to_replace* with *value*.

This docstring was copied from pandas.core.frame.DataFrame.replace.

Some inconsistencies with the Dask version may exist.

Values of the DataFrame are replaced with other values dynamically. This differs from updating with `.loc` or `.iloc`, which require you to specify a location to update with some value.

Parameters

to_replace [str, regex, list, dict, Series, int, float, or None] How to find the values that will be replaced.

- numeric, str or regex:
  - numeric: numeric values equal to *to_replace* will be replaced with *value*
  - str: string exactly matching *to_replace* will be replaced with *value*
  - regex: regexs matching *to_replace* will be replaced with *value*
- list of str, regex, or numeric:
  - First, if *to_replace* and *value* are both lists, they **must** be the same length.
  - Second, if `regex=True` then all of the strings in **both** lists will be interpreted as regexs otherwise they will match directly. This doesn't matter much for *value* since there are only a few possible substitution regexes you can use.
  - str, regex and numeric rules apply as above.
- dict:
  - Dicts can be used to specify different replacement values for different existing values. For example, `{'a': 'b', 'y': 'z'}` replaces the value 'a' with 'b' and 'y' with 'z'. To use a dict in this way the *value* parameter should be *None*.
  - For a DataFrame a dict can specify that different values should be replaced in different columns. For example, `{'a': 1, 'b': 'z'}` looks for the value 1 in column 'a' and the value 'z' in column 'b' and replaces these values with whatever is specified in *value*. The *value* parameter should not be `None` in this case. You can treat this as a special case of passing two lists except that you are specifying the column to search in.
  - For a DataFrame nested dictionaries, e.g., `{'a': {'b': np.nan}}`, are read as follows: look in column 'a' for the value 'b' and replace it with NaN. The *value* parameter should be `None` to use a nested dict in this way. You can nest regular expressions as well. Note that column names (the top-level dictionary keys in a nested dictionary) **cannot** be regular expressions.
- None:

– This means that the *regex* argument must be a string, compiled regular expression, or list, dict, ndarray or Series of such elements. If *value* is also `None` then this **must** be a nested dictionary or Series.

See the examples section for examples of each of these.

value [scalar, dict, list, str, regex, default None] Value to replace any values matching *to_replace* with. For a DataFrame a dict of values can be used to specify which value to use for each column (columns not in the dict will not be filled). Regular expressions, strings and lists or dicts of such objects are also allowed.

inplace [bool, default False (Not supported in Dask)] If True, in place. Note: this will modify any other views on this object (e.g. a column from a DataFrame). Returns the caller if this is True.

limit [int, default None (Not supported in Dask)] Maximum size gap to forward or backward fill.

regex [bool or same types as *to_replace*, default False] Whether to interpret *to_replace* and/or *value* as regular expressions. If this is `True` then *to_replace must* be a string. Alternatively, this could be a regular expression or a list, dict, or array of regular expressions in which case *to_replace* must be `None`.

method [{'pad', 'ffill', 'bfill', *None*} (Not supported in Dask)] The method to use when for replacement, when *to_replace* is a scalar, list or tuple and *value* is `None`.

Changed in version 0.23.0: Added to DataFrame.

Returns

DataFrame Object after replacement.

Raises

AssertionError

- If *regex* is not a `bool` and *to_replace* is not `None`.

TypeError

- If *to_replace* is a `dict` and *value* is not a `list`, `dict`, `ndarray`, or `Series`
- If *to_replace* is `None` and *regex* is not compilable into a regular expression or is a list, dict, ndarray, or Series.
- When replacing multiple `bool` or `datetime64` objects and the arguments to *to_replace* does not match the type of the value being replaced

ValueError

- If a `list` or an `ndarray` is passed to *to_replace* and *value* but they are not the same length.

See also:

`DataFrame.fillna` Fill NA values.

`DataFrame.where` Replace values based on boolean condition.

`Series.str.replace` Simple string replacement.

Notes

- Regex substitution is performed under the hood with `re.sub`. The rules for substitution for `re.sub` are the same.
- Regular expressions will only substitute on strings, meaning you cannot provide, for example, a regular expression matching floating point numbers and expect the columns in your frame that have a numeric dtype to be matched. However, if those floating point numbers *are* strings, then you can do this.
- This method has *a lot* of options. You are encouraged to experiment and play with this method to gain intuition about how it works.
- When dict is used as the *to_replace* value, it is like key(s) in the dict are the to_replace part and value(s) in the dict are the value parameter.

Examples

Scalar ‘to_replace‘ and ‘value‘

```
>>> s = pd.Series([0, 1, 2, 3, 4])  # doctest: +SKIP
>>> s.replace(0, 5)  # doctest: +SKIP
0    5
1    1
2    2
3    3
4    4
dtype: int64
```

```
>>> df = pd.DataFrame({'A': [0, 1, 2, 3, 4],  # doctest: +SKIP
...                    'B': [5, 6, 7, 8, 9],
...                    'C': ['a', 'b', 'c', 'd', 'e']})
>>> df.replace(0, 5)  # doctest: +SKIP
   A  B  C
0  5  5  a
1  1  6  b
2  2  7  c
3  3  8  d
4  4  9  e
```

List-like ‘to_replace‘

```
>>> df.replace([0, 1, 2, 3], 4)  # doctest: +SKIP
   A  B  C
0  4  5  a
1  4  6  b
2  4  7  c
3  4  8  d
4  4  9  e
```

```
>>> df.replace([0, 1, 2, 3], [4, 3, 2, 1])  # doctest: +SKIP
   A  B  C
0  4  5  a
1  3  6  b
2  2  7  c
3  1  8  d
4  4  9  e
```

```
>>> s.replace([1, 2], method='bfill')  # doctest: +SKIP
0    0
1    3
2    3
3    3
4    4
dtype: int64
```

dict-like ‘to_replace‘

```
>>> df.replace({0: 10, 1: 100})  # doctest: +SKIP
     A  B  C
0   10  5  a
1  100  6  b
2    2  7  c
3    3  8  d
4    4  9  e
```

```
>>> df.replace({'A': 0, 'B': 5}, 100)  # doctest: +SKIP
     A    B  C
0  100  100  a
1    1    6  b
2    2    7  c
3    3    8  d
4    4    9  e
```

```
>>> df.replace({'A': {0: 100, 4: 400}})  # doctest: +SKIP
     A  B  C
0  100  5  a
1    1  6  b
2    2  7  c
3    3  8  d
4  400  9  e
```

Regular expression ‘to_replace‘

```
>>> df = pd.DataFrame({'A': ['bat', 'foo', 'bait'],  # doctest: +SKIP
...                    'B': ['abc', 'bar', 'xyz']})
>>> df.replace(to_replace=r'^ba.$', value='new', regex=True)  # doctest:␣
↪+SKIP
      A    B
0   new  abc
1   foo  new
2  bait  xyz
```

```
>>> df.replace({'A': r'^ba.$'}, {'A': 'new'}, regex=True)  # doctest: +SKIP
      A    B
0   new  abc
1   foo  bar
2  bait  xyz
```

```
>>> df.replace(regex=r'^ba.$', value='new')  # doctest: +SKIP
      A    B
0   new  abc
1   foo  new
2  bait  xyz
```

```
>>> df.replace(regex={r'^ba.$': 'new', 'foo': 'xyz'})  # doctest: +SKIP
      A    B
0   new  abc
1   xyz  new
2  bait  xyz
```

```
>>> df.replace(regex=[r'^ba.$', 'foo'], value='new')  # doctest: +SKIP
      A    B
0   new  abc
1   new  new
2  bait  xyz
```

Note that when replacing multiple `bool` or `datetime64` objects, the data types in the *to_replace* parameter must match the data type of the value being replaced:

```
>>> df = pd.DataFrame({'A': [True, False, True],  # doctest: +SKIP
...                    'B': [False, True, False]})
>>> df.replace({'a string': 'new value', True: False})  # raises  # doctest:␣
↪+SKIP
Traceback (most recent call last):
    ...
TypeError: Cannot compare types 'ndarray(dtype=bool)' and 'str'
```

This raises a `TypeError` because one of the `dict` keys is not of the correct type for replacement.

Compare the behavior of `s.replace({'a': None})` and `s.replace('a', None)` to understand the peculiarities of the *to_replace* parameter:

```
>>> s = pd.Series([10, 'a', 'a', 'b', 'a'])  # doctest: +SKIP
```

When one uses a dict as the *to_replace* value, it is like the value(s) in the dict are equal to the *value* parameter. `s.replace({'a': None})` is equivalent to `s.replace(to_replace={'a': None}, value=None, method=None)`:

```
>>> s.replace({'a': None})  # doctest: +SKIP
0      10
1    None
2    None
3       b
4    None
dtype: object
```

When `value=None` and *to_replace* is a scalar, list or tuple, *replace* uses the method parameter (default 'pad') to do the replacement. So this is why the 'a' values are being replaced by 10 in rows 1 and 2 and 'b' in row 4 in this case. The command `s.replace('a', None)` is actually equivalent to `s.replace(to_replace='a', value=None, method='pad')`:

```
>>> s.replace('a', None)  # doctest: +SKIP
0    10
1    10
2    10
3     b
4     b
dtype: object
```

resample(*rule*, *closed=None*, *label=None*)
Resample time-series data.

This docstring was copied from pandas.core.frame.DataFrame.resample.

Some inconsistencies with the Dask version may exist.

Convenience method for frequency conversion and resampling of time series. Object must have a datetime-like index (*DatetimeIndex*, *PeriodIndex*, or *TimedeltaIndex*), or pass datetime-like values to the *on* or *level* keyword.

Parameters

rule [str] The offset string or object representing target conversion.

how [str (Not supported in Dask)] Method for down/re-sampling, default to 'mean' for downsampling.

Deprecated since version 0.18.0: The new syntax is `.resample(...).mean()`, or `.resample(...).apply(<func>)`

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Which axis to use for up- or down-sampling. For *Series* this will default to 0, i.e. along the rows. Must be *DatetimeIndex*, *TimedeltaIndex* or *PeriodIndex*.

fill_method [str, default None (Not supported in Dask)] Filling method for upsampling.

Deprecated since version 0.18.0: The new syntax is `.resample(...).<func>()`, e.g. `.resample(...).pad()`

closed [{'right', 'left'}, default None] Which side of bin interval is closed. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

label [{'right', 'left'}, default None] Which bin edge label to label bucket with. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

convention [{'start', 'end', 's', 'e'}, default 'start' (Not supported in Dask)] For *PeriodIndex* only, controls whether to use the start or end of *rule*.

kind [{'timestamp', 'period'}, optional, default None (Not supported in Dask)] Pass 'timestamp' to convert the resulting index to a *DateTimeIndex* or 'period' to convert it to a *PeriodIndex*. By default the input representation is retained.

loffset [timedelta, default None (Not supported in Dask)] Adjust the resampled time labels.

limit [int, default None (Not supported in Dask)] Maximum size gap when reindexing with *fill_method*.

Deprecated since version 0.18.0.

base [int, default 0 (Not supported in Dask)] For frequencies that evenly subdivide 1 day, the "origin" of the aggregated intervals. For example, for '5min' frequency, base could range from 0 through 4. Defaults to 0.

on [str, optional (Not supported in Dask)] For a DataFrame, column to use instead of index for resampling. Column must be datetime-like.

New in version 0.19.0.

level [str or int, optional (Not supported in Dask)] For a MultiIndex, level (name or number) to use for resampling. *level* must be datetime-like.

New in version 0.19.0.

Returns

Resampler object

See also:

groupby Group by mapping, function, label, or list of labels.

Series.resample Resample a Series.

DataFrame.resample Resample a DataFrame.

Notes

See the user guide for more.

To learn more about the offset strings, please see this link.

Examples

Start by creating a series with 9 one minute timestamps.

```
>>> index = pd.date_range('1/1/2000', periods=9, freq='T')  # doctest: +SKIP
>>> series = pd.Series(range(9), index=index)  # doctest: +SKIP
>>> series  # doctest: +SKIP
2000-01-01 00:00:00    0
2000-01-01 00:01:00    1
2000-01-01 00:02:00    2
2000-01-01 00:03:00    3
2000-01-01 00:04:00    4
2000-01-01 00:05:00    5
2000-01-01 00:06:00    6
2000-01-01 00:07:00    7
2000-01-01 00:08:00    8
Freq: T, dtype: int64
```

Downsample the series into 3 minute bins and sum the values of the timestamps falling into a bin.

```
>>> series.resample('3T').sum()  # doctest: +SKIP
2000-01-01 00:00:00     3
2000-01-01 00:03:00    12
2000-01-01 00:06:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but label each bin using the right edge instead of the left. Please note that the value in the bucket used as the label is not included in the bucket, which it labels. For example, in the original series the bucket `2000-01-01 00:03:00` contains the value 3, but the summed value in the resampled bucket with the label `2000-01-01 00:03:00` does not include 3 (if it did, the summed value would be 6, not 3). To include this value close the right side of the bin interval as illustrated in the example below this one.

```
>>> series.resample('3T', label='right').sum()  # doctest: +SKIP
2000-01-01 00:03:00     3
2000-01-01 00:06:00    12
2000-01-01 00:09:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but close the right side of the bin interval.

```
>>> series.resample('3T', label='right', closed='right').sum()  # doctest:␣
↪+SKIP
2000-01-01 00:00:00     0
2000-01-01 00:03:00     6
2000-01-01 00:06:00    15
2000-01-01 00:09:00    15
Freq: 3T, dtype: int64
```

Upsample the series into 30 second bins.

```
>>> series.resample('30S').asfreq()[0:5]   # Select first 5 rows  # doctest:␣
↪+SKIP
2000-01-01 00:00:00   0.0
2000-01-01 00:00:30   NaN
2000-01-01 00:01:00   1.0
2000-01-01 00:01:30   NaN
2000-01-01 00:02:00   2.0
Freq: 30S, dtype: float64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `pad` method.

```
>>> series.resample('30S').pad()[0:5]  # doctest: +SKIP
2000-01-01 00:00:00    0
2000-01-01 00:00:30    0
2000-01-01 00:01:00    1
2000-01-01 00:01:30    1
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `bfill` method.

```
>>> series.resample('30S').bfill()[0:5]  # doctest: +SKIP
2000-01-01 00:00:00    0
2000-01-01 00:00:30    1
2000-01-01 00:01:00    1
2000-01-01 00:01:30    2
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Pass a custom function via `apply`

```
>>> def custom_resampler(array_like):  # doctest: +SKIP
...     return np.sum(array_like) + 5
...
>>> series.resample('3T').apply(custom_resampler)  # doctest: +SKIP
2000-01-01 00:00:00     8
2000-01-01 00:03:00    17
2000-01-01 00:06:00    26
Freq: 3T, dtype: int64
```

For a Series with a PeriodIndex, the keyword *convention* can be used to control whether to use the start or end of *rule*.

Resample a year by quarter using 'start' *convention*. Values are assigned to the first quarter of the period.

```
>>> s = pd.Series([1, 2], index=pd.period_range('2012-01-01',  # doctest:␣
↪+SKIP
...                                               freq='A',
```

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```
...                                                          periods=2))
>>> s  # doctest: +SKIP
2012    1
2013    2
Freq: A-DEC, dtype: int64
>>> s.resample('Q', convention='start').asfreq()  # doctest: +SKIP
2012Q1    1.0
2012Q2    NaN
2012Q3    NaN
2012Q4    NaN
2013Q1    2.0
2013Q2    NaN
2013Q3    NaN
2013Q4    NaN
Freq: Q-DEC, dtype: float64
```

Resample quarters by month using 'end' *convention*. Values are assigned to the last month of the period.

```
>>> q = pd.Series([1, 2, 3, 4], index=pd.period_range('2018-01-01',  #␣
↪doctest: +SKIP
...                                                          freq='Q',
...                                                          periods=4))
>>> q  # doctest: +SKIP
2018Q1    1
2018Q2    2
2018Q3    3
2018Q4    4
Freq: Q-DEC, dtype: int64
>>> q.resample('M', convention='end').asfreq()  # doctest: +SKIP
2018-03    1.0
2018-04    NaN
2018-05    NaN
2018-06    2.0
2018-07    NaN
2018-08    NaN
2018-09    3.0
2018-10    NaN
2018-11    NaN
2018-12    4.0
Freq: M, dtype: float64
```

For DataFrame objects, the keyword *on* can be used to specify the column instead of the index for resampling.

```
>>> d = dict({'price': [10, 11, 9, 13, 14, 18, 17, 19],  # doctest: +SKIP
...           'volume': [50, 60, 40, 100, 50, 100, 40, 50]})
>>> df = pd.DataFrame(d)  # doctest: +SKIP
>>> df['week_starting'] = pd.date_range('01/01/2018',  # doctest: +SKIP
...                                     periods=8,
...                                     freq='W')
>>> df  # doctest: +SKIP
   price  volume week_starting
0     10      50    2018-01-07
1     11      60    2018-01-14
2      9      40    2018-01-21
3     13     100    2018-01-28
```

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```
4     14       50    2018-02-04
5     18      100    2018-02-11
6     17       40    2018-02-18
7     19       50    2018-02-25
>>> df.resample('M', on='week_starting').mean()   # doctest: +SKIP
               price  volume
week_starting
2018-01-31     10.75    62.5
2018-02-28     17.00    60.0
```

For a DataFrame with MultiIndex, the keyword *level* can be used to specify on which level the resampling needs to take place.

```
>>> days = pd.date_range('1/1/2000', periods=4, freq='D')   # doctest: +SKIP
>>> d2 = dict({'price': [10, 11, 9, 13, 14, 18, 17, 19],   # doctest: +SKIP
...            'volume': [50, 60, 40, 100, 50, 100, 40, 50]})
>>> df2 = pd.DataFrame(d2,   # doctest: +SKIP
...                    index=pd.MultiIndex.from_product([days,
...                                                      ['morning',
...                                                       'afternoon']]
...                                                      ))
>>> df2  # doctest: +SKIP
                      price  volume
2000-01-01 morning       10      50
           afternoon     11      60
2000-01-02 morning        9      40
           afternoon     13     100
2000-01-03 morning       14      50
           afternoon     18     100
2000-01-04 morning       17      40
           afternoon     19      50
>>> df2.resample('D', level=0).sum()   # doctest: +SKIP
            price  volume
2000-01-01     21     110
2000-01-02     22     140
2000-01-03     32     150
2000-01-04     36      90
```

reset_index(*drop=False*)

Reset the index to the default index.

Note that unlike in `pandas`, the reset `dask.dataframe` index will not be monotonically increasing from 0. Instead, it will restart at 0 for each partition (e.g. `index1 = [0, ..., 10], index2 = [0, ...]`). This is due to the inability to statically know the full length of the index.

For DataFrame with multi-level index, returns a new DataFrame with labeling information in the columns under the index names, defaulting to 'level_0', 'level_1', etc. if any are None. For a standard index, the index name will be used (if set), otherwise a default 'index' or 'level_0' (if 'index' is already taken) will be used.

Parameters

drop [boolean, default False] Do not try to insert index into dataframe columns.

rfloordiv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Integer division of dataframe and other, element-wise (binary operator *rfloordiv*).

Equivalent to `other // dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *floordiv*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],  # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
```

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```
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

rmod(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Modulo of dataframe and other, element-wise (binary operator *rmod*).

Equivalent to `other % dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *mod*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],  # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multiindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multiindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multiindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

rmul(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Multiplication of dataframe and other, element-wise (binary operator *rmul*).

Equivalent to `other * dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *mul*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div`	Divide DataFrames (float division).
`DataFrame.truediv`	Divide DataFrames (float division).
`DataFrame.floordiv`	Divide DataFrames (integer division).
`DataFrame.mod`	Calculate modulo (remainder after division).
`DataFrame.pow`	Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],  # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle          -1      358
triangle         2      178
rectangle        3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle          -1      358
triangle         2      178
rectangle        3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle          -1      359
triangle         2      179
rectangle        3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
```

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```
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

rolling(*window*, *min_periods=None*, *center=False*, *win_type=None*, *axis=0*)

Provides rolling transformations.

Parameters

window [int, str, offset] Size of the moving window. This is the number of observations used for calculating the statistic. When not using a `DatetimeIndex`, the window size must not be so large as to span more than one adjacent partition. If using an offset or offset alias like '5D', the data must have a `DatetimeIndex`

Changed in version 0.15.0: Now accepts offsets and string offset aliases

min_periods [int, default None] Minimum number of observations in window required to have a value (otherwise result is NA).

center [boolean, default False] Set the labels at the center of the window.

win_type [string, default None] Provide a window type. The recognized window types are identical to pandas.

axis [int, default 0]

Returns

a Rolling object on which to call a method to compute a statistic

round(*decimals=0*)

Round a DataFrame to a variable number of decimal places.

This docstring was copied from pandas.core.frame.DataFrame.round.

Some inconsistencies with the Dask version may exist.

Parameters

decimals [int, dict, Series] Number of decimal places to round each column to. If an int is given, round each column to the same number of places. Otherwise dict and Series round to variable numbers of places. Column names should be in the keys if *decimals* is a dict-like, or in the index if *decimals* is a Series. Any columns not included in *decimals* will be left as is. Elements of *decimals* which are not columns of the input will be ignored.

Returns

DataFrame

See also:

`numpy.around`, `Series.round`

Examples

```
>>> df = pd.DataFrame(np.random.random([3, 3]),  # doctest: +SKIP
...      columns=['A', 'B', 'C'], index=['first', 'second', 'third'])
>>> df  # doctest: +SKIP
               A         B         C
first   0.028208  0.992815  0.173891
second  0.038683  0.645646  0.577595
third   0.877076  0.149370  0.491027
>>> df.round(2)  # doctest: +SKIP
           A     B     C
first   0.03  0.99  0.17
second  0.04  0.65  0.58
third   0.88  0.15  0.49
>>> df.round({'A': 1, 'C': 2})  # doctest: +SKIP
          A         B     C
first   0.0  0.992815  0.17
second  0.0  0.645646  0.58
third   0.9  0.149370  0.49
>>> decimals = pd.Series([1, 0, 2], index=['A', 'B', 'C'])  # doctest: +SKIP
>>> df.round(decimals)  # doctest: +SKIP
          A  B     C
first   0.0  1  0.17
second  0.0  1  0.58
third   0.9  0  0.49
```

rpow(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Exponential power of dataframe and other, element-wise (binary operator *rpow*).

Equivalent to `other ** dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *pow*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div`	Divide DataFrames (float division).
`DataFrame.truediv`	Divide DataFrames (float division).
`DataFrame.floordiv`	Divide DataFrames (integer division).
`DataFrame.mod`	Calculate modulo (remainder after division).
`DataFrame.pow`	Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],  # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
```

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```
  pentagon         5      540
  hexagon          6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

rsub(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Subtraction of dataframe and other, element-wise (binary operator *rsub*).

Equivalent to `other - dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *sub*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
```

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```
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},   # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                             'degrees': [360, 180, 360, 360, 540, 720]},
...                            index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                   ['circle', 'triangle', 'rectangle',
...                                    'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

rtruediv(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Floating division of dataframe and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / dataframe`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *truediv*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],  # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
```

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```
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                              'degrees': [360, 180, 360, 360, 540, 720]},
...                             index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                    ['circle', 'triangle', 'rectangle',
...                                     'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

sample(*n=None*, *frac=None*, *replace=False*, *random_state=None*)

Random sample of items

Parameters

n [int, optional] Number of items to return is not supported by dask. Use frac instead.

frac [float, optional] Fraction of axis items to return.

replace [boolean, optional] Sample with or without replacement. Default = False.

random_state [int or `np.random.RandomState`] If int we create a new RandomState with this as the seed Otherwise we draw from the passed RandomState

See also:

DataFrame.random_split, pandas.DataFrame.sample

select_dtypes(*include=None*, *exclude=None*)

Return a subset of the DataFrame's columns based on the column dtypes.

This docstring was copied from pandas.core.frame.DataFrame.select_dtypes.

Some inconsistencies with the Dask version may exist.

Parameters

include, exclude [scalar or list-like] A selection of dtypes or strings to be included/excluded. At least one of these parameters must be supplied.

Returns

subset [DataFrame] The subset of the frame including the dtypes in `include` and excluding the dtypes in `exclude`.

Raises

ValueError

- If both of `include` and `exclude` are empty
- If `include` and `exclude` have overlapping elements
- If any kind of string dtype is passed in.

Notes

- To select all *numeric* types, use `np.number` or `'number'`
- To select strings you must use the `object` dtype, but note that this will return *all* object dtype columns
- See the numpy dtype hierarchy
- To select datetimes, use `np.datetime64`, `'datetime'` or `'datetime64'`
- To select timedeltas, use `np.timedelta64`, `'timedelta'` or `'timedelta64'`
- To select Pandas categorical dtypes, use `'category'`
- To select Pandas datetimetz dtypes, use `'datetimetz'` (new in 0.20.0) or `'datetime64[ns, tz]'`

Examples

```
>>> df = pd.DataFrame({'a': [1, 2] * 3,  # doctest: +SKIP
...                    'b': [True, False] * 3,
...                    'c': [1.0, 2.0] * 3})
>>> df  # doctest: +SKIP
        a      b  c
0       1   True  1.0
1       2  False  2.0
2       1   True  1.0
3       2  False  2.0
4       1   True  1.0
5       2  False  2.0
```

```
>>> df.select_dtypes(include='bool')  # doctest: +SKIP
   b
0  True
1  False
2  True
3  False
4  True
5  False
```

```
>>> df.select_dtypes(include=['float64'])  # doctest: +SKIP
   c
0  1.0
1  2.0
2  1.0
3  2.0
4  1.0
5  2.0
```

```
>>> df.select_dtypes(exclude=['int'])  # doctest: +SKIP
       b    c
0   True  1.0
1  False  2.0
2   True  1.0
3  False  2.0
4   True  1.0
5  False  2.0
```

sem(*axis=None*, *skipna=None*, *ddof=1*, *split_every=False*)

Return unbiased standard error of the mean over requested axis.

This docstring was copied from pandas.core.frame.DataFrame.sem.

Some inconsistencies with the Dask version may exist.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

sem [Series or DataFrame (if level specified)]

set_index(*other*, *drop=True*, *sorted=False*, *npartitions=None*, *divisions=None*, *inplace=False*, ***kwargs*)

Set the DataFrame index (row labels) using an existing column.

This realigns the dataset to be sorted by a new column. This can have a significant impact on performance, because joins, groupbys, lookups, etc. are all much faster on that column. However, this performance increase comes with a cost, sorting a parallel dataset requires expensive shuffles. Often we `set_index` once directly after data ingest and filtering and then perform many cheap computations off of the sorted dataset.

This function operates exactly like `pandas.set_index` except with different performance costs (dask dataframe `set_index` is much more expensive). Under normal operation this function does an initial pass over the index column to compute approximate qunatiles to serve as future divisions. It then passes over the data a second time, splitting up each input partition into several pieces and sharing those pieces to all of the output partitions now in sorted order.

In some cases we can alleviate those costs, for example if your dataset is sorted already then we can avoid making many small pieces or if you know good values to split the new index column then we can avoid the initial pass over the data. For example if your new index is a datetime index and your data is already sorted by day then this entire operation can be done for free. You can control these options with the following parameters.

Parameters

df: Dask DataFrame

index: string or Dask Series

npartitions: int, None, or 'auto' The ideal number of output partitions. If None use the same as the input. If 'auto' then decide by memory use.

shuffle: string, optional Either `'disk'` for single-node operation or `'tasks'` for distributed operation. Will be inferred by your current scheduler.

sorted: bool, optional If the index column is already sorted in increasing order. Defaults to False

divisions: list, optional Known values on which to separate index values of the partitions. See https://docs.dask.org/en/latest/dataframe-design.html#partitions Defaults to computing this with a single pass over the data. Note that if `sorted=True`, specified divisions are assumed to match the existing partitions in the data. If `sorted=False`, you should leave divisions empty and call `repartition` after `set_index`.

inplace [bool, optional] Modifying the DataFrame in place is not supported by Dask. Defaults to False.

compute: bool Whether or not to trigger an immediate computation. Defaults to False. Note, that even if you set `compute=False`, an immediate computation will still be triggered if `divisions` is `None`.

Examples

```
>>> df2 = df.set_index('x')  # doctest: +SKIP
>>> df2 = df.set_index(d.x)  # doctest: +SKIP
>>> df2 = df.set_index(d.timestamp, sorted=True)  # doctest: +SKIP
```

A common case is when we have a datetime column that we know to be sorted and is cleanly divided by day. We can set this index for free by specifying both that the column is pre-sorted and the particular divisions along which is is separated

```
>>> import pandas as pd
>>> divisions = pd.date_range('2000', '2010', freq='1D')
>>> df2 = df.set_index('timestamp', sorted=True, divisions=divisions)  #␣
↪doctest: +SKIP
```

shape
Return a tuple representing the dimensionality of the DataFrame.

The number of rows is a Delayed result. The number of columns is a concrete integer.

Examples

```
>>> df.size  # doctest: +SKIP
(Delayed('int-07f06075-5ecc-4d77-817e-63c69a9188a8'), 2)
```

shift (*periods=1*, *freq=None*, *axis=0*)
Shift index by desired number of periods with an optional time *freq*.

This docstring was copied from pandas.core.frame.DataFrame.shift.

Some inconsistencies with the Dask version may exist.

When *freq* is not passed, shift the index without realigning the data. If *freq* is passed (in this case, the index must be date or datetime, or it will raise a *NotImplementedError*), the index will be increased using the periods and the *freq*.

Parameters

periods [int] Number of periods to shift. Can be positive or negative.

freq [DateOffset, tseries.offsets, timedelta, or str, optional] Offset to use from the tseries module or time rule (e.g. 'EOM'). If *freq* is specified then the index values are shifted but the data is not realigned. That is, use *freq* if you would like to extend the index when shifting and preserve the original data.

axis [{0 or 'index', 1 or 'columns', None}, default None] Shift direction.

fill_value [object, optional (Not supported in Dask)] The scalar value to use for newly introduced missing values. the default depends on the dtype of *self*. For numeric data, `np.nan` is used. For datetime, timedelta, or period data, etc. `NaT` is used. For extension dtypes, `self.dtype.na_value` is used.

Changed in version 0.24.0.

Returns

DataFrame Copy of input object, shifted.

See also:

`Index.shift` Shift values of Index.

`DatetimeIndex.shift` Shift values of DatetimeIndex.

`PeriodIndex.shift` Shift values of PeriodIndex.

`tshift` Shift the time index, using the index's frequency if available.

Examples

```
>>> df = pd.DataFrame({'Col1': [10, 20, 15, 30, 45],  # doctest: +SKIP
...                    'Col2': [13, 23, 18, 33, 48],
...                    'Col3': [17, 27, 22, 37, 52]})
```

```
>>> df.shift(periods=3)  # doctest: +SKIP
   Col1  Col2  Col3
0   NaN   NaN   NaN
1   NaN   NaN   NaN
2   NaN   NaN   NaN
3  10.0  13.0  17.0
4  20.0  23.0  27.0
```

```
>>> df.shift(periods=1, axis='columns')  # doctest: +SKIP
   Col1  Col2  Col3
0   NaN  10.0  13.0
1   NaN  20.0  23.0
2   NaN  15.0  18.0
3   NaN  30.0  33.0
4   NaN  45.0  48.0
```

```
>>> df.shift(periods=3, fill_value=0)  # doctest: +SKIP
   Col1  Col2  Col3
0     0     0     0
1     0     0     0
2     0     0     0
3    10    13    17
4    20    23    27
```

size

Size of the Series or DataFrame as a Delayed object.

Examples

```
>>> series.size  # doctest: +SKIP
dd.Scalar<size-ag..., dtype=int64>
```

squeeze(*axis=None*)

Squeeze 1 dimensional axis objects into scalars.

This docstring was copied from pandas.core.frame.DataFrame.squeeze.

Some inconsistencies with the Dask version may exist.

Series or DataFrames with a single element are squeezed to a scalar. DataFrames with a single column or a single row are squeezed to a Series. Otherwise the object is unchanged.

This method is most useful when you don't know if your object is a Series or DataFrame, but you do know it has just a single column. In that case you can safely call *squeeze* to ensure you have a Series.

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default None] A specific axis to squeeze. By default, all length-1 axes are squeezed.

New in version 0.20.0.

Returns

DataFrame, Series, or scalar The projection after squeezing *axis* or all the axes.

See also:

Series.iloc Integer-location based indexing for selecting scalars.

DataFrame.iloc Integer-location based indexing for selecting Series.

Series.to_frame Inverse of DataFrame.squeeze for a single-column DataFrame.

Examples

```
>>> primes = pd.Series([2, 3, 5, 7])  # doctest: +SKIP
```

Slicing might produce a Series with a single value:

```
>>> even_primes = primes[primes % 2 == 0]  # doctest: +SKIP
>>> even_primes  # doctest: +SKIP
0    2
dtype: int64
```

```
>>> even_primes.squeeze()  # doctest: +SKIP
2
```

Squeezing objects with more than one value in every axis does nothing:

```
>>> odd_primes = primes[primes % 2 == 1]  # doctest: +SKIP
>>> odd_primes  # doctest: +SKIP
1    3
2    5
3    7
dtype: int64
```

```
>>> odd_primes.squeeze()  # doctest: +SKIP
1    3
2    5
3    7
dtype: int64
```

Squeezing is even more effective when used with DataFrames.

```
>>> df = pd.DataFrame([[1, 2], [3, 4]], columns=['a', 'b'])  # doctest: +SKIP
>>> df  # doctest: +SKIP
   a  b
0  1  2
1  3  4
```

Slicing a single column will produce a DataFrame with the columns having only one value:

```
>>> df_a = df[['a']]  # doctest: +SKIP
>>> df_a  # doctest: +SKIP
   a
0  1
1  3
```

So the columns can be squeezed down, resulting in a Series:

```
>>> df_a.squeeze('columns')  # doctest: +SKIP
0    1
1    3
Name: a, dtype: int64
```

Slicing a single row from a single column will produce a single scalar DataFrame:

```
>>> df_0a = df.loc[df.index < 1, ['a']]  # doctest: +SKIP
>>> df_0a  # doctest: +SKIP
   a
0  1
```

Squeezing the rows produces a single scalar Series:

```
>>> df_0a.squeeze('rows')  # doctest: +SKIP
a    1
Name: 0, dtype: int64
```

Squeezing all axes wil project directly into a scalar:

```
>>> df_0a.squeeze()  # doctest: +SKIP
1
```

std(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)
Return sample standard deviation over requested axis.

This docstring was copied from pandas.core.frame.DataFrame.std.

Some inconsistencies with the Dask version may exist.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

std [Series or DataFrame (if level specified)]

sub(*other*, *axis='columns'*, *level=None*, *fill_value=None*)
Subtraction of dataframe and other, element-wise (binary operator *sub*).

Equivalent to `dataframe - other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rsub*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add` Add DataFrames.

`DataFrame.sub` Subtract DataFrames.

`DataFrame.mul` Multiply DataFrames.

`DataFrame.div` Divide DataFrames (float division).

`DataFrame.truediv` Divide DataFrames (float division).

`DataFrame.floordiv` Divide DataFrames (integer division).

`DataFrame.mod` Calculate modulo (remainder after division).

`DataFrame.pow` Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],   # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
```

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```
triangle        9       NaN
rectangle      16       NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                                'degrees': [360, 180, 360, 360, 540, 720]},
...                               index=[['A', 'A', 'A', 'B', 'B', 'B'],
...                                      ['circle', 'triangle', 'rectangle',
...                                       'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

sum(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*, *min_count=None*)
Return the sum of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.sum.

Some inconsistencies with the Dask version may exist.

This is equivalent to the method `numpy.sum`.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

sum [Series or DataFrame (if level specified)]

See also:

Series.sum Return the sum.

Series.min Return the minimum.

Series.max Return the maximum.

Series.idxmin Return the index of the minimum.

Series.idxmax Return the index of the maximum.

DataFrame.min Return the sum over the requested axis.

DataFrame.min Return the minimum over the requested axis.

DataFrame.max Return the maximum over the requested axis.

DataFrame.idxmin Return the index of the minimum over the requested axis.

DataFrame.idxmax Return the index of the maximum over the requested axis.

Examples

```
>>> idx = pd.MultiIndex.from_arrays([  # doctest: +SKIP
...     ['warm', 'warm', 'cold', 'cold'],
...     ['dog', 'falcon', 'fish', 'spider']],
...     names=['blooded', 'animal'])
>>> s = pd.Series([4, 2, 0, 8], name='legs', index=idx)  # doctest: +SKIP
>>> s  # doctest: +SKIP
blooded  animal
warm     dog       4
         falcon    2
cold     fish      0
         spider    8
Name: legs, dtype: int64
```

```
>>> s.sum()  # doctest: +SKIP
14
```

Sum using level names, as well as indices.

```
>>> s.sum(level='blooded')  # doctest: +SKIP
blooded
warm    6
cold    8
Name: legs, dtype: int64
```

```
>>> s.sum(level=0)  # doctest: +SKIP
blooded
warm    6
cold    8
Name: legs, dtype: int64
```

By default, the sum of an empty or all-NA Series is `0`.

```
>>> pd.Series([]).sum()  # min_count=0 is the default  # doctest: +SKIP
0.0
```

This can be controlled with the `min_count` parameter. For example, if you'd like the sum of an empty series to be NaN, pass `min_count=1`.

```
>>> pd.Series([]).sum(min_count=1)  # doctest: +SKIP
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).sum()  # doctest: +SKIP
0.0
```

```
>>> pd.Series([np.nan]).sum(min_count=1)  # doctest: +SKIP
nan
```

tail(*n=5*, *compute=True*)
Last n rows of the dataset

Caveat, the only checks the last n rows of the last partition.

to_bag(*index=False*)
Create Dask Bag from a Dask DataFrame

Parameters

index [bool, optional] If True, the elements are tuples of `(index, value)`, otherwise they're just the `value`. Default is False.

Examples

```
>>> bag = df.to_bag()  # doctest: +SKIP
```

to_csv(*filename*, ***kwargs*)
Store Dask DataFrame to CSV files

One filename per partition will be created. You can specify the filenames in a variety of ways.

Use a globstring:

```
>>> df.to_csv('/path/to/data/export-*.csv')
```

The * will be replaced by the increasing sequence 0, 1, 2, …

```
/path/to/data/export-0.csv
/path/to/data/export-1.csv
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> df.to_csv('/path/to/data/export-*.csv', name_function=name)  # doctest:␣
↪+SKIP
```

```
/path/to/data/export-2015-01-01.csv
/path/to/data/export-2015-01-02.csv
...
```

You can also provide an explicit list of paths:

```
>>> paths = ['/path/to/data/alice.csv', '/path/to/data/bob.csv', ...]
>>> df.to_csv(paths)
```

Parameters

filename [string] Path glob indicating the naming scheme for the output files

name_function [callable, default None] Function accepting an integer (partition index) and producing a string to replace the asterisk in the given filename globstring. Should preserve the lexicographic order of partitions. Not supported when *single_file* is *True*.

single_file [bool, default False] Whether to save everything into a single CSV file. Under the single file mode, each partition is appended at the end of the specified CSV file. Note that not all filesystems support the append mode and thus the single file mode, especially on cloud storage systems such as S3 or GCS. A warning will be issued when writing to a file that is not backed by a local filesystem.

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access. Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly automatically

sep [character, default ','] Field delimiter for the output file

na_rep [string, default ''] Missing data representation

float_format [string, default None] Format string for floating point numbers

columns [sequence, optional] Columns to write

header [boolean or list of string, default True] Write out column names. If a list of string is given it is assumed to be aliases for the column names

header_first_partition_only [boolean, default None] If set to *True*, only write the header row in the first output file. By default, headers are written to all partitions under the multiple file mode (*single_file* is *False*) and written only once under the single file mode (*single_file* is *True*). It must not be *False* under the single file mode.

index [boolean, default True] Write row names (index)

index_label [string or sequence, or False, default None] Column label for index column(s) if desired. If None is given, and *header* and *index* are True, then the index names are used. A sequence should be given if the DataFrame uses MultiIndex. If False do not print fields for index names. Use index_label=False for easier importing in R

nanRep [None] deprecated, use na_rep

mode [str] Python write mode, default 'w'

encoding [string, optional] A string representing the encoding to use in the output file, defaults to 'ascii' on Python 2 and 'utf-8' on Python 3.

compression [string, optional] a string representing the compression to use in the output file, allowed values are 'gzip', 'bz2', 'xz', only used when the first argument is a filename

line_terminator [string, default '\n'] The newline character or character sequence to use in the output file

quoting [optional constant from csv module] defaults to csv.QUOTE_MINIMAL

quotechar [string (length 1), default '"'] character used to quote fields

doublequote [boolean, default True] Control quoting of *quotechar* inside a field

escapechar [string (length 1), default None] character used to escape *sep* and *quotechar* when appropriate

chunksize [int or None] rows to write at a time

tupleize_cols [boolean, default False] write multi_index columns as a list of tuples (if True) or new (expanded format) if False)

date_format [string, default None] Format string for datetime objects

decimal: string, default '.' Character recognized as decimal separator. E.g. use ',' for European data

storage_options: dict Parameters passed on to the backend filesystem class.

Returns

The names of the file written if they were computed right away

If not, the delayed tasks associated to the writing of the files

Raises

ValueError If *header_first_partition_only* is set to *False* or *name_function* is specified when *single_file* is *True*.

`to_dask_array`(*lengths=None*)

Convert a dask DataFrame to a dask array.

Parameters

lengths [bool or Sequence of ints, optional] How to determine the chunks sizes for the output array. By default, the output array will have unknown chunk lengths along the first axis, which can cause some later operations to fail.

- True : immediately compute the length of each partition

- Sequence : a sequence of integers to use for the chunk sizes on the first axis. These values are *not* validated for correctness, beyond ensuring that the number of items matches the number of partitions.

to_delayed(*optimize_graph=True*)

Convert into a list of `dask.delayed` objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

dask.dataframe.from_delayed

Examples

```
>>> partitions = df.to_delayed()  # doctest: +SKIP
```

to_hdf(*path_or_buf*, *key*, *mode='a'*, *append=False*, ***kwargs*)

Store Dask Dataframe to Hierarchical Data Format (HDF) files

This is a parallel version of the Pandas function of the same name. Please see the Pandas docstring for more detailed information about shared keyword arguments.

This function differs from the Pandas version by saving the many partitions of a Dask DataFrame in parallel, either to many files, or to many datasets within the same file. You may specify this parallelism with an asterix `*` within the filename or datapath, and an optional `name_function`. The asterix will be replaced with an increasing sequence of integers starting from `0` or with the result of calling `name_function` on each of those integers.

This function only supports the Pandas `'table'` format, not the more specialized `'fixed'` format.

Parameters

path [string, pathlib.Path] Path to a target filename. Supports strings, `pathlib.Path`, or any object implementing the `__fspath__` protocol. May contain a `*` to denote many filenames.

key [string] Datapath within the files. May contain a `*` to denote many locations

name_function [function] A function to convert the `*` in the above options to a string. Should take in a number from 0 to the number of partitions and return a string. (see examples below)

compute [bool] Whether or not to execute immediately. If False then this returns a `dask.Delayed` value.

lock [Lock, optional] Lock to use to prevent concurrency issues. By default a `threading.Lock`, `multiprocessing.Lock` or `SerializableLock` will be used depending on your scheduler if a lock is required. See dask.utils.get_scheduler_lock for more information about lock selection.

scheduler [string] The scheduler to use, like “threads” or “processes”

****other:** See pandas.to_hdf for more information

Returns

filenames [list] Returned if `compute` is True. List of file names that each partition is saved to.

delayed [dask.Delayed] Returned if `compute` is False. Delayed object to execute `to_hdf` when computed.

See also:

read_hdf, *to_parquet*

Examples

Save Data to a single file

```
>>> df.to_hdf('output.hdf', '/data')            # doctest: +SKIP
```

Save data to multiple datapaths within the same file:

```
>>> df.to_hdf('output.hdf', '/data-*')          # doctest: +SKIP
```

Save data to multiple files:

```
>>> df.to_hdf('output-*.hdf', '/data')          # doctest: +SKIP
```

Save data to multiple files, using the multiprocessing scheduler:

```
>>> df.to_hdf('output-*.hdf', '/data', scheduler='processes') # doctest:␣
↪+SKIP
```

Specify custom naming scheme. This writes files as '2000-01-01.hdf', '2000-01-02.hdf', '2000-01-03.hdf', etc..

```
>>> from datetime import date, timedelta
>>> base = date(year=2000, month=1, day=1)
>>> def name_function(i):
...     ''' Convert integer 0 to n to a string '''
...     return base + timedelta(days=i)
```

```
>>> df.to_hdf('*.hdf', '/data', name_function=name_function) # doctest: +SKIP
```

`to_html`(*max_rows=5*)

Render a DataFrame as an HTML table.

Parameters

buf [StringIO-like, optional (Not supported in Dask)] Buffer to write to.

columns [sequence, optional, default None (Not supported in Dask)] The subset of columns to write. Writes all columns by default.

col_space [int, optional (Not supported in Dask)] The minimum width of each column.

header [bool, optional (Not supported in Dask)] Whether to print column labels, default True.

index [bool, optional, default True (Not supported in Dask)] Whether to print index (row) labels.

na_rep [str, optional, default 'NaN' (Not supported in Dask)] String representation of NAN to use.

formatters [list or dict of one-param. functions, optional (Not supported in Dask)] Formatter functions to apply to columns' elements by position or name. The result of each function must be a unicode string. List must be of length equal to the number of columns.

float_format [one-parameter function, optional, default None (Not supported in Dask)] Formatter function to apply to columns' elements if they are floats. The result of this function must be a unicode string.

sparsify [bool, optional, default True (Not supported in Dask)] Set to False for a DataFrame with a hierarchical index to print every multiindex key at each row.

index_names [bool, optional, default True (Not supported in Dask)] Prints the names of the indexes.

justify [str, default None (Not supported in Dask)] How to justify the column labels. If None uses the option from the print configuration (controlled by set_option), 'right' out of the box. Valid values are

This docstring was copied from pandas.core.frame.DataFrame.to_html.

Some inconsistencies with the Dask version may exist.

- left
- right
- center
- justify
- justify-all
- start
- end
- inherit
- match-parent
- initial
- unset.

max_rows [int, optional] Maximum number of rows to display in the console.

max_cols [int, optional (Not supported in Dask)] Maximum number of columns to display in the console.

show_dimensions [bool, default False (Not supported in Dask)] Display DataFrame dimensions (number of rows by number of columns).

decimal [str, default '.' (Not supported in Dask)] Character recognized as decimal separator, e.g. ',' in Europe.

New in version 0.18.0.

bold_rows [bool, default True (Not supported in Dask)] Make the row labels bold in the output.

classes [str or list or tuple, default None (Not supported in Dask)] CSS class(es) to apply to the resulting html table.

escape [bool, default True (Not supported in Dask)] Convert the characters <, >, and & to HTML-safe sequences.

notebook [{True, False}, default False (Not supported in Dask)] Whether the generated HTML is for IPython Notebook.

border [int (Not supported in Dask)] A `border=border` attribute is included in the opening <*table*> tag. Default `pd.options.html.border`.

New in version 0.19.0.

table_id [str, optional (Not supported in Dask)] A css id is included in the opening <*table*> tag if specified.

New in version 0.23.0.

render_links [bool, default False (Not supported in Dask)] Convert URLs to HTML links.

New in version 0.24.0.

Returns

str (or unicode, depending on data and options) String representation of the dataframe.

See also:

`to_string` Convert DataFrame to a string.

`to_json` (*filename*, **args*, ***kwargs*)
See dd.to_json docstring for more information

`to_parquet` (*path*, **args*, ***kwargs*)
Store Dask.dataframe to Parquet files

Parameters

df [dask.dataframe.DataFrame]

path [string or pathlib.Path] Destination directory for data. Prepend with protocol like `s3://` or `hdfs://` for remote data.

engine [{'auto', 'fastparquet', 'pyarrow'}, default 'auto'] Parquet library to use. If only one library is installed, it will use that one; if both, it will use 'fastparquet'.

compression [string or dict, optional] Either a string like `"snappy"` or a dictionary mapping column names to compressors like `{"name": "gzip", "values": "snappy"}`. The default is `"default"`, which uses the default compression for whichever engine is selected.

write_index [boolean, optional] Whether or not to write the index. Defaults to True.

append [bool, optional] If False (default), construct data-set from scratch. If True, add new row-group(s) to an existing data-set. In the latter case, the data-set must exist, and the schema must match the input data.

ignore_divisions [bool, optional] If False (default) raises error when previous divisions overlap with the new appended divisions. Ignored if append=False.

partition_on [list, optional] Construct directory-based partitioning by splitting on these fields' values. Each dask partition will result in one or more datafiles, there will be no global groupby.

storage_options [dict, optional] Key/value pairs to be passed on to the file-system backend, if any.

write_metadata_file [bool, optional] Whether to write the special "_metadata" file.

compute [bool, optional] If True (default) then the result is computed immediately. If False then a `dask.delayed` object is returned for future computation.

****kwargs :** Extra options to be passed on to the specific backend.

See also:

read_parquet Read parquet data to dask.dataframe

Notes

Each partition will be written to a separate file.

Examples

```
>>> df = dd.read_csv(...)  # doctest: +SKIP
>>> dd.to_parquet(df, '/path/to/output/',...)  # doctest: +SKIP
```

to_records (*index=False*, *lengths=None*)

Create Dask Array from a Dask Dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

See also:

`dask.dataframe._Frame.values`, *dask.dataframe.from_dask_array*

Examples

```
>>> df.to_records()  # doctest: +SKIP
dask.array<to_records, shape=(nan,), dtype=(numpy.record, [('ind', '<f8'), (
↪'x', 'O'), ('y', '<i8')]), chunksize=(nan,), chunktype=numpy.ndarray>  #␣
↪noqa: E501
```

to_string (*max_rows=5*)

Render a DataFrame to a console-friendly tabular output.

Parameters

buf [StringIO-like, optional (Not supported in Dask)] Buffer to write to.

columns [sequence, optional, default None (Not supported in Dask)] The subset of columns to write. Writes all columns by default.

col_space [int, optional (Not supported in Dask)] The minimum width of each column.

header [bool, optional (Not supported in Dask)] Write out the column names. If a list of strings is given, it is assumed to be aliases for the column names.

index [bool, optional, default True (Not supported in Dask)] Whether to print index (row) labels.

na_rep [str, optional, default 'NaN' (Not supported in Dask)] String representation of NAN to use.

formatters [list or dict of one-param. functions, optional (Not supported in Dask)] Formatter functions to apply to columns' elements by position or name. The result of each function must be a unicode string. List must be of length equal to the number of columns.

float_format [one-parameter function, optional, default None (Not supported in Dask)] Formatter function to apply to columns' elements if they are floats. The result of this function must be a unicode string.

sparsify [bool, optional, default True (Not supported in Dask)] Set to False for a DataFrame with a hierarchical index to print every multiindex key at each row.

index_names [bool, optional, default True (Not supported in Dask)] Prints the names of the indexes.

justify [str, default None (Not supported in Dask)] How to justify the column labels. If None uses the option from the print configuration (controlled by set_option), 'right' out of the box. Valid values are

This docstring was copied from pandas.core.frame.DataFrame.to_string.

Some inconsistencies with the Dask version may exist.

- left
- right
- center
- justify
- justify-all
- start
- end
- inherit
- match-parent
- initial
- unset.

max_rows [int, optional] Maximum number of rows to display in the console.

max_cols [int, optional (Not supported in Dask)] Maximum number of columns to display in the console.

show_dimensions [bool, default False (Not supported in Dask)] Display DataFrame dimensions (number of rows by number of columns).

decimal [str, default '.' (Not supported in Dask)] Character recognized as decimal separator, e.g. ',' in Europe.

New in version 0.18.0.

line_width [int, optional (Not supported in Dask)] Width to wrap a line in characters.

Returns

str (or unicode, depending on data and options) String representation of the dataframe.

See also:

`to_html` Convert DataFrame to HTML.

Examples

```
>>> d = {'col1': [1, 2, 3], 'col2': [4, 5, 6]}  # doctest: +SKIP
>>> df = pd.DataFrame(d)  # doctest: +SKIP
>>> print(df.to_string())  # doctest: +SKIP
   col1  col2
0     1     4
1     2     5
2     3     6
```

`to_timestamp`(*freq=None*, *how='start'*, *axis=0*)

Cast to DatetimeIndex of timestamps, at *beginning* of period.

This docstring was copied from pandas.core.frame.DataFrame.to_timestamp.

Some inconsistencies with the Dask version may exist.

Parameters

freq [string, default frequency of PeriodIndex] Desired frequency

how [{'s', 'e', 'start', 'end'}] Convention for converting period to timestamp; start of period vs. end

axis [{0 or 'index', 1 or 'columns'}, default 0] The axis to convert (the index by default)

copy [boolean, default True (Not supported in Dask)] If false then underlying input data is not copied

Returns

df [DataFrame with DatetimeIndex]

`truediv`(*other*, *axis='columns'*, *level=None*, *fill_value=None*)

Floating division of dataframe and other, element-wise (binary operator *truediv*).

Equivalent to `dataframe / other`, but with support to substitute a fill_value for missing data in one of the inputs. With reverse version, *rtruediv*.

Among flexible wrappers (*add*, *sub*, *mul*, *div*, *mod*, *pow*) to arithmetic operators: +, -, *, /, //, %, **.

Parameters

other [scalar, sequence, Series, or DataFrame] Any single or multiple element data structure, or list-like object.

axis [{0 or 'index', 1 or 'columns'}] Whether to compare by the index (0 or 'index') or columns (1 or 'columns'). For Series input, axis to match Series index on.

level [int or label] Broadcast across a level, matching Index values on the passed MultiIndex level.

fill_value [float or None, default None] Fill existing missing (NaN) values, and any new element needed for successful DataFrame alignment, with this value before computation. If data in both corresponding DataFrame locations is missing the result will be missing.

Returns

DataFrame Result of the arithmetic operation.

See also:

`DataFrame.add`	Add DataFrames.
`DataFrame.sub`	Subtract DataFrames.
`DataFrame.mul`	Multiply DataFrames.
`DataFrame.div`	Divide DataFrames (float division).
`DataFrame.truediv`	Divide DataFrames (float division).
`DataFrame.floordiv`	Divide DataFrames (integer division).
`DataFrame.mod`	Calculate modulo (remainder after division).
`DataFrame.pow`	Calculate exponential power.

Notes

Mismatched indices will be unioned together.

Examples

```
>>> df = pd.DataFrame({'angles': [0, 3, 4],  # doctest: +SKIP
...                    'degrees': [360, 180, 360]},
...                   index=['circle', 'triangle', 'rectangle'])
>>> df  # doctest: +SKIP
           angles  degrees
circle          0      360
triangle        3      180
rectangle       4      360
```

Add a scalar with operator version which return the same results.

```
>>> df + 1  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

```
>>> df.add(1)  # doctest: +SKIP
           angles  degrees
circle          1      361
triangle        4      181
rectangle       5      361
```

Divide by constant with reverse version.

```
>>> df.div(10)  # doctest: +SKIP
           angles  degrees
circle        0.0     36.0
triangle      0.3     18.0
rectangle     0.4     36.0
```

```
>>> df.rdiv(10)  # doctest: +SKIP
             angles   degrees
circle          inf  0.027778
triangle   3.333333  0.055556
rectangle  2.500000  0.027778
```

Subtract a list and Series by axis with operator version.

```
>>> df - [1, 2]  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub([1, 2], axis='columns')  # doctest: +SKIP
           angles  degrees
circle         -1      358
triangle        2      178
rectangle       3      358
```

```
>>> df.sub(pd.Series([1, 1, 1], index=['circle', 'triangle', 'rectangle']),
↪# doctest: +SKIP
...        axis='index')
           angles  degrees
circle         -1      359
triangle        2      179
rectangle       3      359
```

Multiply a DataFrame of different shape with operator version.

```
>>> other = pd.DataFrame({'angles': [0, 3, 4]},  # doctest: +SKIP
...                      index=['circle', 'triangle', 'rectangle'])
>>> other  # doctest: +SKIP
           angles
circle          0
triangle        3
rectangle       4
```

```
>>> df * other  # doctest: +SKIP
           angles  degrees
circle          0      NaN
triangle        9      NaN
rectangle      16      NaN
```

```
>>> df.mul(other, fill_value=0)  # doctest: +SKIP
           angles  degrees
circle          0      0.0
triangle        9      0.0
rectangle      16      0.0
```

Divide by a MultiIndex by level.

```
>>> df_multindex = pd.DataFrame({'angles': [0, 3, 4, 4, 5, 6],  # doctest:␣
↪+SKIP
...                             'degrees': [360, 180, 360, 360, 540, 720]},
...                            index=[['A', 'A', 'A', 'B', 'B', 'B'],
```

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```
...                                        ['circle', 'triangle', 'rectangle',
...                                         'square', 'pentagon', 'hexagon']])
>>> df_multindex  # doctest: +SKIP
             angles  degrees
A circle          0      360
  triangle        3      180
  rectangle       4      360
B square          4      360
  pentagon        5      540
  hexagon         6      720
```

```
>>> df.div(df_multindex, level=1, fill_value=0)  # doctest: +SKIP
             angles  degrees
A circle        NaN      1.0
  triangle      1.0      1.0
  rectangle     1.0      1.0
B square        0.0      0.0
  pentagon      0.0      0.0
  hexagon       0.0      0.0
```

values
Return a dask.array of the values of this dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

var(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)
Return unbiased variance over requested axis.

This docstring was copied from pandas.core.frame.DataFrame.var.

Some inconsistencies with the Dask version may exist.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

var [Series or DataFrame (if level specified)]

visualize(*filename='mydask'*, *format=None*, *optimize_graph=False*, ***kwargs*)
Render the computation of this object's task graph using graphviz.

Requires `graphviz` to be installed.

Parameters

filename [str or None, optional] The name (without an extension) of the file to write to disk. If *filename* is None, no file will be written, and we communicate with dot using only pipes.

format [{'png', 'pdf', 'dot', 'svg', 'jpeg', 'jpg'}, optional] Format in which to write output file. Default is 'png'.

optimize_graph [bool, optional] If True, the graph is optimized before rendering. Otherwise, the graph is displayed as is. Default is False.

color: {None, 'order'}, optional Options to color nodes. Provide `cmap=` keyword for additional colormap

****kwargs** Additional keyword arguments to forward to `to_graphviz`.

Returns

result [IPython.diplay.Image, IPython.display.SVG, or None] See dask.dot.dot_graph for more information.

See also:

`dask.base.visualize`, `dask.dot.dot_graph`

Notes

For more information on optimization see here:

https://docs.dask.org/en/latest/optimize.html

Examples

```
>>> x.visualize(filename='dask.pdf')  # doctest: +SKIP
>>> x.visualize(filename='dask.pdf', color='order')  # doctest: +SKIP
```

where(*cond*, *other=nan*)

Replace values where the condition is False.

This docstring was copied from pandas.core.frame.DataFrame.where.

Some inconsistencies with the Dask version may exist.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is True, keep the original value. Where False, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is False are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

axis [int, default None (Not supported in Dask)] Alignment axis if needed.

level [int, default None (Not supported in Dask)] Alignment level if needed.

errors [str, {'raise', 'ignore'}, default *raise* (Not supported in Dask)] Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

- *raise* : allow exceptions to be raised.
- *ignore* : suppress exceptions. On error return original object.

try_cast [boolean, default False (Not supported in Dask)] Try to cast the result back to the input type (if possible).

raise_on_error [boolean, default True (Not supported in Dask)] Whether to raise on invalid data types (e.g. trying to where on strings).

Deprecated since version 0.21.0: Use *errors*.

Returns

wh [same type as caller]

See also:

`DataFrame.mask()` Return an object of same shape as self.

Notes

The where method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `True` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for `DataFrame.where()` differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `where` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))  # doctest: +SKIP
>>> s.where(s > 0)  # doctest: +SKIP
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
dtype: float64
```

```
>>> s.mask(s > 0)  # doctest: +SKIP
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

```
>>> s.where(s > 1, 10)  # doctest: +SKIP
0    10
1    10
2    2
3    3
4    4
dtype: int64
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])  #␣
↪doctest: +SKIP
>>> m = df % 3 == 0  # doctest: +SKIP
>>> df.where(m, -df)  # doctest: +SKIP
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)  # doctest: +SKIP
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)  # doctest: +SKIP
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
```

Series Methods

class dask.dataframe.**Series**(*dsk*, *name*, *meta*, *divisions*)

Parallel Pandas Series

Do not use this class directly. Instead use functions like `dd.read_csv`, `dd.read_parquet`, or `dd.from_pandas`.

Parameters

dsk: dict The dask graph to compute this Series

_name: str The key prefix that specifies which keys in the dask comprise this particular Series

meta: pandas.Series An empty `pandas.Series` with names, dtypes, and index matching the expected output.

divisions: tuple of index values Values along which we partition our blocks on the index

See also:

dask.dataframe.DataFrame

abs()

Return a Series/DataFrame with absolute numeric value of each element.

This docstring was copied from pandas.core.frame.DataFrame.abs.

Some inconsistencies with the Dask version may exist.

This function only applies to elements that are all numeric.

Returns

abs Series/DataFrame containing the absolute value of each element.

See also:

`numpy.absolute` Calculate the absolute value element-wise.

Notes

For `complex` inputs, `1.2 + 1j`, the absolute value is $\sqrt{a^2 + b^2}$.

Examples

Absolute numeric values in a Series.

```
>>> s = pd.Series([-1.10, 2, -3.33, 4])  # doctest: +SKIP
>>> s.abs()  # doctest: +SKIP
0    1.10
1    2.00
2    3.33
3    4.00
dtype: float64
```

Absolute numeric values in a Series with complex numbers.

```
>>> s = pd.Series([1.2 + 1j])  # doctest: +SKIP
>>> s.abs()  # doctest: +SKIP
0    1.56205
dtype: float64
```

Absolute numeric values in a Series with a Timedelta element.

```
>>> s = pd.Series([pd.Timedelta('1 days')])  # doctest: +SKIP
>>> s.abs()  # doctest: +SKIP
0   1 days
dtype: timedelta64[ns]
```

Select rows with data closest to certain value using argsort (from StackOverflow).

```
>>> df = pd.DataFrame({  # doctest: +SKIP
...     'a': [4, 5, 6, 7],
...     'b': [10, 20, 30, 40],
...     'c': [100, 50, -30, -50]
... })
>>> df  # doctest: +SKIP
     a    b    c
0    4   10  100
1    5   20   50
2    6   30  -30
3    7   40  -50
```

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```
>>> df.loc[(df.c - 43).abs().argsort()]  # doctest: +SKIP
     a   b    c
1    5  20   50
0    4  10  100
2    6  30  -30
3    7  40  -50
```

add(*other*, *level=None*, *fill_value=None*, *axis=0*)

Addition of series and other, element-wise (binary operator *add*).

Equivalent to `series + other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

`Series.radd`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

align(*other*, *join='outer'*, *axis=None*, *fill_value=None*)
Align two objects on their axes with the specified join method for each axis Index.

This docstring was copied from pandas.core.series.Series.align.

Some inconsistencies with the Dask version may exist.

Parameters

other [DataFrame or Series]

join [{'outer', 'inner', 'left', 'right'}, default 'outer']

axis [allowed axis of the other object, default None] Align on index (0), columns (1), or both (None)

level [int or level name, default None (Not supported in Dask)] Broadcast across a level, matching Index values on the passed MultiIndex level

copy [boolean, default True (Not supported in Dask)] Always returns new objects. If copy=False and no reindexing is required then original objects are returned.

fill_value [scalar, default np.NaN] Value to use for missing values. Defaults to NaN, but can be any "compatible" value

method [{'backfill', 'bfill', 'pad', 'ffill', None}, default None (Not supported in Dask)] Method to use for filling holes in reindexed Series pad / ffill: propagate last valid observation forward to next valid backfill / bfill: use NEXT valid observation to fill gap

limit [int, default None (Not supported in Dask)] If method is specified, this is the maximum number of consecutive NaN values to forward/backward fill. In other words, if there is a gap with more than this number of consecutive NaNs, it will only be partially filled. If method is not specified, this is the maximum number of entries along the entire axis where NaNs will be filled. Must be greater than 0 if not None.

fill_axis [{0 or 'index'}, default 0 (Not supported in Dask)] Filling axis, method and limit

broadcast_axis [{0 or 'index'}, default None (Not supported in Dask)] Broadcast values along this axis, if aligning two objects of different dimensions

Returns

(left, right) [(Series, type of other)] Aligned objects

all(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return whether all elements are True, potentially over an axis.

This docstring was copied from pandas.core.frame.DataFrame.all.

Some inconsistencies with the Dask version may exist.

Returns True unless there at least one element within a series or along a Dataframe axis that is False or equivalent (e.g. zero or empty).

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.

- None : reduce all axes, return a scalar.

bool_only [bool, default None (Not supported in Dask)] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

skipna [bool, default True] Exclude NA/null values. If the entire row/column is NA and skipna is True, then the result will be True, as for an empty row/column. If skipna is False, then NA are treated as True, because these are not equal to zero.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

Series or DataFrame If level is specified, then, DataFrame is returned; otherwise, Series is returned.

See also:

`Series.all` Return True if all elements are True.

`DataFrame.any` Return True if one (or more) elements are True.

Examples

Series

```
>>> pd.Series([True, True]).all()  # doctest: +SKIP
True
>>> pd.Series([True, False]).all()  # doctest: +SKIP
False
>>> pd.Series([]).all()  # doctest: +SKIP
True
>>> pd.Series([np.nan]).all()  # doctest: +SKIP
True
>>> pd.Series([np.nan]).all(skipna=False)  # doctest: +SKIP
True
```

DataFrames

Create a dataframe from a dictionary.

```
>>> df = pd.DataFrame({'col1': [True, True], 'col2': [True, False]})  #␣
↪doctest: +SKIP
>>> df  # doctest: +SKIP
   col1   col2
0  True   True
1  True  False
```

Default behaviour checks if column-wise values all return True.

```
>>> df.all()  # doctest: +SKIP
col1     True
col2    False
dtype: bool
```

Specify `axis='columns'` to check if row-wise values all return True.

```
>>> df.all(axis='columns')  # doctest: +SKIP
0     True
1    False
dtype: bool
```

Or `axis=None` for whether every value is True.

```
>>> df.all(axis=None)  # doctest: +SKIP
False
```

any (*axis=None*, *skipna=True*, *split_every=False*, *out=None*)

Return whether any element is True, potentially over an axis.

This docstring was copied from pandas.core.frame.DataFrame.any.

Some inconsistencies with the Dask version may exist.

Returns False unless there at least one element within a series or along a Dataframe axis that is True or equivalent (e.g. non-zero or non-empty).

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default 0] Indicate which axis or axes should be reduced.

- 0 / 'index' : reduce the index, return a Series whose index is the original column labels.
- 1 / 'columns' : reduce the columns, return a Series whose index is the original index.
- None : reduce all axes, return a scalar.

bool_only [bool, default None (Not supported in Dask)] Include only boolean columns. If None, will attempt to use everything, then use only boolean data. Not implemented for Series.

skipna [bool, default True] Exclude NA/null values. If the entire row/column is NA and skipna is True, then the result will be False, as for an empty row/column. If skipna is False, then NA are treated as True, because these are not equal to zero.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

****kwargs** [any, default None] Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

Series or DataFrame If level is specified, then, DataFrame is returned; otherwise, Series is returned.

See also:

`numpy.any` Numpy version of this method.

`Series.any` Return whether any element is True.

`Series.all` Return whether all elements are True.

`DataFrame.any` Return whether any element is True over requested axis.

DataFrame.all Return whether all elements are True over requested axis.

Examples

Series

For Series input, the output is a scalar indicating whether any element is True.

```
>>> pd.Series([False, False]).any()  # doctest: +SKIP
False
>>> pd.Series([True, False]).any()  # doctest: +SKIP
True
>>> pd.Series([]).any()  # doctest: +SKIP
False
>>> pd.Series([np.nan]).any()  # doctest: +SKIP
False
>>> pd.Series([np.nan]).any(skipna=False)  # doctest: +SKIP
True
```

DataFrame

Whether each column contains at least one True element (the default).

```
>>> df = pd.DataFrame({"A": [1, 2], "B": [0, 2], "C": [0, 0]})  # doctest:␣
↪+SKIP
>>> df  # doctest: +SKIP
   A  B  C
0  1  0  0
1  2  2  0
```

```
>>> df.any()  # doctest: +SKIP
A     True
B     True
C    False
dtype: bool
```

Aggregating over the columns.

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 2]})  # doctest: +SKIP
>>> df  # doctest: +SKIP
       A  B
0   True  1
1  False  2
```

```
>>> df.any(axis='columns')  # doctest: +SKIP
0    True
1    True
dtype: bool
```

```
>>> df = pd.DataFrame({"A": [True, False], "B": [1, 0]})  # doctest: +SKIP
>>> df  # doctest: +SKIP
       A  B
0   True  1
1  False  0
```

```
>>> df.any(axis='columns')  # doctest: +SKIP
0    True
1    False
dtype: bool
```

Aggregating over the entire DataFrame with `axis=None`.

```
>>> df.any(axis=None)  # doctest: +SKIP
True
```

any for an empty DataFrame is an empty Series.

```
>>> pd.DataFrame([]).any()  # doctest: +SKIP
Series([], dtype: bool)
```

append(*other*, *interleave_partitions=False*)

Concatenate two or more Series.

This docstring was copied from pandas.core.series.Series.append.

Some inconsistencies with the Dask version may exist.

Parameters

to_append [Series or list/tuple of Series (Not supported in Dask)]

ignore_index [boolean, default False (Not supported in Dask)] If True, do not use the index labels.

New in version 0.19.0.

verify_integrity [boolean, default False (Not supported in Dask)] If True, raise Exception on creating index with duplicates

Returns

appended [Series]

See also:

`concat` General function to concatenate DataFrame, Series or Panel objects.

Notes

Iteratively appending to a Series can be more computationally intensive than a single concatenate. A better solution is to append values to a list and then concatenate the list with the original Series all at once.

Examples

```
>>> s1 = pd.Series([1, 2, 3])  # doctest: +SKIP
>>> s2 = pd.Series([4, 5, 6])  # doctest: +SKIP
>>> s3 = pd.Series([4, 5, 6], index=[3,4,5])  # doctest: +SKIP
>>> s1.append(s2)  # doctest: +SKIP
0    1
1    2
2    3
0    4
1    5
```

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```
2    6
dtype: int64
```

```
>>> s1.append(s3)  # doctest: +SKIP
0    1
1    2
2    3
3    4
4    5
5    6
dtype: int64
```

With *ignore_index* set to True:

```
>>> s1.append(s2, ignore_index=True)  # doctest: +SKIP
0    1
1    2
2    3
3    4
4    5
5    6
dtype: int64
```

With *verify_integrity* set to True:

```
>>> s1.append(s2, verify_integrity=True)  # doctest: +SKIP
Traceback (most recent call last):
...
ValueError: Indexes have overlapping values: [0, 1, 2]
```

apply (*func*, *convert_dtype=True*, *meta='__no_default__'*, *args=()*, ***kwds*)

Parallel version of pandas.Series.apply

Parameters

func [function] Function to apply

convert_dtype [boolean, default True] Try to find better dtype for elementwise function results. If False, leave as dtype=object.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

args [tuple] Positional arguments to pass to function in addition to the value.

Additional keyword arguments will be passed as keywords to the function.

Returns

applied [Series or DataFrame if func returns a Series.]

See also:

`dask.Series.map_partitions`

Examples

```
>>> import dask.dataframe as dd
>>> s = pd.Series(range(5), name='x')
>>> ds = dd.from_pandas(s, npartitions=2)
```

Apply a function elementwise across the Series, passing in extra arguments in `args` and `kwargs`:

```
>>> def myadd(x, a, b=1):
...     return x + a + b
>>> res = ds.apply(myadd, args=(2,), b=1.5)  # doctest: +SKIP
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with name `'x'`, and dtype `float64`:

```
>>> res = ds.apply(myadd, args=(2,), b=1.5, meta=('x', 'f8'))
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ds.apply(lambda x: x + 1, meta=ds)
```

astype(*dtype*)

Cast a pandas object to a specified dtype `dtype`.

This docstring was copied from pandas.core.frame.DataFrame.astype.

Some inconsistencies with the Dask version may exist.

Parameters

dtype [data type, or dict of column name -> data type] Use a numpy.dtype or Python type to cast entire pandas object to the same type. Alternatively, use {col: dtype, …}, where col is a column label and dtype is a numpy.dtype or Python type to cast one or more of the DataFrame's columns to column-specific types.

copy [bool, default True (Not supported in Dask)] Return a copy when `copy=True` (be very careful setting `copy=False` as changes to values then may propagate to other pandas objects).

errors [{'raise', 'ignore'}, default 'raise' (Not supported in Dask)] Control raising of exceptions on invalid data for provided dtype.

- `raise` : allow exceptions to be raised
- `ignore` : suppress exceptions. On error return original object

New in version 0.20.0.

kwargs [keyword arguments to pass on to the constructor]

Returns

casted [same type as caller]

See also:

`to_datetime` Convert argument to datetime.

`to_timedelta` Convert argument to timedelta.

`to_numeric` Convert argument to a numeric type.

`numpy.ndarray.astype` Cast a numpy array to a specified type.

Examples

```
>>> ser = pd.Series([1, 2], dtype='int32')  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    1
1    2
dtype: int32
>>> ser.astype('int64')  # doctest: +SKIP
0    1
1    2
dtype: int64
```

Convert to categorical type:

```
>>> ser.astype('category')  # doctest: +SKIP
0    1
1    2
dtype: category
Categories (2, int64): [1, 2]
```

Convert to ordered categorical type with custom ordering:

```
>>> cat_dtype = pd.api.types.CategoricalDtype(  # doctest: +SKIP
...                     categories=[2, 1], ordered=True)
>>> ser.astype(cat_dtype)  # doctest: +SKIP
0    1
1    2
dtype: category
Categories (2, int64): [2 < 1]
```

Note that using `copy=False` and changing data on a new pandas object may propagate changes:

```
>>> s1 = pd.Series([1,2])  # doctest: +SKIP
>>> s2 = s1.astype('int64', copy=False)  # doctest: +SKIP
>>> s2[0] = 10  # doctest: +SKIP
>>> s1  # note that s1[0] has changed too  # doctest: +SKIP
0    10
1     2
dtype: int64
```

autocorr(*lag=1*, *split_every=False*)

Compute the lag-N autocorrelation.

This docstring was copied from pandas.core.series.Series.autocorr.

Some inconsistencies with the Dask version may exist.

This method computes the Pearson correlation between the Series and its shifted self.

Parameters

lag [int, default 1] Number of lags to apply before performing autocorrelation.

Returns

float The Pearson correlation between self and self.shift(lag).

See also:

`Series.corr` Compute the correlation between two Series.

`Series.shift` Shift index by desired number of periods.

`DataFrame.corr` Compute pairwise correlation of columns.

`DataFrame.corrwith` Compute pairwise correlation between rows or columns of two DataFrame objects.

Notes

If the Pearson correlation is not well defined return 'NaN'.

Examples

```
>>> s = pd.Series([0.25, 0.5, 0.2, -0.05])  # doctest: +SKIP
>>> s.autocorr()  # doctest: +ELLIPSIS, +SKIP
0.10355...
>>> s.autocorr(lag=2)  # doctest: +ELLIPSIS, +SKIP
-0.99999...
```

If the Pearson correlation is not well defined, then 'NaN' is returned.

```
>>> s = pd.Series([1, 0, 0, 0])  # doctest: +SKIP
>>> s.autocorr()  # doctest: +SKIP
nan
```

between (*left*, *right*, *inclusive=True*)

Return boolean Series equivalent to left <= series <= right.

This docstring was copied from pandas.core.series.Series.between.

Some inconsistencies with the Dask version may exist.

This function returns a boolean vector containing *True* wherever the corresponding Series element is between the boundary values *left* and *right*. NA values are treated as *False*.

Parameters

left [scalar] Left boundary.

right [scalar] Right boundary.

inclusive [bool, default True] Include boundaries.

Returns

Series Each element will be a boolean.

See also:

`Series.gt` Greater than of series and other.

`Series.lt` Less than of series and other.

Notes

This function is equivalent to `(left <= ser) & (ser <= right)`

Examples

```
>>> s = pd.Series([2, 0, 4, 8, np.nan])  # doctest: +SKIP
```

Boundary values are included by default:

```
>>> s.between(1, 4)  # doctest: +SKIP
0     True
1    False
2     True
3    False
4    False
dtype: bool
```

With *inclusive* set to `False` boundary values are excluded:

```
>>> s.between(1, 4, inclusive=False)  # doctest: +SKIP
0     True
1    False
2    False
3    False
4    False
dtype: bool
```

left and *right* can be any scalar value:

```
>>> s = pd.Series(['Alice', 'Bob', 'Carol', 'Eve'])  # doctest: +SKIP
>>> s.between('Anna', 'Daniel')  # doctest: +SKIP
0    False
1     True
2     True
3    False
dtype: bool
```

`bfill`(*axis=None*, *limit=None*)
Synonym for `DataFrame.fillna()` with `method='bfill'`.

`clear_divisions`()
Forget division information

`clip`(*lower=None*, *upper=None*, *out=None*)
Trim values at input threshold(s).

This docstring was copied from pandas.core.series.Series.clip.

Some inconsistencies with the Dask version may exist.

Assigns values outside boundary to boundary values. Thresholds can be singular values or array like, and in the latter case the clipping is performed element-wise in the specified axis.

Parameters

lower [float or array_like, default None] Minimum threshold value. All values below this threshold will be set to it.

upper [float or array_like, default None] Maximum threshold value. All values above this threshold will be set to it.

axis [int or string axis name, optional (Not supported in Dask)] Align object with lower and upper along the given axis.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

New in version 0.21.0.

***args, **kwargs** Additional keywords have no effect but might be accepted for compatibility with numpy.

Returns

Series or DataFrame Same type as calling object with the values outside the clip boundaries replaced

Examples

```
>>> data = {'col_0': [9, -3, 0, -1, 5], 'col_1': [-2, -7, 6, 8, -5]}  #␣
↪doctest: +SKIP
>>> df = pd.DataFrame(data)  # doctest: +SKIP
>>> df  # doctest: +SKIP
   col_0  col_1
0      9     -2
1     -3     -7
2      0      6
3     -1      8
4      5     -5
```

Clips per column using lower and upper thresholds:

```
>>> df.clip(-4, 6)  # doctest: +SKIP
   col_0  col_1
0      6     -2
1     -3     -4
2      0      6
3     -1      6
4      5     -4
```

Clips using specific lower and upper thresholds per column element:

```
>>> t = pd.Series([2, -4, -1, 6, 3])  # doctest: +SKIP
>>> t  # doctest: +SKIP
0    2
1   -4
2   -1
3    6
4    3
dtype: int64
```

```
>>> df.clip(t, t + 4, axis=0)  # doctest: +SKIP
   col_0  col_1
0      6      2
1     -3     -4
2      0      3
```

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```
3       6       8
4       5       3
```

clip_lower(*threshold*)

Trim values below a given threshold.

This docstring was copied from pandas.core.series.Series.clip_lower.

Some inconsistencies with the Dask version may exist.

Deprecated since version 0.24.0: Use clip(lower=threshold) instead.

Elements below the *threshold* will be changed to match the *threshold* value(s). Threshold can be a single value or an array, in the latter case it performs the truncation element-wise.

Parameters

threshold [numeric or array-like] Minimum value allowed. All values below threshold will be set to this value.

- float : every value is compared to *threshold*.
- array-like : The shape of *threshold* should match the object it's compared to. When *self* is a Series, *threshold* should be the length. When *self* is a DataFrame, *threshold* should 2-D and the same shape as *self* for `axis=None`, or 1-D and the same length as the axis being compared.

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Align *self* with *threshold* along the given axis.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

New in version 0.21.0.

Returns

Series or DataFrame Original data with values trimmed.

See also:

`Series.clip` General purpose method to trim Series values to given threshold(s).

`DataFrame.clip` General purpose method to trim DataFrame values to given threshold(s).

Examples

Series single threshold clipping:

```
>>> s = pd.Series([5, 6, 7, 8, 9])  # doctest: +SKIP
>>> s.clip(lower=8)  # doctest: +SKIP
0    8
1    8
2    8
3    8
4    9
dtype: int64
```

Series clipping element-wise using an array of thresholds. *threshold* should be the same length as the Series.

```
>>> elemwise_thresholds = [4, 8, 7, 2, 5]  # doctest: +SKIP
>>> s.clip(lower=elemwise_thresholds)  # doctest: +SKIP
0    5
1    8
2    7
3    8
4    9
dtype: int64
```

DataFrames can be compared to a scalar.

```
>>> df = pd.DataFrame({"A": [1, 3, 5], "B": [2, 4, 6]})  # doctest: +SKIP
>>> df  # doctest: +SKIP
   A  B
0  1  2
1  3  4
2  5  6
```

```
>>> df.clip(lower=3)  # doctest: +SKIP
   A  B
0  3  3
1  3  4
2  5  6
```

Or to an array of values. By default, *threshold* should be the same shape as the DataFrame.

```
>>> df.clip(lower=np.array([[3, 4], [2, 2], [6, 2]]))  # doctest: +SKIP
   A  B
0  3  4
1  3  4
2  6  6
```

Control how *threshold* is broadcast with *axis*. In this case *threshold* should be the same length as the axis specified by *axis*.

```
>>> df.clip(lower=[3, 3, 5], axis='index')  # doctest: +SKIP
   A  B
0  3  3
1  3  4
2  5  6
```

```
>>> df.clip(lower=[4, 5], axis='columns')  # doctest: +SKIP
   A  B
0  4  5
1  4  5
2  5  6
```

clip_upper(*threshold*)

Trim values above a given threshold.

This docstring was copied from pandas.core.series.Series.clip_upper.

Some inconsistencies with the Dask version may exist.

Deprecated since version 0.24.0: Use clip(upper=threshold) instead.

Elements above the *threshold* will be changed to match the *threshold* value(s). Threshold can be a single value or an array, in the latter case it performs the truncation element-wise.

Parameters

threshold [numeric or array-like] Maximum value allowed. All values above threshold will be set to this value.

- float : every value is compared to *threshold*.
- array-like : The shape of *threshold* should match the object it's compared to. When *self* is a Series, *threshold* should be the length. When *self* is a DataFrame, *threshold* should 2-D and the same shape as *self* for `axis=None`, or 1-D and the same length as the axis being compared.

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Align object with *threshold* along the given axis.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

New in version 0.21.0.

Returns

Series or DataFrame Original data with values trimmed.

See also:

`Series.clip` General purpose method to trim Series values to given threshold(s).

`DataFrame.clip` General purpose method to trim DataFrame values to given threshold(s).

Examples

```
>>> s = pd.Series([1, 2, 3, 4, 5])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    1
1    2
2    3
3    4
4    5
dtype: int64
```

```
>>> s.clip(upper=3)  # doctest: +SKIP
0    1
1    2
2    3
3    3
4    3
dtype: int64
```

```
>>> elemwise_thresholds = [5, 4, 3, 2, 1]  # doctest: +SKIP
>>> elemwise_thresholds  # doctest: +SKIP
[5, 4, 3, 2, 1]
```

```
>>> s.clip(upper=elemwise_thresholds)  # doctest: +SKIP
0    1
1    2
2    3
3    2
```

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```
4    1
dtype: int64
```

combine(*other*, *func*, *fill_value=None*)

Combine the Series with a Series or scalar according to *func*.

This docstring was copied from pandas.core.series.Series.combine.

Some inconsistencies with the Dask version may exist.

Combine the Series and *other* using *func* to perform elementwise selection for combined Series. *fill_value* is assumed when value is missing at some index from one of the two objects being combined.

Parameters

other [Series or scalar] The value(s) to be combined with the *Series*.

func [function] Function that takes two scalars as inputs and returns an element.

fill_value [scalar, optional] The value to assume when an index is missing from one Series or the other. The default specifies to use the appropriate NaN value for the underlying dtype of the Series.

Returns

Series The result of combining the Series with the other object.

See also:

Series.combine_first Combine Series values, choosing the calling Series' values first.

Examples

Consider 2 Datasets `s1` and `s2` containing highest clocked speeds of different birds.

```
>>> s1 = pd.Series({'falcon': 330.0, 'eagle': 160.0})  # doctest: +SKIP
>>> s1  # doctest: +SKIP
falcon    330.0
eagle     160.0
dtype: float64
>>> s2 = pd.Series({'falcon': 345.0, 'eagle': 200.0, 'duck': 30.0})  #␣
↪doctest: +SKIP
>>> s2  # doctest: +SKIP
falcon    345.0
eagle     200.0
duck       30.0
dtype: float64
```

Now, to combine the two datasets and view the highest speeds of the birds across the two datasets

```
>>> s1.combine(s2, max)  # doctest: +SKIP
duck        NaN
eagle     200.0
falcon    345.0
dtype: float64
```

In the previous example, the resulting value for duck is missing, because the maximum of a NaN and a float is a NaN. So, in the example, we set `fill_value=0`, so the maximum value returned will be the value from some dataset.

```
>>> s1.combine(s2, max, fill_value=0)  # doctest: +SKIP
duck        30.0
eagle      200.0
falcon     345.0
dtype: float64
```

combine_first(*other*)

Combine Series values, choosing the calling Series's values first.

This docstring was copied from pandas.core.series.Series.combine_first.

Some inconsistencies with the Dask version may exist.

Parameters

other [Series] The value(s) to be combined with the *Series*.

Returns

Series The result of combining the Series with the other object.

See also:

Series.combine Perform elementwise operation on two Series using a given function.

Notes

Result index will be the union of the two indexes.

Examples

```
>>> s1 = pd.Series([1, np.nan])  # doctest: +SKIP
>>> s2 = pd.Series([3, 4])  # doctest: +SKIP
>>> s1.combine_first(s2)  # doctest: +SKIP
0    1.0
1    4.0
dtype: float64
```

compute(***kwargs*)

Compute this dask collection

This turns a lazy Dask collection into its in-memory equivalent. For example a Dask.array turns into a `numpy.array()` and a Dask.dataframe turns into a Pandas dataframe. The entire dataset must fit into memory before calling this operation.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

See also:

`dask.base.compute`

copy()

Make a copy of the dataframe

This is strictly a shallow copy of the underlying computational graph. It does not affect the underlying data

corr(*other*, *method='pearson'*, *min_periods=None*, *split_every=False*)

Compute correlation with *other* Series, excluding missing values.

This docstring was copied from pandas.core.series.Series.corr.

Some inconsistencies with the Dask version may exist.

Parameters

other [Series]

method [{'pearson', 'kendall', 'spearman'} or callable]

- pearson : standard correlation coefficient
- kendall : Kendall Tau correlation coefficient
- spearman : Spearman rank correlation
- **callable: callable with input two 1d ndarray** and returning a float .. version-added:: 0.24.0

min_periods [int, optional] Minimum number of observations needed to have a valid result

Returns

correlation [float]

Examples

```
>>> histogram_intersection = lambda a, b: np.minimum(a, b  # doctest: +SKIP
... ).sum().round(decimals=1)
>>> s1 = pd.Series([.2, .0, .6, .2])  # doctest: +SKIP
>>> s2 = pd.Series([.3, .6, .0, .1])  # doctest: +SKIP
>>> s1.corr(s2, method=histogram_intersection)  # doctest: +SKIP
0.3
```

count(*split_every=False*)

Return number of non-NA/null observations in the Series.

This docstring was copied from pandas.core.series.Series.count.

Some inconsistencies with the Dask version may exist.

Parameters

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a smaller Series

Returns

nobs [int or Series (if level specified)]

cov(*other*, *min_periods=None*, *split_every=False*)

Compute covariance with Series, excluding missing values.

This docstring was copied from pandas.core.series.Series.cov.

Some inconsistencies with the Dask version may exist.

Parameters

other [Series]

min_periods [int, optional] Minimum number of observations needed to have a valid result

Returns

covariance [float]

Normalized by N-1 (unbiased estimator).

cummax (*axis=None*, *skipna=True*, *out=None*)

Return cumulative maximum over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cummax.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative maximum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummax [Series or DataFrame]

See also:

core.window.Expanding.max Similar functionality but ignores `NaN` values.

DataFrame.max Return the maximum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummax()  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3    5.0
4    5.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummax(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the maximum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummax()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  3.0  1.0
```

To iterate over columns and find the maximum in each row, use `axis=1`

```
>>> df.cummax(axis=1)  # doctest: +SKIP
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  1.0
```

cummin(*axis=None*, *skipna=True*, *out=None*)

Return cumulative minimum over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cummin.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative minimum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cummin [Series or DataFrame]

See also:

`core.window.Expanding.min` Similar functionality but ignores `NaN` values.

`DataFrame.min` Return the minimum over DataFrame axis.

`DataFrame.cummax` Return cumulative maximum over DataFrame axis.

`DataFrame.cummin` Return cumulative minimum over DataFrame axis.

`DataFrame.cumsum` Return cumulative sum over DataFrame axis.

`DataFrame.cumprod` Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cummin()  # doctest: +SKIP
0    2.0
1    NaN
2    2.0
3   -1.0
4   -1.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cummin(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the minimum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cummin()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  2.0  NaN
2  1.0  0.0
```

To iterate over columns and find the minimum in each row, use `axis=1`

```
>>> df.cummin(axis=1)  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

cumprod(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative product over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cumprod.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative product.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumprod [Series or DataFrame]

See also:

core.window.Expanding.prod Similar functionality but ignores `NaN` values.

DataFrame.prod Return the product over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

`DataFrame.cumprod` Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumprod()  # doctest: +SKIP
0     2.0
1     NaN
2    10.0
3   -10.0
4    -0.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumprod(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the product in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumprod()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  6.0  NaN
2  6.0  0.0
```

To iterate over columns and find the product in each row, use `axis=1`

```
>>> df.cumprod(axis=1)  # doctest: +SKIP
     A    B
0  2.0  2.0
1  3.0  NaN
2  1.0  0.0
```

cumsum(*axis=None*, *skipna=True*, *dtype=None*, *out=None*)

Return cumulative sum over a DataFrame or Series axis.

This docstring was copied from pandas.core.frame.DataFrame.cumsum.

Some inconsistencies with the Dask version may exist.

Returns a DataFrame or Series of the same size containing the cumulative sum.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] The index or the name of the axis. 0 is equivalent to None or 'index'.

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

***args, **kwargs :** Additional keywords have no effect but might be accepted for compatibility with NumPy.

Returns

cumsum [Series or DataFrame]

See also:

core.window.Expanding.sum Similar functionality but ignores `NaN` values.

DataFrame.sum Return the sum over DataFrame axis.

DataFrame.cummax Return cumulative maximum over DataFrame axis.

DataFrame.cummin Return cumulative minimum over DataFrame axis.

DataFrame.cumsum Return cumulative sum over DataFrame axis.

DataFrame.cumprod Return cumulative product over DataFrame axis.

Examples

Series

```
>>> s = pd.Series([2, np.nan, 5, -1, 0])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0    2.0
1    NaN
2    5.0
3   -1.0
4    0.0
dtype: float64
```

By default, NA values are ignored.

```
>>> s.cumsum()  # doctest: +SKIP
0    2.0
1    NaN
2    7.0
3    6.0
4    6.0
dtype: float64
```

To include NA values in the operation, use `skipna=False`

```
>>> s.cumsum(skipna=False)  # doctest: +SKIP
0    2.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

DataFrame

```
>>> df = pd.DataFrame([[2.0, 1.0],  # doctest: +SKIP
...                    [3.0, np.nan],
...                    [1.0, 0.0]],
...                    columns=list('AB'))
>>> df  # doctest: +SKIP
     A    B
0  2.0  1.0
1  3.0  NaN
2  1.0  0.0
```

By default, iterates over rows and finds the sum in each column. This is equivalent to `axis=None` or `axis='index'`.

```
>>> df.cumsum()  # doctest: +SKIP
     A    B
0  2.0  1.0
1  5.0  NaN
2  6.0  1.0
```

To iterate over columns and find the sum in each row, use `axis=1`

```
>>> df.cumsum(axis=1)  # doctest: +SKIP
     A    B
0  2.0  3.0
1  3.0  NaN
2  1.0  1.0
```

describe(*split_every=False*, *percentiles=None*, *percentiles_method='default'*, *include=None*, *exclude=None*)

Generate descriptive statistics that summarize the central tendency, dispersion and shape of a dataset's distribution, excluding `NaN` values.

This docstring was copied from pandas.core.frame.DataFrame.describe.

Some inconsistencies with the Dask version may exist.

Analyzes both numeric and object series, as well as `DataFrame` column sets of mixed data types. The output will vary depending on what is provided. Refer to the notes below for more detail.

Parameters

percentiles [list-like of numbers, optional] The percentiles to include in the output. All should fall between 0 and 1. The default is `[.25, .5, .75]`, which returns the 25th, 50th, and 75th percentiles.

include ['all', list-like of dtypes or None (default), optional] A white list of data types to include in the result. Ignored for `Series`. Here are the options:

- 'all' : All columns of the input will be included in the output.
- A list-like of dtypes : Limits the results to the provided data types. To limit the result to numeric types submit `numpy.number`. To limit it instead to object columns submit the `numpy.object` data type. Strings can also be used in the style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To select pandas categorical columns, use `'category'`
- None (default) : The result will include all numeric columns.

exclude [list-like of dtypes or None (default), optional,] A black list of data types to omit from the result. Ignored for `Series`. Here are the options:

- A list-like of dtypes : Excludes the provided data types from the result. To exclude numeric types submit `numpy.number`. To exclude object columns submit the data type `numpy.object`. Strings can also be used in the style of `select_dtypes` (e.g. `df.describe(include=['O'])`). To exclude pandas categorical columns, use `'category'`
- None (default) : The result will exclude nothing.

Returns

Series or DataFrame Summary statistics of the Series or Dataframe provided.

See also:

`DataFrame.count` Count number of non-NA/null observations.

`DataFrame.max` Maximum of the values in the object.

`DataFrame.min` Minimum of the values in the object.

`DataFrame.mean` Mean of the values.

`DataFrame.std` Standard deviation of the obersvations.

`DataFrame.select_dtypes` Subset of a DataFrame including/excluding columns based on their dtype.

Notes

For numeric data, the result's index will include `count`, `mean`, `std`, `min`, `max` as well as lower, `50` and upper percentiles. By default the lower percentile is `25` and the upper percentile is `75`. The `50` percentile is the same as the median.

For object data (e.g. strings or timestamps), the result's index will include `count`, `unique`, `top`, and `freq`. The `top` is the most common value. The `freq` is the most common value's frequency. Timestamps also include the `first` and `last` items.

If multiple object values have the highest count, then the `count` and `top` results will be arbitrarily chosen from among those with the highest count.

For mixed data types provided via a `DataFrame`, the default is to return only an analysis of numeric columns. If the dataframe consists only of object and categorical data without any numeric columns, the default is to return an analysis of both the object and categorical columns. If `include='all'` is provided as an option, the result will include a union of attributes of each type.

The *include* and *exclude* parameters can be used to limit which columns in a `DataFrame` are analyzed for the output. The parameters are ignored when analyzing a `Series`.

Examples

Describing a numeric `Series`.

```
>>> s = pd.Series([1, 2, 3])  # doctest: +SKIP
>>> s.describe()  # doctest: +SKIP
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
75%      2.5
max      3.0
dtype: float64
```

Describing a categorical `Series`.

```
>>> s = pd.Series(['a', 'a', 'b', 'c'])  # doctest: +SKIP
>>> s.describe()  # doctest: +SKIP
count     4
unique    3
top       a
freq      2
dtype: object
```

Describing a timestamp `Series`.

```
>>> s = pd.Series([  # doctest: +SKIP
...   np.datetime64("2000-01-01"),
...   np.datetime64("2010-01-01"),
...   np.datetime64("2010-01-01")
... ])
>>> s.describe()  # doctest: +SKIP
count                       3
unique                      2
top       2010-01-01 00:00:00
freq                        2
first     2000-01-01 00:00:00
last      2010-01-01 00:00:00
dtype: object
```

Describing a `DataFrame`. By default only numeric fields are returned.

```
>>> df = pd.DataFrame({'categorical': pd.Categorical(['d','e','f']),  #␣
↪doctest: +SKIP
...                    'numeric': [1, 2, 3],
...                    'object': ['a', 'b', 'c']
...                   })
```

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```
>>> df.describe()  # doctest: +SKIP
       numeric
count      3.0
mean       2.0
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Describing all columns of a `DataFrame` regardless of data type.

```
>>> df.describe(include='all')  # doctest: +SKIP
        categorical  numeric object
count            3      3.0      3
unique           3      NaN      3
top              f      NaN      c
freq             1      NaN      1
mean           NaN      2.0    NaN
std            NaN      1.0    NaN
min            NaN      1.0    NaN
25%            NaN      1.5    NaN
50%            NaN      2.0    NaN
75%            NaN      2.5    NaN
max            NaN      3.0    NaN
```

Describing a column from a `DataFrame` by accessing it as an attribute.

```
>>> df.numeric.describe()  # doctest: +SKIP
count    3.0
mean     2.0
std      1.0
min      1.0
25%      1.5
50%      2.0
75%      2.5
max      3.0
Name: numeric, dtype: float64
```

Including only numeric columns in a `DataFrame` description.

```
>>> df.describe(include=[np.number])  # doctest: +SKIP
       numeric
count      3.0
mean       2.0
std        1.0
min        1.0
25%        1.5
50%        2.0
75%        2.5
max        3.0
```

Including only string columns in a `DataFrame` description.

```
>>> df.describe(include=[np.object])  # doctest: +SKIP
       object
```

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```
count       3
unique      3
top         c
freq        1
```

Including only categorical columns from a `DataFrame` description.

```
>>> df.describe(include=['category'])  # doctest: +SKIP
       categorical
count            3
unique           3
top              f
freq             1
```

Excluding numeric columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.number])  # doctest: +SKIP
       categorical object
count            3      3
unique           3      3
top              f      c
freq             1      1
```

Excluding object columns from a `DataFrame` description.

```
>>> df.describe(exclude=[np.object])  # doctest: +SKIP
       categorical  numeric
count            3      3.0
unique           3      NaN
top              f      NaN
freq             1      NaN
mean           NaN      2.0
std            NaN      1.0
min            NaN      1.0
25%            NaN      1.5
50%            NaN      2.0
75%            NaN      2.5
max            NaN      3.0
```

diff(*periods=1*, *axis=0*)

First discrete difference of element.

This docstring was copied from pandas.core.frame.DataFrame.diff.

Some inconsistencies with the Dask version may exist.

Note: Pandas currently uses an `object`-dtype column to represent boolean data with missing values. This can cause issues for boolean-specific operations, like `|`. To enable boolean- specific operations, at the cost of metadata that doesn't match pandas, use `.astype(bool)` after the `shift`.

Calculates the difference of a DataFrame element compared with another element in the DataFrame (default is the element in the same column of the previous row).

Parameters

periods [int, default 1] Periods to shift for calculating difference, accepts negative values.

axis [{0 or 'index', 1 or 'columns'}, default 0] Take difference over rows (0) or columns (1).

New in version 0.16.1..

Returns

diffed [DataFrame]

See also:

Series.diff First discrete difference for a Series.

DataFrame.pct_change Percent change over given number of periods.

DataFrame.shift Shift index by desired number of periods with an optional time freq.

Examples

Difference with previous row

```
>>> df = pd.DataFrame({'a': [1, 2, 3, 4, 5, 6],  # doctest: +SKIP
...                    'b': [1, 1, 2, 3, 5, 8],
...                    'c': [1, 4, 9, 16, 25, 36]})
>>> df  # doctest: +SKIP
   a  b   c
0  1  1   1
1  2  1   4
2  3  2   9
3  4  3  16
4  5  5  25
5  6  8  36
```

```
>>> df.diff()  # doctest: +SKIP
     a    b     c
0  NaN  NaN   NaN
1  1.0  0.0   3.0
2  1.0  1.0   5.0
3  1.0  1.0   7.0
4  1.0  2.0   9.0
5  1.0  3.0  11.0
```

Difference with previous column

```
>>> df.diff(axis=1)  # doctest: +SKIP
    a    b     c
0 NaN  0.0   0.0
1 NaN -1.0   3.0
2 NaN -1.0   7.0
3 NaN -1.0  13.0
4 NaN  0.0  20.0
5 NaN  2.0  28.0
```

Difference with 3rd previous row

```
>>> df.diff(periods=3)  # doctest: +SKIP
     a    b     c
0  NaN  NaN   NaN
```

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```
1  NaN  NaN   NaN
2  NaN  NaN   NaN
3  3.0  2.0  15.0
4  3.0  4.0  21.0
5  3.0  6.0  27.0
```

Difference with following row

```
>>> df.diff(periods=-1)  # doctest: +SKIP
     a    b     c
0 -1.0  0.0  -3.0
1 -1.0 -1.0  -5.0
2 -1.0 -1.0  -7.0
3 -1.0 -2.0  -9.0
4 -1.0 -3.0 -11.0
5  NaN  NaN   NaN
```

div (*other*, *level=None*, *fill_value=None*, *axis=0*)

Floating division of series and other, element-wise (binary operator *truediv*).

Equivalent to `series / other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.rtruediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
```

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```
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

divide(*other*, *level=None*, *fill_value=None*, *axis=0*)

Floating division of series and other, element-wise (binary operator *truediv*).

Equivalent to `series / other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

Series.rtruediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
```

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```
c    1.0
d    1.0
e    NaN
dtype: float64
```

drop_duplicates(*subset=None*, *split_every=None*, *split_out=1*, ***kwargs*)

Return DataFrame with duplicate rows removed, optionally only considering certain columns.

This docstring was copied from pandas.core.frame.DataFrame.drop_duplicates.

Some inconsistencies with the Dask version may exist.

Parameters

subset [column label or sequence of labels, optional] Only consider certain columns for identifying duplicates, by default use all of the columns

keep [{'first', 'last', False}, default 'first' (Not supported in Dask)]

- `first` : Drop duplicates except for the first occurrence.
- `last` : Drop duplicates except for the last occurrence.
- False : Drop all duplicates.

inplace [boolean, default False (Not supported in Dask)] Whether to drop duplicates in place or to return a copy

Returns

deduplicated [DataFrame]

dropna()

Return a new Series with missing values removed.

This docstring was copied from pandas.core.series.Series.dropna.

Some inconsistencies with the Dask version may exist.

See the User Guide for more on which values are considered missing, and how to work with missing data.

Parameters

axis [{0 or 'index'}, default 0 (Not supported in Dask)] There is only one axis to drop values from.

inplace [bool, default False (Not supported in Dask)] If True, do operation inplace and return None.

****kwargs** Not in use.

Returns

Series Series with NA entries dropped from it.

See also:

Series.isna Indicate missing values.

Series.notna Indicate existing (non-missing) values.

Series.fillna Replace missing values.

DataFrame.dropna Drop rows or columns which contain NA values.

Index.dropna Drop missing indices.

Examples

```
>>> ser = pd.Series([1., 2., np.nan])  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    1.0
1    2.0
2    NaN
dtype: float64
```

Drop NA values from a Series.

```
>>> ser.dropna()  # doctest: +SKIP
0    1.0
1    2.0
dtype: float64
```

Keep the Series with valid entries in the same variable.

```
>>> ser.dropna(inplace=True)  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    1.0
1    2.0
dtype: float64
```

Empty strings are not considered NA values. `None` is considered an NA value.

```
>>> ser = pd.Series([np.NaN, 2, pd.NaT, '', None, 'I stay'])  # doctest:␣
↪+SKIP
>>> ser  # doctest: +SKIP
0       NaN
1         2
2       NaT
3
4      None
5    I stay
dtype: object
>>> ser.dropna()  # doctest: +SKIP
1         2
3
5    I stay
dtype: object
```

dt
Namespace of datetime methods

dtype
Return data type

eq(*other*, *level=None*, *fill_value=None*, *axis=0*)
Equal to of series and other, element-wise (binary operator *eq*).

Equivalent to `series == other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

`ffill`(*axis=None*, *limit=None*)
Synonym for `DataFrame.fillna()` with `method='ffill'`.

`fillna`(*value=None*, *method=None*, *limit=None*, *axis=None*)
Fill NA/NaN values using the specified method.

This docstring was copied from pandas.core.frame.DataFrame.fillna.

Some inconsistencies with the Dask version may exist.

Parameters

value [scalar, dict, Series, or DataFrame] Value to use to fill holes (e.g. 0), alternately a dict/Series/DataFrame of values specifying which value to use for each index (for a Series) or column (for a DataFrame). (values not in the dict/Series/DataFrame will not be filled). This value cannot be a list.

method [{'backfill', 'bfill', 'pad', 'ffill', None}, default None] Method to use for filling holes in reindexed Series pad / ffill: propagate last valid observation forward to next valid backfill / bfill: use NEXT valid observation to fill gap

axis [{0 or 'index', 1 or 'columns'}]

inplace [boolean, default False (Not supported in Dask)] If True, fill in place. Note: this will modify any other views on this object, (e.g. a no-copy slice for a column in a DataFrame).

limit [int, default None] If method is specified, this is the maximum number of consecutive NaN values to forward/backward fill. In other words, if there is a gap with more than this number of consecutive NaNs, it will only be partially filled. If method is not specified, this is the maximum number of entries along the entire axis where NaNs will be filled. Must be greater than 0 if not None.

downcast [dict, default is None (Not supported in Dask)] a dict of item->dtype of what to downcast if possible, or the string 'infer' which will try to downcast to an appropriate equal type (e.g. float64 to int64 if possible)

Returns

filled [DataFrame]

See also:

`interpolate` Fill NaN values using interpolation.

`reindex`, `asfreq`

Examples

```
>>> df = pd.DataFrame([[np.nan, 2, np.nan, 0],  # doctest: +SKIP
...                    [3, 4, np.nan, 1],
...                    [np.nan, np.nan, np.nan, 5],
...                    [np.nan, 3, np.nan, 4]],
...                    columns=list('ABCD'))
>>> df  # doctest: +SKIP
     A    B   C  D
0  NaN  2.0 NaN  0
1  3.0  4.0 NaN  1
2  NaN  NaN NaN  5
3  NaN  3.0 NaN  4
```

Replace all NaN elements with 0s.

```
>>> df.fillna(0)  # doctest: +SKIP
    A   B   C   D
0   0.0 2.0 0.0 0
1   3.0 4.0 0.0 1
2   0.0 0.0 0.0 5
3   0.0 3.0 0.0 4
```

We can also propagate non-null values forward or backward.

```
>>> df.fillna(method='ffill')  # doctest: +SKIP
    A   B   C   D
0   NaN 2.0 NaN 0
1   3.0 4.0 NaN 1
2   3.0 4.0 NaN 5
3   3.0 3.0 NaN 4
```

Replace all NaN elements in column 'A', 'B', 'C', and 'D', with 0, 1, 2, and 3 respectively.

```
>>> values = {'A': 0, 'B': 1, 'C': 2, 'D': 3}  # doctest: +SKIP
>>> df.fillna(value=values)  # doctest: +SKIP
    A   B   C   D
0   0.0 2.0 2.0 0
1   3.0 4.0 2.0 1
2   0.0 1.0 2.0 5
3   0.0 3.0 2.0 4
```

Only replace the first NaN element.

```
>>> df.fillna(value=values, limit=1)  # doctest: +SKIP
    A   B   C   D
0   0.0 2.0 2.0 0
1   3.0 4.0 NaN 1
2   NaN 1.0 NaN 5
3   NaN 3.0 NaN 4
```

first (*offset*)

Convenience method for subsetting initial periods of time series data based on a date offset.

This docstring was copied from pandas.core.frame.DataFrame.first.

Some inconsistencies with the Dask version may exist.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [same type as caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

last Select final periods of time series based on a date offset.

at_time Select values at a particular time of the day.

between_time Select values between particular times of the day.

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')  # doctest: +SKIP
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)  # doctest: +SKIP
>>> ts  # doctest: +SKIP
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the first 3 days:

```
>>> ts.first('3D')  # doctest: +SKIP
            A
2018-04-09  1
2018-04-11  2
```

Notice the data for 3 first calender days were returned, not the first 3 days observed in the dataset, and therefore data for 2018-04-13 was not returned.

floordiv(*other*, *level=None*, *fill_value=None*, *axis=0*)

Integer division of series and other, element-wise (binary operator *floordiv*).

Equivalent to `series // other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

Series.rfloordiv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

ge (*other*, *level=None*, *fill_value=None*, *axis=0*)

Greater than or equal to of series and other, element-wise (binary operator *ge*).

Equivalent to `series >= other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

get_partition (*n*)

Get a dask DataFrame/Series representing the *nth* partition.

groupby (*by=None*, ***kwargs*)

Group DataFrame or Series using a mapper or by a Series of columns.

This docstring was copied from pandas.core.series.Series.groupby.

Some inconsistencies with the Dask version may exist.

A groupby operation involves some combination of splitting the object, applying a function, and combining the results. This can be used to group large amounts of data and compute operations on these groups.

Parameters

by [mapping, function, label, or list of labels] Used to determine the groups for the groupby. If `by` is a function, it's called on each value of the object's index. If a dict or Series is passed, the Series or dict VALUES will be used to determine the groups (the Series' values are first aligned; see `.align()` method). If an ndarray is passed, the values are used as-is determine the groups. A label or list of labels may be passed to group by the columns in `self`. Notice that a tuple is interpreted a (single) key.

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Split along rows (0) or columns (1).

level [int, level name, or sequence of such, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), group by a particular level or levels.

as_index [bool, default True (Not supported in Dask)] For aggregated output, return object with group labels as the index. Only relevant for DataFrame input. as_index=False is effectively "SQL-style" grouped output.

sort [bool, default True (Not supported in Dask)] Sort group keys. Get better performance by turning this off. Note this does not influence the order of observations within each group. Groupby preserves the order of rows within each group.

group_keys [bool, default True (Not supported in Dask)] When calling apply, add group keys to index to identify pieces.

squeeze [bool, default False (Not supported in Dask)] Reduce the dimensionality of the return type if possible, otherwise return a consistent type.

observed [bool, default False (Not supported in Dask)] This only applies if any of the groupers are Categoricals. If True: only show observed values for categorical groupers. If False: show all values for categorical groupers.

New in version 0.23.0.

****kwargs** Optional, only accepts keyword argument 'mutated' and is passed to groupby.

Returns

DataFrameGroupBy or SeriesGroupBy Depends on the calling object and returns groupby object that contains information about the groups.

See also:

`resample` Convenience method for frequency conversion and resampling of time series.

Notes

See the user guide for more.

Examples

```
>>> df = pd.DataFrame({'Animal' : ['Falcon', 'Falcon',  # doctest: +SKIP
...                                'Parrot', 'Parrot'],
...                    'Max Speed' : [380., 370., 24., 26.]})
>>> df  # doctest: +SKIP
   Animal  Max Speed
0  Falcon      380.0
1  Falcon      370.0
2  Parrot       24.0
3  Parrot       26.0
>>> df.groupby(['Animal']).mean()  # doctest: +SKIP
        Max Speed
Animal
Falcon      375.0
Parrot       25.0
```

Hierarchical Indexes

We can groupby different levels of a hierarchical index using the *level* parameter:

```
>>> arrays = [['Falcon', 'Falcon', 'Parrot', 'Parrot'],  # doctest: +SKIP
...           ['Capitve', 'Wild', 'Capitve', 'Wild']]
>>> index = pd.MultiIndex.from_arrays(arrays, names=('Animal', 'Type'))  #␣
↪doctest: +SKIP
>>> df = pd.DataFrame({'Max Speed' : [390., 350., 30., 20.]},  # doctest:␣
↪+SKIP
...                   index=index)
>>> df  # doctest: +SKIP
                Max Speed
Animal Type
Falcon Capitve      390.0
       Wild         350.0
Parrot Capitve       30.0
       Wild          20.0
>>> df.groupby(level=0).mean()  # doctest: +SKIP
        Max Speed
Animal
Falcon      370.0
Parrot       25.0
>>> df.groupby(level=1).mean()  # doctest: +SKIP
         Max Speed
Type
Capitve      210.0
Wild         185.0
```

gt (*other*, *level=None*, *fill_value=None*, *axis=0*)

Greater than of series and other, element-wise (binary operator *gt*).

Equivalent to `series > other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

head(*n=5*, *npartitions=1*, *compute=True*)
First n rows of the dataset

Parameters

n [int, optional] The number of rows to return. Default is 5.

npartitions [int, optional] Elements are only taken from the first `npartitions`, with a default of 1. If there are fewer than `n` rows in the first `npartitions` a warning will be raised and any found rows returned. Pass -1 to use all partitions.

compute [bool, optional] Whether to compute the result, default is True.

idxmax(*axis=None*, *skipna=True*, *split_every=False*)
Return index of first occurrence of maximum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmax.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmax [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmax

Notes

This method is the DataFrame version of `ndarray.argmax`.

idxmin(*axis=None*, *skipna=True*, *split_every=False*)

Return index of first occurrence of minimum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmin.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmin [Series]

Raises

ValueError

- If the row/column is empty

See also:

Series.idxmin

Notes

This method is the DataFrame version of `ndarray.argmin`.

index

Return dask Index instance

isin(*values*)

Check whether *values* are contained in Series.

This docstring was copied from pandas.core.series.Series.isin.

Some inconsistencies with the Dask version may exist.

Return a boolean Series showing whether each element in the Series matches an element in the passed sequence of *values* exactly.

Parameters

values [set or list-like] The sequence of values to test. Passing in a single string will raise a `TypeError`. Instead, turn a single string into a list of one element.

New in version 0.18.1: Support for values as a set.

Returns

isin [Series (bool dtype)]

Raises

TypeError

- If *values* is a string

See also:

DataFrame.isin Equivalent method on DataFrame.

Examples

```
>>> s = pd.Series(['lama', 'cow', 'lama', 'beetle', 'lama',  # doctest: +SKIP
...                'hippo'], name='animal')
>>> s.isin(['cow', 'lama'])  # doctest: +SKIP
0     True
1     True
2     True
3    False
4     True
5    False
Name: animal, dtype: bool
```

Passing a single string as `s.isin('lama')` will raise an error. Use a list of one element instead:

```
>>> s.isin(['lama'])  # doctest: +SKIP
0     True
1    False
2     True
3    False
4     True
5    False
Name: animal, dtype: bool
```

isna()

Detect missing values.

This docstring was copied from pandas.core.frame.DataFrame.isna.

Some inconsistencies with the Dask version may exist.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.isnull Alias of isna.

DataFrame.notna Boolean inverse of isna.

DataFrame.dropna Omit axes labels with missing values.

isna Top-level isna.

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],  # doctest: +SKIP
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df  # doctest: +SKIP
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25                Joker
```

```
>>> df.isna()  # doctest: +SKIP
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()  # doctest: +SKIP
0    False
1    False
2     True
dtype: bool
```

isnull()

Detect missing values.

This docstring was copied from pandas.core.frame.DataFrame.isnull.

Some inconsistencies with the Dask version may exist.

Return a boolean same-sized object indicating if the values are NA. NA values, such as None or `numpy.NaN`, gets mapped to True values. Everything else gets mapped to False values. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`).

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.isnull Alias of isna.

DataFrame.notna Boolean inverse of isna.

DataFrame.dropna Omit axes labels with missing values.

isna Top-level isna.

Examples

Show which entries in a DataFrame are NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],  # doctest: +SKIP
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df  # doctest: +SKIP
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25              Joker
```

```
>>> df.isna()  # doctest: +SKIP
     age   born   name    toy
0  False   True  False   True
1  False  False  False  False
2   True  False  False  False
```

Show which entries in a Series are NA.

```
>>> ser = pd.Series([5, 6, np.NaN])  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.isna()  # doctest: +SKIP
0    False
1    False
2     True
dtype: bool
```

iteritems()

Lazily iterate over (index, value) tuples.

known_divisions

Whether divisions are already known

last (*offset*)

Convenience method for subsetting final periods of time series data based on a date offset.

This docstring was copied from pandas.core.frame.DataFrame.last.

Some inconsistencies with the Dask version may exist.

Parameters

offset [string, DateOffset, dateutil.relativedelta]

Returns

subset [same type as caller]

Raises

TypeError If the index is not a `DatetimeIndex`

See also:

first Select initial periods of time series based on a date offset.

at_time Select values at a particular time of the day.

between_time Select values between particular times of the day.

Examples

```
>>> i = pd.date_range('2018-04-09', periods=4, freq='2D')   # doctest: +SKIP
>>> ts = pd.DataFrame({'A': [1,2,3,4]}, index=i)   # doctest: +SKIP
>>> ts  # doctest: +SKIP
            A
2018-04-09  1
2018-04-11  2
2018-04-13  3
2018-04-15  4
```

Get the rows for the last 3 days:

```
>>> ts.last('3D')  # doctest: +SKIP
            A
2018-04-13  3
2018-04-15  4
```

Notice the data for 3 last calender days were returned, not the last 3 observed days in the dataset, and therefore data for 2018-04-11 was not returned.

le (*other*, *level=None*, *fill_value=None*, *axis=0*)

Less than or equal to of series and other, element-wise (binary operator *le*).

Equivalent to `series <= other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

loc

Purely label-location based indexer for selection by label.

```
>>> df.loc["b"]  # doctest: +SKIP
>>> df.loc["b":"d"]  # doctest: +SKIP
```

lt (*other*, *level=None*, *fill_value=None*, *axis=0*)

Less than of series and other, element-wise (binary operator *lt*).

Equivalent to `series < other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

map(*arg*, *na_action=None*, *meta='__no_default__'*)

Map values of Series according to input correspondence.

This docstring was copied from pandas.core.series.Series.map.

Some inconsistencies with the Dask version may exist.

Used for substituting each value in a Series with another value, that may be derived from a function, a `dict` or a *`Series`*.

Parameters

arg [function, dict, or Series] Mapping correspondence.

na_action [{None, 'ignore'}, default None] If 'ignore', propagate NaN values, without passing them to the mapping correspondence.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

Series Same index as caller.

See also:

Series.apply For applying more complex functions on a Series.

DataFrame.apply Apply a function row-/column-wise.

DataFrame.applymap Apply a function elementwise on a whole DataFrame.

Notes

When `arg` is a dictionary, values in Series that are not in the dictionary (as keys) are converted to `NaN`. However, if the dictionary is a `dict` subclass that defines `__missing__` (i.e. provides a method for default values), then this default is used rather than `NaN`.

Examples

```
>>> s = pd.Series(['cat', 'dog', np.nan, 'rabbit'])  # doctest: +SKIP
>>> s  # doctest: +SKIP
0      cat
1      dog
2      NaN
3   rabbit
dtype: object
```

`map` accepts a `dict` or a `Series`. Values that are not found in the `dict` are converted to `NaN`, unless the dict has a default value (e.g. `defaultdict`):

```
>>> s.map({'cat': 'kitten', 'dog': 'puppy'})  # doctest: +SKIP
0   kitten
1    puppy
2      NaN
3      NaN
dtype: object
```

It also accepts a function:

```
>>> s.map('I am a {}'.format)  # doctest: +SKIP
0       I am a cat
1       I am a dog
2       I am a nan
3    I am a rabbit
dtype: object
```

To avoid applying the function to missing values (and keep them as `NaN`) `na_action='ignore'` can be used:

```
>>> s.map('I am a {}'.format, na_action='ignore')  # doctest: +SKIP
0     I am a cat
1     I am a dog
2            NaN
3  I am a rabbit
dtype: object
```

map_overlap (*func*, *before*, *after*, **args*, ***kwargs*)

Apply a function to each partition, sharing rows with adjacent partitions.

This can be useful for implementing windowing functions such as `df.rolling(...).mean()` or `df.diff()`.

Parameters

func [function] Function applied to each partition.

before [int] The number of rows to prepend to partition `i` from the end of partition `i - 1`.

after [int] The number of rows to append to partition `i` from the beginning of partition `i + 1`.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Notes

Given positive integers `before` and `after`, and a function `func`, `map_overlap` does the following:

1. Prepend `before` rows to each partition `i` from the end of partition `i - 1`. The first partition has no rows prepended.
2. Append `after` rows to each partition `i` from the beginning of partition `i + 1`. The last partition has no rows appended.
3. Apply `func` to each partition, passing in any extra `args` and `kwargs` if provided.
4. Trim `before` rows from the beginning of all but the first partition.
5. Trim `after` rows from the end of all but the last partition.

Note that the index and divisions are assumed to remain unchanged.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 4, 7, 11],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

A rolling sum with a trailing moving window of size 2 can be computed by overlapping 2 rows before each partition, and then mapping calls to `df.rolling(2).sum()`:

```
>>> ddf.compute()
    x    y
0   1  1.0
1   2  2.0
2   4  3.0
3   7  4.0
4  11  5.0
>>> ddf.map_overlap(lambda df: df.rolling(2).sum(), 2, 0).compute()
      x    y
0   NaN  NaN
1   3.0  3.0
2   6.0  5.0
3  11.0  7.0
4  18.0  9.0
```

The pandas `diff` method computes a discrete difference shifted by a number of periods (can be positive or negative). This can be implemented by mapping calls to `df.diff` to each partition after prepending/appending that many rows, depending on sign:

```
>>> def diff(df, periods=1):
...     before, after = (periods, 0) if periods > 0 else (0, -periods)
...     return df.map_overlap(lambda df, periods=1: df.diff(periods),
...                           periods, 0, periods=periods)
>>> diff(ddf, 1).compute()
     x    y
0  NaN  NaN
1  1.0  1.0
2  2.0  1.0
3  3.0  1.0
4  4.0  1.0
```

If you have a `DatetimeIndex`, you can use a `pd.Timedelta` for time- based windows.

```
>>> ts = pd.Series(range(10), index=pd.date_range('2017', periods=10))
>>> dts = dd.from_pandas(ts, npartitions=2)
>>> dts.map_overlap(lambda df: df.rolling('2D').sum(),
...                 pd.Timedelta('2D'), 0).compute()
2017-01-01     0.0
2017-01-02     1.0
2017-01-03     3.0
2017-01-04     5.0
2017-01-05     7.0
2017-01-06     9.0
2017-01-07    11.0
2017-01-08    13.0
2017-01-09    15.0
2017-01-10    17.0
dtype: float64
```

`map_partitions` (*func*, **args*, ***kwargs*)

Apply Python function on each DataFrame partition.

Note that the index and divisions are assumed to remain unchanged.

Parameters

func [function] Function applied to each partition.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*. Arguments and keywords may contain `Scalar`, `Delayed` or regular python objects. DataFrame-like args (both dask and pandas) will be repartitioned to align (if necessary) before applying the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Examples

Given a DataFrame, Series, or Index, such as:

```
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': [1, 2, 3, 4, 5],
...                    'y': [1., 2., 3., 4., 5.]})
>>> ddf = dd.from_pandas(df, npartitions=2)
```

One can use `map_partitions` to apply a function on each partition. Extra arguments and keywords can optionally be provided, and will be passed to the function after the partition.

Here we apply a function with arguments and keywords to a DataFrame, resulting in a Series:

```
>>> def myadd(df, a, b=1):
...     return df.x + df.y + a + b
>>> res = ddf.map_partitions(myadd, 1, b=2)
>>> res.dtype
dtype('float64')
```

By default, dask tries to infer the output metadata by running your provided function on some fake data. This works well in many cases, but can sometimes be expensive, or even fail. To avoid this, you can manually specify the output metadata with the `meta` keyword. This can be specified in many forms, for more information see `dask.dataframe.utils.make_meta`.

Here we specify the output is a Series with no name, and dtype `float64`:

```
>>> res = ddf.map_partitions(myadd, 1, b=2, meta=(None, 'f8'))
```

Here we map a function that takes in a DataFrame, and returns a DataFrame with a new column:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y))
>>> res.dtypes
x      int64
y    float64
z    float64
dtype: object
```

As before, the output metadata can also be specified manually. This time we pass in a `dict`, as the output is a DataFrame:

```
>>> res = ddf.map_partitions(lambda df: df.assign(z=df.x * df.y),
...                          meta={'x': 'i8', 'y': 'f8', 'z': 'f8'})
```

In the case where the metadata doesn't change, you can also pass in the object itself directly:

```
>>> res = ddf.map_partitions(lambda df: df.head(), meta=df)
```

Also note that the index and divisions are assumed to remain unchanged. If the function you're mapping changes the index/divisions, you'll need to clear them afterwards:

```
>>> ddf.map_partitions(func).clear_divisions()  # doctest: +SKIP
```

mask(*cond*, *other=nan*)

Replace values where the condition is True.

This docstring was copied from pandas.core.frame.DataFrame.mask.

Some inconsistencies with the Dask version may exist.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is False, keep the original value. Where True, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is True are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

axis [int, default None (Not supported in Dask)] Alignment axis if needed.

level [int, default None (Not supported in Dask)] Alignment level if needed.

errors [str, {'raise', 'ignore'}, default *raise* (Not supported in Dask)] Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

- *raise* : allow exceptions to be raised.
- *ignore* : suppress exceptions. On error return original object.

try_cast [boolean, default False (Not supported in Dask)] Try to cast the result back to the input type (if possible).

raise_on_error [boolean, default True (Not supported in Dask)] Whether to raise on invalid data types (e.g. trying to where on strings).

Deprecated since version 0.21.0: Use *errors*.

Returns

wh [same type as caller]

See also:

`DataFrame.where()` Return an object of same shape as self.

Notes

The mask method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `False` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for *`DataFrame.where()`* differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `mask` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))  # doctest: +SKIP
>>> s.where(s > 0)  # doctest: +SKIP
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
dtype: float64
```

```
>>> s.mask(s > 0)  # doctest: +SKIP
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

```
>>> s.where(s > 1, 10)  # doctest: +SKIP
0    10
1    10
2    2
3    3
4    4
dtype: int64
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])  #␣
↪doctest: +SKIP
>>> m = df % 3 == 0  # doctest: +SKIP
>>> df.where(m, -df)  # doctest: +SKIP
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)  # doctest: +SKIP
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)  # doctest: +SKIP
```

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```
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
```

max (*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return the maximum of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.max.

Some inconsistencies with the Dask version may exist.

If you want the *index* of the maximum, use `idxmax`. This is the equivalent of the `numpy.ndarray` method `argmax`.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

max [Series or DataFrame (if level specified)]

See also:

`Series.sum` Return the sum.

`Series.min` Return the minimum.

`Series.max` Return the maximum.

`Series.idxmin` Return the index of the minimum.

`Series.idxmax` Return the index of the maximum.

`DataFrame.min` Return the sum over the requested axis.

`DataFrame.min` Return the minimum over the requested axis.

`DataFrame.max` Return the maximum over the requested axis.

`DataFrame.idxmin` Return the index of the minimum over the requested axis.

`DataFrame.idxmax` Return the index of the maximum over the requested axis.

Examples

```
>>> idx = pd.MultiIndex.from_arrays([  # doctest: +SKIP
...     ['warm', 'warm', 'cold', 'cold'],
...     ['dog', 'falcon', 'fish', 'spider']],
...     names=['blooded', 'animal'])
>>> s = pd.Series([4, 2, 0, 8], name='legs', index=idx)  # doctest: +SKIP
>>> s  # doctest: +SKIP
blooded  animal
warm     dog       4
         falcon    2
cold     fish      0
         spider    8
Name: legs, dtype: int64
```

```
>>> s.max()  # doctest: +SKIP
8
```

Max using level names, as well as indices.

```
>>> s.max(level='blooded')  # doctest: +SKIP
blooded
warm    4
cold    8
Name: legs, dtype: int64
```

```
>>> s.max(level=0)  # doctest: +SKIP
blooded
warm    4
cold    8
Name: legs, dtype: int64
```

mean(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*)
Return the mean of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.mean.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

mean [Series or DataFrame (if level specified)]

memory_usage(*index=True*, *deep=False*)
Return the memory usage of the Series.

This docstring was copied from pandas.core.series.Series.memory_usage.

Some inconsistencies with the Dask version may exist.

The memory usage can optionally include the contribution of the index and of elements of *object* dtype.

Parameters

index [bool, default True] Specifies whether to include the memory usage of the Series index.

deep [bool, default False] If True, introspect the data deeply by interrogating *object* dtypes for system-level memory consumption, and include it in the returned value.

Returns

int Bytes of memory consumed.

See also:

`numpy.ndarray.nbytes` Total bytes consumed by the elements of the array.

`DataFrame.memory_usage` Bytes consumed by a DataFrame.

Examples

```
>>> s = pd.Series(range(3))  # doctest: +SKIP
>>> s.memory_usage()  # doctest: +SKIP
104
```

Not including the index gives the size of the rest of the data, which is necessarily smaller:

```
>>> s.memory_usage(index=False)  # doctest: +SKIP
24
```

The memory footprint of *object* values is ignored by default:

```
>>> s = pd.Series(["a", "b"])  # doctest: +SKIP
>>> s.values  # doctest: +SKIP
array(['a', 'b'], dtype=object)
>>> s.memory_usage()  # doctest: +SKIP
96
>>> s.memory_usage(deep=True)  # doctest: +SKIP
212
```

min(*axis=None*, *skipna=True*, *split_every=False*, *out=None*)
Return the minimum of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.min.

Some inconsistencies with the Dask version may exist.

If you want the *index* of the minimum, use `idxmin`. This is the equivalent of the `numpy.ndarray` method `argmin`.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

min [Series or DataFrame (if level specified)]

See also:

`Series.sum` Return the sum.

`Series.min` Return the minimum.

`Series.max` Return the maximum.

`Series.idxmin` Return the index of the minimum.

`Series.idxmax` Return the index of the maximum.

`DataFrame.min` Return the sum over the requested axis.

`DataFrame.min` Return the minimum over the requested axis.

`DataFrame.max` Return the maximum over the requested axis.

`DataFrame.idxmin` Return the index of the minimum over the requested axis.

`DataFrame.idxmax` Return the index of the maximum over the requested axis.

Examples

```
>>> idx = pd.MultiIndex.from_arrays([  # doctest: +SKIP
...     ['warm', 'warm', 'cold', 'cold'],
...     ['dog', 'falcon', 'fish', 'spider']],
...     names=['blooded', 'animal'])
>>> s = pd.Series([4, 2, 0, 8], name='legs', index=idx)  # doctest: +SKIP
>>> s  # doctest: +SKIP
blooded  animal
warm     dog       4
         falcon    2
cold     fish      0
         spider    8
Name: legs, dtype: int64
```

```
>>> s.min()  # doctest: +SKIP
0
```

Min using level names, as well as indices.

```
>>> s.min(level='blooded')  # doctest: +SKIP
blooded
warm    2
cold    0
Name: legs, dtype: int64
```

```
>>> s.min(level=0)  # doctest: +SKIP
blooded
warm    2
cold    0
Name: legs, dtype: int64
```

mod(*other*, *level=None*, *fill_value=None*, *axis=0*)
Modulo of series and other, element-wise (binary operator *mod*).

Equivalent to `series % other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

Series.rmod

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

mul(*other*, *level=None*, *fill_value=None*, *axis=0*)
Multiplication of series and other, element-wise (binary operator *mul*).

Equivalent to `series * other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

`Series.rmul`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

nbytes
Number of bytes

ndim
Return dimensionality

ne(*other*, *level=None*, *fill_value=None*, *axis=0*)
Not equal to of series and other, element-wise (binary operator *ne*).

Equivalent to `series != other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

`Series.None`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

`nlargest`(*n=5*, *split_every=None*)

Return the largest *n* elements.

This docstring was copied from pandas.core.series.Series.nlargest.

Some inconsistencies with the Dask version may exist.

Parameters

n [int, default 5] Return this many descending sorted values.

keep [{'first', 'last', 'all'}, default 'first' (Not supported in Dask)] When there are duplicate values that cannot all fit in a Series of *n* elements:

- `first` : take the first occurrences based on the index order
- `last` : take the last occurrences based on the index order
- **`all`** [keep all occurrences. This can result in a Series of] size larger than *n*.

Returns

Series The *n* largest values in the Series, sorted in decreasing order.

See also:

`Series.nsmallest` Get the *n* smallest elements.

`Series.sort_values` Sort Series by values.

`Series.head` Return the first *n* rows.

Notes

Faster than `.sort_values(ascending=False).head(n)` for small *n* relative to the size of the `Series` object.

Examples

```
>>> countries_population = {"Italy": 59000000, "France": 65000000,   #␣
↪doctest: +SKIP
...                          "Malta": 434000, "Maldives": 434000,
...                          "Brunei": 434000, "Iceland": 337000,
...                          "Nauru": 11300, "Tuvalu": 11300,
...                          "Anguilla": 11300, "Monserat": 5200}
>>> s = pd.Series(countries_population)   # doctest: +SKIP
>>> s  # doctest: +SKIP
Italy       59000000
France      65000000
Malta         434000
Maldives      434000
Brunei        434000
Iceland       337000
Nauru          11300
Tuvalu         11300
Anguilla       11300
Monserat        5200
dtype: int64
```

The *n* largest elements where `n=5` by default.

```
>>> s.nlargest()  # doctest: +SKIP
France      65000000
Italy       59000000
Malta         434000
Maldives      434000
Brunei        434000
dtype: int64
```

The *n* largest elements where `n=3`. Default *keep* value is 'first' so Malta will be kept.

```
>>> s.nlargest(3)  # doctest: +SKIP
France    65000000
Italy     59000000
Malta       434000
dtype: int64
```

The *n* largest elements where `n=3` and keeping the last duplicates. Brunei will be kept since it is the last with value 434000 based on the index order.

```
>>> s.nlargest(3, keep='last')  # doctest: +SKIP
France      65000000
Italy       59000000
Brunei        434000
dtype: int64
```

The *n* largest elements where `n=3` with all duplicates kept. Note that the returned Series has five elements due to the three duplicates.

```
>>> s.nlargest(3, keep='all')  # doctest: +SKIP
France      65000000
Italy       59000000
Malta         434000
Maldives      434000
Brunei        434000
dtype: int64
```

notnull()

Detect existing (non-missing) values.

This docstring was copied from pandas.core.frame.DataFrame.notnull.

Some inconsistencies with the Dask version may exist.

Return a boolean same-sized object indicating if the values are not NA. Non-missing values get mapped to True. Characters such as empty strings `''` or `numpy.inf` are not considered NA values (unless you set `pandas.options.mode.use_inf_as_na = True`). NA values, such as None or `numpy.NaN`, get mapped to False values.

Returns

DataFrame Mask of bool values for each element in DataFrame that indicates whether an element is not an NA value.

See also:

DataFrame.notnull Alias of notna.

DataFrame.isna Boolean inverse of notna.

DataFrame.dropna Omit axes labels with missing values.

notna Top-level notna.

Examples

Show which entries in a DataFrame are not NA.

```
>>> df = pd.DataFrame({'age': [5, 6, np.NaN],  # doctest: +SKIP
...                    'born': [pd.NaT, pd.Timestamp('1939-05-27'),
...                             pd.Timestamp('1940-04-25')],
...                    'name': ['Alfred', 'Batman', ''],
...                    'toy': [None, 'Batmobile', 'Joker']})
>>> df  # doctest: +SKIP
   age       born    name        toy
0  5.0        NaT  Alfred       None
1  6.0 1939-05-27  Batman  Batmobile
2  NaN 1940-04-25                Joker
```

```
>>> df.notna()  # doctest: +SKIP
     age   born  name    toy
0   True  False  True  False
1   True   True  True   True
2  False   True  True   True
```

Show which entries in a Series are not NA.

```
>>> ser = pd.Series([5, 6, np.NaN])  # doctest: +SKIP
>>> ser  # doctest: +SKIP
0    5.0
1    6.0
2    NaN
dtype: float64
```

```
>>> ser.notna()  # doctest: +SKIP
0     True
1     True
2    False
dtype: bool
```

npartitions
Return number of partitions

nsmallest (*n=5*, *split_every=None*)
Return the smallest *n* elements.

This docstring was copied from pandas.core.series.Series.nsmallest.

Some inconsistencies with the Dask version may exist.

Parameters

n [int, default 5] Return this many ascending sorted values.

keep [{'first', 'last', 'all'}, default 'first' (Not supported in Dask)] When there are duplicate values that cannot all fit in a Series of *n* elements:

- `first` : take the first occurrences based on the index order
- `last` : take the last occurrences based on the index order
- **`all`** [keep all occurrences. This can result in a Series of] size larger than *n*.

Returns

Series The *n* smallest values in the Series, sorted in increasing order.

See also:

Series.nlargest Get the *n* largest elements.

Series.sort_values Sort Series by values.

Series.head Return the first *n* rows.

Notes

Faster than `.sort_values().head(n)` for small *n* relative to the size of the `Series` object.

Examples

```
>>> countries_population = {"Italy": 59000000, "France": 65000000,  #␣
↪doctest: +SKIP
...                         "Brunei": 434000, "Malta": 434000,
...                         "Maldives": 434000, "Iceland": 337000,
...                         "Nauru": 11300, "Tuvalu": 11300,
...                         "Anguilla": 11300, "Monserat": 5200}
>>> s = pd.Series(countries_population)  # doctest: +SKIP
>>> s  # doctest: +SKIP
Italy       59000000
France      65000000
Brunei        434000
Malta         434000
Maldives      434000
Iceland       337000
Nauru          11300
Tuvalu         11300
Anguilla       11300
Monserat        5200
dtype: int64
```

The *n* largest elements where `n=5` by default.

```
>>> s.nsmallest()  # doctest: +SKIP
Monserat      5200
Nauru        11300
Tuvalu       11300
Anguilla     11300
Iceland     337000
dtype: int64
```

The *n* smallest elements where `n=3`. Default *keep* value is 'first' so Nauru and Tuvalu will be kept.

```
>>> s.nsmallest(3)  # doctest: +SKIP
Monserat     5200
Nauru       11300
Tuvalu      11300
dtype: int64
```

The *n* smallest elements where `n=3` and keeping the last duplicates. Anguilla and Tuvalu will be kept since they are the last with value 11300 based on the index order.

```
>>> s.nsmallest(3, keep='last')  # doctest: +SKIP
Monserat     5200
Anguilla    11300
```

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```
Tuvalu      11300
dtype: int64
```

The *n* smallest elements where `n=3` with all duplicates kept. Note that the returned Series has four elements due to the three duplicates.

```
>>> s.nsmallest(3, keep='all')  # doctest: +SKIP
Monserat     5200
Nauru       11300
Tuvalu      11300
Anguilla    11300
dtype: int64
```

nunique(*split_every=None*)

Return number of unique elements in the object.

This docstring was copied from pandas.core.series.Series.nunique.

Some inconsistencies with the Dask version may exist.

Excludes NA values by default.

Parameters

dropna [boolean, default True (Not supported in Dask)] Don't include NaN in the count.

Returns

nunique [int]

nunique_approx(*split_every=None*)

Approximate number of unique rows.

This method uses the HyperLogLog algorithm for cardinality estimation to compute the approximate number of unique rows. The approximate error is 0.406%.

Parameters

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used. Default is 8.

Returns

a float representing the approximate number of elements

partitions

Slice dataframe by partitions

This allows partitionwise slicing of a Dask Dataframe. You can perform normal Numpy-style slicing but now rather than slice elements of the array you slice along partitions so, for example, `df.partitions[:5]` produces a new Dask Dataframe of the first five partitions.

Returns

A Dask DataFrame

Examples

```
>>> df.partitions[0]  # doctest: +SKIP
>>> df.partitions[:3]  # doctest: +SKIP
>>> df.partitions[::10]  # doctest: +SKIP
```

persist(***kwargs*)

Persist this dask collection into memory

This turns a lazy Dask collection into a Dask collection with the same metadata, but now with the results fully computed or actively computing in the background.

The action of function differs significantly depending on the active task scheduler. If the task scheduler supports asynchronous computing, such as is the case of the dask.distributed scheduler, then persist will return *immediately* and the return value's task graph will contain Dask Future objects. However if the task scheduler only supports blocking computation then the call to persist will *block* and the return value's task graph will contain concrete Python results.

This function is particularly useful when using distributed systems, because the results will be kept in distributed memory, rather than returned to the local process as with compute.

Parameters

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

****kwargs** Extra keywords to forward to the scheduler function.

Returns

New dask collections backed by in-memory data

See also:

`dask.base.persist`

pipe(*func*, **args*, ***kwargs*)

Apply func(self, *args, **kwargs).

This docstring was copied from pandas.core.frame.DataFrame.pipe.

Some inconsistencies with the Dask version may exist.

Parameters

func [function] function to apply to the NDFrame. `args`, and `kwargs` are passed into `func`. Alternatively a `(callable, data_keyword)` tuple where `data_keyword` is a string indicating the keyword of `callable` that expects the NDFrame.

args [iterable, optional] positional arguments passed into `func`.

kwargs [mapping, optional] a dictionary of keyword arguments passed into `func`.

Returns

object [the return type of `func`.]

See also:

`DataFrame.apply`, *`DataFrame.applymap`*, *`Series.map`*

Notes

Use `.pipe` when chaining together functions that expect Series, DataFrames or GroupBy objects. Instead of writing

```
>>> f(g(h(df), arg1=a), arg2=b, arg3=c)  # doctest: +SKIP
```

You can write

```
>>> (df.pipe(h)  # doctest: +SKIP
...    .pipe(g, arg1=a)
...    .pipe(f, arg2=b, arg3=c)
... )
```

If you have a function that takes the data as (say) the second argument, pass a tuple indicating which keyword expects the data. For example, suppose `f` takes its data as `arg2`:

```
>>> (df.pipe(h)  # doctest: +SKIP
...    .pipe(g, arg1=a)
...    .pipe((f, 'arg2'), arg1=a, arg3=c)
...  )
```

pow(*other*, *level=None*, *fill_value=None*, *axis=0*)

Exponential power of series and other, element-wise (binary operator *pow*).

Equivalent to `series ** other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

`Series.rpow`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
```

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```
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

prod(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*, *min_count=None*)
Return the product of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.prod.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

prod [Series or DataFrame (if level specified)]

Examples

By default, the product of an empty or all-NA Series is `1`

```
>>> pd.Series([]).prod()  # doctest: +SKIP
1.0
```

This can be controlled with the `min_count` parameter

```
>>> pd.Series([]).prod(min_count=1)  # doctest: +SKIP
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).prod()  # doctest: +SKIP
1.0
```

```
>>> pd.Series([np.nan]).prod(min_count=1)  # doctest: +SKIP
nan
```

quantile(*q=0.5*, *method='default'*)
Approximate quantiles of Series

Parameters

q [list/array of floats, default 0.5 (50%)] Iterable of numbers ranging from 0 to 1 for the desired quantiles

method [{'default', 'tdigest', 'dask'}, optional] What method to use. By default will use dask's internal custom algorithm (`'dask'`). If set to `'tdigest'` will use tdigest for floats and ints and fallback to the `'dask'` otherwise.

radd(*other*, *level=None*, *fill_value=None*, *axis=0*)
Addition of series and other, element-wise (binary operator *radd*).

Equivalent to `other + series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.add

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
```

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```
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

random_split (*frac*, *random_state=None*)

Pseudorandomly split dataframe into different pieces row-wise

Parameters

frac [list] List of floats that should sum to one.

random_state: int or np.random.RandomState If int create a new RandomState with this as the seed

Otherwise draw from the passed RandomState

See also:

`dask.DataFrame.sample`

Examples

50/50 split

```
>>> a, b = df.random_split([0.5, 0.5])  # doctest: +SKIP
```

80/10/10 split, consistent random_state

```
>>> a, b, c = df.random_split([0.8, 0.1, 0.1], random_state=123)  # doctest:␣
↪+SKIP
```

rdiv (*other*, *level=None*, *fill_value=None*, *axis=0*)

Floating division of series and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

`Series.truediv`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

reduction(*chunk*, *aggregate=None*, *combine=None*, *meta='__no_default__'*, *token=None*, *split_every=None*, *chunk_kwargs=None*, *aggregate_kwargs=None*, *combine_kwargs=None*, ***kwargs*)
Generic row-wise reductions.

Parameters

chunk [callable] Function to operate on each partition. Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

aggregate [callable, optional] Function to operate on the concatenated result of `chunk`. If not specified, defaults to `chunk`. Used to do the final aggregation in a tree reduction.

The input to `aggregate` depends on the output of `chunk`. If the output of `chunk` is a:

- scalar: Input is a Series, with one row per partition.
- Series: Input is a DataFrame, with one row per partition. Columns are the rows in the output series.
- DataFrame: Input is a DataFrame, with one row per partition. Columns are the columns in the output dataframes.

Should return a `pandas.DataFrame`, `pandas.Series`, or a scalar.

combine [callable, optional] Function to operate on intermediate concatenated results of `chunk` in a tree-reduction. If not provided, defaults to `aggregate`. The input/output requirements should match that of `aggregate` described above.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a dict of {name: dtype} or iterable of (name, dtype) can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of (name, dtype) can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing meta is recommended. For more information, see dask.dataframe.utils.make_meta.

token [str, optional] The name to use for the output keys.

split_every [int, optional] Group partitions into groups of this size while performing a tree-reduction. If set to False, no tree-reduction will be used, and all intermediates will be concatenated and passed to aggregate. Default is 8.

chunk_kwargs [dict, optional] Keyword arguments to pass on to chunk only.

aggregate_kwargs [dict, optional] Keyword arguments to pass on to aggregate only.

combine_kwargs [dict, optional] Keyword arguments to pass on to combine only.

kwargs : All remaining keywords will be passed to chunk, combine, and aggregate.

Examples

```
>>> import pandas as pd
>>> import dask.dataframe as dd
>>> df = pd.DataFrame({'x': range(50), 'y': range(50, 100)})
>>> ddf = dd.from_pandas(df, npartitions=4)
```

Count the number of rows in a DataFrame. To do this, count the number of rows in each partition, then sum the results:

```
>>> res = ddf.reduction(lambda x: x.count(),
...                     aggregate=lambda x: x.sum())
>>> res.compute()
x     50
y     50
dtype: int64
```

Count the number of rows in a Series with elements greater than or equal to a value (provided via a keyword).

```
>>> def count_greater(x, value=0):
...     return (x >= value).sum()
>>> res = ddf.x.reduction(count_greater, aggregate=lambda x: x.sum(),
...                       chunk_kwargs={'value': 25})
>>> res.compute()
25
```

Aggregate both the sum and count of a Series at the same time:

```
>>> def sum_and_count(x):
...     return pd.Series({'count': x.count(), 'sum': x.sum()},
...                      index=['count', 'sum'])
>>> res = ddf.x.reduction(sum_and_count, aggregate=lambda x: x.sum())
>>> res.compute()
count      50
sum      1225
dtype: int64
```

Doing the same, but for a DataFrame. Here `chunk` returns a DataFrame, meaning the input to `aggregate` is a DataFrame with an index with non-unique entries for both 'x' and 'y'. We groupby the index, and sum each group to get the final result.

```
>>> def sum_and_count(x):
...     return pd.DataFrame({'count': x.count(), 'sum': x.sum()},
...                         columns=['count', 'sum'])
>>> res = ddf.reduction(sum_and_count,
...                     aggregate=lambda x: x.groupby(level=0).sum())
>>> res.compute()
   count   sum
x     50  1225
y     50  3725
```

rename(*index=None*, *inplace=False*, *sorted_index=False*)
Alter Series index labels or name

Function / dict values must be unique (1-to-1). Labels not contained in a dict / Series will be left as-is. Extra labels listed don't throw an error.

Alternatively, change `Series.name` with a scalar value.

Parameters

index [scalar, hashable sequence, dict-like or callable, optional] If dict-like or callable, the transformation is applied to the index. Scalar or hashable sequence-like will alter the `Series.name` attribute.

inplace [boolean, default False] Whether to return a new Series or modify this one in-place.

sorted_index [bool, default False] If true, the output `Series` will have known divisions inferred from the input series and the transformation. Ignored for non-callable/dict-like `index` or when the input series has unknown divisions. Note that this may only be set to `True` if you know that the transformed index is monotonicly increasing. Dask will check that transformed divisions are monotonic, but cannot check all the values between divisions, so incorrectly setting this can result in bugs.

Returns

renamed [Series]

See also:

`pandas.Series.rename`

repartition(*divisions=None*, *npartitions=None*, *partition_size=None*, *freq=None*, *force=False*)
Repartition dataframe along new divisions

Parameters

divisions [list, optional] List of partitions to be used. Only used if npartitions and partition_size isn't specified.

npartitions [int, optional] Number of partitions of output. Only used if partition_size isn't specified.

partition_size: int or string, optional Max number of bytes of memory for each partition. Use numbers or strings like 5MB. If specified npartitions and divisions will be ignored.

> **Warning:** This keyword argument triggers computation to determine the memory size of each partition, which may be expensive.

freq [str, pd.Timedelta] A period on which to partition timeseries data like `'7D'` or `'12h'` or `pd.Timedelta(hours=12)`. Assumes a datetime index.

force [bool, default False] Allows the expansion of the existing divisions. If False then the new divisions lower and upper bounds must be the same as the old divisions.

Notes

Exactly one of *divisions*, *npartitions*, *partition_size*, or *freq* should be specified. A `ValueError` will be raised when that is not the case.

Examples

```
>>> df = df.repartition(npartitions=10)  # doctest: +SKIP
>>> df = df.repartition(divisions=[0, 5, 10, 20])  # doctest: +SKIP
>>> df = df.repartition(freq='7d')  # doctest: +SKIP
```

replace(*to_replace=None*, *value=None*, *regex=False*)

Replace values given in *to_replace* with *value*.

This docstring was copied from pandas.core.frame.DataFrame.replace.

Some inconsistencies with the Dask version may exist.

Values of the DataFrame are replaced with other values dynamically. This differs from updating with `.loc` or `.iloc`, which require you to specify a location to update with some value.

Parameters

to_replace [str, regex, list, dict, Series, int, float, or None] How to find the values that will be replaced.

- numeric, str or regex:
  - numeric: numeric values equal to *to_replace* will be replaced with *value*
  - str: string exactly matching *to_replace* will be replaced with *value*
  - regex: regexs matching *to_replace* will be replaced with *value*
- list of str, regex, or numeric:
  - First, if *to_replace* and *value* are both lists, they **must** be the same length.
  - Second, if `regex=True` then all of the strings in **both** lists will be interpreted as regexs otherwise they will match directly. This doesn't matter much for *value* since there are only a few possible substitution regexes you can use.
  - str, regex and numeric rules apply as above.
- dict:
  - Dicts can be used to specify different replacement values for different existing values. For example, `{'a': 'b', 'y': 'z'}` replaces the value 'a' with 'b' and 'y' with 'z'. To use a dict in this way the *value* parameter should be *None*.

- For a DataFrame a dict can specify that different values should be replaced in different columns. For example, `{'a': 1, 'b': 'z'}` looks for the value 1 in column 'a' and the value 'z' in column 'b' and replaces these values with whatever is specified in *value*. The *value* parameter should not be `None` in this case. You can treat this as a special case of passing two lists except that you are specifying the column to search in.
- For a DataFrame nested dictionaries, e.g., `{'a': {'b': np.nan}}`, are read as follows: look in column 'a' for the value 'b' and replace it with NaN. The *value* parameter should be `None` to use a nested dict in this way. You can nest regular expressions as well. Note that column names (the top-level dictionary keys in a nested dictionary) **cannot** be regular expressions.

• None:

- This means that the *regex* argument must be a string, compiled regular expression, or list, dict, ndarray or Series of such elements. If *value* is also `None` then this **must** be a nested dictionary or Series.

See the examples section for examples of each of these.

value [scalar, dict, list, str, regex, default None] Value to replace any values matching *to_replace* with. For a DataFrame a dict of values can be used to specify which value to use for each column (columns not in the dict will not be filled). Regular expressions, strings and lists or dicts of such objects are also allowed.

inplace [bool, default False (Not supported in Dask)] If True, in place. Note: this will modify any other views on this object (e.g. a column from a DataFrame). Returns the caller if this is True.

limit [int, default None (Not supported in Dask)] Maximum size gap to forward or backward fill.

regex [bool or same types as *to_replace*, default False] Whether to interpret *to_replace* and/or *value* as regular expressions. If this is `True` then *to_replace must* be a string. Alternatively, this could be a regular expression or a list, dict, or array of regular expressions in which case *to_replace* must be `None`.

method [{'pad', 'ffill', 'bfill', *None*} (Not supported in Dask)] The method to use when for replacement, when *to_replace* is a scalar, list or tuple and *value* is `None`.

Changed in version 0.23.0: Added to DataFrame.

Returns

DataFrame Object after replacement.

Raises

AssertionError

• If *regex* is not a `bool` and *to_replace* is not `None`.

TypeError

• If *to_replace* is a `dict` and *value* is not a `list`, `dict`, `ndarray`, or `Series`

• If *to_replace* is `None` and *regex* is not compilable into a regular expression or is a list, dict, ndarray, or Series.

• When replacing multiple `bool` or `datetime64` objects and the arguments to *to_replace* does not match the type of the value being replaced

ValueError

- If a `list` or an `ndarray` is passed to *to_replace* and *value* but they are not the same length.

See also:

`DataFrame.fillna` Fill NA values.

`DataFrame.where` Replace values based on boolean condition.

`Series.str.replace` Simple string replacement.

Notes

- Regex substitution is performed under the hood with `re.sub`. The rules for substitution for `re.sub` are the same.
- Regular expressions will only substitute on strings, meaning you cannot provide, for example, a regular expression matching floating point numbers and expect the columns in your frame that have a numeric dtype to be matched. However, if those floating point numbers *are* strings, then you can do this.
- This method has *a lot* of options. You are encouraged to experiment and play with this method to gain intuition about how it works.
- When dict is used as the *to_replace* value, it is like key(s) in the dict are the to_replace part and value(s) in the dict are the value parameter.

Examples

Scalar ‘to_replace‘ and ‘value‘

```
>>> s = pd.Series([0, 1, 2, 3, 4])  # doctest: +SKIP
>>> s.replace(0, 5)  # doctest: +SKIP
0    5
1    1
2    2
3    3
4    4
dtype: int64
```

```
>>> df = pd.DataFrame({'A': [0, 1, 2, 3, 4],  # doctest: +SKIP
...                    'B': [5, 6, 7, 8, 9],
...                    'C': ['a', 'b', 'c', 'd', 'e']})
>>> df.replace(0, 5)  # doctest: +SKIP
   A  B  C
0  5  5  a
1  1  6  b
2  2  7  c
3  3  8  d
4  4  9  e
```

List-like ‘to_replace‘

```
>>> df.replace([0, 1, 2, 3], 4)  # doctest: +SKIP
   A  B  C
0  4  5  a
1  4  6  b
```

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```
2  4  7  c
3  4  8  d
4  4  9  e
```

```
>>> df.replace([0, 1, 2, 3], [4, 3, 2, 1])  # doctest: +SKIP
   A  B  C
0  4  5  a
1  3  6  b
2  2  7  c
3  1  8  d
4  4  9  e
```

```
>>> s.replace([1, 2], method='bfill')  # doctest: +SKIP
0    0
1    3
2    3
3    3
4    4
dtype: int64
```

dict-like ‘to_replace‘

```
>>> df.replace({0: 10, 1: 100})  # doctest: +SKIP
     A  B  C
0   10  5  a
1  100  6  b
2    2  7  c
3    3  8  d
4    4  9  e
```

```
>>> df.replace({'A': 0, 'B': 5}, 100)  # doctest: +SKIP
     A    B  C
0  100  100  a
1    1    6  b
2    2    7  c
3    3    8  d
4    4    9  e
```

```
>>> df.replace({'A': {0: 100, 4: 400}})  # doctest: +SKIP
     A  B  C
0  100  5  a
1    1  6  b
2    2  7  c
3    3  8  d
4  400  9  e
```

Regular expression ‘to_replace‘

```
>>> df = pd.DataFrame({'A': ['bat', 'foo', 'bait'],  # doctest: +SKIP
...                    'B': ['abc', 'bar', 'xyz']})
>>> df.replace(to_replace=r'^ba.$', value='new', regex=True)  # doctest:␣
↪+SKIP
      A    B
0   new  abc
1   foo  new
```

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```
2  bait  xyz
```

```
>>> df.replace({'A': r'^ba.$'}, {'A': 'new'}, regex=True)  # doctest: +SKIP
      A    B
0   new  abc
1   foo  bar
2  bait  xyz
```

```
>>> df.replace(regex=r'^ba.$', value='new')  # doctest: +SKIP
      A    B
0   new  abc
1   foo  new
2  bait  xyz
```

```
>>> df.replace(regex={r'^ba.$': 'new', 'foo': 'xyz'})  # doctest: +SKIP
      A    B
0   new  abc
1   xyz  new
2  bait  xyz
```

```
>>> df.replace(regex=[r'^ba.$', 'foo'], value='new')  # doctest: +SKIP
      A    B
0   new  abc
1   new  new
2  bait  xyz
```

Note that when replacing multiple `bool` or `datetime64` objects, the data types in the *to_replace* parameter must match the data type of the value being replaced:

```
>>> df = pd.DataFrame({'A': [True, False, True],  # doctest: +SKIP
...                    'B': [False, True, False]})
>>> df.replace({'a string': 'new value', True: False})  # raises  # doctest:␣
↪+SKIP
Traceback (most recent call last):
    ...
TypeError: Cannot compare types 'ndarray(dtype=bool)' and 'str'
```

This raises a `TypeError` because one of the `dict` keys is not of the correct type for replacement.

Compare the behavior of `s.replace({'a': None})` and `s.replace('a', None)` to understand the peculiarities of the *to_replace* parameter:

```
>>> s = pd.Series([10, 'a', 'a', 'b', 'a'])  # doctest: +SKIP
```

When one uses a dict as the *to_replace* value, it is like the value(s) in the dict are equal to the *value* parameter. `s.replace({'a': None})` is equivalent to `s.replace(to_replace={'a': None}, value=None, method=None)`:

```
>>> s.replace({'a': None})  # doctest: +SKIP
0      10
1    None
2    None
3       b
4    None
dtype: object
```

When `value=None` and *to_replace* is a scalar, list or tuple, *replace* uses the method parameter (default 'pad') to do the replacement. So this is why the 'a' values are being replaced by 10 in rows 1 and 2 and 'b' in row 4 in this case. The command `s.replace('a', None)` is actually equivalent to `s.replace(to_replace='a', value=None, method='pad')`:

```
>>> s.replace('a', None)  # doctest: +SKIP
0    10
1    10
2    10
3     b
4     b
dtype: object
```

resample(*rule*, *closed=None*, *label=None*)

Resample time-series data.

This docstring was copied from pandas.core.frame.DataFrame.resample.

Some inconsistencies with the Dask version may exist.

Convenience method for frequency conversion and resampling of time series. Object must have a datetime-like index (*DatetimeIndex*, *PeriodIndex*, or *TimedeltaIndex*), or pass datetime-like values to the *on* or *level* keyword.

Parameters

rule [str] The offset string or object representing target conversion.

how [str (Not supported in Dask)] Method for down/re-sampling, default to 'mean' for downsampling.

Deprecated since version 0.18.0: The new syntax is `.resample(...).mean()`, or `.resample(...).apply(<func>)`

axis [{0 or 'index', 1 or 'columns'}, default 0 (Not supported in Dask)] Which axis to use for up- or down-sampling. For *Series* this will default to 0, i.e. along the rows. Must be *DatetimeIndex*, *TimedeltaIndex* or *PeriodIndex*.

fill_method [str, default None (Not supported in Dask)] Filling method for upsampling.

Deprecated since version 0.18.0: The new syntax is `.resample(...).<func>()`, e.g. `.resample(...).pad()`

closed [{'right', 'left'}, default None] Which side of bin interval is closed. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

label [{'right', 'left'}, default None] Which bin edge label to label bucket with. The default is 'left' for all frequency offsets except for 'M', 'A', 'Q', 'BM', 'BA', 'BQ', and 'W' which all have a default of 'right'.

convention [{'start', 'end', 's', 'e'}, default 'start' (Not supported in Dask)] For *PeriodIndex* only, controls whether to use the start or end of *rule*.

kind [{'timestamp', 'period'}, optional, default None (Not supported in Dask)] Pass 'timestamp' to convert the resulting index to a *DateTimeIndex* or 'period' to convert it to a *PeriodIndex*. By default the input representation is retained.

loffset [timedelta, default None (Not supported in Dask)] Adjust the resampled time labels.

limit [int, default None (Not supported in Dask)] Maximum size gap when reindexing with *fill_method*.

Deprecated since version 0.18.0.

base [int, default 0 (Not supported in Dask)] For frequencies that evenly subdivide 1 day, the "origin" of the aggregated intervals. For example, for '5min' frequency, base could range from 0 through 4. Defaults to 0.

on [str, optional (Not supported in Dask)] For a DataFrame, column to use instead of index for resampling. Column must be datetime-like.

New in version 0.19.0.

level [str or int, optional (Not supported in Dask)] For a MultiIndex, level (name or number) to use for resampling. *level* must be datetime-like.

New in version 0.19.0.

Returns

Resampler object

See also:

`groupby` Group by mapping, function, label, or list of labels.

`Series.resample` Resample a Series.

`DataFrame.resample` Resample a DataFrame.

Notes

See the user guide for more.

To learn more about the offset strings, please see this link.

Examples

Start by creating a series with 9 one minute timestamps.

```
>>> index = pd.date_range('1/1/2000', periods=9, freq='T')  # doctest: +SKIP
>>> series = pd.Series(range(9), index=index)  # doctest: +SKIP
>>> series  # doctest: +SKIP
2000-01-01 00:00:00    0
2000-01-01 00:01:00    1
2000-01-01 00:02:00    2
2000-01-01 00:03:00    3
2000-01-01 00:04:00    4
2000-01-01 00:05:00    5
2000-01-01 00:06:00    6
2000-01-01 00:07:00    7
2000-01-01 00:08:00    8
Freq: T, dtype: int64
```

Downsample the series into 3 minute bins and sum the values of the timestamps falling into a bin.

```
>>> series.resample('3T').sum()  # doctest: +SKIP
2000-01-01 00:00:00     3
2000-01-01 00:03:00    12
2000-01-01 00:06:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but label each bin using the right edge instead of the left. Please note that the value in the bucket used as the label is not included in the bucket, which it labels. For example, in the original series the bucket `2000-01-01 00:03:00` contains the value 3, but the summed value in the resampled bucket with the label `2000-01-01 00:03:00` does not include 3 (if it did, the summed value would be 6, not 3). To include this value close the right side of the bin interval as illustrated in the example below this one.

```
>>> series.resample('3T', label='right').sum()  # doctest: +SKIP
2000-01-01 00:03:00     3
2000-01-01 00:06:00    12
2000-01-01 00:09:00    21
Freq: 3T, dtype: int64
```

Downsample the series into 3 minute bins as above, but close the right side of the bin interval.

```
>>> series.resample('3T', label='right', closed='right').sum()  # doctest:␣
↪+SKIP
2000-01-01 00:00:00     0
2000-01-01 00:03:00     6
2000-01-01 00:06:00    15
2000-01-01 00:09:00    15
Freq: 3T, dtype: int64
```

Upsample the series into 30 second bins.

```
>>> series.resample('30S').asfreq()[0:5]   # Select first 5 rows  # doctest:␣
↪+SKIP
2000-01-01 00:00:00   0.0
2000-01-01 00:00:30   NaN
2000-01-01 00:01:00   1.0
2000-01-01 00:01:30   NaN
2000-01-01 00:02:00   2.0
Freq: 30S, dtype: float64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `pad` method.

```
>>> series.resample('30S').pad()[0:5]  # doctest: +SKIP
2000-01-01 00:00:00    0
2000-01-01 00:00:30    0
2000-01-01 00:01:00    1
2000-01-01 00:01:30    1
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Upsample the series into 30 second bins and fill the `NaN` values using the `bfill` method.

```
>>> series.resample('30S').bfill()[0:5]  # doctest: +SKIP
2000-01-01 00:00:00    0
2000-01-01 00:00:30    1
2000-01-01 00:01:00    1
2000-01-01 00:01:30    2
2000-01-01 00:02:00    2
Freq: 30S, dtype: int64
```

Pass a custom function via `apply`

```
>>> def custom_resampler(array_like):  # doctest: +SKIP
...     return np.sum(array_like) + 5
...
>>> series.resample('3T').apply(custom_resampler)  # doctest: +SKIP
2000-01-01 00:00:00     8
2000-01-01 00:03:00    17
2000-01-01 00:06:00    26
Freq: 3T, dtype: int64
```

For a Series with a PeriodIndex, the keyword *convention* can be used to control whether to use the start or end of *rule*.

Resample a year by quarter using 'start' *convention*. Values are assigned to the first quarter of the period.

```
>>> s = pd.Series([1, 2], index=pd.period_range('2012-01-01',  # doctest:␣
↪+SKIP
...                                                 freq='A',
...                                                 periods=2))
>>> s  # doctest: +SKIP
2012    1
2013    2
Freq: A-DEC, dtype: int64
>>> s.resample('Q', convention='start').asfreq()  # doctest: +SKIP
2012Q1    1.0
2012Q2    NaN
2012Q3    NaN
2012Q4    NaN
2013Q1    2.0
2013Q2    NaN
2013Q3    NaN
2013Q4    NaN
Freq: Q-DEC, dtype: float64
```

Resample quarters by month using 'end' *convention*. Values are assigned to the last month of the period.

```
>>> q = pd.Series([1, 2, 3, 4], index=pd.period_range('2018-01-01',  #␣
↪doctest: +SKIP
...                                                       freq='Q',
...                                                       periods=4))
>>> q  # doctest: +SKIP
2018Q1    1
2018Q2    2
2018Q3    3
2018Q4    4
Freq: Q-DEC, dtype: int64
>>> q.resample('M', convention='end').asfreq()  # doctest: +SKIP
2018-03    1.0
2018-04    NaN
2018-05    NaN
2018-06    2.0
2018-07    NaN
2018-08    NaN
2018-09    3.0
2018-10    NaN
2018-11    NaN
2018-12    4.0
Freq: M, dtype: float64
```

For DataFrame objects, the keyword *on* can be used to specify the column instead of the index for resampling.

```
>>> d = dict({'price': [10, 11, 9, 13, 14, 18, 17, 19],  # doctest: +SKIP
...           'volume': [50, 60, 40, 100, 50, 100, 40, 50]})
>>> df = pd.DataFrame(d)  # doctest: +SKIP
>>> df['week_starting'] = pd.date_range('01/01/2018',  # doctest: +SKIP
...                                     periods=8,
...                                     freq='W')
>>> df  # doctest: +SKIP
   price  volume week_starting
0     10      50    2018-01-07
1     11      60    2018-01-14
2      9      40    2018-01-21
3     13     100    2018-01-28
4     14      50    2018-02-04
5     18     100    2018-02-11
6     17      40    2018-02-18
7     19      50    2018-02-25
>>> df.resample('M', on='week_starting').mean()  # doctest: +SKIP
               price  volume
week_starting
2018-01-31     10.75    62.5
2018-02-28     17.00    60.0
```

For a DataFrame with MultiIndex, the keyword *level* can be used to specify on which level the resampling needs to take place.

```
>>> days = pd.date_range('1/1/2000', periods=4, freq='D')  # doctest: +SKIP
>>> d2 = dict({'price': [10, 11, 9, 13, 14, 18, 17, 19],  # doctest: +SKIP
...            'volume': [50, 60, 40, 100, 50, 100, 40, 50]})
>>> df2 = pd.DataFrame(d2,  # doctest: +SKIP
...                    index=pd.MultiIndex.from_product([days,
...                                                     ['morning',
...                                                      'afternoon']]
...                                                     ))
>>> df2  # doctest: +SKIP
                      price  volume
2000-01-01 morning       10      50
           afternoon     11      60
2000-01-02 morning        9      40
           afternoon     13     100
2000-01-03 morning       14      50
           afternoon     18     100
2000-01-04 morning       17      40
           afternoon     19      50
>>> df2.resample('D', level=0).sum()  # doctest: +SKIP
            price  volume
2000-01-01     21     110
2000-01-02     22     140
2000-01-03     32     150
2000-01-04     36      90
```

reset_index(*drop=False*)

Reset the index to the default index.

Note that unlike in `pandas`, the reset `dask.dataframe` index will not be monotonically increasing from 0. Instead, it will restart at 0 for each partition (e.g. `index1 = [0, ..., 10], index2 = [0, ...]`). This is due to the inability to statically know the full length of the index.

For DataFrame with multi-level index, returns a new DataFrame with labeling information in the columns under the index names, defaulting to 'level_0', 'level_1', etc. if any are None. For a standard index, the index name will be used (if set), otherwise a default 'index' or 'level_0' (if 'index' is already taken) will be used.

Parameters

drop [boolean, default False] Do not try to insert index into dataframe columns.

rfloordiv(*other*, *level=None*, *fill_value=None*, *axis=0*)

Integer division of series and other, element-wise (binary operator *rfloordiv*).

Equivalent to `other // series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.floordiv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rmod(*other*, *level=None*, *fill_value=None*, *axis=0*)

Modulo of series and other, element-wise (binary operator *rmod*).

Equivalent to `other % series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

Series.mod

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rmul(*other*, *level=None*, *fill_value=None*, *axis=0*)

Multiplication of series and other, element-wise (binary operator *rmul*).

Equivalent to `other * series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.mul

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rolling(*window*, *min_periods=None*, *center=False*, *win_type=None*, *axis=0*)
Provides rolling transformations.

Parameters

window [int, str, offset] Size of the moving window. This is the number of observations used for calculating the statistic. When not using a `DatetimeIndex`, the window size must not be so large as to span more than one adjacent partition. If using an offset or offset alias like '5D', the data must have a `DatetimeIndex`

Changed in version 0.15.0: Now accepts offsets and string offset aliases

min_periods [int, default None] Minimum number of observations in window required to have a value (otherwise result is NA).

center [boolean, default False] Set the labels at the center of the window.

win_type [string, default None] Provide a window type. The recognized window types are identical to pandas.

axis [int, default 0]

Returns

a Rolling object on which to call a method to compute a statistic

round(*decimals=0*)

Round each value in a Series to the given number of decimals.

This docstring was copied from pandas.core.series.Series.round.

Some inconsistencies with the Dask version may exist.

Parameters

decimals [int] Number of decimal places to round to (default: 0). If decimals is negative, it specifies the number of positions to the left of the decimal point.

Returns

Series object

See also:

`numpy.around`, *`DataFrame.round`*

rpow(*other, level=None, fill_value=None, axis=0*)

Exponential power of series and other, element-wise (binary operator *rpow*).

Equivalent to `other ** series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

`Series.pow`

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
```

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```
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rsub(*other*, *level=None*, *fill_value=None*, *axis=0*)
Subtraction of series and other, element-wise (binary operator *rsub*).

Equivalent to `other - series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

Series.sub

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
```

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```
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

rtruediv(*other*, *level=None*, *fill_value=None*, *axis=0*)

Floating division of series and other, element-wise (binary operator *rtruediv*).

Equivalent to `other / series`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed MultiIndex level

Returns

result [Series]

See also:

Series.truediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
```

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```
c    1.0
d    1.0
e    NaN
dtype: float64
```

sample(*n=None*, *frac=None*, *replace=False*, *random_state=None*)
Random sample of items

Parameters

n [int, optional] Number of items to return is not supported by dask. Use frac instead.

frac [float, optional] Fraction of axis items to return.

replace [boolean, optional] Sample with or without replacement. Default = False.

random_state [int or `np.random.RandomState`] If int we create a new RandomState with this as the seed Otherwise we draw from the passed RandomState

See also:

DataFrame.random_split, `pandas.DataFrame.sample`

sem(*axis=None*, *skipna=None*, *ddof=1*, *split_every=False*)
Return unbiased standard error of the mean over requested axis.

This docstring was copied from pandas.core.frame.DataFrame.sem.

Some inconsistencies with the Dask version may exist.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

sem [Series or DataFrame (if level specified)]

shape
Return a tuple representing the dimensionality of a Series.

The single element of the tuple is a Delayed result.

Examples

```
>>> series.shape  # doctest: +SKIP
# (dd.Scalar<size-ag..., dtype=int64>,)
```

shift (*periods=1*, *freq=None*, *axis=0*)

Shift index by desired number of periods with an optional time *freq*.

This docstring was copied from pandas.core.frame.DataFrame.shift.

Some inconsistencies with the Dask version may exist.

When *freq* is not passed, shift the index without realigning the data. If *freq* is passed (in this case, the index must be date or datetime, or it will raise a *NotImplementedError*), the index will be increased using the periods and the *freq*.

Parameters

periods [int] Number of periods to shift. Can be positive or negative.

freq [DateOffset, tseries.offsets, timedelta, or str, optional] Offset to use from the tseries module or time rule (e.g. 'EOM'). If *freq* is specified then the index values are shifted but the data is not realigned. That is, use *freq* if you would like to extend the index when shifting and preserve the original data.

axis [{0 or 'index', 1 or 'columns', None}, default None] Shift direction.

fill_value [object, optional (Not supported in Dask)] The scalar value to use for newly introduced missing values. the default depends on the dtype of *self*. For numeric data, `np.nan` is used. For datetime, timedelta, or period data, etc. `NaT` is used. For extension dtypes, `self.dtype.na_value` is used.

Changed in version 0.24.0.

Returns

DataFrame Copy of input object, shifted.

See also:

`Index.shift` Shift values of Index.

`DatetimeIndex.shift` Shift values of DatetimeIndex.

`PeriodIndex.shift` Shift values of PeriodIndex.

`tshift` Shift the time index, using the index's frequency if available.

Examples

```
>>> df = pd.DataFrame({'Col1': [10, 20, 15, 30, 45],  # doctest: +SKIP
...                    'Col2': [13, 23, 18, 33, 48],
...                    'Col3': [17, 27, 22, 37, 52]})
```

```
>>> df.shift(periods=3)  # doctest: +SKIP
   Col1  Col2  Col3
0   NaN   NaN   NaN
1   NaN   NaN   NaN
2   NaN   NaN   NaN
3  10.0  13.0  17.0
4  20.0  23.0  27.0
```

```
>>> df.shift(periods=1, axis='columns')  # doctest: +SKIP
   Col1  Col2  Col3
0   NaN  10.0  13.0
```

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```
1   NaN  20.0  23.0
2   NaN  15.0  18.0
3   NaN  30.0  33.0
4   NaN  45.0  48.0
```

```
>>> df.shift(periods=3, fill_value=0)  # doctest: +SKIP
   Col1  Col2  Col3
0     0     0     0
1     0     0     0
2     0     0     0
3    10    13    17
4    20    23    27
```

size

Size of the Series or DataFrame as a Delayed object.

Examples

```
>>> series.size  # doctest: +SKIP
dd.Scalar<size-ag..., dtype=int64>
```

squeeze()

Squeeze 1 dimensional axis objects into scalars.

This docstring was copied from pandas.core.series.Series.squeeze.

Some inconsistencies with the Dask version may exist.

Series or DataFrames with a single element are squeezed to a scalar. DataFrames with a single column or a single row are squeezed to a Series. Otherwise the object is unchanged.

This method is most useful when you don't know if your object is a Series or DataFrame, but you do know it has just a single column. In that case you can safely call *squeeze* to ensure you have a Series.

Parameters

axis [{0 or 'index', 1 or 'columns', None}, default None (Not supported in Dask)] A specific axis to squeeze. By default, all length-1 axes are squeezed.

New in version 0.20.0.

Returns

DataFrame, Series, or scalar The projection after squeezing *axis* or all the axes.

See also:

Series.iloc Integer-location based indexing for selecting scalars.

DataFrame.iloc Integer-location based indexing for selecting Series.

Series.to_frame Inverse of DataFrame.squeeze for a single-column DataFrame.

Examples

```
>>> primes = pd.Series([2, 3, 5, 7])  # doctest: +SKIP
```

Slicing might produce a Series with a single value:

```
>>> even_primes = primes[primes % 2 == 0]  # doctest: +SKIP
>>> even_primes  # doctest: +SKIP
0    2
dtype: int64
```

```
>>> even_primes.squeeze()  # doctest: +SKIP
2
```

Squeezing objects with more than one value in every axis does nothing:

```
>>> odd_primes = primes[primes % 2 == 1]  # doctest: +SKIP
>>> odd_primes  # doctest: +SKIP
1    3
2    5
3    7
dtype: int64
```

```
>>> odd_primes.squeeze()  # doctest: +SKIP
1    3
2    5
3    7
dtype: int64
```

Squeezing is even more effective when used with DataFrames.

```
>>> df = pd.DataFrame([[1, 2], [3, 4]], columns=['a', 'b'])  # doctest: +SKIP
>>> df  # doctest: +SKIP
   a  b
0  1  2
1  3  4
```

Slicing a single column will produce a DataFrame with the columns having only one value:

```
>>> df_a = df[['a']]  # doctest: +SKIP
>>> df_a  # doctest: +SKIP
   a
0  1
1  3
```

So the columns can be squeezed down, resulting in a Series:

```
>>> df_a.squeeze('columns')  # doctest: +SKIP
0    1
1    3
Name: a, dtype: int64
```

Slicing a single row from a single column will produce a single scalar DataFrame:

```
>>> df_0a = df.loc[df.index < 1, ['a']]  # doctest: +SKIP
>>> df_0a  # doctest: +SKIP
   a
0  1
```

Squeezing the rows produces a single scalar Series:

```
>>> df_0a.squeeze('rows')  # doctest: +SKIP
a    1
Name: 0, dtype: int64
```

Squeezing all axes wil project directly into a scalar:

```
>>> df_0a.squeeze()  # doctest: +SKIP
1
```

std(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)

Return sample standard deviation over requested axis.

This docstring was copied from pandas.core.frame.DataFrame.std.

Some inconsistencies with the Dask version may exist.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

std [Series or DataFrame (if level specified)]

str

Namespace for string methods

sub(*other*, *level=None*, *fill_value=None*, *axis=0*)

Subtraction of series and other, element-wise (binary operator *sub*).

Equivalent to `series - other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

Series.rsub

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

sum(*axis=None*, *skipna=True*, *split_every=False*, *dtype=None*, *out=None*, *min_count=None*)
Return the sum of the values for the requested axis.

This docstring was copied from pandas.core.frame.DataFrame.sum.

Some inconsistencies with the Dask version may exist.

This is equivalent to the method `numpy.sum`.

Parameters

axis [{index (0), columns (1)}] Axis for the function to be applied on.

skipna [bool, default True] Exclude NA/null values when computing the result.

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series.

numeric_only [bool, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

min_count [int, default 0] The required number of valid values to perform the operation. If fewer than `min_count` non-NA values are present the result will be NA.

New in version 0.22.0: Added with the default being 0. This means the sum of an all-NA or empty Series is 0, and the product of an all-NA or empty Series is 1.

****kwargs** Additional keyword arguments to be passed to the function.

Returns

sum [Series or DataFrame (if level specified)]

See also:

Series.sum	Return the sum.
Series.min	Return the minimum.
Series.max	Return the maximum.
Series.idxmin	Return the index of the minimum.
Series.idxmax	Return the index of the maximum.
DataFrame.min	Return the sum over the requested axis.
DataFrame.min	Return the minimum over the requested axis.
DataFrame.max	Return the maximum over the requested axis.
DataFrame.idxmin	Return the index of the minimum over the requested axis.
DataFrame.idxmax	Return the index of the maximum over the requested axis.

Examples

```
>>> idx = pd.MultiIndex.from_arrays([  # doctest: +SKIP
...     ['warm', 'warm', 'cold', 'cold'],
...     ['dog', 'falcon', 'fish', 'spider']],
...     names=['blooded', 'animal'])
>>> s = pd.Series([4, 2, 0, 8], name='legs', index=idx)  # doctest: +SKIP
>>> s  # doctest: +SKIP
blooded  animal
warm     dog       4
         falcon    2
cold     fish      0
         spider    8
Name: legs, dtype: int64
```

```
>>> s.sum()  # doctest: +SKIP
14
```

Sum using level names, as well as indices.

```
>>> s.sum(level='blooded')  # doctest: +SKIP
blooded
warm    6
cold    8
Name: legs, dtype: int64
```

```
>>> s.sum(level=0)  # doctest: +SKIP
blooded
warm    6
cold    8
Name: legs, dtype: int64
```

By default, the sum of an empty or all-NA Series is `0`.

```
>>> pd.Series([]).sum()  # min_count=0 is the default  # doctest: +SKIP
0.0
```

This can be controlled with the `min_count` parameter. For example, if you'd like the sum of an empty series to be NaN, pass `min_count=1`.

```
>>> pd.Series([]).sum(min_count=1)  # doctest: +SKIP
nan
```

Thanks to the `skipna` parameter, `min_count` handles all-NA and empty series identically.

```
>>> pd.Series([np.nan]).sum()  # doctest: +SKIP
0.0
```

```
>>> pd.Series([np.nan]).sum(min_count=1)  # doctest: +SKIP
nan
```

tail(*n=5*, *compute=True*)
Last n rows of the dataset

Caveat, the only checks the last n rows of the last partition.

to_bag(*index=False*)
Create a Dask Bag from a Series

to_csv(*filename*, ***kwargs*)
Store Dask DataFrame to CSV files

One filename per partition will be created. You can specify the filenames in a variety of ways.

Use a globstring:

```
>>> df.to_csv('/path/to/data/export-*.csv')
```

The * will be replaced by the increasing sequence 0, 1, 2, …

```
/path/to/data/export-0.csv
/path/to/data/export-1.csv
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> df.to_csv('/path/to/data/export-*.csv', name_function=name)  # doctest:␣
↪+SKIP
```

```
/path/to/data/export-2015-01-01.csv
/path/to/data/export-2015-01-02.csv
...
```

You can also provide an explicit list of paths:

```
>>> paths = ['/path/to/data/alice.csv', '/path/to/data/bob.csv', ...]
>>> df.to_csv(paths)
```

Parameters

filename [string] Path glob indicating the naming scheme for the output files

name_function [callable, default None] Function accepting an integer (partition index) and producing a string to replace the asterisk in the given filename globstring. Should preserve the lexicographic order of partitions. Not supported when *single_file* is *True*.

single_file [bool, default False] Whether to save everything into a single CSV file. Under the single file mode, each partition is appended at the end of the specified CSV file. Note that not all filesystems support the append mode and thus the single file mode, especially on cloud storage systems such as S3 or GCS. A warning will be issued when writing to a file that is not backed by a local filesystem.

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access. Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly automatically

sep [character, default ','] Field delimiter for the output file

na_rep [string, default ''] Missing data representation

float_format [string, default None] Format string for floating point numbers

columns [sequence, optional] Columns to write

header [boolean or list of string, default True] Write out column names. If a list of string is given it is assumed to be aliases for the column names

header_first_partition_only [boolean, default None] If set to *True*, only write the header row in the first output file. By default, headers are written to all partitions under the multiple file mode (*single_file* is *False*) and written only once under the single file mode (*single_file* is *True*). It must not be *False* under the single file mode.

index [boolean, default True] Write row names (index)

index_label [string or sequence, or False, default None] Column label for index column(s) if desired. If None is given, and *header* and *index* are True, then the index names are used. A sequence should be given if the DataFrame uses MultiIndex. If False do not print fields for index names. Use index_label=False for easier importing in R

nanRep [None] deprecated, use na_rep

mode [str] Python write mode, default 'w'

encoding [string, optional] A string representing the encoding to use in the output file, defaults to 'ascii' on Python 2 and 'utf-8' on Python 3.

compression [string, optional] a string representing the compression to use in the output file, allowed values are 'gzip', 'bz2', 'xz', only used when the first argument is a filename

line_terminator [string, default '\n'] The newline character or character sequence to use in the output file

quoting [optional constant from csv module] defaults to csv.QUOTE_MINIMAL

quotechar [string (length 1), default '"'] character used to quote fields

doublequote [boolean, default True] Control quoting of *quotechar* inside a field

escapechar [string (length 1), default None] character used to escape *sep* and *quotechar* when appropriate

chunksize [int or None] rows to write at a time

tupleize_cols [boolean, default False] write multi_index columns as a list of tuples (if True) or new (expanded format) if False)

date_format [string, default None] Format string for datetime objects

decimal: string, default '.' Character recognized as decimal separator. E.g. use ',' for European data

storage_options: dict Parameters passed on to the backend filesystem class.

Returns

The names of the file written if they were computed right away

If not, the delayed tasks associated to the writing of the files

Raises

ValueError If *header_first_partition_only* is set to *False* or *name_function* is specified when *single_file* is *True*.

`to_dask_array`(*lengths=None*)

Convert a dask DataFrame to a dask array.

Parameters

lengths [bool or Sequence of ints, optional] How to determine the chunks sizes for the output array. By default, the output array will have unknown chunk lengths along the first axis, which can cause some later operations to fail.

- True : immediately compute the length of each partition
- Sequence : a sequence of integers to use for the chunk sizes on the first axis. These values are *not* validated for correctness, beyond ensuring that the number of items matches the number of partitions.

`to_delayed`(*optimize_graph=True*)

Convert into a list of `dask.delayed` objects, one per partition.

Parameters

optimize_graph [bool, optional] If True [default], the graph is optimized before converting into `dask.delayed` objects.

See also:

`dask.dataframe.from_delayed`

Examples

```
>>> partitions = df.to_delayed()  # doctest: +SKIP
```

to_frame (*name=None*)

Convert Series to DataFrame.

This docstring was copied from pandas.core.series.Series.to_frame.

Some inconsistencies with the Dask version may exist.

Parameters

name [object, default None] The passed name should substitute for the series name (if it has one).

Returns

data_frame [DataFrame]

to_hdf (*path_or_buf*, *key*, *mode='a'*, *append=False*, ***kwargs*)

Store Dask Dataframe to Hierarchical Data Format (HDF) files

This is a parallel version of the Pandas function of the same name. Please see the Pandas docstring for more detailed information about shared keyword arguments.

This function differs from the Pandas version by saving the many partitions of a Dask DataFrame in parallel, either to many files, or to many datasets within the same file. You may specify this parallelism with an asterix `*` within the filename or datapath, and an optional `name_function`. The asterix will be replaced with an increasing sequence of integers starting from `0` or with the result of calling `name_function` on each of those integers.

This function only supports the Pandas `'table'` format, not the more specialized `'fixed'` format.

Parameters

path [string, pathlib.Path] Path to a target filename. Supports strings, `pathlib.Path`, or any object implementing the `__fspath__` protocol. May contain a `*` to denote many filenames.

key [string] Datapath within the files. May contain a `*` to denote many locations

name_function [function] A function to convert the `*` in the above options to a string. Should take in a number from 0 to the number of partitions and return a string. (see examples below)

compute [bool] Whether or not to execute immediately. If False then this returns a `dask.Delayed` value.

lock [Lock, optional] Lock to use to prevent concurrency issues. By default a `threading.Lock`, `multiprocessing.Lock` or `SerializableLock` will be used depending on your scheduler if a lock is required. See dask.utils.get_scheduler_lock for more information about lock selection.

scheduler [string] The scheduler to use, like "threads" or "processes"

****other:** See pandas.to_hdf for more information

Returns

filenames [list] Returned if `compute` is True. List of file names that each partition is saved to.

delayed [dask.Delayed] Returned if `compute` is False. Delayed object to execute `to_hdf` when computed.

See also:

read_hdf, *to_parquet*

Examples

Save Data to a single file

```
>>> df.to_hdf('output.hdf', '/data')            # doctest: +SKIP
```

Save data to multiple datapaths within the same file:

```
>>> df.to_hdf('output.hdf', '/data-*')          # doctest: +SKIP
```

Save data to multiple files:

```
>>> df.to_hdf('output-*.hdf', '/data')          # doctest: +SKIP
```

Save data to multiple files, using the multiprocessing scheduler:

```
>>> df.to_hdf('output-*.hdf', '/data', scheduler='processes') # doctest:␣
↪+SKIP
```

Specify custom naming scheme. This writes files as '2000-01-01.hdf', '2000-01-02.hdf', '2000-01-03.hdf', etc..

```
>>> from datetime import date, timedelta
>>> base = date(year=2000, month=1, day=1)
>>> def name_function(i):
...     ''' Convert integer 0 to n to a string '''
...     return base + timedelta(days=i)
```

```
>>> df.to_hdf('*.hdf', '/data', name_function=name_function) # doctest: +SKIP
```

`to_json` (*filename*, **args*, ***kwargs*)
See dd.to_json docstring for more information

`to_string` (*max_rows=5*)
Render a string representation of the Series.

This docstring was copied from pandas.core.series.Series.to_string.

Some inconsistencies with the Dask version may exist.

Parameters

buf [StringIO-like, optional (Not supported in Dask)] buffer to write to

na_rep [string, optional (Not supported in Dask)] string representation of NAN to use, default 'NaN'

float_format [one-parameter function, optional (Not supported in Dask)] formatter function to apply to columns' elements if they are floats default None

header [boolean, default True (Not supported in Dask)] Add the Series header (index name)

index [bool, optional (Not supported in Dask)] Add index (row) labels, default True

length [boolean, default False (Not supported in Dask)] Add the Series length

dtype [boolean, default False (Not supported in Dask)] Add the Series dtype

name [boolean, default False (Not supported in Dask)] Add the Series name if not None

max_rows [int, optional] Maximum number of rows to show before truncating. If None, show all.

Returns

formatted [string (if not buffer passed)]

to_timestamp (*freq=None*, *how='start'*, *axis=0*)

Cast to DatetimeIndex of timestamps, at *beginning* of period.

This docstring was copied from pandas.core.frame.DataFrame.to_timestamp.

Some inconsistencies with the Dask version may exist.

Parameters

freq [string, default frequency of PeriodIndex] Desired frequency

how [{'s', 'e', 'start', 'end'}] Convention for converting period to timestamp; start of period vs. end

axis [{0 or 'index', 1 or 'columns'}, default 0] The axis to convert (the index by default)

copy [boolean, default True (Not supported in Dask)] If false then underlying input data is not copied

Returns

df [DataFrame with DatetimeIndex]

truediv (*other*, *level=None*, *fill_value=None*, *axis=0*)

Floating division of series and other, element-wise (binary operator *truediv*).

Equivalent to `series / other`, but with support to substitute a fill_value for missing data in one of the inputs.

Parameters

other [Series or scalar value]

fill_value [None or float value, default None (NaN)] Fill existing missing (NaN) values, and any new element needed for successful Series alignment, with this value before computation. If data in both corresponding Series locations is missing the result will be missing

level [int or name] Broadcast across a level, matching Index values on the passed Multi-Index level

Returns

result [Series]

See also:

Series.rtruediv

Examples

```
>>> a = pd.Series([1, 1, 1, np.nan], index=['a', 'b', 'c', 'd'])  # doctest:␣
↪+SKIP
>>> a  # doctest: +SKIP
a    1.0
b    1.0
c    1.0
d    NaN
dtype: float64
>>> b = pd.Series([1, np.nan, 1, np.nan], index=['a', 'b', 'd', 'e'])  #␣
↪doctest: +SKIP
>>> b  # doctest: +SKIP
a    1.0
b    NaN
d    1.0
e    NaN
dtype: float64
>>> a.add(b, fill_value=0)  # doctest: +SKIP
a    2.0
b    1.0
c    1.0
d    1.0
e    NaN
dtype: float64
```

unique(*split_every=None*, *split_out=1*)
Return Series of unique values in the object. Includes NA values.

Returns

uniques [Series]

value_counts(*split_every=None*, *split_out=1*)
Return a Series containing counts of unique values.

This docstring was copied from pandas.core.series.Series.value_counts.

Some inconsistencies with the Dask version may exist.

The resulting object will be in descending order so that the first element is the most frequently-occurring element. Excludes NA values by default.

Parameters

normalize [boolean, default False (Not supported in Dask)] If True then the object returned will contain the relative frequencies of the unique values.

sort [boolean, default True (Not supported in Dask)] Sort by values.

ascending [boolean, default False (Not supported in Dask)] Sort in ascending order.

bins [integer, optional (Not supported in Dask)] Rather than count values, group them into half-open bins, a convenience for `pd.cut`, only works with numeric data.

dropna [boolean, default True (Not supported in Dask)] Don't include counts of NaN.

Returns

counts [Series]

See also:

Series.count Number of non-NA elements in a Series.

DataFrame.count Number of non-NA elements in a DataFrame.

Examples

```
>>> index = pd.Index([3, 1, 2, 3, 4, np.nan])  # doctest: +SKIP
>>> index.value_counts()  # doctest: +SKIP
3.0    2
4.0    1
2.0    1
1.0    1
dtype: int64
```

With *normalize* set to *True*, returns the relative frequency by dividing all values by the sum of values.

```
>>> s = pd.Series([3, 1, 2, 3, 4, np.nan])  # doctest: +SKIP
>>> s.value_counts(normalize=True)  # doctest: +SKIP
3.0    0.4
4.0    0.2
2.0    0.2
1.0    0.2
dtype: float64
```

bins

Bins can be useful for going from a continuous variable to a categorical variable; instead of counting unique apparitions of values, divide the index in the specified number of half-open bins.

```
>>> s.value_counts(bins=3)  # doctest: +SKIP
(2.0, 3.0]      2
(0.996, 2.0]    2
(3.0, 4.0]      1
dtype: int64
```

dropna

With *dropna* set to *False* we can also see NaN index values.

```
>>> s.value_counts(dropna=False)  # doctest: +SKIP
3.0    2
NaN    1
4.0    1
2.0    1
1.0    1
dtype: int64
```

values
Return a dask.array of the values of this dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

var(*axis=None*, *skipna=True*, *ddof=1*, *split_every=False*, *dtype=None*, *out=None*)
Return unbiased variance over requested axis.

This docstring was copied from pandas.core.frame.DataFrame.var.

Some inconsistencies with the Dask version may exist.

Normalized by N-1 by default. This can be changed using the ddof argument

Parameters

axis [{index (0), columns (1)}]

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA

level [int or level name, default None (Not supported in Dask)] If the axis is a MultiIndex (hierarchical), count along a particular level, collapsing into a Series

ddof [int, default 1] Delta Degrees of Freedom. The divisor used in calculations is N - ddof, where N represents the number of elements.

numeric_only [boolean, default None (Not supported in Dask)] Include only float, int, boolean columns. If None, will attempt to use everything, then use only numeric data. Not implemented for Series.

Returns

var [Series or DataFrame (if level specified)]

visualize (*filename='mydask'*, *format=None*, *optimize_graph=False*, ***kwargs*)

Render the computation of this object's task graph using graphviz.

Requires `graphviz` to be installed.

Parameters

filename [str or None, optional] The name (without an extension) of the file to write to disk. If *filename* is None, no file will be written, and we communicate with dot using only pipes.

format [{'png', 'pdf', 'dot', 'svg', 'jpeg', 'jpg'}, optional] Format in which to write output file. Default is 'png'.

optimize_graph [bool, optional] If True, the graph is optimized before rendering. Otherwise, the graph is displayed as is. Default is False.

color: {None, 'order'}, optional Options to color nodes. Provide `cmap=` keyword for additional colormap

****kwargs** Additional keyword arguments to forward to `to_graphviz`.

Returns

result [IPython.diplay.Image, IPython.display.SVG, or None] See dask.dot.dot_graph for more information.

See also:

`dask.base.visualize`, `dask.dot.dot_graph`

Notes

For more information on optimization see here:

https://docs.dask.org/en/latest/optimize.html

Examples

```
>>> x.visualize(filename='dask.pdf')  # doctest: +SKIP
>>> x.visualize(filename='dask.pdf', color='order')  # doctest: +SKIP
```

where(*cond*, *other=nan*)

Replace values where the condition is False.

This docstring was copied from pandas.core.frame.DataFrame.where.

Some inconsistencies with the Dask version may exist.

Parameters

cond [boolean NDFrame, array-like, or callable] Where *cond* is True, keep the original value. Where False, replace with corresponding value from *other*. If *cond* is callable, it is computed on the NDFrame and should return boolean NDFrame or array. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as cond.

other [scalar, NDFrame, or callable] Entries where *cond* is False are replaced with corresponding value from *other*. If other is callable, it is computed on the NDFrame and should return scalar or NDFrame. The callable must not change input NDFrame (though pandas doesn't check it).

New in version 0.18.1: A callable can be used as other.

inplace [boolean, default False (Not supported in Dask)] Whether to perform the operation in place on the data.

axis [int, default None (Not supported in Dask)] Alignment axis if needed.

level [int, default None (Not supported in Dask)] Alignment level if needed.

errors [str, {'raise', 'ignore'}, default *raise* (Not supported in Dask)] Note that currently this parameter won't affect the results and will always coerce to a suitable dtype.

- *raise* : allow exceptions to be raised.
- *ignore* : suppress exceptions. On error return original object.

try_cast [boolean, default False (Not supported in Dask)] Try to cast the result back to the input type (if possible).

raise_on_error [boolean, default True (Not supported in Dask)] Whether to raise on invalid data types (e.g. trying to where on strings).

Deprecated since version 0.21.0: Use *errors*.

Returns

wh [same type as caller]

See also:

`DataFrame.mask()` Return an object of same shape as self.

Notes

The where method is an application of the if-then idiom. For each element in the calling DataFrame, if `cond` is `True` the element is used; otherwise the corresponding element from the DataFrame `other` is used.

The signature for `DataFrame.where()` differs from `numpy.where()`. Roughly `df1.where(m, df2)` is equivalent to `np.where(m, df1, df2)`.

For further details and examples see the `where` documentation in indexing.

Examples

```
>>> s = pd.Series(range(5))  # doctest: +SKIP
>>> s.where(s > 0)  # doctest: +SKIP
0    NaN
1    1.0
2    2.0
3    3.0
4    4.0
dtype: float64
```

```
>>> s.mask(s > 0)  # doctest: +SKIP
0    0.0
1    NaN
2    NaN
3    NaN
4    NaN
dtype: float64
```

```
>>> s.where(s > 1, 10)  # doctest: +SKIP
0    10
1    10
2    2
3    3
4    4
dtype: int64
```

```
>>> df = pd.DataFrame(np.arange(10).reshape(-1, 2), columns=['A', 'B'])  #␣
↪doctest: +SKIP
>>> m = df % 3 == 0  # doctest: +SKIP
>>> df.where(m, -df)  # doctest: +SKIP
   A  B
0  0 -1
1 -2  3
2 -4 -5
3  6 -7
4 -8  9
>>> df.where(m, -df) == np.where(m, df, -df)  # doctest: +SKIP
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
>>> df.where(m, -df) == df.mask(~m, -df)  # doctest: +SKIP
      A     B
0  True  True
1  True  True
2  True  True
3  True  True
4  True  True
```

DataFrameGroupBy

class dask.dataframe.groupby.**DataFrameGroupBy**(*df*, *by=None*, *slice=None*, *group_keys=True*)

agg(*arg*, *split_every=None*, *split_out=1*)

Aggregate using one or more operations over the specified axis.

This docstring was copied from pandas.core.groupby.generic.DataFrameGroupBy.agg.

Some inconsistencies with the Dask version may exist.

Parameters

func [function, str, list or dict] Function to use for aggregating the data. If a function, must either work when passed a DataFrame or when passed to DataFrame.apply.

Accepted combinations are:

- function
- string function name
- list of functions and/or function names, e.g. `[np.sum, 'mean']`
- dict of axis labels -> functions, function names or list of such.

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

DataFrame, Series or scalar if DataFrame.agg is called with a single function, returns a Series if DataFrame.agg is called with several functions, returns a DataFrame if Series.agg is called with single function, returns a scalar if Series.agg is called with several functions, returns a Series

See also:

`pandas.DataFrame.groupby.apply`, `pandas.DataFrame.groupby.transform`, `pandas.DataFrame.aggregate`

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> df = pd.DataFrame({'A': [1, 1, 2, 2],  # doctest: +SKIP
...                    'B': [1, 2, 3, 4],
...                    'C': np.random.randn(4)})
```

```
>>> df  # doctest: +SKIP
   A  B         C
0  1  1  0.362838
1  1  2  0.227877
2  2  3  1.267767
3  2  4 -0.562860
```

The aggregation is for each column.

```
>>> df.groupby('A').agg('min')  # doctest: +SKIP
   B         C
A
1  1  0.227877
2  3 -0.562860
```

Multiple aggregations

```
>>> df.groupby('A').agg(['min', 'max'])  # doctest: +SKIP
    B             C
  min max       min       max
A
1   1   2  0.227877  0.362838
2   3   4 -0.562860  1.267767
```

Select a column for aggregation

```
>>> df.groupby('A').B.agg(['min', 'max'])  # doctest: +SKIP
   min  max
A
1    1    2
2    3    4
```

Different aggregations per column

```
>>> df.groupby('A').agg({'B': ['min', 'max'], 'C': 'sum'})  # doctest: +SKIP
    B             C
  min max       sum
A
1   1   2  0.590716
2   3   4  0.704907
```

aggregate(*arg*, *split_every=None*, *split_out=1*)
Aggregate using one or more operations over the specified axis.

This docstring was copied from pandas.core.groupby.generic.DataFrameGroupBy.aggregate.

Some inconsistencies with the Dask version may exist.

Parameters

func [function, str, list or dict] Function to use for aggregating the data. If a function, must either work when passed a DataFrame or when passed to DataFrame.apply.

Accepted combinations are:

- function
- string function name
- list of functions and/or function names, e.g. `[np.sum, 'mean']`
- dict of axis labels -> functions, function names or list of such.

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

DataFrame, Series or scalar if DataFrame.agg is called with a single function, returns a Series if DataFrame.agg is called with several functions, returns a DataFrame if Series.agg is called with single function, returns a scalar if Series.agg is called with several functions, returns a Series

See also:

`pandas.DataFrame.groupby.apply`, `pandas.DataFrame.groupby.transform`, `pandas.DataFrame.aggregate`

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> df = pd.DataFrame({'A': [1, 1, 2, 2],  # doctest: +SKIP
...                    'B': [1, 2, 3, 4],
...                    'C': np.random.randn(4)})
```

```
>>> df  # doctest: +SKIP
   A  B         C
0  1  1  0.362838
1  1  2  0.227877
2  2  3  1.267767
3  2  4 -0.562860
```

The aggregation is for each column.

```
>>> df.groupby('A').agg('min')  # doctest: +SKIP
   B         C
A
1  1  0.227877
2  3 -0.562860
```

Multiple aggregations

```
>>> df.groupby('A').agg(['min', 'max'])  # doctest: +SKIP
    B             C
  min max       min       max
A
1   1   2  0.227877  0.362838
2   3   4 -0.562860  1.267767
```

Select a column for aggregation

```
>>> df.groupby('A').B.agg(['min', 'max'])  # doctest: +SKIP
   min  max
A
1    1    2
2    3    4
```

Different aggregations per column

```
>>> df.groupby('A').agg({'B': ['min', 'max'], 'C': 'sum'})  # doctest: +SKIP
    B             C
  min max       sum
A
1   1   2  0.590716
2   3   4  0.704907
```

apply (*func*, **args*, ***kwargs*)
Parallel version of pandas GroupBy.apply

This mimics the pandas version except for the following:

1. If the grouper does not align with the index then this causes a full shuffle. The order of rows within each group may not be preserved.
2. Dask's GroupBy.apply is not appropriate for aggregations. For custom aggregations, use `dask.dataframe.groupby.Aggregation`.

Warning: Pandas' groupby-apply can be used to to apply arbitrary functions, including aggregations that result in one row per group. Dask's groupby-apply will apply `func` once to each partition-group pair, so when `func` is a reduction you'll end up with one row per partition-group pair. To apply a custom aggregation with Dask, use `dask.dataframe.groupby.Aggregation`.

Parameters

func: function Function to apply

args, kwargs [Scalar, Delayed or object] Arguments and keywords to pass to the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

applied [Series or DataFrame depending on columns keyword]

corr (*ddof=1*, *split_every=None*, *split_out=1*)
Compute pairwise correlation of columns, excluding NA/null values.

This docstring was copied from pandas.core.frame.DataFrame.corr.

Some inconsistencies with the Dask version may exist.

Groupby correlation: corr(X, Y) = cov(X, Y) / (std_x * std_y)

Parameters

method [{'pearson', 'kendall', 'spearman'} or callable (Not supported in Dask)]

- pearson : standard correlation coefficient
- kendall : Kendall Tau correlation coefficient

- spearman : Spearman rank correlation
- **callable: callable with input two 1d ndarrays** and returning a float .. version-added:: 0.24.0

min_periods [int, optional (Not supported in Dask)] Minimum number of observations required per pair of columns to have a valid result. Currently only available for pearson and spearman correlation

Returns

y [DataFrame]

See also:

`DataFrame.corrwith`, `Series.corr`

Examples

```
>>> histogram_intersection = lambda a, b: np.minimum(a, b  # doctest: +SKIP
... ).sum().round(decimals=1)
>>> df = pd.DataFrame([(.2, .3), (.0, .6), (.6, .0), (.2, .1)],  # doctest:␣
↪+SKIP
...                   columns=['dogs', 'cats'])
>>> df.corr(method=histogram_intersection)  # doctest: +SKIP
      dogs  cats
dogs   1.0   0.3
cats   0.3   1.0
```

count (*split_every=None*, *split_out=1*)
Compute count of group, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.count.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

cov (*ddof=1*, *split_every=None*, *split_out=1*, *std=False*)
Compute pairwise covariance of columns, excluding NA/null values.

This docstring was copied from pandas.core.frame.DataFrame.cov.

Some inconsistencies with the Dask version may exist.

Groupby covariance is accomplished by

1. Computing intermediate values for sum, count, and the product of all columns: a b c -> a*a, a*b, b*b, b*c, c*c.
2. The values are then aggregated and the final covariance value is calculated: cov(X, Y) = X*Y - Xbar * Ybar

When *std* is True calculate Correlation

Compute the pairwise covariance among the series of a DataFrame. The returned data frame is the covariance matrix of the columns of the DataFrame.

Both NA and null values are automatically excluded from the calculation. (See the note below about bias from missing values.) A threshold can be set for the minimum number of observations for each value created. Comparisons with observations below this threshold will be returned as `NaN`.

This method is generally used for the analysis of time series data to understand the relationship between different measures across time.

Parameters

min_periods [int, optional (Not supported in Dask)] Minimum number of observations required per pair of columns to have a valid result.

Returns

DataFrame The covariance matrix of the series of the DataFrame.

See also:

`pandas.Series.cov` Compute covariance with another Series.

`pandas.core.window.EWM.cov` Exponential weighted sample covariance.

`pandas.core.window.Expanding.cov` Expanding sample covariance.

`pandas.core.window.Rolling.cov` Rolling sample covariance.

Notes

Returns the covariance matrix of the DataFrame's time series. The covariance is normalized by N-1.

For DataFrames that have Series that are missing data (assuming that data is missing at random) the returned covariance matrix will be an unbiased estimate of the variance and covariance between the member Series.

However, for many applications this estimate may not be acceptable because the estimate covariance matrix is not guaranteed to be positive semi-definite. This could lead to estimate correlations having absolute values which are greater than one, and/or a non-invertible covariance matrix. See Estimation of covariance matrices for more details.

Examples

```
>>> df = pd.DataFrame([(1, 2), (0, 3), (2, 0), (1, 1)],  # doctest: +SKIP
...                   columns=['dogs', 'cats'])
>>> df.cov()  # doctest: +SKIP
          dogs      cats
dogs  0.666667 -1.000000
cats -1.000000  1.666667
```

```
>>> np.random.seed(42)  # doctest: +SKIP
>>> df = pd.DataFrame(np.random.randn(1000, 5),  # doctest: +SKIP
...                   columns=['a', 'b', 'c', 'd', 'e'])
>>> df.cov()  # doctest: +SKIP
          a         b         c         d         e
a  0.998438 -0.020161  0.059277 -0.008943  0.014144
b -0.020161  1.059352 -0.008543 -0.024738  0.009826
c  0.059277 -0.008543  1.010670 -0.001486 -0.000271
d -0.008943 -0.024738 -0.001486  0.921297 -0.013692
e  0.014144  0.009826 -0.000271 -0.013692  0.977795
```

Minimum number of periods

This method also supports an optional `min_periods` keyword that specifies the required minimum number of non-NA observations for each column pair in order to have a valid result:

```
>>> np.random.seed(42)  # doctest: +SKIP
>>> df = pd.DataFrame(np.random.randn(20, 3),  # doctest: +SKIP
...                   columns=['a', 'b', 'c'])
>>> df.loc[df.index[:5], 'a'] = np.nan  # doctest: +SKIP
>>> df.loc[df.index[5:10], 'b'] = np.nan  # doctest: +SKIP
>>> df.cov(min_periods=12)  # doctest: +SKIP
          a         b         c
a  0.316741       NaN -0.150812
b       NaN  1.248003  0.191417
c -0.150812  0.191417  0.895202
```

cumcount (*axis=None*)

Number each item in each group from 0 to the length of that group - 1.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.cumcount.

Some inconsistencies with the Dask version may exist.

Essentially this is equivalent to

```
>>> self.apply(lambda x: pd.Series(np.arange(len(x)), x.index))  # doctest:␣
↪+SKIP
```

Parameters

ascending [bool, default True (Not supported in Dask)] If False, number in reverse, from length of group - 1 to 0.

See also:

ngroup Number the groups themselves.

Examples

```
>>> df = pd.DataFrame([['a'], ['a'], ['a'], ['b'], ['b'], ['a']],  #␣
↪doctest: +SKIP
...                   columns=['A'])
>>> df  # doctest: +SKIP
   A
0  a
1  a
2  a
3  b
4  b
5  a
>>> df.groupby('A').cumcount()  # doctest: +SKIP
0    0
1    1
2    2
3    0
4    1
5    3
dtype: int64
>>> df.groupby('A').cumcount(ascending=False)  # doctest: +SKIP
0    3
1    2
```

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```
2    1
3    1
4    0
5    0
dtype: int64
```

cumprod(*axis=0*)

Cumulative product for each group.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.cumprod.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

cumsum(*axis=0*)

Cumulative sum for each group.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.cumsum.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

first(*split_every=None*, *split_out=1*)

Compute first of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

get_group(*key*)

Constructs NDFrame from group with provided name.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.get_group.

Some inconsistencies with the Dask version may exist.

Parameters

name [object (Not supported in Dask)] the name of the group to get as a DataFrame

obj [NDFrame, default None (Not supported in Dask)] the NDFrame to take the DataFrame out of. If it is None, the object groupby was called on will be used

Returns

group [same type as obj]

idxmax(*split_every=None*, *split_out=1*, *axis=None*, *skipna=True*)

Return index of first occurrence of maximum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmax.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmax [Series]

Raises

ValueError

- If the row/column is empty

See also:

`Series.idxmax`

Notes

This method is the DataFrame version of `ndarray.argmax`.

idxmin(*split_every=None*, *split_out=1*, *axis=None*, *skipna=True*)

Return index of first occurrence of minimum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmin.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmin [Series]

Raises

ValueError

- If the row/column is empty

See also:

`Series.idxmin`

Notes

This method is the DataFrame version of `ndarray.argmin`.

last(*split_every=None*, *split_out=1*)

Compute last of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

max(*split_every=None*, *split_out=1*)

Compute max of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

mean(*split_every=None*, *split_out=1*)

Compute mean of groups, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.mean.

Some inconsistencies with the Dask version may exist.

Returns

pandas.Series or pandas.DataFrame

See also:

`pandas.Series.`, `pandas.DataFrame.`, `pandas.Panel.`

Examples

```
>>> df = pd.DataFrame({'A': [1, 1, 2, 1, 2],  # doctest: +SKIP
...                    'B': [np.nan, 2, 3, 4, 5],
...                    'C': [1, 2, 1, 1, 2]}, columns=['A', 'B', 'C'])
```

Groupby one column and return the mean of the remaining columns in each group.

```
>>> df.groupby('A').mean()  # doctest: +SKIP
>>>
     B         C
A
1  3.0  1.333333
2  4.0  1.500000
```

Groupby two columns and return the mean of the remaining column.

```
>>> df.groupby(['A', 'B']).mean()  # doctest: +SKIP
>>>
       C
A B
1 2.0  2
  4.0  1
2 3.0  1
  5.0  2
```

Groupby one column and return the mean of only particular column in the group.

```
>>> df.groupby('A')['B'].mean()  # doctest: +SKIP
>>>
A
1    3.0
2    4.0
Name: B, dtype: float64
```

`min`(*split_every=None*, *split_out=1*)
Compute min of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

`prod`(*split_every=None*, *split_out=1*, *min_count=None*)
Compute prod of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

`size`(*split_every=None*, *split_out=1*)
Compute group sizes.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.size.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

std(*ddof=1*, *split_every=None*, *split_out=1*)

Compute standard deviation of groups, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.std.

Some inconsistencies with the Dask version may exist.

For multiple groupings, the result index will be a MultiIndex.

Parameters

ddof [integer, default 1] degrees of freedom

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

sum(*split_every=None*, *split_out=1*, *min_count=None*)

Compute sum of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

transform(*func*, **args*, ***kwargs*)

Parallel version of pandas GroupBy.transform

This mimics the pandas version except for the following:

1. If the grouper does not align with the index then this causes a full shuffle. The order of rows within each group may not be preserved.
2. Dask's GroupBy.transform is not appropriate for aggregations. For custom aggregations, use *`dask.dataframe.groupby.Aggregation`*.

Warning: Pandas' groupby-transform can be used to to apply arbitrary functions, including aggregations that result in one row per group. Dask's groupby-transform will apply `func` once to each partition-group pair, so when `func` is a reduction you'll end up with one row per partition-group pair. To apply a custom aggregation with Dask, use *`dask.dataframe.groupby.Aggregation`*.

Parameters

func: function Function to apply

args, kwargs [Scalar, Delayed or object] Arguments and keywords to pass to the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

applied [Series or DataFrame depending on columns keyword]

var(*ddof=1*, *split_every=None*, *split_out=1*)

Compute variance of groups, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.var.

Some inconsistencies with the Dask version may exist.

For multiple groupings, the result index will be a MultiIndex.

Parameters

ddof [integer, default 1] degrees of freedom

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

SeriesGroupBy

class `dask.dataframe.groupby.`**`SeriesGroupBy`**(*df*, *by=None*, *slice=None*, ***kwargs*)

agg(*arg*, *split_every=None*, *split_out=1*)

Aggregate using one or more operations over the specified axis.

This docstring was copied from pandas.core.groupby.generic.SeriesGroupBy.agg.

Some inconsistencies with the Dask version may exist.

Parameters

func [function, str, list or dict] Function to use for aggregating the data. If a function, must either work when passed a Series or when passed to Series.apply.

Accepted combinations are:

- function
- string function name
- list of functions and/or function names, e.g. `[np.sum, 'mean']`
- dict of axis labels -> functions, function names or list of such.

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

DataFrame, Series or scalar if DataFrame.agg is called with a single function, returns a Series if DataFrame.agg is called with several functions, returns a DataFrame if Series.agg is called with single function, returns a scalar if Series.agg is called with several functions, returns a Series

See also:

`pandas.Series.groupby.apply`, `pandas.Series.groupby.transform`, `pandas.Series.aggregate`

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> s = pd.Series([1, 2, 3, 4])  # doctest: +SKIP
```

```
>>> s  # doctest: +SKIP
0    1
1    2
2    3
3    4
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).min()  # doctest: +SKIP
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg('min')  # doctest: +SKIP
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg(['min', 'max'])  # doctest: +SKIP
   min  max
1    1    2
2    3    4
```

aggregate(*arg*, *split_every=None*, *split_out=1*)

Aggregate using one or more operations over the specified axis.

This docstring was copied from pandas.core.groupby.generic.SeriesGroupBy.aggregate.

Some inconsistencies with the Dask version may exist.

Parameters

func [function, str, list or dict] Function to use for aggregating the data. If a function, must either work when passed a Series or when passed to Series.apply.

Accepted combinations are:

- function
- string function name
- list of functions and/or function names, e.g. `[np.sum, 'mean']`
- dict of axis labels -> functions, function names or list of such.

***args** Positional arguments to pass to *func*.

****kwargs** Keyword arguments to pass to *func*.

Returns

DataFrame, Series or scalar if DataFrame.agg is called with a single function, returns a Series if DataFrame.agg is called with several functions, returns a DataFrame if Series.agg is called with single function, returns a scalar if Series.agg is called with several functions, returns a Series

See also:

pandas.Series.groupby.apply, pandas.Series.groupby.transform, pandas.Series.aggregate

Notes

agg is an alias for *aggregate*. Use the alias.

A passed user-defined-function will be passed a Series for evaluation.

Examples

```
>>> s = pd.Series([1, 2, 3, 4])  # doctest: +SKIP
```

```
>>> s  # doctest: +SKIP
0    1
1    2
2    3
3    4
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).min()  # doctest: +SKIP
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg('min')  # doctest: +SKIP
1    1
2    3
dtype: int64
```

```
>>> s.groupby([1, 1, 2, 2]).agg(['min', 'max'])  # doctest: +SKIP
   min  max
1    1    2
2    3    4
```

apply (*func*, **args*, ***kwargs*)
Parallel version of pandas GroupBy.apply

This mimics the pandas version except for the following:

1. If the grouper does not align with the index then this causes a full shuffle. The order of rows within each group may not be preserved.
2. Dask's GroupBy.apply is not appropriate for aggregations. For custom aggregations, use *dask.dataframe.groupby.Aggregation*.

Warning: Pandas' groupby-apply can be used to to apply arbitrary functions, including aggregations that result in one row per group. Dask's groupby-apply will apply `func` once to each partition-group pair, so when `func` is a reduction you'll end up with one row per partition-group pair. To apply a custom aggregation with Dask, use *dask.dataframe.groupby.Aggregation*.

Parameters

func: function Function to apply

args, kwargs [Scalar, Delayed or object] Arguments and keywords to pass to the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

applied [Series or DataFrame depending on columns keyword]

corr(*ddof=1*, *split_every=None*, *split_out=1*)

Compute pairwise correlation of columns, excluding NA/null values.

This docstring was copied from pandas.core.frame.DataFrame.corr.

Some inconsistencies with the Dask version may exist.

Groupby correlation: corr(X, Y) = cov(X, Y) / (std_x * std_y)

Parameters

method [{'pearson', 'kendall', 'spearman'} or callable (Not supported in Dask)]

- pearson : standard correlation coefficient
- kendall : Kendall Tau correlation coefficient
- spearman : Spearman rank correlation
- **callable: callable with input two 1d ndarrays** and returning a float .. versionadded:: 0.24.0

min_periods [int, optional (Not supported in Dask)] Minimum number of observations required per pair of columns to have a valid result. Currently only available for pearson and spearman correlation

Returns

y [DataFrame]

See also:

`DataFrame.corrwith`, `Series.corr`

Examples

```
>>> histogram_intersection = lambda a, b: np.minimum(a, b  # doctest: +SKIP
... ).sum().round(decimals=1)
>>> df = pd.DataFrame([(.2, .3), (.0, .6), (.6, .0), (.2, .1)],  # doctest:␣
↪+SKIP
...                   columns=['dogs', 'cats'])
>>> df.corr(method=histogram_intersection)  # doctest: +SKIP
      dogs cats
dogs   1.0  0.3
cats   0.3  1.0
```

count (*split_every=None*, *split_out=1*)

Compute count of group, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.count.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

cov (*ddof=1*, *split_every=None*, *split_out=1*, *std=False*)

Compute pairwise covariance of columns, excluding NA/null values.

This docstring was copied from pandas.core.frame.DataFrame.cov.

Some inconsistencies with the Dask version may exist.

Groupby covariance is accomplished by

1. Computing intermediate values for sum, count, and the product of all columns: a b c -> a*a, a*b, b*b, b*c, c*c.
2. The values are then aggregated and the final covariance value is calculated: cov(X, Y) = X*Y - Xbar * Ybar

When *std* is True calculate Correlation

Compute the pairwise covariance among the series of a DataFrame. The returned data frame is the covariance matrix of the columns of the DataFrame.

Both NA and null values are automatically excluded from the calculation. (See the note below about bias from missing values.) A threshold can be set for the minimum number of observations for each value created. Comparisons with observations below this threshold will be returned as `NaN`.

This method is generally used for the analysis of time series data to understand the relationship between different measures across time.

Parameters

min_periods [int, optional (Not supported in Dask)] Minimum number of observations required per pair of columns to have a valid result.

Returns

DataFrame The covariance matrix of the series of the DataFrame.

See also:

`pandas.Series.cov` Compute covariance with another Series.

`pandas.core.window.EWM.cov` Exponential weighted sample covariance.

`pandas.core.window.Expanding.cov` Expanding sample covariance.

`pandas.core.window.Rolling.cov` Rolling sample covariance.

Notes

Returns the covariance matrix of the DataFrame's time series. The covariance is normalized by N-1.

For DataFrames that have Series that are missing data (assuming that data is missing at random) the returned covariance matrix will be an unbiased estimate of the variance and covariance between the member Series.

However, for many applications this estimate may not be acceptable because the estimate covariance matrix is not guaranteed to be positive semi-definite. This could lead to estimate correlations having absolute values which are greater than one, and/or a non-invertible covariance matrix. See Estimation of covariance matrices for more details.

Examples

```
>>> df = pd.DataFrame([(1, 2), (0, 3), (2, 0), (1, 1)],  # doctest: +SKIP
...                   columns=['dogs', 'cats'])
>>> df.cov()  # doctest: +SKIP
          dogs      cats
dogs  0.666667 -1.000000
cats -1.000000  1.666667
```

```
>>> np.random.seed(42)  # doctest: +SKIP
>>> df = pd.DataFrame(np.random.randn(1000, 5),  # doctest: +SKIP
...                   columns=['a', 'b', 'c', 'd', 'e'])
>>> df.cov()  # doctest: +SKIP
          a         b         c         d         e
a  0.998438 -0.020161  0.059277 -0.008943  0.014144
b -0.020161  1.059352 -0.008543 -0.024738  0.009826
c  0.059277 -0.008543  1.010670 -0.001486 -0.000271
d -0.008943 -0.024738 -0.001486  0.921297 -0.013692
e  0.014144  0.009826 -0.000271 -0.013692  0.977795
```

Minimum number of periods

This method also supports an optional `min_periods` keyword that specifies the required minimum number of non-NA observations for each column pair in order to have a valid result:

```
>>> np.random.seed(42)  # doctest: +SKIP
>>> df = pd.DataFrame(np.random.randn(20, 3),  # doctest: +SKIP
...                   columns=['a', 'b', 'c'])
>>> df.loc[df.index[:5], 'a'] = np.nan  # doctest: +SKIP
>>> df.loc[df.index[5:10], 'b'] = np.nan  # doctest: +SKIP
>>> df.cov(min_periods=12)  # doctest: +SKIP
          a         b         c
a  0.316741       NaN -0.150812
b       NaN  1.248003  0.191417
c -0.150812  0.191417  0.895202
```

cumcount (*axis=None*)

Number each item in each group from 0 to the length of that group - 1.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.cumcount.

Some inconsistencies with the Dask version may exist.

Essentially this is equivalent to

```
>>> self.apply(lambda x: pd.Series(np.arange(len(x)), x.index))  # doctest:␣
↪+SKIP
```

Parameters

ascending [bool, default True (Not supported in Dask)] If False, number in reverse, from length of group - 1 to 0.

See also:

ngroup Number the groups themselves.

Examples

```
>>> df = pd.DataFrame([['a'], ['a'], ['a'], ['b'], ['b'], ['a']],  #␣
↪doctest: +SKIP
...                   columns=['A'])
>>> df  # doctest: +SKIP
   A
0  a
1  a
2  a
3  b
4  b
5  a
>>> df.groupby('A').cumcount()  # doctest: +SKIP
0    0
1    1
2    2
3    0
4    1
5    3
dtype: int64
>>> df.groupby('A').cumcount(ascending=False)  # doctest: +SKIP
0    3
1    2
2    1
3    1
4    0
5    0
dtype: int64
```

cumprod (*axis=0*)

Cumulative product for each group.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.cumprod.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

cumsum (*axis=0*)

Cumulative sum for each group.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.cumsum.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

first (*split_every=None, split_out=1*)

Compute first of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

get_group(*key*)

Constructs NDFrame from group with provided name.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.get_group.

Some inconsistencies with the Dask version may exist.

Parameters

name [object (Not supported in Dask)] the name of the group to get as a DataFrame

obj [NDFrame, default None (Not supported in Dask)] the NDFrame to take the DataFrame out of. If it is None, the object groupby was called on will be used

Returns

group [same type as obj]

idxmax(*split_every=None*, *split_out=1*, *axis=None*, *skipna=True*)

Return index of first occurrence of maximum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmax.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmax [Series]

Raises

ValueError

- If the row/column is empty

See also:

`Series.idxmax`

Notes

This method is the DataFrame version of `ndarray.argmax`.

idxmin(*split_every=None*, *split_out=1*, *axis=None*, *skipna=True*)

Return index of first occurrence of minimum over requested axis. NA/null values are excluded.

This docstring was copied from pandas.core.frame.DataFrame.idxmin.

Some inconsistencies with the Dask version may exist.

Parameters

axis [{0 or 'index', 1 or 'columns'}, default 0] 0 or 'index' for row-wise, 1 or 'columns' for column-wise

skipna [boolean, default True] Exclude NA/null values. If an entire row/column is NA, the result will be NA.

Returns

idxmin [Series]

Raises

ValueError

- If the row/column is empty

See also:

`Series.idxmin`

Notes

This method is the DataFrame version of `ndarray.argmin`.

`last`(*split_every=None*, *split_out=1*)
Compute last of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

`max`(*split_every=None*, *split_out=1*)
Compute max of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

`mean`(*split_every=None*, *split_out=1*)
Compute mean of groups, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.mean.

Some inconsistencies with the Dask version may exist.

Returns

pandas.Series or pandas.DataFrame

See also:

`pandas.Series.`, `pandas.DataFrame.`, `pandas.Panel.`

Examples

```
>>> df = pd.DataFrame({'A': [1, 1, 2, 1, 2],  # doctest: +SKIP
...                    'B': [np.nan, 2, 3, 4, 5],
...                    'C': [1, 2, 1, 1, 2]}, columns=['A', 'B', 'C'])
```

Groupby one column and return the mean of the remaining columns in each group.

```
>>> df.groupby('A').mean()  # doctest: +SKIP
>>>
     B         C
A
1  3.0  1.333333
2  4.0  1.500000
```

Groupby two columns and return the mean of the remaining column.

```
>>> df.groupby(['A', 'B']).mean()  # doctest: +SKIP
>>>
       C
A B
```

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```
1 2.0  2
  4.0  1
2 3.0  1
  5.0  2
```

Groupby one column and return the mean of only particular column in the group.

```
>>> df.groupby('A')['B'].mean()  # doctest: +SKIP
>>>
A
1    3.0
2    4.0
Name: B, dtype: float64
```

min(*split_every=None*, *split_out=1*)
Compute min of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

prod(*split_every=None*, *split_out=1*, *min_count=None*)
Compute prod of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

size(*split_every=None*, *split_out=1*)
Compute group sizes.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.size.

Some inconsistencies with the Dask version may exist.

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

std(*ddof=1*, *split_every=None*, *split_out=1*)
Compute standard deviation of groups, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.std.

Some inconsistencies with the Dask version may exist.

For multiple groupings, the result index will be a MultiIndex.

Parameters

ddof [integer, default 1] degrees of freedom

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

sum(*split_every=None*, *split_out=1*, *min_count=None*)
Compute sum of group values See Also ——— pandas.Series.groupby pandas.DataFrame.groupby pandas.Panel.groupby

transform(*func*, **args*, ***kwargs*)
Parallel version of pandas GroupBy.transform

This mimics the pandas version except for the following:

1. If the grouper does not align with the index then this causes a full shuffle. The order of rows within each group may not be preserved.

2. Dask's GroupBy.transform is not appropriate for aggregations. For custom aggregations, use *dask.dataframe.groupby.Aggregation*.

Warning: Pandas' groupby-transform can be used to to apply arbitrary functions, including aggregations that result in one row per group. Dask's groupby-transform will apply `func` once to each partition-group pair, so when `func` is a reduction you'll end up with one row per partition-group pair. To apply a custom aggregation with Dask, use *dask.dataframe.groupby.Aggregation*.

Parameters

func: function Function to apply

args, kwargs [Scalar, Delayed or object] Arguments and keywords to pass to the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

applied [Series or DataFrame depending on columns keyword]

var(*ddof=1*, *split_every=None*, *split_out=1*)
Compute variance of groups, excluding missing values.

This docstring was copied from pandas.core.groupby.groupby.GroupBy.var.

Some inconsistencies with the Dask version may exist.

For multiple groupings, the result index will be a MultiIndex.

Parameters

ddof [integer, default 1] degrees of freedom

See also:

`pandas.Series.groupby`, `pandas.DataFrame.groupby`, `pandas.Panel.groupby`

Custom Aggregation

class dask.dataframe.groupby.**Aggregation**(*name*, *chunk*, *agg*, *finalize=None*)
User defined groupby-aggregation.

This class allows users to define their own custom aggregation in terms of operations on Pandas dataframes in a map-reduce style. You need to specify what operation to do on each chunk of data, how to combine those chunks of data together, and then how to finalize the result.

See *Aggregate* for more.

Parameters

name [str] the name of the aggregation. It should be unique, since intermediate result will be identified by this name.

chunk [callable] a function that will be called with the grouped column of each partition. It can either return a single series or a tuple of series. The index has to be equal to the groups.

agg [callable] a function that will be called to aggregate the results of each chunk. Again the argument(s) will be grouped series. If `chunk` returned a tuple, `agg` will be called with all of them as individual positional arguments.

finalize [callable] an optional finalizer that will be called with the results from the aggregation.

Examples

We could implement `sum` as follows:

```
>>> custom_sum = dd.Aggregation(
...     name='custom_sum',
...     chunk=lambda s: s.sum(),
...     agg=lambda s0: s0.sum()
... )  # doctest: +SKIP
>>> df.groupby('g').agg(custom_sum)  # doctest: +SKIP
```

We can implement `mean` as follows:

```
>>> custom_mean = dd.Aggregation(
...     name='custom_mean',
...     chunk=lambda s: (s.count(), s.sum()),
...     agg=lambda count, sum: (count.sum(), sum.sum()),
...     finalize=lambda count, sum: sum / count,
... )  # doctest: +SKIP
>>> df.groupby('g').agg(custom_mean)  # doctest: +SKIP
```

Though of course, both of these are built-in and so you don't need to implement them yourself.

Storage and Conversion

`dask.dataframe.`**`read_csv`**(*urlpath*, *blocksize=64000000*, *collection=True*, *lineterminator=None*, *compression=None*, *sample=256000*, *enforce=False*, *assume_missing=False*, *storage_options=None*, *include_path_column=False*, ***kwargs*)

Read CSV files into a Dask.DataFrame

This parallelizes the `pandas.read_csv()` function in the following ways:

- It supports loading many files at once using globstrings:

```
>>> df = dd.read_csv('myfiles.*.csv')  # doctest: +SKIP
```

- In some cases it can break up large files:

```
>>> df = dd.read_csv('largefile.csv', blocksize=25e6)  # 25MB chunks  #␣
↪doctest: +SKIP
```

- It can read CSV files from external resources (e.g. S3, HDFS) by providing a URL:

```
>>> df = dd.read_csv('s3://bucket/myfiles.*.csv')  # doctest: +SKIP
>>> df = dd.read_csv('hdfs:///myfiles.*.csv')  # doctest: +SKIP
>>> df = dd.read_csv('hdfs://namenode.example.com/myfiles.*.csv')  #␣
↪doctest: +SKIP
```

Internally `dd.read_csv` uses `pandas.read_csv()` and supports many of the same keyword arguments with the same performance guarantees. See the docstring for `pandas.read_csv()` for more information on available keyword arguments.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

blocksize [str, int or None, optional] Number of bytes by which to cut up larger files. Default value is computed based on available physical memory and the number of cores. If `None`, use a single block for each file. Can be a number like 64000000 or a string like "64MB"

collection [boolean, optional] Return a dask.dataframe if True or list of dask.delayed objects if False

sample [int, optional] Number of bytes to use when determining dtypes

assume_missing [bool, optional] If True, all integer columns that aren't specified in `dtype` are assumed to contain missing values, and are converted to floats. Default is False.

storage_options [dict, optional] Extra options that make sense for a particular storage connection, e.g. host, port, username, password, etc.

include_path_column [bool or str, optional] Whether or not to include the path to each particular file. If True a new column is added to the dataframe called `path`. If str, sets new column name. Default is False.

****kwargs** Extra keyword arguments to forward to `pandas.read_csv()`.

Notes

Dask dataframe tries to infer the `dtype` of each column by reading a sample from the start of the file (or of the first file if it's a glob). Usually this works fine, but if the `dtype` is different later in the file (or in other files) this can cause issues. For example, if all the rows in the sample had integer dtypes, but later on there was a `NaN`, then this would error at compute time. To fix this, you have a few options:

- Provide explicit dtypes for the offending columns using the `dtype` keyword. This is the recommended solution.
- Use the `assume_missing` keyword to assume that all columns inferred as integers contain missing values, and convert them to floats.
- Increase the size of the sample using the `sample` keyword.

It should also be noted that this function may fail if a CSV file includes quoted strings that contain the line terminator. To get around this you can specify `blocksize=None` to not split files into multiple partitions, at the cost of reduced parallelism.

`dask.dataframe.`**`read_table`**(*urlpath*, *blocksize=64000000*, *collection=True*, *lineterminator=None*, *compression=None*, *sample=256000*, *enforce=False*, *assume_missing=False*, *storage_options=None*, *include_path_column=False*, ***kwargs*)

Read delimited files into a Dask.DataFrame

This parallelizes the `pandas.read_table()` function in the following ways:

- It supports loading many files at once using globstrings:

```
>>> df = dd.read_table('myfiles.*.csv')  # doctest: +SKIP
```

- In some cases it can break up large files:

```
>>> df = dd.read_table('largefile.csv', blocksize=25e6)  # 25MB chunks  #␣
↪doctest: +SKIP
```

- It can read CSV files from external resources (e.g. S3, HDFS) by providing a URL:

```
>>> df = dd.read_table('s3://bucket/myfiles.*.csv')  # doctest: +SKIP
>>> df = dd.read_table('hdfs:///myfiles.*.csv')  # doctest: +SKIP
>>> df = dd.read_table('hdfs://namenode.example.com/myfiles.*.csv')  #␣
↪doctest: +SKIP
```

Internally `dd.read_table` uses `pandas.read_table()` and supports many of the same keyword arguments with the same performance guarantees. See the docstring for `pandas.read_table()` for more information on available keyword arguments.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

blocksize [str, int or None, optional] Number of bytes by which to cut up larger files. Default value is computed based on available physical memory and the number of cores. If `None`, use a single block for each file. Can be a number like 64000000 or a string like "64MB"

collection [boolean, optional] Return a dask.dataframe if True or list of dask.delayed objects if False

sample [int, optional] Number of bytes to use when determining dtypes

assume_missing [bool, optional] If True, all integer columns that aren't specified in `dtype` are assumed to contain missing values, and are converted to floats. Default is False.

storage_options [dict, optional] Extra options that make sense for a particular storage connection, e.g. host, port, username, password, etc.

include_path_column [bool or str, optional] Whether or not to include the path to each particular file. If True a new column is added to the dataframe called `path`. If str, sets new column name. Default is False.

****kwargs** Extra keyword arguments to forward to `pandas.read_table()`.

Notes

Dask dataframe tries to infer the `dtype` of each column by reading a sample from the start of the file (or of the first file if it's a glob). Usually this works fine, but if the `dtype` is different later in the file (or in other files) this can cause issues. For example, if all the rows in the sample had integer dtypes, but later on there was a `NaN`, then this would error at compute time. To fix this, you have a few options:

- Provide explicit dtypes for the offending columns using the `dtype` keyword. This is the recommended solution.
- Use the `assume_missing` keyword to assume that all columns inferred as integers contain missing values, and convert them to floats.

- Increase the size of the sample using the `sample` keyword.

It should also be noted that this function may fail if a delimited file includes quoted strings that contain the line terminator. To get around this you can specify `blocksize=None` to not split files into multiple partitions, at the cost of reduced parallelism.

`dask.dataframe.`**`read_fwf`**(*urlpath*, *blocksize=64000000*, *collection=True*, *lineterminator=None*, *compression=None*, *sample=256000*, *enforce=False*, *assume_missing=False*, *storage_options=None*, *include_path_column=False*, ***kwargs*)

Read fixed-width files into a Dask.DataFrame

This parallelizes the `pandas.read_fwf()` function in the following ways:

- It supports loading many files at once using globstrings:

```
>>> df = dd.read_fwf('myfiles.*.csv')  # doctest: +SKIP
```

- In some cases it can break up large files:

```
>>> df = dd.read_fwf('largefile.csv', blocksize=25e6)  # 25MB chunks  #␣
↪doctest: +SKIP
```

- It can read CSV files from external resources (e.g. S3, HDFS) by providing a URL:

```
>>> df = dd.read_fwf('s3://bucket/myfiles.*.csv')  # doctest: +SKIP
>>> df = dd.read_fwf('hdfs:///myfiles.*.csv')  # doctest: +SKIP
>>> df = dd.read_fwf('hdfs://namenode.example.com/myfiles.*.csv')  #␣
↪doctest: +SKIP
```

Internally `dd.read_fwf` uses `pandas.read_fwf()` and supports many of the same keyword arguments with the same performance guarantees. See the docstring for `pandas.read_fwf()` for more information on available keyword arguments.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

blocksize [str, int or None, optional] Number of bytes by which to cut up larger files. Default value is computed based on available physical memory and the number of cores. If `None`, use a single block for each file. Can be a number like 64000000 or a string like "64MB"

collection [boolean, optional] Return a dask.dataframe if True or list of dask.delayed objects if False

sample [int, optional] Number of bytes to use when determining dtypes

assume_missing [bool, optional] If True, all integer columns that aren't specified in `dtype` are assumed to contain missing values, and are converted to floats. Default is False.

storage_options [dict, optional] Extra options that make sense for a particular storage connection, e.g. host, port, username, password, etc.

include_path_column [bool or str, optional] Whether or not to include the path to each particular file. If True a new column is added to the dataframe called `path`. If str, sets new column name. Default is False.

****kwargs** Extra keyword arguments to forward to `pandas.read_fwf()`.

Notes

Dask dataframe tries to infer the `dtype` of each column by reading a sample from the start of the file (or of the first file if it's a glob). Usually this works fine, but if the `dtype` is different later in the file (or in other files) this can cause issues. For example, if all the rows in the sample had integer dtypes, but later on there was a `NaN`, then this would error at compute time. To fix this, you have a few options:

- Provide explicit dtypes for the offending columns using the `dtype` keyword. This is the recommended solution.
- Use the `assume_missing` keyword to assume that all columns inferred as integers contain missing values, and convert them to floats.
- Increase the size of the sample using the `sample` keyword.

It should also be noted that this function may fail if a fixed-width file includes quoted strings that contain the line terminator. To get around this you can specify `blocksize=None` to not split files into multiple partitions, at the cost of reduced parallelism.

`dask.dataframe.`**`read_parquet`**(*path*, *columns=None*, *filters=None*, *categories=None*, *index=None*, *storage_options=None*, *engine='auto'*, *gather_statistics=None*, ***kwargs*)

Read a Parquet file into a Dask DataFrame

This reads a directory of Parquet data into a Dask.dataframe, one file per partition. It selects the index among the sorted columns if any exist.

Parameters

path [string or list] Source directory for data, or path(s) to individual parquet files. Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

columns [string, list or None (default)] Field name(s) to read in as columns in the output. By default all non-index fields will be read (as determined by the pandas parquet metadata, if present). Provide a single field name instead of a list to read in the data as a Series.

filters [list]

List of filters to apply, like `[('x', '>', 0), ...]`. This implements row-group (partition) -level filtering only, i.e., to

prevent the loading of some chunks of the data, and only if relevant statistics have been included in the metadata.

index [string, list, False or None (default)] Field name(s) to use as the output frame index. By default will be inferred from the pandas parquet file metadata (if present). Use False to read all fields as columns.

categories [list, dict or None] For any fields listed here, if the parquet encoding is Dictionary, the column will be created with dtype category. Use only if it is guaranteed that the column is encoded as dictionary in all row-groups. If a list, assumes up to 2**16-1 labels; if a dict, specify the number of labels expected; if None, will load categories automatically for data written by dask/fastparquet, not otherwise.

storage_options [dict] Key/value pairs to be passed on to the file-system backend, if any.

engine [{'auto', 'fastparquet', 'pyarrow'}, default 'auto'] Parquet reader library to use. If only one library is installed, it will use that one; if both, it will use 'fastparquet'

gather_statistics [bool or None (default).] Gather the statistics for each dataset partition. By default, this will only be done if the _metadata file is available. Otherwise, statistics will only be gathered if True, because the footer of every file will be parsed (which is very slow on some systems).

****kwargs: dict (of dicts)** Passthrough key-word arguments for read backend. The top-level keys correspond to the appropriate operation type, and the second level corresponds to the kwargs that will be passed on to the underlying *pyarrow* or *fastparquet* function. Supported top-level keys: 'dataset' (for opening a *pyarrow* dataset), 'file' (for opening a *fastparquet ParquetFile*), and 'read' (for the backend read function)

See also:

to_parquet

Examples

```
>>> df = dd.read_parquet('s3://bucket/my-parquet-data')  # doctest: +SKIP
```

dask.dataframe.**read_orc**(*path*, *columns=None*, *storage_options=None*)

Read dataframe from ORC file(s)

Parameters

path: str or list(str) Location of file(s), which can be a full URL with protocol specifier, and may include glob character if a single string.

columns: None or list(str) Columns to load. If None, loads all.

storage_options: None or dict Further parameters to pass to the bytes backend.

Returns

Dask.DataFrame (even if there is only one column)

Examples

```
>>> df = dd.read_orc('https://github.com/apache/orc/raw/'
...                  'master/examples/demo-11-zlib.orc')  # doctest: +SKIP
```

dask.dataframe.**read_hdf**(*pattern*, *key*, *start=0*, *stop=None*, *columns=None*, *chunksize=1000000*, *sorted_index=False*, *lock=True*, *mode='a'*)

Read HDF files into a Dask DataFrame

Read hdf files into a dask dataframe. This function is like `pandas.read_hdf`, except it can read from a single large file, or from multiple files, or from multiple keys from the same file.

Parameters

pattern [string, pathlib.Path, list] File pattern (string), pathlib.Path, buffer to read from, or list of file paths. Can contain wildcards.

key [group identifier in the store. Can contain wildcards]

start [optional, integer (defaults to 0), row number to start at]

stop [optional, integer (defaults to None, the last row), row number to] stop at

columns [list of columns, optional] A list of columns that if not None, will limit the return columns (default is None)

chunksize [positive integer, optional] Maximal number of rows per partition (default is 1000000).

sorted_index [boolean, optional] Option to specify whether or not the input hdf files have a sorted index (default is False).

lock [boolean, optional] Option to use a lock to prevent concurrency issues (default is True).

mode [{'a', 'r', 'r+'}, default 'a'. Mode to use when opening file(s).]

'r' Read-only; no data can be modified.

'a' Append; an existing file is opened for reading and writing, and if the file does not exist it is created.

'r+' It is similar to 'a', but the file must already exist.

Returns

dask.DataFrame

Examples

Load single file

```
>>> dd.read_hdf('myfile.1.hdf5', '/x')  # doctest: +SKIP
```

Load multiple files

```
>>> dd.read_hdf('myfile.*.hdf5', '/x')  # doctest: +SKIP
```

```
>>> dd.read_hdf(['myfile.1.hdf5', 'myfile.2.hdf5'], '/x')  # doctest: +SKIP
```

Load multiple datasets

```
>>> dd.read_hdf('myfile.1.hdf5', '/*')  # doctest: +SKIP
```

`dask.dataframe.`**`read_json`**(*url_path, orient='records', lines=None, storage_options=None, blocksize=None, sample=1048576, encoding='utf-8', errors='strict', compression='infer', meta=None, engine=<function read_json>, **kwargs*)

Create a dataframe from a set of JSON files

This utilises `pandas.read_json()`, and most parameters are passed through - see its docstring.

Differences: orient is 'records' by default, with lines=True; this is appropriate for line-delimited "JSON-lines" data, the kind of JSON output that is most common in big-data scenarios, and which can be chunked when reading (see `read_json()`). All other options require blocksize=None, i.e., one partition per input file.

Parameters

url_path: str, list of str Location to read from. If a string, can include a glob character to find a set of file names. Supports protocol specifications such as `"s3://"`.

encoding, errors: The text encoding to implement, e.g., "utf-8" and how to respond to errors in the conversion (see `str.encode()`).

orient, lines, kwargs passed to pandas; if not specified, lines=True when orient='records', False otherwise.

storage_options: dict Passed to backend file-system implementation

blocksize: None or int If None, files are not blocked, and you get one partition per input file. If int, which can only be used for line-delimited JSON files, each partition will be approximately this size in bytes, to the nearest newline character.

sample: int Number of bytes to pre-load, to provide an empty dataframe structure to any blocks wihout data. Only relevant is using blocksize.

encoding, errors: Text conversion, `see bytes.decode()`

compression [string or None] String like 'gzip' or 'xz'.

engine [function object, default `pd.read_json`] The underlying function that dask will use to read JSON files. By default, this will be the pandas JSON reader (`pd.read_json`).

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

Returns

dask.DataFrame

Examples

Load single file

```
>>> dd.read_json('myfile.1.json')  # doctest: +SKIP
```

Load multiple files

```
>>> dd.read_json('myfile.*.json')  # doctest: +SKIP
```

```
>>> dd.read_json(['myfile.1.json', 'myfile.2.json'])  # doctest: +SKIP
```

Load large line-delimited JSON files using partitions of approx 256MB size

>> dd.read_json('data/file*.csv', blocksize=2**28)

`dask.dataframe.`**`read_sql_table`**(*table, uri, index_col, divisions=None, npartitions=None, limits=None, columns=None, bytes_per_chunk=268435456, head_rows=5, schema=None, meta=None, engine_kwargs=None, **kwargs*)

Create dataframe from an SQL table.

If neither divisions or npartitions is given, the memory footprint of the first few rows will be determined, and partitions of size ~256MB will be used.

Parameters

table [string or sqlalchemy expression] Select columns from here.

uri [string] Full sqlalchemy URI for the database connection

index_col [string] Column which becomes the index, and defines the partitioning. Should be a indexed column in the SQL server, and any orderable type. If the type is number or time, then partition boundaries can be inferred from npartitions or bytes_per_chunk; otherwide must supply explicit `divisions=`. `index_col` could be a function to return a value, e.g., `sql.func.abs(sql.column('value')).label('abs(value)')`. Labeling columns created by functions or arithmetic operations is required.

divisions: sequence Values of the index column to split the table by. If given, this will override npartitions and bytes_per_chunk. The divisions are the value boundaries of the index column used to define the partitions. For example, `divisions=list('acegikmoqsuwz')` could be used to partition a string column lexographically into 12 partitions, with the implicit assumption that each partition contains similar numbers of records.

npartitions [int] Number of partitions, if divisions is not given. Will split the values of the index column linearly between limits, if given, or the column max/min. The index column must be numeric or time for this to work

limits: 2-tuple or None Manually give upper and lower range of values for use with npartitions; if None, first fetches max/min from the DB. Upper limit, if given, is inclusive.

columns [list of strings or None] Which columns to select; if None, gets all; can include sqlalchemy functions, e.g., `sql.func.abs(sql.column('value')).label('abs(value)')`. Labeling columns created by functions or arithmetic operations is recommended.

bytes_per_chunk [int] If both divisions and npartitions is None, this is the target size of each partition, in bytes

head_rows [int] How many rows to load for inferring the data-types, unless passing meta

meta [empty DataFrame or None] If provided, do not attempt to infer dtypes, but use these, coercing all chunks on load

schema [str or None] If using a table name, pass this to sqlalchemy to select which DB schema to use within the URI connection

engine_kwargs [dict or None] Specific db engine parameters for sqlalchemy

kwargs [dict] Additional parameters to pass to *pd.read_sql()*

Returns

dask.dataframe

Examples

```
>>> df = dd.read_sql_table('accounts', 'sqlite:///path/to/bank.db',
...                  npartitions=10, index_col='id')  # doctest: +SKIP
```

`dask.dataframe.`**`from_array`**(*x*, *chunksize=50000*, *columns=None*)

Read any slicable array into a Dask Dataframe

Uses getitem syntax to pull slices out of the array. The array need not be a NumPy array but must support slicing syntax

x[50000:100000]

and have 2 dimensions:

x.ndim == 2

or have a record dtype:

x.dtype == [('name', 'O'), ('balance', 'i8')] `dask.dataframe.`**`from_pandas`**`(`*data*, *npartitions=None*, *chunksize=None*, *sort=True*, *name=None*`)`

Construct a Dask DataFrame from a Pandas DataFrame

This splits an in-memory Pandas dataframe into several parts and constructs a dask.dataframe from those parts on which Dask.dataframe can operate in parallel.

Note that, despite parallelism, Dask.dataframe may not always be faster than Pandas. We recommend that you stay with Pandas for as long as possible before switching to Dask.dataframe.

Parameters

data [pandas.DataFrame or pandas.Series] The DataFrame/Series with which to construct a Dask DataFrame/Series

npartitions [int, optional] The number of partitions of the index to create. Note that depending on the size and index of the dataframe, the output may have fewer partitions than requested.

chunksize [int, optional] The number of rows per index partition to use.

sort: bool Sort input first to obtain cleanly divided partitions or don't sort and don't get cleanly divided partitions

name: string, optional An optional keyname for the dataframe. Defaults to hashing the input

Returns

dask.DataFrame or dask.Series A dask DataFrame/Series partitioned along the index

Raises

TypeError If something other than a `pandas.DataFrame` or `pandas.Series` is passed in.

See also:

`from_array` Construct a dask.DataFrame from an array that has record dtype

`read_csv` Construct a dask.DataFrame from a CSV file

Examples

```
>>> df = pd.DataFrame(dict(a=list('aabbcc'), b=list(range(6))),
...                   index=pd.date_range(start='20100101', periods=6))
>>> ddf = from_pandas(df, npartitions=3)
>>> ddf.divisions  # doctest: +NORMALIZE_WHITESPACE
(Timestamp('2010-01-01 00:00:00', freq='D'),
 Timestamp('2010-01-03 00:00:00', freq='D'),
 Timestamp('2010-01-05 00:00:00', freq='D'),
 Timestamp('2010-01-06 00:00:00', freq='D'))
>>> ddf = from_pandas(df.a, npartitions=3)  # Works with Series too!
>>> ddf.divisions  # doctest: +NORMALIZE_WHITESPACE
(Timestamp('2010-01-01 00:00:00', freq='D'),
 Timestamp('2010-01-03 00:00:00', freq='D'),
 Timestamp('2010-01-05 00:00:00', freq='D'),
 Timestamp('2010-01-06 00:00:00', freq='D'))
```

`dask.dataframe.`**`from_bcolz`**`(`*x*, *chunksize=None*, *categorize=True*, *index=None*, *lock=<unlocked _thread.lock object>*, ***kwargs*`)`

Read BColz CTable into a Dask Dataframe

BColz is a fast on-disk compressed column store with careful attention given to compression. https://bcolz.readthedocs.io/en/latest/

Parameters

x [bcolz.ctable]

chunksize [int, optional] The size(rows) of blocks to pull out from ctable.

categorize [bool, defaults to True] Automatically categorize all string dtypes

index [string, optional] Column to make the index

lock: bool or Lock Lock to use when reading or False for no lock (not-thread-safe)

See also:

from_array more generic function not optimized for bcolz

`dask.dataframe.`**`from_dask_array`**`(`*x*, *columns=None*, *index=None*`)`

Create a Dask DataFrame from a Dask Array.

Converts a 2d array into a DataFrame and a 1d array into a Series.

Parameters

x [da.Array]

columns [list or string] list of column names if DataFrame, single string if Series

index [dask.dataframe.Index, optional] An optional *dask* Index to use for the output Series or DataFrame.

The default output index depends on whether *x* has any unknown chunks. If there are any unknown chunks, the output has `None` for all the divisions (one per chunk). If all the chunks are known, a default index with known divsions is created.

Specifying *index* can be useful if you're conforming a Dask Array to an existing dask Series or DataFrame, and you would like the indices to match.

See also:

`dask.bag.to_dataframe` from dask.bag

`dask.dataframe._Frame.values` Reverse conversion

`dask.dataframe._Frame.to_records` Reverse conversion

Examples

```
>>> import dask.array as da
>>> import dask.dataframe as dd
>>> x = da.ones((4, 2), chunks=(2, 2))
>>> df = dd.io.from_dask_array(x, columns=['a', 'b'])
>>> df.compute()
     a    b
0  1.0  1.0
1  1.0  1.0
2  1.0  1.0
3  1.0  1.0
```

`dask.dataframe.`**`from_delayed`**(*dfs*, *meta=None*, *divisions=None*, *prefix='from-delayed'*, *verify_meta=True*)

Create Dask DataFrame from many Dask Delayed objects

Parameters

dfs [list of Delayed] An iterable of `dask.delayed.Delayed` objects, such as come from `dask.delayed` These comprise the individual partitions of the resulting dataframe.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

divisions [tuple, str, optional] Partition boundaries along the index. For tuple, see https://docs.dask.org/en/latest/dataframe-design.html#partitions For string 'sorted' will compute the delayed values to find index values. Assumes that the indexes are mutually sorted. If None, then won't use index information

prefix [str, optional] Prefix to prepend to the keys.

verify_meta [bool, optional] If True check that the partitions have consistent metadata, defaults to True.

`dask.dataframe.`**`to_records`**(*df*)

Create Dask Array from a Dask Dataframe

Warning: This creates a dask.array without precise shape information. Operations that depend on shape information, like slicing or reshaping, will not work.

See also:

`dask.dataframe._Frame.values`, *`dask.dataframe.from_dask_array`*

Examples

```
>>> df.to_records()  # doctest: +SKIP
dask.array<to_records, shape=(nan,), dtype=(numpy.record, [('ind', '<f8'), ('x',
↪'O'), ('y', '<i8')]), chunksize=(nan,), chunktype=numpy.ndarray>  # noqa: E501
```

`dask.dataframe.`**`to_csv`**(*df*, *filename*, *single_file=False*, *encoding='utf-8'*, *mode='wt'*, *name_function=None*, *compression=None*, *compute=True*, *scheduler=None*, *storage_options=None*, *header_first_partition_only=None*, ***kwargs*)

Store Dask DataFrame to CSV files

One filename per partition will be created. You can specify the filenames in a variety of ways.

Use a globstring:

```
>>> df.to_csv('/path/to/data/export-*.csv')
```

The * will be replaced by the increasing sequence 0, 1, 2, …

```
/path/to/data/export-0.csv
/path/to/data/export-1.csv
```

Use a globstring and a `name_function=` keyword argument. The name_function function should expect an integer and produce a string. Strings produced by name_function must preserve the order of their respective partition indices.

```
>>> from datetime import date, timedelta
>>> def name(i):
...     return str(date(2015, 1, 1) + i * timedelta(days=1))
```

```
>>> name(0)
'2015-01-01'
>>> name(15)
'2015-01-16'
```

```
>>> df.to_csv('/path/to/data/export-*.csv', name_function=name)  # doctest: +SKIP
```

```
/path/to/data/export-2015-01-01.csv
/path/to/data/export-2015-01-02.csv
...
```

You can also provide an explicit list of paths:

```
>>> paths = ['/path/to/data/alice.csv', '/path/to/data/bob.csv', ...]
>>> df.to_csv(paths)
```

Parameters

filename [string] Path glob indicating the naming scheme for the output files

name_function [callable, default None] Function accepting an integer (partition index) and producing a string to replace the asterisk in the given filename globstring. Should preserve the lexicographic order of partitions. Not supported when *single_file* is *True*.

single_file [bool, default False] Whether to save everything into a single CSV file. Under the single file mode, each partition is appended at the end of the specified CSV file. Note that not all filesystems support the append mode and thus the single file mode, especially on cloud storage systems such as S3 or GCS. A warning will be issued when writing to a file that is not backed by a local filesystem.

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access. Filenames with extensions corresponding to known compression algorithms (gz, bz2) will be compressed accordingly automatically

sep [character, default ','] Field delimiter for the output file

na_rep [string, default ''] Missing data representation

float_format [string, default None] Format string for floating point numbers

columns [sequence, optional] Columns to write

header [boolean or list of string, default True] Write out column names. If a list of string is given it is assumed to be aliases for the column names

header_first_partition_only [boolean, default None] If set to *True*, only write the header row in the first output file. By default, headers are written to all partitions under the multiple file mode (*single_file* is *False*) and written only once under the single file mode (*single_file* is *True*). It must not be *False* under the single file mode.

index [boolean, default True] Write row names (index)

index_label [string or sequence, or False, default None] Column label for index column(s) if desired. If None is given, and *header* and *index* are True, then the index names are used. A sequence should be given if the DataFrame uses MultiIndex. If False do not print fields for index names. Use index_label=False for easier importing in R

nanRep [None] deprecated, use na_rep

mode [str] Python write mode, default 'w'

encoding [string, optional] A string representing the encoding to use in the output file, defaults to 'ascii' on Python 2 and 'utf-8' on Python 3.

compression [string, optional] a string representing the compression to use in the output file, allowed values are 'gzip', 'bz2', 'xz', only used when the first argument is a filename

line_terminator [string, default '\n'] The newline character or character sequence to use in the output file

quoting [optional constant from csv module] defaults to csv.QUOTE_MINIMAL

quotechar [string (length 1), default '"'] character used to quote fields

doublequote [boolean, default True] Control quoting of *quotechar* inside a field

escapechar [string (length 1), default None] character used to escape *sep* and *quotechar* when appropriate

chunksize [int or None] rows to write at a time

tupleize_cols [boolean, default False] write multi_index columns as a list of tuples (if True) or new (expanded format) if False)

date_format [string, default None] Format string for datetime objects

decimal: string, default '.' Character recognized as decimal separator. E.g. use ',' for European data

storage_options: dict Parameters passed on to the backend filesystem class.

Returns

The names of the file written if they were computed right away

If not, the delayed tasks associated to the writing of the files

Raises

ValueError If *header_first_partition_only* is set to *False* or *name_function* is specified when *single_file* is *True*.

`dask.dataframe.`**`to_bag`**(*df*, *index=False*)

Create Dask Bag from a Dask DataFrame

Parameters

index [bool, optional] If True, the elements are tuples of `(index, value)`, otherwise they're just the `value`. Default is False.

Examples

```
>>> bag = df.to_bag()  # doctest: +SKIP
```

`dask.dataframe.to_hdf`(*df, path, key, mode='a', append=False, scheduler=None, name_function=None, compute=True, lock=None, dask_kwargs={}, **kwargs*)

Store Dask Dataframe to Hierarchical Data Format (HDF) files

This is a parallel version of the Pandas function of the same name. Please see the Pandas docstring for more detailed information about shared keyword arguments.

This function differs from the Pandas version by saving the many partitions of a Dask DataFrame in parallel, either to many files, or to many datasets within the same file. You may specify this parallelism with an asterix `*` within the filename or datapath, and an optional `name_function`. The asterix will be replaced with an increasing sequence of integers starting from `0` or with the result of calling `name_function` on each of those integers.

This function only supports the Pandas `'table'` format, not the more specialized `'fixed'` format.

Parameters

path [string, pathlib.Path] Path to a target filename. Supports strings, `pathlib.Path`, or any object implementing the `__fspath__` protocol. May contain a `*` to denote many filenames.

key [string] Datapath within the files. May contain a `*` to denote many locations

name_function [function] A function to convert the `*` in the above options to a string. Should take in a number from 0 to the number of partitions and return a string. (see examples below)

compute [bool] Whether or not to execute immediately. If False then this returns a `dask.Delayed` value.

lock [Lock, optional] Lock to use to prevent concurrency issues. By default a `threading.Lock`, `multiprocessing.Lock` or `SerializableLock` will be used depending on your scheduler if a lock is required. See dask.utils.get_scheduler_lock for more information about lock selection.

scheduler [string] The scheduler to use, like "threads" or "processes"

****other:** See pandas.to_hdf for more information

Returns

filenames [list] Returned if `compute` is True. List of file names that each partition is saved to.

delayed [dask.Delayed] Returned if `compute` is False. Delayed object to execute `to_hdf` when computed.

See also:

`read_hdf`, *`to_parquet`*

Examples

Save Data to a single file

```
>>> df.to_hdf('output.hdf', '/data')            # doctest: +SKIP
```

Save data to multiple datapaths within the same file:

```
>>> df.to_hdf('output.hdf', '/data-*')          # doctest: +SKIP
```

Save data to multiple files:

```
>>> df.to_hdf('output-*.hdf', '/data')          # doctest: +SKIP
```

Save data to multiple files, using the multiprocessing scheduler:

```
>>> df.to_hdf('output-*.hdf', '/data', scheduler='processes') # doctest: +SKIP
```

Specify custom naming scheme. This writes files as '2000-01-01.hdf', '2000-01-02.hdf', '2000-01-03.hdf', etc..

```
>>> from datetime import date, timedelta
>>> base = date(year=2000, month=1, day=1)
>>> def name_function(i):
...     ''' Convert integer 0 to n to a string '''
...     return base + timedelta(days=i)
```

```
>>> df.to_hdf('*.hdf', '/data', name_function=name_function) # doctest: +SKIP
```

`dask.dataframe.`**`to_parquet`**(*df*, *path*, *engine='auto'*, *compression='default'*, *write_index=True*, *append=False*, *ignore_divisions=False*, *partition_on=None*, *storage_options=None*, *write_metadata_file=True*, *compute=True*, ***kwargs*)

Store Dask.dataframe to Parquet files

Parameters

df [dask.dataframe.DataFrame]

path [string or pathlib.Path] Destination directory for data. Prepend with protocol like `s3://` or `hdfs://` for remote data.

engine [{'auto', 'fastparquet', 'pyarrow'}, default 'auto'] Parquet library to use. If only one library is installed, it will use that one; if both, it will use 'fastparquet'.

compression [string or dict, optional] Either a string like `"snappy"` or a dictionary mapping column names to compressors like `{"name": "gzip", "values": "snappy"}`. The default is `"default"`, which uses the default compression for whichever engine is selected.

write_index [boolean, optional] Whether or not to write the index. Defaults to True.

append [bool, optional] If False (default), construct data-set from scratch. If True, add new row-group(s) to an existing data-set. In the latter case, the data-set must exist, and the schema must match the input data.

ignore_divisions [bool, optional] If False (default) raises error when previous divisions overlap with the new appended divisions. Ignored if append=False.

partition_on [list, optional] Construct directory-based partitioning by splitting on these fields' values. Each dask partition will result in one or more datafiles, there will be no global groupby.

storage_options [dict, optional] Key/value pairs to be passed on to the file-system backend, if any.

write_metadata_file [bool, optional] Whether to write the special "_metadata" file.

compute [bool, optional] If True (default) then the result is computed immediately. If False then a `dask.delayed` object is returned for future computation.

****kwargs :** Extra options to be passed on to the specific backend.

See also:

read_parquet Read parquet data to dask.dataframe

Notes

Each partition will be written to a separate file.

Examples

```
>>> df = dd.read_csv(...)  # doctest: +SKIP
>>> dd.to_parquet(df, '/path/to/output/',...)  # doctest: +SKIP
```

`dask.dataframe.`**`to_json`**`(`*df*, *url_path*, *orient='records'*, *lines=None*, *storage_options=None*, *compute=True*, *encoding='utf-8'*, *errors='strict'*, *compression=None*, ***kwargs*`)`

Write dataframe into JSON text files

This utilises `pandas.DataFrame.to_json()`, and most parameters are passed through - see its docstring.

Differences: orient is 'records' by default, with lines=True; this produces the kind of JSON output that is most common in big-data applications, and which can be chunked when reading (see `read_json()`).

Parameters

df: dask.DataFrame Data to save

url_path: str, list of str Location to write to. If a string, and there are more than one partitions in df, should include a glob character to expand into a set of file names, or provide a `name_function=` parameter. Supports protocol specifications such as `"s3://"`.

encoding, errors: The text encoding to implement, e.g., "utf-8" and how to respond to errors in the conversion (see `str.encode()`).

orient, lines, kwargs passed to pandas; if not specified, lines=True when orient='records', False otherwise.

storage_options: dict Passed to backend file-system implementation

compute: bool If true, immediately executes. If False, returns a set of delayed objects, which can be computed at a later time.

encoding, errors: Text conversion, `see str.encode()`

compression [string or None] String like 'gzip' or 'xz'.

Rolling

`dask.dataframe.rolling.`**`map_overlap`**`(`*func*, *df*, *before*, *after*, **args*, ***kwargs*`)`

Apply a function to each partition, sharing rows with adjacent partitions.

Parameters

func [function] Function applied to each partition.

df [dd.DataFrame, dd.Series]

before [int or timedelta] The rows to prepend to partition `i` from the end of partition `i - 1`.

after [int or timedelta] The rows to append to partition `i` from the beginning of partition `i + 1`.

args, kwargs : Arguments and keywords to pass to the function. The partition will be the first argument, and these will be passed *after*.

See also:

`dd.DataFrame.map_overlap`

Dask Metadata

Other functions

`dask.dataframe.`**`compute`**`(`**args*, ***kwargs*`)`

Compute several dask collections at once.

Parameters

args [object] Any number of objects. If it is a dask object, it's computed and the result is returned. By default, python builtin collections are also traversed to look for dask objects (for more information see the `traverse` keyword). Non-dask arguments are passed through unchanged.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `compute`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the optimizations for each collection are applied before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

Examples

```
>>> import dask.array as da
>>> a = da.arange(10, chunks=2).sum()
>>> b = da.arange(10, chunks=2).mean()
>>> compute(a, b)
(45, 4.5)
```

By default, dask objects inside python collections will also be computed:

```
>>> compute({'a': a, 'b': b, 'c': 1})  # doctest: +SKIP
({'a': 45, 'b': 4.5, 'c': 1},)
```

`dask.dataframe.`**`map_partitions`**`(`*func*, **args*, ***kwargs*`)`

Apply Python function on each DataFrame partition.

Parameters

func [function] Function applied to each partition.

args, kwargs : Arguments and keywords to pass to the function. At least one of the args should be a Dask.dataframe. Arguments and keywords may contain `Scalar`, `Delayed` or regular python objects. DataFrame-like args (both dask and pandas) will be repartitioned to align (if necessary) before applying the function.

meta [pd.DataFrame, pd.Series, dict, iterable, tuple, optional] An empty `pd.DataFrame` or `pd.Series` that matches the dtypes and column names of the output. This metadata is necessary for many algorithms in dask dataframe to work. For ease of use, some alternative inputs are also available. Instead of a `DataFrame`, a `dict` of `{name: dtype}` or iterable of `(name, dtype)` can be provided (note that the order of the names should match the order of the columns). Instead of a series, a tuple of `(name, dtype)` can be used. If not provided, dask will try to infer the metadata. This may lead to unexpected results, so providing `meta` is recommended. For more information, see `dask.dataframe.utils.make_meta`.

`dask.dataframe.`**`to_datetime`**`(`*arg*, *errors='raise'*, *dayfirst=False*, *yearfirst=False*, *utc=None*, *box=True*, *format=None*, *exact=True*, *unit=None*, *infer_datetime_format=False*, *origin='unix'*, *cache=False*`)`

Convert argument to datetime.

Parameters

arg [integer, float, string, datetime, list, tuple, 1-d array, Series] New in version 0.18.1: or DataFrame/dict-like

errors [{'ignore', 'raise', 'coerce'}, default 'raise']

- If 'raise', then invalid parsing will raise an exception
- If 'coerce', then invalid parsing will be set as NaT
- If 'ignore', then invalid parsing will return the input

dayfirst [boolean, default False] Specify a date parse order if *arg* is str or its list-likes. If True, parses dates with the day first, eg 10/11/12 is parsed as 2012-11-10. Warning: dayfirst=True is not strict, but will prefer to parse with day first (this is a known bug, based on dateutil behavior).

yearfirst [boolean, default False] Specify a date parse order if *arg* is str or its list-likes.

- If True parses dates with the year first, eg 10/11/12 is parsed as 2010-11-12.
- If both dayfirst and yearfirst are True, yearfirst is preceded (same as dateutil).

Warning: yearfirst=True is not strict, but will prefer to parse with year first (this is a known bug, based on dateutil behavior).

New in version 0.16.1.

utc [boolean, default None] Return UTC DatetimeIndex if True (converting any tz-aware datetime.datetime objects as well).

box [boolean, default True]

- If True returns a DatetimeIndex or Index-like object
- If False returns ndarray of values.

format [string, default None] strftime to parse time, eg "%d/%m/%Y", note that "%f" will parse all the way up to nanoseconds.

exact [boolean, True by default]

- If True, require an exact format match.

- If False, allow the format to match anywhere in the target string.

unit [string, default 'ns'] unit of the arg (D,s,ms,us,ns) denote the unit, which is an integer or float number. This will be based off the origin. Example, with unit='ms' and origin='unix' (the default), this would calculate the number of milliseconds to the unix epoch start.

infer_datetime_format [boolean, default False] If True and no *format* is given, attempt to infer the format of the datetime strings, and if it can be inferred, switch to a faster method of parsing them. In some cases this can increase the parsing speed by ~5-10x.

origin [scalar, default is 'unix'] Define the reference date. The numeric values would be parsed as number of units (defined by *unit*) since this reference date.

- If 'unix' (or POSIX) time; origin is set to 1970-01-01.
- If 'julian', unit must be 'D', and origin is set to beginning of Julian Calendar. Julian day number 0 is assigned to the day starting at noon on January 1, 4713 BC.
- If Timestamp convertible, origin is set to Timestamp identified by origin.

New in version 0.20.0.

cache [boolean, default False] If True, use a cache of unique, converted dates to apply the datetime conversion. May produce significant speed-up when parsing duplicate date strings, especially ones with timezone offsets.

New in version 0.23.0.

Returns

ret [datetime if parsing succeeded.] Return type depends on input:

- list-like: DatetimeIndex
- Series: Series of datetime64 dtype
- scalar: Timestamp

In case when it is not possible to return designated types (e.g. when any element of input is before Timestamp.min or after Timestamp.max) return will have datetime.datetime type (or corresponding array/Series).

See also:

`pandas.DataFrame.astype` Cast argument to a specified dtype.

`pandas.to_timedelta` Convert argument to timedelta.

Examples

Assembling a datetime from multiple columns of a DataFrame. The keys can be common abbreviations like ['year', 'month', 'day', 'minute', 'second', 'ms', 'us', 'ns']) or plurals of the same

```
>>> df = pd.DataFrame({'year': [2015, 2016],
                       'month': [2, 3],
                       'day': [4, 5]})
>>> pd.to_datetime(df)
0   2015-02-04
1   2016-03-05
dtype: datetime64[ns]
```

If a date does not meet the timestamp limitations, passing errors='ignore' will return the original input instead of raising any exception.

Passing errors='coerce' will force an out-of-bounds date to NaT, in addition to forcing non-dates (or non-parseable dates) to NaT.

```
>>> pd.to_datetime('13000101', format='%Y%m%d', errors='ignore')
datetime.datetime(1300, 1, 1, 0, 0)
>>> pd.to_datetime('13000101', format='%Y%m%d', errors='coerce')
NaT
```

Passing infer_datetime_format=True can often-times speedup a parsing if its not an ISO8601 format exactly, but in a regular format.

```
>>> s = pd.Series(['3/11/2000', '3/12/2000', '3/13/2000']*1000)
```

```
>>> s.head()
0    3/11/2000
1    3/12/2000
2    3/13/2000
3    3/11/2000
4    3/12/2000
dtype: object
```

```
>>> %timeit pd.to_datetime(s,infer_datetime_format=True)
100 loops, best of 3: 10.4 ms per loop
```

```
>>> %timeit pd.to_datetime(s,infer_datetime_format=False)
1 loop, best of 3: 471 ms per loop
```

Using a unix epoch time

```
>>> pd.to_datetime(1490195805, unit='s')
Timestamp('2017-03-22 15:16:45')
>>> pd.to_datetime(1490195805433502912, unit='ns')
Timestamp('2017-03-22 15:16:45.433502912')
```

Warning: For float arg, precision rounding might happen. To prevent unexpected behavior use a fixed-width exact type.

Using a non-unix epoch origin

```
>>> pd.to_datetime([1, 2, 3], unit='D',
                   origin=pd.Timestamp('1960-01-01'))
0    1960-01-02
1    1960-01-03
2    1960-01-04
```

`dask.dataframe.multi.`**`concat`**(*dfs*, *axis=0*, *join='outer'*, *interleave_partitions=False*)

Concatenate DataFrames along rows.

- When axis=0 (default), concatenate DataFrames row-wise:
  - If all divisions are known and ordered, concatenate DataFrames keeping divisions. When divisions are not ordered, specifying interleave_partition=True allows concatenate divisions each by each.

    - If any of division is unknown, concatenate DataFrames resetting its division to unknown (None)

- When axis=1, concatenate DataFrames column-wise:
    - Allowed if all divisions are known.
    - If any of division is unknown, it raises ValueError.

Parameters

dfs [list] List of dask.DataFrames to be concatenated

axis [{0, 1, 'index', 'columns'}, default 0] The axis to concatenate along

join [{'inner', 'outer'}, default 'outer'] How to handle indexes on other axis

interleave_partitions [bool, default False] Whether to concatenate DataFrames ignoring its order. If True, every divisions are concatenated each by each.

Notes

This differs in from `pd.concat` in the when concatenating Categoricals with different categories. Pandas currently coerces those to objects before concatenating. Coercing to objects is very expensive for large arrays, so dask preserves the Categoricals by taking the union of the categories.

Examples

If all divisions are known and ordered, divisions are kept.

```
>>> a                                                    # doctest: +SKIP
dd.DataFrame<x, divisions=(1, 3, 5)>
>>> b                                                    # doctest: +SKIP
dd.DataFrame<y, divisions=(6, 8, 10)>
>>> dd.concat([a, b])                                    # doctest: +SKIP
dd.DataFrame<concat-..., divisions=(1, 3, 6, 8, 10)>
```

Unable to concatenate if divisions are not ordered.

```
>>> a                                                    # doctest: +SKIP
dd.DataFrame<x, divisions=(1, 3, 5)>
>>> b                                                    # doctest: +SKIP
dd.DataFrame<y, divisions=(2, 3, 6)>
>>> dd.concat([a, b])                                    # doctest: +SKIP
ValueError: All inputs have known divisions which cannot be concatenated
in order. Specify interleave_partitions=True to ignore order
```

Specify interleave_partitions=True to ignore the division order.

```
>>> dd.concat([a, b], interleave_partitions=True)    # doctest: +SKIP
dd.DataFrame<concat-..., divisions=(1, 2, 3, 5, 6)>
```

If any of division is unknown, the result division will be unknown

```
>>> a                                                    # doctest: +SKIP
dd.DataFrame<x, divisions=(None, None)>
>>> b                                                    # doctest: +SKIP
dd.DataFrame<y, divisions=(1, 4, 10)>
```

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```
>>> dd.concat([a, b])                                  # doctest: +SKIP
dd.DataFrame<concat-..., divisions=(None, None, None, None)>
```

Different categoricals are unioned

>> dd.concat([# doctest: +SKIP ... dd.from_pandas(pd.Series(['a', 'b'], dtype='category'), 1), ... dd.from_pandas(pd.Series(['a', 'c'], dtype='category'), 1), ...], interleave_partitions=True).dtype CategoricalDtype(categories=['a', 'b', 'c'], ordered=False)

`dask.dataframe.multi.`**`merge`**(*left*, *right*, *how='inner'*, *on=None*, *left_on=None*, *right_on=None*, *left_index=False*, *right_index=False*, *sort=False*, *suffixes=('_x', '_y')*, *copy=True*, *indicator=False*, *validate=None*)

Merge DataFrame or named Series objects with a database-style join.

The join is done on columns or indexes. If joining columns on columns, the DataFrame indexes *will be ignored*. Otherwise if joining indexes on indexes or indexes on a column or columns, the index will be passed on.

Parameters

left [DataFrame]

right [DataFrame or named Series] Object to merge with.

how [{'left', 'right', 'outer', 'inner'}, default 'inner'] Type of merge to be performed.

- left: use only keys from left frame, similar to a SQL left outer join; preserve key order.
- right: use only keys from right frame, similar to a SQL right outer join; preserve key order.
- outer: use union of keys from both frames, similar to a SQL full outer join; sort keys lexicographically.
- inner: use intersection of keys from both frames, similar to a SQL inner join; preserve the order of the left keys.

on [label or list] Column or index level names to join on. These must be found in both DataFrames. If *on* is None and not merging on indexes then this defaults to the intersection of the columns in both DataFrames.

left_on [label or list, or array-like] Column or index level names to join on in the left DataFrame. Can also be an array or list of arrays of the length of the left DataFrame. These arrays are treated as if they are columns.

right_on [label or list, or array-like] Column or index level names to join on in the right DataFrame. Can also be an array or list of arrays of the length of the right DataFrame. These arrays are treated as if they are columns.

left_index [bool, default False] Use the index from the left DataFrame as the join key(s). If it is a MultiIndex, the number of keys in the other DataFrame (either the index or a number of columns) must match the number of levels.

right_index [bool, default False] Use the index from the right DataFrame as the join key. Same caveats as left_index.

sort [bool, default False] Sort the join keys lexicographically in the result DataFrame. If False, the order of the join keys depends on the join type (how keyword).

suffixes [tuple of (str, str), default ('_x', '_y')] Suffix to apply to overlapping column names in the left and right side, respectively. To raise an exception on overlapping columns use (False, False).

copy [bool, default True] If False, avoid copy if possible.

indicator [bool or str, default False] If True, adds a column to output DataFrame called "_merge" with information on the source of each row. If string, column with information on source of each row will be added to output DataFrame, and column will be named value of string. Information column is Categorical-type and takes on a value of "left_only" for observations whose merge key only appears in 'left' DataFrame, "right_only" for observations whose merge key only appears in 'right' DataFrame, and "both" if the observation's merge key is found in both.

validate [str, optional] If specified, checks if merge is of specified type.

- "one_to_one" or "1:1": check if merge keys are unique in both left and right datasets.
- "one_to_many" or "1:m": check if merge keys are unique in left dataset.
- "many_to_one" or "m:1": check if merge keys are unique in right dataset.
- "many_to_many" or "m:m": allowed, but does not result in checks.

New in version 0.21.0.

Returns

DataFrame A DataFrame of the two merged objects.

See also:

`merge_ordered` Merge with optional filling/interpolation.

`merge_asof` Merge on nearest keys.

`DataFrame.join` Similar method using indices.

Notes

Support for specifying index levels as the *on*, *left_on*, and *right_on* parameters was added in version 0.23.0 Support for merging named Series objects was added in version 0.24.0

Examples

```
>>> df1 = pd.DataFrame({'lkey': ['foo', 'bar', 'baz', 'foo'],
...                     'value': [1, 2, 3, 5]})
>>> df2 = pd.DataFrame({'rkey': ['foo', 'bar', 'baz', 'foo'],
...                     'value': [5, 6, 7, 8]})
>>> df1
    lkey value
0   foo      1
1   bar      2
2   baz      3
3   foo      5
>>> df2
    rkey value
0   foo      5
1   bar      6
2   baz      7
3   foo      8
```

Merge df1 and df2 on the lkey and rkey columns. The value columns have the default suffixes, _x and _y, appended.

```
>>> df1.merge(df2, left_on='lkey', right_on='rkey')
  lkey  value_x rkey  value_y
0  foo        1  foo        5
1  foo        1  foo        8
2  foo        5  foo        5
3  foo        5  foo        8
4  bar        2  bar        6
5  baz        3  baz        7
```

Merge DataFrames df1 and df2 with specified left and right suffixes appended to any overlapping columns.

```
>>> df1.merge(df2, left_on='lkey', right_on='rkey',
...           suffixes=('_left', '_right'))
  lkey  value_left rkey  value_right
0  foo           1  foo            5
1  foo           1  foo            8
2  foo           5  foo            5
3  foo           5  foo            8
4  bar           2  bar            6
5  baz           3  baz            7
```

Merge DataFrames df1 and df2, but raise an exception if the DataFrames have any overlapping columns.

```
>>> df1.merge(df2, left_on='lkey', right_on='rkey', suffixes=(False, False))
Traceback (most recent call last):
...
ValueError: columns overlap but no suffix specified:
    Index(['value'], dtype='object')
```

dask.dataframe.multi.**merge_asof**(*left*, *right*, *on=None*, *left_on=None*, *right_on=None*, *left_index=False*, *right_index=False*, *by=None*, *left_by=None*, *right_by=None*, *suffixes=('_x', '_y')*, *tolerance=None*, *allow_exact_matches=True*, *direction='backward'*)

Perform an asof merge. This is similar to a left-join except that we match on nearest key rather than equal keys.

Both DataFrames must be sorted by the key.

For each row in the left DataFrame:

- A "backward" search selects the last row in the right DataFrame whose 'on' key is less than or equal to the left's key.
- A "forward" search selects the first row in the right DataFrame whose 'on' key is greater than or equal to the left's key.
- A "nearest" search selects the row in the right DataFrame whose 'on' key is closest in absolute distance to the left's key.

The default is "backward" and is compatible in versions below 0.20.0. The direction parameter was added in version 0.20.0 and introduces "forward" and "nearest".

Optionally match on equivalent keys with 'by' before searching with 'on'.

New in version 0.19.0.

Parameters

left [DataFrame]

right [DataFrame]

on [label] Field name to join on. Must be found in both DataFrames. The data MUST be ordered. Furthermore this must be a numeric column, such as datetimelike, integer, or float. On or left_on/right_on must be given.

left_on [label] Field name to join on in left DataFrame.

right_on [label] Field name to join on in right DataFrame.

left_index [boolean] Use the index of the left DataFrame as the join key.

New in version 0.19.2.

right_index [boolean] Use the index of the right DataFrame as the join key.

New in version 0.19.2.

by [column name or list of column names] Match on these columns before performing merge operation.

left_by [column name] Field names to match on in the left DataFrame.

New in version 0.19.2.

right_by [column name] Field names to match on in the right DataFrame.

New in version 0.19.2.

suffixes [2-length sequence (tuple, list, . . .)] Suffix to apply to overlapping column names in the left and right side, respectively.

tolerance [integer or Timedelta, optional, default None] Select asof tolerance within this range; must be compatible with the merge index.

allow_exact_matches [boolean, default True]

- If True, allow matching with the same 'on' value (i.e. less-than-or-equal-to / greater-than-or-equal-to)
- If False, don't match the same 'on' value (i.e., strictly less-than / strictly greater-than)

direction ['backward' (default), 'forward', or 'nearest'] Whether to search for prior, subsequent, or closest matches.

New in version 0.20.0.

Returns

merged [DataFrame]

See also:

merge, merge_ordered

Examples

```
>>> left = pd.DataFrame({'a': [1, 5, 10], 'left_val': ['a', 'b', 'c']})
>>> left
    a left_val
0   1        a
1   5        b
2  10        c
```

```
>>> right = pd.DataFrame({'a': [1, 2, 3, 6, 7],
...                       'right_val': [1, 2, 3, 6, 7]})
>>> right
   a  right_val
0  1          1
1  2          2
2  3          3
3  6          6
4  7          7
```

```
>>> pd.merge_asof(left, right, on='a')
    a left_val  right_val
0   1        a          1
1   5        b          3
2  10        c          7
```

```
>>> pd.merge_asof(left, right, on='a', allow_exact_matches=False)
    a left_val  right_val
0   1        a        NaN
1   5        b        3.0
2  10        c        7.0
```

```
>>> pd.merge_asof(left, right, on='a', direction='forward')
    a left_val  right_val
0   1        a        1.0
1   5        b        6.0
2  10        c        NaN
```

```
>>> pd.merge_asof(left, right, on='a', direction='nearest')
    a left_val  right_val
0   1        a          1
1   5        b          6
2  10        c          7
```

We can use indexed DataFrames as well.

```
>>> left = pd.DataFrame({'left_val': ['a', 'b', 'c']}, index=[1, 5, 10])
>>> left
   left_val
1         a
5         b
10        c
```

```
>>> right = pd.DataFrame({'right_val': [1, 2, 3, 6, 7]},
...                      index=[1, 2, 3, 6, 7])
>>> right
   right_val
1          1
2          2
3          3
6          6
7          7
```

```
>>> pd.merge_asof(left, right, left_index=True, right_index=True)
   left_val  right_val
```

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```
1          a          1
5          b          3
10         c          7
```

Here is a real-world times-series example

```
>>> quotes
                     time ticker     bid     ask
0 2016-05-25 13:30:00.023   GOOG  720.50  720.93
1 2016-05-25 13:30:00.023   MSFT   51.95   51.96
2 2016-05-25 13:30:00.030   MSFT   51.97   51.98
3 2016-05-25 13:30:00.041   MSFT   51.99   52.00
4 2016-05-25 13:30:00.048   GOOG  720.50  720.93
5 2016-05-25 13:30:00.049   AAPL   97.99   98.01
6 2016-05-25 13:30:00.072   GOOG  720.50  720.88
7 2016-05-25 13:30:00.075   MSFT   52.01   52.03
```

```
>>> trades
                     time ticker   price  quantity
0 2016-05-25 13:30:00.023   MSFT   51.95        75
1 2016-05-25 13:30:00.038   MSFT   51.95       155
2 2016-05-25 13:30:00.048   GOOG  720.77       100
3 2016-05-25 13:30:00.048   GOOG  720.92       100
4 2016-05-25 13:30:00.048   AAPL   98.00       100
```

By default we are taking the asof of the quotes

```
>>> pd.merge_asof(trades, quotes,
...                           on='time',
...                           by='ticker')
                     time ticker   price  quantity     bid     ask
0 2016-05-25 13:30:00.023   MSFT   51.95        75   51.95   51.96
1 2016-05-25 13:30:00.038   MSFT   51.95       155   51.97   51.98
2 2016-05-25 13:30:00.048   GOOG  720.77       100  720.50  720.93
3 2016-05-25 13:30:00.048   GOOG  720.92       100  720.50  720.93
4 2016-05-25 13:30:00.048   AAPL   98.00       100     NaN     NaN
```

We only asof within 2ms between the quote time and the trade time

```
>>> pd.merge_asof(trades, quotes,
...                           on='time',
...                           by='ticker',
...                           tolerance=pd.Timedelta('2ms'))
                     time ticker   price  quantity     bid     ask
0 2016-05-25 13:30:00.023   MSFT   51.95        75   51.95   51.96
1 2016-05-25 13:30:00.038   MSFT   51.95       155     NaN     NaN
2 2016-05-25 13:30:00.048   GOOG  720.77       100  720.50  720.93
3 2016-05-25 13:30:00.048   GOOG  720.92       100  720.50  720.93
4 2016-05-25 13:30:00.048   AAPL   98.00       100     NaN     NaN
```

We only asof within 10ms between the quote time and the trade time and we exclude exact matches on time. However *prior* data will propagate forward

```
>>> pd.merge_asof(trades, quotes,
...                           on='time',
...                           by='ticker',
```

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```
...                           tolerance=pd.Timedelta('10ms'),
...                           allow_exact_matches=False)
                     time ticker   price  quantity     bid     ask
0 2016-05-25 13:30:00.023   MSFT   51.95        75     NaN     NaN
1 2016-05-25 13:30:00.038   MSFT   51.95       155   51.97   51.98
2 2016-05-25 13:30:00.048   GOOG  720.77       100     NaN     NaN
3 2016-05-25 13:30:00.048   GOOG  720.92       100     NaN     NaN
4 2016-05-25 13:30:00.048   AAPL   98.00       100     NaN     NaN
```

`dask.dataframe.reshape.`**`get_dummies`**(*data*, *prefix=None*, *prefix_sep='_'*, *dummy_na=False*, *columns=None*, *sparse=False*, *drop_first=False*, *dtype=<class 'numpy.uint8'>*, ***kwargs*)

Convert categorical variable into dummy/indicator variables.

Data must have category dtype to infer result's `columns`.

Parameters

data [Series, or DataFrame] For Series, the dtype must be categorical. For DataFrame, at least one column must be categorical.

prefix [string, list of strings, or dict of strings, default None] String to append DataFrame column names. Pass a list with length equal to the number of columns when calling get_dummies on a DataFrame. Alternatively, *prefix* can be a dictionary mapping column names to prefixes.

prefix_sep [string, default '_'] If appending prefix, separator/delimiter to use. Or pass a list or dictionary as with *prefix.*

dummy_na [bool, default False] Add a column to indicate NaNs, if False NaNs are ignored.

columns [list-like, default None] Column names in the DataFrame to be encoded. If *columns* is None then all the columns with *category* dtype will be converted.

sparse [bool, default False] Whether the dummy columns should be sparse or not. Returns SparseDataFrame if *data* is a Series or if all columns are included. Otherwise returns a DataFrame with some SparseBlocks.

New in version 0.18.2.

drop_first [bool, default False] Whether to get k-1 dummies out of k categorical levels by removing the first level.

dtype [dtype, default np.uint8] Data type for new columns. Only a single dtype is allowed. Only valid if pandas is 0.23.0 or newer.

New in version 0.18.2.

Returns

dummies [DataFrame]

See also:

`pandas.get_dummies`

Examples

Dask's version only works with Categorical data, as this is the only way to know the output shape without computing all the data.

```
>>> import pandas as pd
>>> import dask.dataframe as dd
>>> s = dd.from_pandas(pd.Series(list('abca')), npartitions=2)
>>> dd.get_dummies(s)
Traceback (most recent call last):
    ...
NotImplementedError: `get_dummies` with non-categorical dtypes is not supported...
```

With categorical data:

```
>>> s = dd.from_pandas(pd.Series(list('abca'), dtype='category'), npartitions=2)
>>> dd.get_dummies(s)  # doctest: +NORMALIZE_WHITESPACE
Dask DataFrame Structure:
                   a      b      c
npartitions=2
0              uint8  uint8  uint8
2                ...    ...    ...
3                ...    ...    ...
Dask Name: get_dummies, 4 tasks
>>> dd.get_dummies(s).compute()  # doctest: +ELLIPSIS
   a  b  c
0  1  0  0
1  0  1  0
2  0  0  1
3  1  0  0
```

`dask.dataframe.reshape.`**`pivot_table`**(*df*, *index=None*, *columns=None*, *values=None*, *aggfunc='mean'*)

Create a spreadsheet-style pivot table as a DataFrame. Target `columns` must have category dtype to infer result's `columns`. `index`, `columns`, `values` and `aggfunc` must be all scalar.

Parameters

df [DataFrame]

index [scalar] column to be index

columns [scalar] column to be columns

values [scalar] column to aggregate

aggfunc [{'mean', 'sum', 'count'}, default 'mean']

Returns

table [DataFrame]

See also:

`pandas.DataFrame.pivot_table`

`dask.dataframe.reshape.`**`melt`**(*frame*, *id_vars=None*, *value_vars=None*, *var_name=None*, *value_name='value'*, *col_level=None*)

Unpivots a DataFrame from wide format to long format, optionally leaving identifier variables set.

This function is useful to massage a DataFrame into a format where one or more columns are identifier variables (`id_vars`), while all other columns, considered measured variables (`value_vars`), are "unpivoted" to the row axis, leaving just two non-identifier columns, 'variable' and 'value'.

Parameters

frame [DataFrame]

id_vars [tuple, list, or ndarray, optional] Column(s) to use as identifier variables.

value_vars [tuple, list, or ndarray, optional] Column(s) to unpivot. If not specified, uses all columns that are not set as *id_vars*.

var_name [scalar] Name to use for the 'variable' column. If None it uses `frame.columns.name` or 'variable'.

value_name [scalar, default 'value'] Name to use for the 'value' column.

col_level [int or string, optional] If columns are a MultiIndex then use this level to melt.

Returns

DataFrame Unpivoted DataFrame.

See also:

`pandas.DataFrame.melt`

3.9.2 Create and Store Dask DataFrames

Dask can create DataFrames from various data storage formats like CSV, HDF, Apache Parquet, and others. For most formats, this data can live on various storage systems including local disk, network file systems (NFS), the Hadoop File System (HDFS), and Amazon's S3 (excepting HDF, which is only available on POSIX like file systems).

See the Overview section for an in depth discussion of `dask.dataframe` scope, use, and limitations.

API

The following functions provide access to convert between Dask DataFrames, file formats, and other Dask or Python collections.

File Formats:

read_csv(urlpath[, blocksize, collection, . . .])	Read CSV files into a Dask.DataFrame
read_parquet(path[, columns, filters, . . .])	Read a Parquet file into a Dask DataFrame
read_hdf(pattern, key[, start, stop, . . .])	Read HDF files into a Dask DataFrame
read_orc(path[, columns, storage_options])	Read dataframe from ORC file(s)
read_json(url_path[, orient, lines, . . .])	Create a dataframe from a set of JSON files
read_sql_table(table, uri, index_col[, . . .])	Create dataframe from an SQL table.
read_table(urlpath[, blocksize, collection, . . .])	Read delimited files into a Dask.DataFrame
read_fwf(urlpath[, blocksize, collection, . . .])	Read fixed-width files into a Dask.DataFrame
from_bcolz(x[, chunksize, categorize, . . .])	Read BColz CTable into a Dask Dataframe
from_array(x[, chunksize, columns])	Read any slicable array into a Dask Dataframe
to_csv(df, filename[, single_file, . . .])	Store Dask DataFrame to CSV files
to_parquet(df, path[, engine, compression, . . .])	Store Dask.dataframe to Parquet files
to_hdf(df, path, key[, mode, append, . . .])	Store Dask Dataframe to Hierarchical Data Format (HDF) files

Dask Collections:

from_delayed(dfs[, meta, divisions, prefix, . . .])	Create Dask DataFrame from many Dask Delayed objects
from_dask_array(x[, columns, index])	Create a Dask DataFrame from a Dask Array.

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dask.bag.core.Bag.to_dataframe([meta, columns])	Create Dask Dataframe from a Dask Bag.
DataFrame.to_delayed([optimize_graph])	Convert into a list of `dask.delayed` objects, one per partition.
to_records(df)	Create Dask Array from a Dask Dataframe
to_bag(df[, index])	Create Dask Bag from a Dask DataFrame

Pandas:

from_pandas(data[, npartitions, chunksize, . . .])	Construct a Dask DataFrame from a Pandas DataFrame

Locations

For text, CSV, and Apache Parquet formats, data can come from local disk, the Hadoop File System, S3FS, or other sources, by prepending the filenames with a protocol:

```
>>> df = dd.read_csv('my-data-*.csv')
>>> df = dd.read_csv('hdfs:///path/to/my-data-*.csv')
>>> df = dd.read_csv('s3://bucket-name/my-data-*.csv')
```

For remote systems like HDFS or S3, credentials may be an issue. Usually, these are handled by configuration files on disk (such as a `.boto` file for S3), but in some cases you may want to pass storage-specific options through to the storage backend. You can do this with the `storage_options=` keyword:

```
>>> df = dd.read_csv('s3://bucket-name/my-data-*.csv',
...                  storage_options={'anon': True})
```

Dask Delayed

For more complex situations not covered by the functions above, you may want to use *dask.delayed*, which lets you construct Dask DataFrames out of arbitrary Python function calls that load DataFrames. This can allow you to handle new formats easily or bake in particular logic around loading data if, for example, your data is stored with some special format.

See *documentation on using dask.delayed with collections* or an example notebook showing how to create a Dask DataFrame from a nested directory structure of Feather files (as a stand in for any custom file format).

Dask delayed is particularly useful when simple `map` operations aren't sufficient to capture the complexity of your data layout.

From Raw Dask Graphs

This section is mainly for developers wishing to extend `dask.dataframe`. It discusses internal API not normally needed by users. Everything below can be done just as effectively with *dask.delayed* described just above. You should never need to create a DataFrame object by hand.

To construct a DataFrame manually from a dask graph you need the following information:

1. Dask: a Dask graph with keys like `{(name, 0): ..., (name, 1): ...}` as well as any other tasks on which those tasks depend. The tasks corresponding to `(name, i)` should produce `pandas.DataFrame` objects that correspond to the columns and divisions information discussed below
2. Name: the special name used above

3. Columns: a list of column names
4. Divisions: a list of index values that separate the different partitions. Alternatively, if you don't know the divisions (this is common), you can provide a list of `[None, None, None, ...]` with as many partitions as you have plus one. For more information, see the Partitions section in the *DataFrame documentation*

As an example, we build a DataFrame manually that reads several CSV files that have a datetime index separated by day. Note that you should **never** do this. The `dd.read_csv` function does this for you:

```
dsk = {('mydf', 0): (pd.read_csv, 'data/2000-01-01.csv'),
       ('mydf', 1): (pd.read_csv, 'data/2000-01-02.csv'),
       ('mydf', 2): (pd.read_csv, 'data/2000-01-03.csv')}
name = 'mydf'
columns = ['price', 'name', 'id']
divisions = [Timestamp('2000-01-01 00:00:00'),
             Timestamp('2000-01-02 00:00:00'),
             Timestamp('2000-01-03 00:00:00'),
             Timestamp('2000-01-03 23:59:59')]

df = dd.DataFrame(dsk, name, columns, divisions)
```

3.9.3 Best Practices

It is easy to get started with Dask DataFrame, but using it *well* does require some experience. This page contains suggestions for best practices, and includes solutions to common problems.

Use Pandas

For data that fits into RAM, Pandas can often be faster and easier to use than Dask DataFrame. While "Big Data" tools can be exciting, they are almost always worse than normal data tools while those remain appropriate.

Reduce, and then use Pandas

Similar to above, even if you have a large dataset there may be a point in your computation where you've reduced things to a more manageable level. You may want to switch to Pandas at this point.

```
df = dd.read_parquet('my-giant-file.parquet')
df = df[df.name == 'Alice']              # Select a subsection
result = df.groupby('id').value.mean()   # Reduce to a smaller size
result = result.compute()                # Convert to Pandas dataframe
result...                                # Continue working with Pandas
```

Pandas Performance Tips Apply to Dask DataFrame

Usual Pandas performance tips like avoiding apply, using vectorized operations, using categoricals, etc., all apply equally to Dask DataFrame. See Modern Pandas by Tom Augspurger for a good read on this topic.

Use the Index

Dask DataFrame can be optionally sorted along a single index column. Some operations against this column can be very fast. For example, if your dataset is sorted by time, you can quickly select data for a particular day, perform time series joins, etc. You can check if your data is sorted by looking at the `df.known_divisions` attribute. You can set an index column using the `.set_index(column_name)` method. This operation is expensive though, so use it sparingly (see below):

```
df = df.set_index('timestamp')  # set the index to make some operations fast

df.loc['2001-01-05':'2001-01-12']  # this is very fast if you have an index
df.merge(df2, left_index=True, right_index=True)  # this is also very fast
```

For more information, see documentation on *dataframe partitions*.

Avoid Full-Data Shuffling

Setting an index is an important but expensive operation (see above). You should do it infrequently and you should persist afterwards (see below).

Some operations like `set_index` and `merge/join` are harder to do in a parallel or distributed setting than if they are in-memory on a single machine. In particular, *shuffling operations* that rearrange data become much more communication intensive. For example, if your data is arranged by customer ID but now you want to arrange it by time, all of your partitions will have to talk to each other to exchange shards of data. This can be an intensive process, particularly on a cluster.

So, definitely set the index but try do so infrequently. After you set the index, you may want to `persist` your data if you are on a cluster:

```
df = df.set_index('column_name')  # do this infrequently
```

Additionally, `set_index` has a few options that can accelerate it in some situations. For example, if you know that your dataset is sorted or you already know the values by which it is divided, you can provide these to accelerate the `set_index` operation. For more information, see the set_index docstring.

```
df2 = df.set_index(d.timestamp, sorted=True)
```

Persist Intelligently

Note: This section is only relevant to users on distributed systems.

Often DataFrame workloads look like the following:

1. Load data from files
2. Filter data to a particular subset
3. Shuffle data to set an intelligent index
4. Several complex queries on top of this indexed data

It is often ideal to load, filter, and shuffle data once and keep this result in memory. Afterwards, each of the several complex queries can be based off of this in-memory data rather than have to repeat the full load-filter-shuffle process each time. To do this, use the client.persist method:

```
df = dd.read_csv('s3://bucket/path/to/*.csv')
df = df[df.balance < 0]
df = client.persist(df)

df = df.set_index('timestamp')
```

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```
df = client.persist(df)

>>> df.customer_id.nunique().compute()
18452844

>>> df.groupby(df.city).size().compute()
...
```

Persist is important because Dask DataFrame is *lazy by default*. It is a way of telling the cluster that it should start executing the computations that you have defined so far, and that it should try to keep those results in memory. You will get back a new DataFrame that is semantically equivalent to your old DataFrame, but now points to running data. Your old DataFrame still points to lazy computations:

```
# Don't do this
client.persist(df)  # persist doesn't change the input in-place

# Do this instead
df = client.persist(df)  # replace your old lazy DataFrame
```

Repartition to Reduce Overhead

Your Dask DataFrame is split up into many Pandas DataFrames. We sometimes call these "partitions", and often the number of partitions is decided for you. For example, it might be the number of CSV files from which you are reading. However, over time, as you reduce or increase the size of your pandas DataFrames by filtering or joining, it may be wise to reconsider how many partitions you need. There is a cost to having too many or having too few.

Partitions should fit comfortably in memory (smaller than a gigabyte) but also not be too many. Every operation on every partition takes the central scheduler a few hundred microseconds to process. If you have a few thousand tasks this is barely noticeable, but it is nice to reduce the number if possible.

A common situation is that you load lots of data into reasonably sized partitions (Dask's defaults make decent choices), but then you filter down your dataset to only a small fraction of the original. At this point, it is wise to regroup your many small partitions into a few larger ones. You can do this by using the `repartition` method:

```
df = dd.read_csv('s3://bucket/path/to/*.csv')
df = df[df.name == 'Alice']  # only 1/100th of the data
df = df.repartition(npartitions=df.npartitions // 100)

df = df.persist()  # if on a distributed system
```

This helps to reduce overhead and increase the effectiveness of vectorized Pandas operations. You should aim for partitions that have around 100MB of data each.

Additionally, reducing partitions is very helpful just before shuffling, which creates `n log(n)` tasks relative to the number of partitions. DataFrames with less than 100 partitions are much easier to shuffle than DataFrames with tens of thousands.

Joins

Joining two DataFrames can be either very expensive or very cheap depending on the situation. It is cheap in the following cases:

1. Joining a Dask DataFrame with a Pandas DataFrame
2. Joining a Dask DataFrame with another Dask DataFrame of a single partition

3. Joining Dask DataFrames along their indexes

Also, it is expensive in the following case:

1. Joining Dask DataFrames along columns that are not their index

The expensive case requires a shuffle. This is fine, and Dask DataFrame will complete the job well, but it will be more expensive than a typical linear-time operation:

```
dd.merge(a, pandas_df)  # fast
dd.merge(a, b, left_index=True, right_index=True)  # fast
dd.merge(a, b, left_index=True, right_on='id')  # half-fast, half-slow
dd.merge(a, b, left_on='id', right_on='id')  # slow
```

For more information see *Joins*.

Store Data in Apache Parquet Format

HDF5 is a popular choice for Pandas users with high performance needs. We encourage Dask DataFrame users to *store and load data* using Parquet instead. Apache Parquet is a columnar binary format that is easy to split into multiple files (easier for parallel loading) and is generally much simpler to deal with than HDF5 (from the library's perspective). It is also a common format used by other big data systems like Apache Spark and Apache Impala, and so it is useful to interchange with other systems:

```
df.to_parquet('path/to/my-results/')
df = dd.read_parquet('path/to/my-results/')
```

Dask supports reading parquet files with different engine implementations of the Apache Parquet format for Python:

```
df1 = dd.read_parquet('path/to/my-results/', engine='fastparquet')
df2 = dd.read_parquet('path/to/my-results/', engine='pyarrow')
```

These libraries can be installed using:

```
conda install fastparquet pyarrow -c conda-forge
```

fastparquet is a Python-based implementation that uses the Numba Python-to-LLVM compiler. PyArrow is part of the Apache Arrow project and uses the C++ implementation of Apache Parquet.

3.9.4 Internal Design

Dask DataFrames coordinate many Pandas DataFrames/Series arranged along an index. We define a Dask DataFrame object with the following components:

- A Dask graph with a special set of keys designating partitions, such as `('x', 0), ('x', 1), ...`
- A name to identify which keys in the Dask graph refer to this DataFrame, such as `'x'`
- An empty Pandas object containing appropriate metadata (e.g. column names, dtypes, etc.)
- A sequence of partition boundaries along the index called `divisions`

Metadata

Many DataFrame operations rely on knowing the name and dtype of columns. To keep track of this information, all Dask DataFrame objects have a `_meta` attribute which contains an empty Pandas object with the same dtypes and names. For example:

```
>>> df = pd.DataFrame({'a': [1, 2, 3], 'b': ['x', 'y', 'z']})
>>> ddf = dd.from_pandas(df, npartitions=2)
>>> ddf._meta
Empty DataFrame
Columns: [a, b]
Index: []
>>> ddf._meta.dtypes
a     int64
b    object
dtype: object
```

Internally, Dask DataFrame does its best to propagate this information through all operations, so most of the time a user shouldn't have to worry about this. Usually this is done by evaluating the operation on a small sample of fake data, which can be found on the `_meta_nonempty` attribute:

```
>>> ddf._meta_nonempty
   a    b
0  1  foo
1  1  foo
```

Sometimes this operation may fail in user defined functions (e.g. when using `DataFrame.apply`), or may be prohibitively expensive. For these cases, many functions support an optional `meta` keyword, which allows specifying the metadata directly, avoiding the inference step. For convenience, this supports several options:

1. A Pandas object with appropriate dtypes and names. If not empty, an empty slice will be taken:

```
>>> ddf.map_partitions(foo, meta=pd.DataFrame({'a': [1], 'b': [2]}))
```

2. A description of the appropriate names and dtypes. This can take several forms:

   - A `dict` of `{name: dtype}` or an iterable of `(name, dtype)` specifies a DataFrame. Note that order is important: the order of the names in `meta` should match the order of the columns
   - A tuple of `(name, dtype)` specifies a series
   - A dtype object or string (e.g. `'f8'`) specifies a scalar

This keyword is available on all functions/methods that take user provided callables (e.g. `DataFrame.map_partitions`, `DataFrame.apply`, etc...), as well as many creation functions (e.g. `dd.from_delayed`).

Partitions

Internally, a Dask DataFrame is split into many partitions, where each partition is one Pandas DataFrame. These DataFrames are split vertically along the index. When our index is sorted and we know the values of the divisions of our partitions, then we can be clever and efficient with expensive algorithms (e.g. groupby's, joins, etc...).

For example, if we have a time-series index, then our partitions might be divided by month: all of January will live in one partition while all of February will live in the next. In these cases, operations like `loc`, `groupby`, and `join/merge` along the index can be *much* more efficient than would otherwise be possible in parallel. You can view the number of partitions and divisions of your DataFrame with the following fields:

```
>>> df.npartitions
4
>>> df.divisions
['2015-01-01', '2015-02-01', '2015-03-01', '2015-04-01', '2015-04-31']
```

Divisions includes the minimum value of every partition's index and the maximum value of the last partition's index. In the example above, if the user searches for a specific datetime range, then we know which partitions we need to inspect and which we can drop:

```
>>> df.loc['2015-01-20': '2015-02-10']  # Must inspect first two partitions
```

Often we do not have such information about our partitions. When reading CSV files, for example, we do not know, without extra user input, how the data is divided. In this case `.divisions` will be all `None`:

```
>>> df.divisions
[None, None, None, None, None]
```

In these cases, any operation that requires a cleanly partitioned DataFrame with known divisions will have to perform a sort. This can generally achieved by calling `df.set_index(...)`.

3.9.5 Shuffling for GroupBy and Join

Operations like `groupby`, `join`, and `set_index` have special performance considerations that are different from normal Pandas due to the parallel, larger-than-memory, and distributed nature of Dask DataFrame.

Easy Case

To start off, common groupby operations like `df.groupby(columns).reduction()` for known reductions like `mean, sum, std, var, count, nunique` are all quite fast and efficient, even if partitions are not cleanly divided with known divisions. This is the common case.

Additionally, if divisions are known, then applying an arbitrary function to groups is efficient when the grouping columns include the index.

Joins are also quite fast when joining a Dask DataFrame to a Pandas DataFrame or when joining two Dask DataFrames along their index. No special considerations need to be made when operating in these common cases.

So, if you're doing common groupby and join operations, then you can stop reading this. Everything will scale nicely. Fortunately, this is true most of the time:

```
>>> df.groupby(columns).known_reduction()            # Fast and common case
>>> df.groupby(columns_with_index).apply(user_fn)    # Fast and common case
>>> dask_df.join(pandas_df, on=column)               # Fast and common case
>>> lhs.join(rhs)                                    # Fast and common case
>>> lhs.merge(rhs, on=columns_with_index)            # Fast and common case
```

Difficult Cases

In some cases, such as when applying an arbitrary function to groups (when not grouping on index with known divisions), when joining along non-index columns, or when explicitly setting an unsorted column to be the index, we may need to trigger a full dataset shuffle:

```
>>> df.groupby(columns_no_index).apply(user_fn)   # Requires shuffle
>>> lhs.join(rhs, on=columns_no_index)            # Requires shuffle
>>> df.set_index(column)                          # Requires shuffle
```

A shuffle is necessary when we need to re-sort our data along a new index. For example, if we have banking records that are organized by time and we now want to organize them by user ID, then we'll need to move a lot of data around. In Pandas all of this data fits in memory, so this operation was easy. Now that we don't assume that all data fits in memory, we must be a bit more careful.

Re-sorting the data can be avoided by restricting yourself to the easy cases mentioned above.

Shuffle Methods

There are currently two strategies to shuffle data depending on whether you are on a single machine or on a distributed cluster: shuffle on disk and shuffle over the network.

Shuffle on Disk

When operating on larger-than-memory data on a single machine, we shuffle by dumping intermediate results to disk. This is done using the partd project for on-disk shuffles.

Shuffle over the Network

When operating on a distributed cluster, the Dask workers may not have access to a shared hard drive. In this case, we shuffle data by breaking input partitions into many pieces based on where they will end up and moving these pieces throughout the network. This prolific expansion of intermediate partitions can stress the task scheduler. To manage for many-partitioned datasets we sometimes shuffle in stages, causing undue copies but reducing the `n**2` effect of shuffling to something closer to `n log(n)` with `log(n)` copies.

Selecting methods

Dask will use on-disk shuffling by default, but will switch to task-based distributed shuffling if the default scheduler is set to use a `dask.distributed.Client`, such as would be the case if the user sets the Client as default:

```
client = Client('scheduler:8786', set_as_default=True)
```

Alternatively, if you prefer to avoid defaults, you can configure the global shuffling method by using the `dask.config.set(shuffle=...)` command. This can be done globally:

```
dask.config.set(shuffle='tasks')

df.groupby(...).apply(...)
```

or as a context manager:

```
with dask.config.set(shuffle='tasks'):
    df.groupby(...).apply(...)
```

In addition, `set_index` also accepts a `shuffle` keyword argument that can be used to select either on-disk or task-based shuffling:

```
df.set_index(column, shuffle='disk')
df.set_index(column, shuffle='tasks')
```

3.9.6 Aggregate

Dask supports Pandas' `aggregate` syntax to run multiple reductions on the same groups. Common reductions such as `max`, `sum`, and `mean` are directly supported:

```
>>> df.groupby(columns).aggregate(['sum', 'mean', 'max', 'min'])
```

Dask also supports user defined reductions. To ensure proper performance, the reduction has to be formulated in terms of three independent steps. The `chunk` step is applied to each partition independently and reduces the data within a partition. The `aggregate` combines the within partition results. The optional `finalize` step combines the results returned from the `aggregate` step and should return a single final column. For Dask to recognize the reduction, it has to be passed as an instance of `dask.dataframe.Aggregation`.

For example, `sum` could be implemented as:

```
custom_sum = dd.Aggregation('custom_sum', lambda s: s.sum(), lambda s0: s0.sum())
df.groupby('g').agg(custom_sum)
```

The name argument should be different from existing reductions to avoid data corruption. The arguments to each function are pre-grouped series objects, similar to `df.groupby('g')['value']`.

Many reductions can only be implemented with multiple temporaries. To implement these reductions, the steps should return tuples and expect multiple arguments. A mean function can be implemented as:

```
custom_mean = dd.Aggregation(
    'custom_mean',
    lambda s: (s.count(), s.sum()),
    lambda count, sum: (count.sum(), sum.sum()),
    lambda count, sum: sum / count,
)
df.groupby('g').agg(custom_mean)
```

For example, let's compute the group-wise extent (maximum - minimum) for a DataFrame.

```
>>> df = pd.DataFrame({
...   'a': ['a', 'b', 'a', 'a', 'b'],
...   'b': [0, 1, 0, 2, 5],
>>> })
>>> ddf = dd.from_pandas(df, 2)
```

We define the building blocks to find the maximum and minimum of each chunk, and then the maximum and minimum over all the chunks. We finalize by taking the difference between the Series with the maxima and minima

```
>>> def chunk(grouped):
...     return grouped.max(), grouped.min()

>>> def agg(chunk_maxes, chunk_mins):
...     return chunk_maxes.max(), chunk_mins.min()

>>> def finalize(maxima, minima):
...     return maxima - minima
```

Finally, we create and use the aggregation

```
>>> extent = dd.Aggregation('extent', chunk, agg, finalize=finalize)
>>> ddf.groupby('a').agg(extent).compute()
   b
a
a  2
b  4
```

3.9.7 Joins

DataFrame joins are a common and expensive computation that benefit from a variety of optimizations in different situations. Understanding how your data is laid out and what you're trying to accomplish can have a large impact on performance. This documentation page goes through the various different options and their performance impacts.

Large to Large Unsorted Joins

In the worst case scenario you have two large tables with many partitions each and you want to join them both along a column that may not be sorted.

This can be slow. In this case Dask DataFrame will need to move all of your data around so that rows with matching values in the joining columns are in the same partition. This large-scale movement can create communication costs, and can require a large amount of memory. If enough memory can not be found then Dask will have to read and write data to disk, which may cause other performance costs.

These problems are solvable, but will be significantly slower than many other operations. They are best avoided if possible.

Large to Small Joins

Many join or merge computations combine a large table with one small one. If the small table is either a single partition Dask DataFrame or even just a normal Pandas DataFrame then the computation can proceed in an embarrassingly parallel way, where each partition of the large DataFrame is joined against the single small table. This incurs almost no overhead relative to Pandas joins.

If your smaller table can easily fit in memory, then you might want to ensure that it is a single partition with the following

```
small = small.repartition(npartitions=1)
result = big.merge(small)
```

Sorted Joins

The Pandas merge API supports the `left_index=` and `right_index=` options to perform joins on the index. For Dask DataFrames these keyword options hold special significance if the index has known divisions (see *Partitions*). In this case the DataFrame partitions are aligned along these divisions (which is generally fast) and then an embarrassingly parallel Pandas join happens across partition pairs. This is generally relatively fast.

Sorted or indexed joins are a good solution to the large-large join problem. If you plan to join against a dataset repeatedly then it may be worthwhile to set the index ahead of time, and possibly store the data in a format that maintains that index, like Parquet.

```
left = left.set_index('id').persist()

left.merge(right_one, left_index=True, ...)
left.merge(right_two, left_index=True, ...)
...
```

3.9.8 Indexing into Dask DataFrames

Dask DataFrame supports some of Pandas' indexing behavior.

DataFrame.iloc	Purely integer-location based indexing for selection by position.
DataFrame.loc	Purely label-location based indexer for selection by label.

Label-based Indexing

Just like Pandas, Dask DataFrame supports label-based indexing with the `.loc` accessor for selecting rows or columns, and `__getitem__` (square brackets) for selecting just columns.

Note: To select rows, the DataFrame's divisions must be known (see *Internal Design* and *Best Practices* for more information.)

```
>>> import dask.dataframe as dd
>>> import pandas as pd
>>> df = pd.DataFrame({"A": [1, 2, 3], "B": [3, 4, 5]},
...                   index=['a', 'b', 'c'])
>>> ddf = dd.from_pandas(df, npartitions=2)
>>> ddf
Dask DataFrame Structure:
                   A      B
npartitions=1
a              int64  int64
c                ...    ...
Dask Name: from_pandas, 1 tasks
```

Selecting columns:

```
>>> ddf[['B', 'A']]
Dask DataFrame Structure:
                   B      A
npartitions=1
a              int64  int64
c                ...    ...
Dask Name: getitem, 2 tasks
```

Selecting a single column reduces to a Dask Series:

```
>>> ddf['A']
Dask Series Structure:
npartitions=1
a    int64
c      ...
Name: A, dtype: int64
Dask Name: getitem, 2 tasks
```

Slicing rows and (optionally) columns with `.loc`:

```
>>> ddf.loc[['b', 'c'], ['A']]
Dask DataFrame Structure:
                   A
npartitions=1
b              int64
```

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```
c                ...
Dask Name: loc, 2 tasks
```

Dask DataFrame supports Pandas' partial-string indexing:

```
>>> ts = dd.demo.make_timeseries()
>>> ts
Dask DataFrame Structure:
                   id    name        x        y
npartitions=11
2000-01-31      int64  object  float64  float64
2000-02-29        ...     ...      ...      ...
...               ...     ...      ...      ...
2000-11-30        ...     ...      ...      ...
2000-12-31        ...     ...      ...      ...
Dask Name: make-timeseries, 11 tasks

>>> ts.loc['2000-02-12']
Dask DataFrame Structure:
                                  id    name        x        y
npartitions=1
2000-02-12 00:00:00.000000000  int64  object  float64  float64
2000-02-12 23:59:59.999999999    ...     ...      ...      ...
Dask Name: loc, 12 tasks
```

Positional Indexing

Dask DataFrame does not track the length of partitions, making positional indexing with `.iloc` inefficient for selecting rows. *`DataFrame.iloc()`* only supports indexers where the row indexer is `slice(None)` (which `:` is a shorthand for.)

```
>>> ddf.iloc[:, [1, 0]]
Dask DataFrame Structure:
                   B      A
npartitions=1
a              int64  int64
c                ...    ...
Dask Name: iloc, 2 tasks
```

Trying to select specific rows with `iloc` will raise an exception:

```
>>> ddf.iloc[[0, 2], [1]]
Traceback (most recent call last)
  File "<stdin>", line 1, in <module>
ValueError: 'DataFrame.iloc' does not support slicing rows. The indexer must be a 2-
↪tuple whose first item is 'slice(None)'.
```

3.9.9 Categoricals

Dask DataFrame divides categorical data into two types:

- Known categoricals have the `categories` known statically (on the `_meta` attribute). Each partition **must** have the same categories as found on the `_meta` attribute

- Unknown categoricals don't know the categories statically, and may have different categories in each partition. Internally, unknown categoricals are indicated by the presence of `dd.utils.UNKNOWN_CATEGORIES` in the categories on the `_meta` attribute. Since most DataFrame operations propagate the categories, the known/unknown status should propagate through operations (similar to how `NaN` propagates)

For metadata specified as a description (option 2 above), unknown categoricals are created.

Certain operations are only available for known categoricals. For example, `df.col.cat.categories` would only work if `df.col` has known categories, since the categorical mapping is only known statically on the metadata of known categoricals.

The known/unknown status for a categorical column can be found using the `known` property on the categorical accessor:

```
>>> ddf.col.cat.known
False
```

Additionally, an unknown categorical can be converted to known using `.cat.as_known()`. If you have multiple categorical columns in a DataFrame, you may instead want to use `df.categorize(columns=...)`, which will convert all specified columns to known categoricals. Since getting the categories requires a full scan of the data, using `df.categorize()` is more efficient than calling `.cat.as_known()` for each column (which would result in multiple scans):

```
>>> col_known = ddf.col.cat.as_known()  # use for single column
>>> col_known.cat.known
True
>>> ddf_known = ddf.categorize()        # use for multiple columns
>>> ddf_known.col.cat.known
True
```

To convert a known categorical to an unknown categorical, there is also the `.cat.as_unknown()` method. This requires no computation as it's just a change in the metadata.

Non-categorical columns can be converted to categoricals in a few different ways:

```
# astype operates lazily, and results in unknown categoricals
ddf = ddf.astype({'mycol': 'category', ...})
# or
ddf['mycol'] = ddf.mycol.astype('category')

# categorize requires computation, and results in known categoricals
ddf = ddf.categorize(columns=['mycol', ...])
```

Additionally, with Pandas 0.19.2 and up, `dd.read_csv` and `dd.read_table` can read data directly into unknown categorical columns by specifying a column dtype as `'category'`:

```
>>> ddf = dd.read_csv(..., dtype={col_name: 'category'})
```

Moreover, with Pandas 0.21.0 and up, `dd.read_csv` and `dd.read_table` can read data directly into *known* categoricals by specifying instances of `pd.api.types.CategoricalDtype`:

```
>>> dtype = {'col': pd.api.types.CategoricalDtype(['a', 'b', 'c'])}
>>> ddf = dd.read_csv(..., dtype=dtype)
```

3.9.10 Subclass DataFrames

There are a few projects that subclass or replicate the functionality of Pandas objects:

- GeoPandas: for Geospatial analytics
- PyGDF: for data analysis on GPUs
- . . .

These projects may also want to produce parallel variants of themselves with Dask, and may want to reuse some of the code in Dask DataFrame. This document describes how to do this. It is intended for maintainers of these libraries and not for general users.

Implement dask, name, meta, and divisions

You will need to implement `._meta`, `.dask`, `.divisions`, and `._name` as defined in the *DataFrame design docs*.

Extend Dispatched Methods

If you are going to pass around Pandas-like objects that are not normal Pandas objects, then we ask you to extend a few dispatched methods.

make_meta

This function returns an empty version of one of your non-Dask objects, given a non-empty non-Dask object:

```python
from dask.dataframe import make_meta

@make_meta.register(MyDataFrame)
def make_meta_dataframe(df):
    return df.head(0)


@make_meta.register(MySeries)
def make_meta_series(s):
    return s.head(0)


@make_meta.register(MyIndex)
def make_meta_index(ind):
    return ind[:0]
```

Additionally, you should create a similar function that returns a non-empty version of your non-Dask DataFrame objects filled with a few rows of representative or random data. This is used to guess types when they are not provided. It should expect an empty version of your object with columns, dtypes, index name, and it should return a non-empty version:

```python
from dask.dataframe.utils import meta_nonempty

@meta_nonempty.register(MyDataFrame)
def meta_nonempty_dataframe(df):
    ...
    return MyDataFrame(..., columns=df.columns,
                       index=MyIndex(..., name=df.index.name)


@meta_nonempty.register(MySeries)
def meta_nonempty_series(s):
```

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```
    ...


@meta_nonempty.register(MyIndex)
def meta_nonempty_index(ind):
    ...
```

get_parallel_type

Given a non-Dask DataFrame object, return the Dask equivalent:

```
from dask.dataframe.core import get_parallel_type

@get_parallel_type.register(MyDataFrame)
def get_parallel_type_dataframe(df):
    return MyDaskDataFrame


@get_parallel_type.register(MySeries)
def get_parallel_type_series(s):
    return MyDaskSeries


@get_parallel_type.register(MyIndex)
def get_parallel_type_index(ind):
    return MyDaskIndex
```

concat

Concatenate many of your non-Dask DataFrame objects together. It should expect a list of your objects (homogeneously typed):

```
from dask.dataframe.methods import concat_dispatch

@concat_dispatch.register((MyDataFrame, MySeries, MyIndex))
def concat_pandas(dfs, axis=0, join='outer', uniform=False, filter_warning=True):
    ...
```

Extension Arrays

Rather than subclassing Pandas DataFrames, you may be interested in extending Pandas with Extension Arrays.

All of the first-party extension arrays (those implemented in pandas itself) are supported directly by dask.

Developers implementing third-party extension arrays (outside of pandas) will need to do register their `ExtensionDtype` with Dask so that it works correctly in `dask.dataframe`.

For example, we'll register the *test-only* `DecimalDtype` from pandas test suite.

```
from decimal import Decimal
from dask.dataframe.extensions import make_array_nonempty, make_scalar
from pandas.tests.extension.decimal import DecimalArray, DecimalDtype
```

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```
@make_array_nonempty.register(DecimalDtype)
def _(dtype):
    return DecimalArray._from_sequence([Decimal('0'), Decimal('NaN')],
                                       dtype=dtype)


@make_scalar.register(Decimal)
def _(x):
   return Decimal('1')
```

Internally, Dask will use this to create a small dummy Series for tracking metadata through operations.

```
>>> make_array_nonempty(DecimalDtype())
<DecimalArray>
[Decimal('0'), Decimal('NaN')]
Length: 2, dtype: decimal
```

So you (or your users) can now create and store a dask `DataFrame` or `Series` with your extension array contained within.

```
>>> from decimal import Decimal
>>> import dask.dataframe as dd
>>> import pandas as pd
>>> from pandas.tests.extension.decimal import DecimalArray
>>> ser = pd.Series(DecimalArray([Decimal('0.0')] * 10))
>>> dser = dd.from_pandas(ser, 3)
>>> dser
Dask Series Structure:
npartitions=3
0    decimal
4        ...
8        ...
9        ...
dtype: decimal
Dask Name: from_pandas, 3 tasks
```

Notice the `decimal` dtype.

Accessors

Many extension arrays expose their functionality on Series or DataFrame objects using accessors. Dask provides decorators to register accessors similar to pandas. See the pandas documentation on accessors for more.

`dask.dataframe.extensions.`**`register_dataframe_accessor`**`(`*name*`)`

Register a custom accessor on *`dask.dataframe.DataFrame`*.

See `pandas.api.extensions.register_dataframe_accessor()` for more.

`dask.dataframe.extensions.`**`register_series_accessor`**`(`*name*`)`

Register a custom accessor on *`dask.dataframe.Series`*.

See `pandas.api.extensions.register_series_accessor()` for more.

`dask.dataframe.extensions.`**`register_index_accessor`**`(`*name*`)`

Register a custom accessor on `dask.dataframe.Index`.

See `pandas.api.extensions.register_index_accessor()` for more.

A Dask DataFrame is a large parallel DataFrame composed of many smaller Pandas DataFrames, split along the index. These Pandas DataFrames may live on disk for larger-than-memory computing on a single machine, or on many different machines in a cluster. One Dask DataFrame operation triggers many operations on the constituent Pandas DataFrames.

3.9.11 Design

Dask DataFrames coordinate many Pandas DataFrames/Series arranged along the index. A Dask DataFrame is partitioned *row-wise*, grouping rows by index value for efficiency. These Pandas objects may live on disk or on other machines.

3.9.12 Dask DataFrame copies the Pandas API

Because the `dask.dataframe` application programming interface (API) is a subset of the Pandas API, it should be familiar to Pandas users. There are some slight alterations due to the parallel nature of Dask:

```
>>> import dask.dataframe as dd
>>> df = dd.read_csv('2014-*.csv')
>>> df.head()
   x  y
0  1  a
1  2  b
2  3  c
3  4  a
4  5  b
5  6  c

>>> df2 = df[df.y == 'a'].x + 1
```

As with all Dask collections, one triggers computation by calling the `.compute()` method:

```
>>> df2.compute()
0    2
3    5
Name: x, dtype: int64
```

3.9.13 Common Uses and Anti-Uses

Dask DataFrame is used in situations where Pandas is commonly needed, usually when Pandas fails due to data size or computation speed:

- Manipulating large datasets, even when those datasets don't fit in memory
- Accelerating long computations by using many cores
- Distributed computing on large datasets with standard Pandas operations like groupby, join, and time series computations

Dask DataFrame may not be the best choice in the following situations:

- If your dataset fits comfortably into RAM on your laptop, then you may be better off just using Pandas. There may be simpler ways to improve performance than through parallelism

- If your dataset doesn't fit neatly into the Pandas tabular model, then you might find more use in *dask.bag* or *dask.array*
- If you need functions that are not implemented in Dask DataFrame, then you might want to look at *dask.delayed* which offers more flexibility
- If you need a proper database with all that databases offer you might prefer something like Postgres

3.9.14 Scope

Dask DataFrame covers a well-used portion of the Pandas API. The following class of computations works well:

- **Trivially parallelizable operations (fast):**
  - Element-wise operations: `df.x + df.y`, `df * df`
  - Row-wise selections: `df[df.x > 0]`
  - Loc: `df.loc[4.0:10.5]`
  - Common aggregations: `df.x.max()`, `df.max()`
  - Is in: `df[df.x.isin([1, 2, 3])]`
  - Date time/string accessors: `df.timestamp.month`
- **Cleverly parallelizable operations (fast):**
  - groupby-aggregate (with common aggregations): `df.groupby(df.x).y.max()`, `df.groupby('x').max()`
  - groupby-apply on index: `df.groupby(['idx', 'x']).apply(myfunc)`, where `idx` is the index level name
  - value_counts: `df.x.value_counts()`
  - Drop duplicates: `df.x.drop_duplicates()`
  - Join on index: `dd.merge(df1, df2, left_index=True, right_index=True)` or `dd.merge(df1, df2, on=['idx', 'x'])` where `idx` is the index name for both `df1` and `df2`
  - Join with Pandas DataFrames: `dd.merge(df1, df2, on='id')`
  - Element-wise operations with different partitions / divisions: `df1.x + df2.y`
  - Date time resampling: `df.resample(...)`
  - Rolling averages: `df.rolling(...)`
  - Pearson's correlation: `df[['col1', 'col2']].corr()`
- **Operations requiring a shuffle (slow-ish, unless on index)**
  - Set index: `df.set_index(df.x)`
  - groupby-apply not on index (with anything): `df.groupby(df.x).apply(myfunc)`
  - Join not on the index: `dd.merge(df1, df2, on='name')`

However, Dask DataFrame does not implement the entire Pandas interface. Users expecting this will be disappointed. Notably, Dask DataFrame has the following limitations:

1. Setting a new index from an unsorted column is expensive
2. Many operations like groupby-apply and join on unsorted columns require setting the index, which as mentioned above, is expensive

3. The Pandas API is very large. Dask DataFrame does not attempt to implement many Pandas features or any of the more exotic data structures like NDFrames
4. Operations that were slow on Pandas, like iterating through row-by-row, remain slow on Dask DataFrame

See *DataFrame API documentation* for a more extensive list.

3.9.15 Execution

By default, Dask DataFrame uses the multi-threaded scheduler. This exposes some parallelism when Pandas or the underlying NumPy operations release the global interpreter lock (GIL). Generally, Pandas is more GIL bound than NumPy, so multi-core speed-ups are not as pronounced for Dask DataFrame as they are for Dask Array. This is changing, and the Pandas development team is actively working on releasing the GIL.

When dealing with text data, you may see speedups by switching to the newer *distributed scheduler* either on a cluster or single machine.

3.10 Delayed

3.10.1 API

The `dask.delayed` interface consists of one function, `delayed`:

- `delayed` wraps functions

  Wraps functions. Can be used as a decorator, or around function calls directly (i.e. `delayed(foo)(a, b, c)`). Outputs from functions wrapped in `delayed` are proxy objects of type `Delayed` that contain a graph of all operations done to get to this result.

- `delayed` wraps objects

  Wraps objects. Used to create `Delayed` proxies directly.

`Delayed` objects can be thought of as representing a key in the dask task graph. A `Delayed` supports *most* python operations, each of which creates another `Delayed` representing the result:

- Most operators (`*`, `-`, and so on)
- Item access and slicing (`a[0]`)
- Attribute access (`a.size`)
- Method calls (`a.index(0)`)

Operations that aren't supported include:

- Mutating operators (`a += 1`)
- Mutating magics such as `__setitem__`/`__setattr__` (`a[0] = 1`, `a.foo = 1`)
- Iteration. (`for i in a: ...`)
- Use as a predicate (`if a: ...`)

The last two points in particular mean that `Delayed` objects cannot be used for control flow, meaning that no `Delayed` can appear in a loop or if statement. In other words you can't iterate over a `Delayed` object, or use it as part of a condition in an if statement, but `Delayed` object can be used in a body of a loop or if statement (i.e. the example above is fine, but if `data` was a `Delayed` object it wouldn't be). Even with this limitation, many workflows can easily be parallelized.

delayed	Wraps a function or object to produce a Delayed.

`dask.delayed.`**`delayed`**`()`

Wraps a function or object to produce a `Delayed`.

`Delayed` objects act as proxies for the object they wrap, but all operations on them are done lazily by building up a dask graph internally.

Parameters

obj [object] The function or object to wrap

name [string or hashable, optional] The key to use in the underlying graph for the wrapped object. Defaults to hashing content. Note that this only affects the name of the object wrapped by this call to delayed, and *not* the output of delayed function calls - for that use `dask_key_name=` as described below.

pure [bool, optional] Indicates whether calling the resulting `Delayed` object is a pure operation. If True, arguments to the call are hashed to produce deterministic keys. If not provided, the default is to check the global `delayed_pure` setting, and fallback to `False` if unset.

nout [int, optional] The number of outputs returned from calling the resulting `Delayed` object. If provided, the `Delayed` output of the call can be iterated into `nout` objects, allowing for unpacking of results. By default iteration over `Delayed` objects will error. Note, that `nout=1` expects `obj`, to return a tuple of length 1, and consequently for `nout=0`, `obj` should return an empty tuple.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `delayed`. For large collections this can be expensive. If `obj` doesn't contain any dask objects, set `traverse=False` to avoid doing this traversal.

Examples

Apply to functions to delay execution:

```
>>> def inc(x):
...     return x + 1
```

```
>>> inc(10)
11
```

```
>>> x = delayed(inc, pure=True)(10)
>>> type(x) == Delayed
True
>>> x.compute()
11
```

Can be used as a decorator:

```
>>> @delayed(pure=True)
... def add(a, b):
...     return a + b
>>> add(1, 2).compute()
3
```

`delayed` also accepts an optional keyword `pure`. If False, then subsequent calls will always produce a different `Delayed`. This is useful for non-pure functions (such as `time` or `random`).

```
>>> from random import random
>>> out1 = delayed(random, pure=False)()
>>> out2 = delayed(random, pure=False)()
>>> out1.key == out2.key
False
```

If you know a function is pure (output only depends on the input, with no global state), then you can set `pure=True`. This will attempt to apply a consistent name to the output, but will fallback on the same behavior of `pure=False` if this fails.

```
>>> @delayed(pure=True)
... def add(a, b):
...     return a + b
>>> out1 = add(1, 2)
>>> out2 = add(1, 2)
>>> out1.key == out2.key
True
```

Instead of setting `pure` as a property of the callable, you can also set it contextually using the `delayed_pure` setting. Note that this influences the *call* and not the *creation* of the callable:

```
>>> import dask
>>> @delayed
... def mul(a, b):
...     return a * b
>>> with dask.config.set(delayed_pure=True):
...     print(mul(1, 2).key == mul(1, 2).key)
True
>>> with dask.config.set(delayed_pure=False):
...     print(mul(1, 2).key == mul(1, 2).key)
False
```

The key name of the result of calling a delayed object is determined by hashing the arguments by default. To explicitly set the name, you can use the `dask_key_name` keyword when calling the function:

```
>>> add(1, 2)    # doctest: +SKIP
Delayed('add-3dce7c56edd1ac2614add714086e950f')
>>> add(1, 2, dask_key_name='three')
Delayed('three')
```

Note that objects with the same key name are assumed to have the same result. If you set the names explicitly you should make sure your key names are different for different results.

```
>>> add(1, 2, dask_key_name='three')  # doctest: +SKIP
>>> add(2, 1, dask_key_name='three')  # doctest: +SKIP
>>> add(2, 2, dask_key_name='four')   # doctest: +SKIP
```

`delayed` can also be applied to objects to make operations on them lazy:

```
>>> a = delayed([1, 2, 3])
>>> isinstance(a, Delayed)
True
>>> a.compute()
[1, 2, 3]
```

The key name of a delayed object is hashed by default if pure=True or is generated randomly if pure=False (default). To explicitly set the name, you can use the name keyword:

```
>>> a = delayed([1, 2, 3], name='mylist')
>>> a
Delayed('mylist')
```

Delayed results act as a proxy to the underlying object. Many operators are supported:

```
>>> (a + [1, 2]).compute()
[1, 2, 3, 1, 2]
>>> a[1].compute()
2
```

Method and attribute access also works:

```
>>> a.count(2).compute()
1
```

Note that if a method doesn't exist, no error will be thrown until runtime:

```
>>> res = a.not_a_real_method()
>>> res.compute()  # doctest: +SKIP
AttributeError("'list' object has no attribute 'not_a_real_method'")
```

"Magic" methods (e.g. operators and attribute access) are assumed to be pure, meaning that subsequent calls must return the same results. This behavior is not overrideable through the delayed call, but can be modified using other ways as described below.

To invoke an impure attribute or operator, you'd need to use it in a delayed function with pure=False:

```
>>> class Incrementer(object):
...     def __init__(self):
...         self._n = 0
...     @property
...     def n(self):
...         self._n += 1
...         return self._n
...
>>> x = delayed(Incrementer())
>>> x.n.key == x.n.key
True
>>> get_n = delayed(lambda x: x.n, pure=False)
>>> get_n(x).key == get_n(x).key
False
```

In contrast, methods are assumed to be impure by default, meaning that subsequent calls may return different results. To assume purity, set *pure=True*. This allows sharing of any intermediate values.

```
>>> a.count(2, pure=True).key == a.count(2, pure=True).key
True
```

As with function calls, method calls also respect the global delayed_pure setting and support the dask_key_name keyword:

```
>>> a.count(2, dask_key_name="count_2")
Delayed('count_2')
>>> with dask.config.set(delayed_pure=True):
```

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```
...     print(a.count(2).key == a.count(2).key)
True
```

3.10.2 Working with Collections

Often we want to do a bit of custom work with `dask.delayed` (for example, for complex data ingest), then leverage the algorithms in `dask.array` or `dask.dataframe`, and then switch back to custom work. To this end, all collections support `from_delayed` functions and `to_delayed` methods.

As an example, consider the case where we store tabular data in a custom format not known by Dask DataFrame. This format is naturally broken apart into pieces and we have a function that reads one piece into a Pandas DataFrame. We use `dask.delayed` to lazily read these files into Pandas DataFrames, use `dd.from_delayed` to wrap these pieces up into a single Dask DataFrame, use the complex algorithms within the DataFrame (groupby, join, etc.), and then switch back to `dask.delayed` to save our results back to the custom format:

```
import dask.dataframe as dd
from dask.delayed import delayed

from my_custom_library import load, save

filenames = ...
dfs = [delayed(load)(fn) for fn in filenames]

df = dd.from_delayed(dfs)
df = ... # do work with dask.dataframe

dfs = df.to_delayed()
writes = [delayed(save)(df, fn) for df, fn in zip(dfs, filenames)]

dd.compute(*writes)
```

Data science is often complex, and `dask.delayed` provides a release valve for users to manage this complexity on their own, and solve the last mile problem for custom formats and complex situations.

3.10.3 Best Practices

It is easy to get started with Dask delayed, but using it *well* does require some experience. This page contains suggestions for best practices, and includes solutions to common problems.

Call delayed on the function, not the result

Dask delayed operates on functions like `dask.delayed(f)(x, y)`, not on their results like `dask.delayed(f(x, y))`. When you do the latter, Python first calculates `f(x, y)` before Dask has a chance to step in.

Don't	Do

`# This executes immediately`
 	
`dask.delayed(f(x, y))`
	`# This makes a delayed function, acting␣`
	`↪lazily`
	
	`dask.delayed(f)(x, y)`

Compute on lots of computation at once

To improve parallelism, you want to include lots of computation in each compute call. Ideally, you want to make many `dask.delayed` calls to define your computation and then call `dask.compute` only at the end. It is ok to call `dask.compute` in the middle of your computation as well, but everything will stop there as Dask computes those results before moving forward with your code.

Don't	Do
`# Avoid calling compute repeatedly`	`# Collect many calls for one compute`
`results = []`	`results = []`
`for x in L:`	`for x in L:`
`    y = dask.delayed(f)(x)`	`    y = dask.delayed(f)(x)`
`    results.append(y.compute())`	`    results.append(y)`
`results`	`results = dask.compute(*results)`

Calling *y.compute()* within the loop would await the result of the computation every time, and so inhibit parallelism.

Don't mutate inputs

Your functions should not change the inputs directly.

Don't	Do
`# Mutate inputs in functions`	`# Return new values or copies`
`@dask.delayed`	`@dask.delayed`
`def f(x):`	`def f(x):`
`    x += 1`	`    x = x + 1`
`    return x`	`    return x`

If you need to use a mutable operation, then make a copy within your function first:

```
@dask.delayed
def f(x):
    x = copy(x)
    x += 1
    return x
```

Avoid global state

Ideally, your operations shouldn't rely on global state. Using global state *might* work if you only use threads, but when you move to multiprocessing or distributed computing then you will likely encounter confusing errors.

Don't
```
L = []

# This references global variable L

@dask.delayed
def f(x):
    L.append(x)
```

Don't rely on side effects

Delayed functions only do something if they are computed. You will always need to pass the output to something that eventually calls compute.

Don't	Do

```
# Forget to call compute

dask.delayed(f)(1, 2, 3)

...
```
	```
	# Ensure delayed tasks are computed

	x = dask.delayed(f)(1, 2, 3)
	...
	dask.compute(x, ...)
	```

In the first case here, nothing happens, because `compute()` is never called.

Break up computations into many pieces

Every `dask.delayed` function call is a single operation from Dask's perspective. You achieve parallelism by having many delayed calls, not by using only a single one: Dask will not look inside a function decorated with `@dask.delayed` and parallelize that code internally. To accomplish that, it needs your help to find good places to break up a computation.

Don’t	Do
`# One giant task`	`# Break up into many tasks`
	`@dask.delayed`
`def load(filename):`	`def load(filename):`
`    ...`	`    ...`
	`@dask.delayed`
`def process(filename):`	`def process(filename):`
`    ...`	`    ...`
	`@dask.delayed`
`def save(filename):`	`def save(filename):`
`    ...`	`    ...`
`@dask.delayed`	
`def f(filenames):`	`def f(filenames):`
`    results = []`	`    results = []`
`    for filename in filenames:`	`    for filename in filenames:`
`        data = load(filename)`	`        data = load(filename)`
`        data = process(data)`	`        data = process(data)`
`        result = save(data)`	`        result = save(data)`
`    return results`	`    return results`
`dask.compute(f(filenames))`	`dask.compute(f(filenames))`

The first version only has one delayed task, and so cannot parallelize.

Avoid too many tasks

Every delayed task has an overhead of a few hundred microseconds. Usually this is ok, but it can become a problem if you apply `dask.delayed` too finely. In this case, it’s often best to break up your many tasks into batches or use one of the Dask collections to help you.

Don’t	Do
`# Too mamy tasks`	`# Use collections`
`results = []`	`import dask.bag as db`
`for x in range(10000000):`	`b = db.from_sequence(range(10000000),␣`
`    y = dask.delayed(f)(x)`	`↪npartitions=1000)`
`    results.append(y)`	`b = b.map(f)`
	`...`

Here we use `dask.bag` to automatically batch applying our function. We could also have constructed our own batching as follows

```
def batch(seq):
    sub_results = []
    for x in seq:
```

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```
        sub_results.append(f(x))
    return sub_results

batches = []
for i in range(0, 10000000, 10000):
    result_batch = dask.delayed(batch)(range(i, i + 10000))
    batches.append(result_batch)
```

Here we construct batches where each delayed function call computes for many data points from the original input.

Avoid calling delayed within delayed functions

Often, if you are new to using Dask delayed, you place `dask.delayed` calls everywhere and hope for the best. While this may actually work, it's usually slow and results in hard-to-understand solutions.

Usually you never call `dask.delayed` within `dask.delayed` functions.

Don't	Do

```
# Delayed function calls delayed

@dask.delayed
def process_all(L):
    result = []
    for x in L:
        y = dask.delayed(f)(x)
        result.append(y)
    return result
```
	```
	# Normal function calls delayed


	def process_all(L):
	    result = []
	    for x in L:
	        y = dask.delayed(f)(x)
	        result.append(y)
	    return result
	```

Because the normal function only does delayed work it is very fast and so there is no reason to delay it.

Don't call dask.delayed on other Dask collections

When you place a Dask array or Dask DataFrame into a delayed call, that function will receive the NumPy or Pandas equivalent. Beware that if your array is large, then this might crash your workers.

Instead, it's more common to use methods like `da.map_blocks`

Don't	Do

```
# Call delayed functions on Dask␣
↪collections

import dask.dataframe as dd
df = dd.read_csv('/path/to/*.csv')

dask.delayed(train)(df)
```
	```
	# Use mapping methods if applicable

	import dask.dataframe as dd
	df = dd.read_csv('/path/to/*.csv')

	df.map_partitions(train)
	```

Alternatively, if the procedure doesn't fit into a mapping, you can always turn your arrays or dataframes into *many* delayed objects, for example

```
partitions = df.to_delayed()
delayed_values = [dask.delayed(train)(part)
                  for part in partitions]
```

However, if you don't mind turning your Dask array/DataFrame into a single chunk, then this is ok.

```
dask.delayed(train)(..., y=df.sum())
```

Avoid repeatedly putting large inputs into delayed calls

Every time you pass a concrete result (anything that isn't delayed) Dask will hash it by default to give it a name. This is fairly fast (around 500 MB/s) but can be slow if you do it over and over again. Instead, it is better to delay your data as well.

This is especially important when using a distributed cluster to avoid sending your data separately for each function call.

Don't	Do

`x = np.array(...)  # some large array`
 	
`results = [dask.delayed(train)(x, i)`
`           for i in range(1000)]`
	`x = np.array(...)    # some large array`
	`x = dask.delayed(x)   # delay the data␣`
	`↪once`
	`results = [dask.delayed(train)(x, i)`
	`           for i in range(1000)]`

Every call to `dask.delayed(train)(x, ...)` has to hash the NumPy array `x`, which slows things down.

Do

```
x = np.array(...)  # some large array
x = dask.delayed(x)  # delay the data, hashing once

results = [dask.delayed(train)(x, i) for i in range(1000)]
```

Sometimes problems don't fit into one of the collections like `dask.array` or `dask.dataframe`. In these cases, users can parallelize custom algorithms using the simpler `dask.delayed` interface. This allows one to create graphs directly with a light annotation of normal python code:

```
>>> x = dask.delayed(inc)(1)
>>> y = dask.delayed(inc)(2)
>>> z = dask.delayed(add)(x, y)
>>> z.compute()
5
>>> z.visualize()
```

3.10.4 Example

Sometimes we face problems that are parallelizable, but don't fit into high-level abstractions like Dask Array or Dask DataFrame. Consider the following example:

```python
def inc(x):
    return x + 1

def double(x):
    return x + 2

def add(x, y):
    return x + y

data = [1, 2, 3, 4, 5]

output = []
for x in data:
    a = inc(x)
    b = double(x)
    c = add(a, b)
    output.append(c)

total = sum(output)
```

There is clearly parallelism in this problem (many of the `inc`, `double`, and `add` functions can evaluate independently), but it's not clear how to convert this to a big array or big DataFrame computation.

As written, this code runs sequentially in a single thread. However, we see that a lot of this could be executed in parallel.

The Dask `delayed` function decorates your functions so that they operate *lazily*. Rather than executing your function immediately, it will defer execution, placing the function and its arguments into a task graph.

delayed	Wraps a function or object to produce a `Delayed`.

We slightly modify our code by wrapping functions in `delayed`. This delays the execution of the function and generates a Dask graph instead:

```python
import dask

output = []
for x in data:
    a = dask.delayed(inc)(x)
    b = dask.delayed(double)(x)
    c = dask.delayed(add)(a, b)
    output.append(c)

total = dask.delayed(sum)(output)
```

We used the `dask.delayed` function to wrap the function calls that we want to turn into tasks. None of the `inc`, `double`, `add`, or `sum` calls have happened yet. Instead, the object `total` is a `Delayed` result that contains a task graph of the entire computation. Looking at the graph we see clear opportunities for parallel execution. The Dask schedulers will exploit this parallelism, generally improving performance (although not in this example, because these functions are already very small and fast.)

```python
total.visualize()  # see image to the right
```

We can now compute this lazy result to execute the graph in parallel:

```
>>> total.compute()
45
```

3.10.5 Decorator

It is also common to see the delayed function used as a decorator. Here is a reproduction of our original problem as a parallel code:

```
import dask

@dask.delayed
def inc(x):
    return x + 1

@dask.delayed
def double(x):
    return x + 2

@dask.delayed
def add(x, y):
    return x + y

data = [1, 2, 3, 4, 5]

output = []
for x in data:
    a = inc(x)
    b = double(x)
    c = add(a, b)
    output.append(c)

total = dask.delayed(sum)(output)
```

3.10.6 Real time

Sometimes you want to create and destroy work during execution, launch tasks from other tasks, etc. For this, see the *Futures* interface.

3.10.7 Best Practices

For a list of common problems and recommendations see *Delayed Best Practices*.

3.11 Futures

Dask supports a real-time task framework that extends Python's concurrent.futures interface. This interface is good for arbitrary task scheduling like *dask.delayed*, but is immediate rather than lazy, which provides some more flexibility in situations where the computations may evolve over time.

These features depend on the second generation task scheduler found in dask.distributed (which, despite its name, runs very well on a single machine).

3.11.1 Start Dask Client

You must start a `Client` to use the futures interface. This tracks state among the various worker processes or threads:

```
from dask.distributed import Client

client = Client()  # start local workers as processes
# or
client = Client(processes=False)  # start local workers as threads
```

If you have Bokeh installed, then this starts up a diagnostic dashboard at http://localhost:8787 .

3.11.2 Submit Tasks

`Client.submit`(func, *args[, key, workers, . . .])	Submit a function application to the scheduler
`Client.map`(func, *iterables[, key, workers, . . .])	Map a function on a sequence of arguments
`Future.result`([timeout])	Wait until computation completes, gather result to local process.

You can submit individual tasks using the `submit` method:

```
def inc(x):
    return x + 1

def add(x, y):
    return x + y

a = client.submit(inc, 10)  # calls inc(10) in background thread or process
b = client.submit(inc, 20)  # calls inc(20) in background thread or process
```

The `submit` function returns a `Future`, which refers to a remote result. This result may not yet be completed:

```
>>> a
<Future: status: pending, key: inc-b8aaf26b99466a7a1980efa1ade6701d>
```

Eventually it will complete. The result stays in the remote thread/process/worker until you ask for it back explicitly:

```
>>> a
<Future: status: finished, type: int, key: inc-b8aaf26b99466a7a1980efa1ade6701d>

>>> a.result()  # blocks until task completes and data arrives
11
```

You can pass futures as inputs to submit. Dask automatically handles dependency tracking; once all input futures have completed, they will be moved onto a single worker (if necessary), and then the computation that depends on them will be started. You do not need to wait for inputs to finish before submitting a new task; Dask will handle this automatically:

```
c = client.submit(add, a, b)  # calls add on the results of a and b
```

Similar to Python's `map`, you can use `Client.map` to call the same function and many inputs:

```
futures = client.map(inc, range(1000))
```

However, note that each task comes with about 1ms of overhead. If you want to map a function over a large number of inputs, then you might consider *dask.bag* or *dask.dataframe* instead.

3.11.3 Move Data

`Future.result([timeout])`	Wait until computation completes, gather result to local process.
`Client.gather(futures[, errors, direct, …])`	Gather futures from distributed memory
`Client.scatter(data[, workers, broadcast, …])`	Scatter data into distributed memory

Given any future, you can call the `.result` method to gather the result. This will block until the future is done computing and then transfer the result back to your local process if necessary:

```
>>> c.result()
32
```

You can gather many results concurrently using the `Client.gather` method. This can be more efficient than calling `.result()` on each future sequentially:

```
>>> # results = [future.result() for future in futures]
>>> results = client.gather(futures)  # this can be faster
```

If you have important local data that you want to include in your computation, you can either include it as a normal input to a submit or map call:

```
>>> df = pd.read_csv('training-data.csv')
>>> future = client.submit(my_function, df)
```

Or you can `scatter` it explicitly. Scattering moves your data to a worker and returns a future pointing to that data:

```
>>> remote_df = client.scatter(df)
>>> remote_df
<Future: status: finished, type: DataFrame, key: bbd0ca93589c56ea14af49cba470006e>

>>> future = client.submit(my_function, remote_df)
```

Both of these accomplish the same result, but using scatter can sometimes be faster. This is especially true if you use processes or distributed workers (where data transfer is necessary) and you want to use `df` in many computations. Scattering the data beforehand avoids excessive data movement.

Calling scatter on a list scatters all elements individually. Dask will spread these elements evenly throughout workers in a round-robin fashion:

```
>>> client.scatter([1, 2, 3])
[<Future: status: finished, type: int, key: c0a8a20f903a4915b94db8de3ea63195>,
 <Future: status: finished, type: int, key: 58e78e1b34eb49a68c65b54815d1b158>,
 <Future: status: finished, type: int, key: d3395e15f605bc35ab1bac6341a285e2>]
```

3.11.4 References, Cancellation, and Exceptions

`Future.cancel(**kwargs)`	Cancel request to run this future
`Future.exception([timeout])`	Return the exception of a failed task

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Future.traceback([timeout])	Return the traceback of a failed task
Client.cancel(futures[, asynchronous, force])	Cancel running futures

Dask will only compute and hold onto results for which there are active futures. In this way, your local variables define what is active in Dask. When a future is garbage collected by your local Python session, Dask will feel free to delete that data or stop ongoing computations that were trying to produce it:

```
>>> del future  # deletes remote data once future is garbage collected
```

You can also explicitly cancel a task using the `Future.cancel` or `Client.cancel` methods:

```
>>> future.cancel()  # deletes data even if other futures point to it
```

If a future fails, then Dask will raise the remote exceptions and tracebacks if you try to get the result:

```
def div(x, y):
    return x / y

>>> a = client.submit(div, 1, 0)  # 1 / 0 raises a ZeroDivisionError
>>> a
<Future: status: error, key: div-3601743182196fb56339e584a2bf1039>

>>> a.result()
      1 def div(x, y):
----> 2     return x / y

ZeroDivisionError: division by zero
```

All futures that depend on an erred future also err with the same exception:

```
>>> b = client.submit(inc, a)
>>> b
<Future: status: error, key: inc-15e2e4450a0227fa38ede4d6b1a952db>
```

You can collect the exception or traceback explicitly with the `Future.exception` or `Future.traceback` methods.

3.11.5 Waiting on Futures

as_completed([futures, loop, with_results, . . .])	Return futures in the order in which they complete
wait(fs[, timeout, return_when])	Wait until all/any futures are finished

You can wait on a future or collection of futures using the `wait` function:

```
from dask.distributed import wait

>>> wait(futures)
```

This blocks until all futures are finished or have erred.

You can also iterate over the futures as they complete using the `as_completed` function:

```
from dask.distributed import as_completed
```

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```
futures = client.map(score, x_values)

best = -1
for future in as_completed(futures):
   y = future.result()
   if y > best:
       best = y
```

For greater efficiency, you can also ask `as_completed` to gather the results in the background:

```
for future, result in as_completed(futures, with_results=True):
    # y = future.result()  # don't need this
   ...
```

Or collect all futures in batches that had arrived since the last iteration:

```
for batch in as_completed(futures, with_results=True).batches():
   for future, result in batch:
       ...
```

Additionally, for iterative algorithms, you can add more futures into the `as_completed` iterator *during* iteration:

```
seq = as_completed(futures)

for future in seq:
    y = future.result()
    if condition(y):
        new_future = client.submit(...)
        seq.add(new_future)  # add back into the loop
```

3.11.6 Fire and Forget

fire_and_forget(obj)	Run tasks at least once, even if we release the futures

Sometimes we don't care about gathering the result of a task, and only care about side effects that it might have like writing a result to a file:

```
>>> a = client.submit(load, filename)
>>> b = client.submit(process, a)
>>> c = client.submit(write, b, out_filename)
```

As noted above, Dask will stop work that doesn't have any active futures. It thinks that because no one has a pointer to this data that no one cares. You can tell Dask to compute a task anyway, even if there are no active futures, using the `fire_and_forget` function:

```
from dask.distributed import fire_and_forget

>>> fire_and_forget(c)
```

This is particularly useful when a future may go out of scope, for example, as part of a function:

```
def process(filename):
    out_filename = 'out-' + filename
```

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```
    a = client.submit(load, filename)
    b = client.submit(process, a)
    c = client.submit(write, b, out_filename)
    fire_and_forget(c)
    return  # here we lose the reference to c, but that's now ok

for filename in filenames:
    process(filename)
```

3.11.7 Submit Tasks from Tasks

`get_client`([address, timeout, resolve_address])	Get a client while within a task.
`rejoin`()	Have this thread rejoin the ThreadPoolExecutor
`secede`()	Have this task secede from the worker's thread pool

This is an advanced feature and is rarely necessary in the common case.

Tasks can launch other tasks by getting their own client. This enables complex and highly dynamic workloads:

```
from dask.distributed import get_client

def my_function(x):
    ...

    # Get locally created client
    client = get_client()

    # Do normal client operations, asking cluster for computation
    a = client.submit(...)
    b = client.submit(...)
    a, b = client.gather([a, b])

    return a + b
```

It also allows you to set up long running tasks that watch other resources like sockets or physical sensors:

```
def monitor(device):
   client = get_client()
   while True:
       data = device.read_data()
       future = client.submit(process, data)
       fire_and_forget(future)

for device in devices:
    fire_and_forget(client.submit(monitor))
```

However, each running task takes up a single thread, and so if you launch many tasks that launch other tasks, then it is possible to deadlock the system if you are not careful. You can call the `secede` function from within a task to have it remove itself from the dedicated thread pool into an administrative thread that does not take up a slot within the Dask worker:

```
from dask.distributed import get_client, secede

```

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```
def monitor(device):
   client = get_client()
   secede()  # remove this task from the thread pool
   while True:
       data = device.read_data()
       future = client.submit(process, data)
       fire_and_forget(future)
```

If you intend to do more work in the same thread after waiting on client work, you may want to explicitly block until the thread is able to *rejoin* the thread pool. This allows some control over the number of threads that are created and stops too many threads from being active at once, over-saturating your hardware:

```
def f(n):  # assume that this runs as a task
   client = get_client()

   secede()  # secede while we wait for results to come back
   futures = client.map(func, range(n))
   results = client.gather(futures)

   rejoin()  # block until a slot is open in the thread pool
   result = analyze(results)
   return result
```

Alternatively, you can just use the normal `compute` function *within* a task. This will automatically call `secede` and `rejoin` appropriately:

```
def f(name, fn):
    df = dd.read_csv(fn)  # note that this is a dask collection
    result = df[df.name == name].count()

    # This calls secede
    # Then runs the computation on the cluster (including this worker)
    # Then blocks on rejoin, and finally delivers the answer
    result = result.compute()

    return result
```

3.11.8 Coordination Primitives

`Queue`([name, client, maxsize])	Distributed Queue
`Variable`([name, client, maxsize])	Distributed Global Variable
`Lock`([name, client])	Distributed Centralized Lock
`Pub`(name[, worker, client])	Publish data with Publish-Subscribe pattern
`Sub`(name[, worker, client])	Subscribe to a Publish/Subscribe topic

Sometimes situations arise where tasks, workers, or clients need to coordinate with each other in ways beyond normal task scheduling with futures. In these cases Dask provides additional primitives to help in complex situations.

Dask provides distributed versions of coordination primitives like locks, queues, global variables, and pub-sub systems that, where appropriate, match their in-memory counterparts. These can be used to control access to external resources, track progress of ongoing computations, or share data in side-channels between many workers, clients, and tasks sensibly.

These features are rarely necessary for common use of Dask. We recommend that beginning users stick with using the simpler futures found above (like `Client.submit` and `Client.gather`) rather than embracing needlessly complex techniques.

Queues

Queue([name, client, maxsize])	Distributed Queue

Dask queues follow the API for the standard Python Queue, but now move futures or small messages between clients. Queues serialize sensibly and reconnect themselves on remote clients if necessary:

```
from dask.distributed import Queue

def load_and_submit(filename):
    data = load(filename)
    client = get_client()
    future = client.submit(process, data)
    queue.put(future)

client = Client()

queue = Queue()

for filename in filenames:
    future = client.submit(load_and_submit, filename)
    fire_and_forget(future)

while True:
    future = queue.get()
    print(future.result())
```

Queues can also send small pieces of information, anything that is msgpack encodable (ints, strings, bools, lists, dicts, etc.). This can be useful to send back small scores or administrative messages:

```
def func(x):
    try:
        ...
    except Exception as e:
        error_queue.put(str(e))

error_queue = Queue()
```

Queues are mediated by the central scheduler, and so they are not ideal for sending large amounts of data (everything you send will be routed through a central point). They are well suited to move around small bits of metadata, or futures. These futures may point to much larger pieces of data safely:

```
>>> x = ... # my large numpy array

# Don't do this!
>>> q.put(x)

# Do this instead
>>> future = client.scatter(x)
>>> q.put(future)

# Or use futures for metadata
>>> q.put({'status': 'OK', 'stage=': 1234})
```

If you're looking to move large amounts of data between workers, then you might also want to consider the Pub/Sub system described a few sections below.

Global Variables

`Variable`([name, client, maxsize])	Distributed Global Variable

Variables are like Queues in that they communicate futures and small data between clients. However, variables hold only a single value. You can get or set that value at any time:

```
>>> var = Variable('stopping-criterion')
>>> var.set(False)

>>> var.get()
False
```

This is often used to signal stopping criteria or current parameters between clients.

If you want to share large pieces of information, then scatter the data first:

```
>>> parameters = np.array(...)
>>> future = client.scatter(parameters)
>>> var.set(future)
```

Locks

`Lock`([name, client])	Distributed Centralized Lock

You can also hold onto cluster-wide locks using the `Lock` object. Dask Locks have the same API as normal `threading.Lock` objects, except that they work across the cluster:

```
from dask.distributed import Lock
lock = Lock()

with lock:
    # access protected resource
```

You can manage several locks at the same time. Lock can either be given a consistent name or you can pass the lock object around itself.

Using a consistent name is convenient when you want to lock some known named resource:

```
from dask.distributed import Lock

def load(fn):
    with Lock('the-production-database'):
        # read data from filename using some sensitive source
        return ...

futures = client.map(load, filenames)
```

Passing around a lock works as well and is easier when you want to create short-term locks for a particular situation:

```
from dask.distributed import Lock
lock = Lock()

def load(fn, lock=None):
    with lock:
        # read data from filename using some sensitive source
        return ...

futures = client.map(load, filenames, lock=lock)
```

This can be useful if you want to control concurrent access to some external resource like a database or un-thread-safe library.

Publish-Subscribe

Pub(name[, worker, client])	Publish data with Publish-Subscribe pattern
Sub(name[, worker, client])	Subscribe to a Publish/Subscribe topic

Dask implements the Publish Subscribe pattern, providing an additional channel of communication between ongoing tasks.

class distributed.**Pub**(*name*, *worker=None*, *client=None*)

Publish data with Publish-Subscribe pattern

This allows clients and workers to directly communicate data between each other with a typical Publish-Subscribe pattern. This involves two components,

Pub objects, into which we put data:

```
>>> pub = Pub('my-topic')
>>> pub.put(123)
```

And Sub objects, from which we collect data:

```
>>> sub = Sub('my-topic')
>>> sub.get()
123
```

Many Pub and Sub objects can exist for the same topic. All data sent from any Pub will be sent to all Sub objects on that topic that are currently connected. Pub's and Sub's find each other using the scheduler, but they communicate directly with each other without coordination from the scheduler.

Pubs and Subs use the central scheduler to find each other, but not to mediate the communication. This means that there is very little additional latency or overhead, and they are appropriate for very frequent data transfers. For context, most data transfer first checks with the scheduler to find which workers should participate, and then does direct worker-to-worker transfers. This checking in with the scheduler provides some stability guarantees, but also adds in a few extra network hops. PubSub doesn't do this, and so is faster, but also can easily drop messages if Pubs or Subs disappear without notice.

When using a Pub or Sub from a Client all communications will be routed through the scheduler. This can cause some performance degradation. Pubs and Subs only operate at top-speed when they are both on workers.

Parameters

name: object (msgpack serializable) The name of the group of Pubs and Subs on which to participate

See also:

Sub

Examples

```
>>> pub = Pub('my-topic')
>>> sub = Sub('my-topic')
>>> pub.put([1, 2, 3])
>>> sub.get()
[1, 2, 3]
```

You can also use sub within a for loop:

```
>>> for msg in sub:  # doctest: +SKIP
...     print(msg)
```

or an async for loop

```
>>> async for msg in sub:  # doctest: +SKIP
...     print(msg)
```

Similarly the `.get` method will return an awaitable if used by an async client or within the IOLoop thread of a worker

```
>>> await sub.get()  # doctest: +SKIP
```

You can see the set of connected worker subscribers by looking at the `.subscribers` attribute:

```
>>> pub.subscribers
{'tcp://...': {},
 'tcp://...': {}}
```

put (*msg*)
Publish a message to all subscribers of this topic

3.11.9 Actors

Note: This is an advanced feature and is rarely necessary in the common case.

Note: This is an experimental feature and is subject to change without notice.

Actors allow workers to manage rapidly changing state without coordinating with the central scheduler. This has the advantage of reducing latency (worker-to-worker roundtrip latency is around 1ms), reducing pressure on the centralized scheduler (workers can coordinate actors entirely among each other), and also enabling workflows that require stateful or in-place memory manipulation.

However, these benefits come at a cost. The scheduler is unaware of actors and so they don't benefit from diagnostics, load balancing, or resilience. Once an actor is running on a worker it is forever tied to that worker. If that worker becomes overburdened or dies, then there is no opportunity to recover the workload.

Because Actors avoid the central scheduler they can be high-performing, but not resilient.

Example: Counter

An actor is a class containing both state and methods that is submitted to a worker:

```
class Counter:
    n = 0

    def __init__(self):
        self.n = 0

    def increment(self):
        self.n += 1
        return self.n

from dask.distributed import Client
client = Client()

future = client.submit(Counter, actor=True)
counter = future.result()

>>> counter
<Actor: Counter, key=Counter-afa1cdfb6b4761e616fa2cfab42398c8>
```

Method calls on this object produce `ActorFutures`, which are similar to normal Futures, but interact only with the worker holding the Actor:

```
>>> future = counter.increment()
>>> future
<ActorFuture>

>>> future.result()
1
```

Attribute access is synchronous and blocking:

```
>>> counter.n
1
```

Example: Parameter Server

```
import numpy as np

from dask.distributed import Client
client = Client(processes=False)

class ParameterServer:
    def __init__(self):
        self.data = dict()

    def put(self, key, value):
        self.data[key] = value

    def get(self, key):
        return self.data[key]

ps_future = client.submit(ParameterServer, actor=True)
```

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```
ps = ps_future.result()

ps.put('parameters', np.random.random(1000))

def train(batch, ps):
    params = ps.get('parameters')

for batch in batches:
```

Asynchronous Operation

All operations that require talking to the remote worker are awaitable:

```
async def f():
    future = client.submit(Counter, actor=True)
    counter = await future  # gather actor object locally

    counter.increment()  # send off a request asynchronously
    await counter.increment()  # or wait until it was received

    n = await counter.n  # attribute access also must be awaited
```

3.11.10 API

Client

`Client`([address, loop, timeout, . . .])	Connect to and submit computation to a Dask cluster
`Client.cancel`(futures[, asynchronous, force])	Cancel running futures
`Client.compute`(collections[, sync, . . .])	Compute dask collections on cluster
`Client.gather`(futures[, errors, direct, . . .])	Gather futures from distributed memory
`Client.get`(dsk, keys[, restrictions, . . .])	Compute dask graph
`Client.get_dataset`(name, **kwargs)	Get named dataset from the scheduler
`Client.get_executor`(**kwargs)	Return a concurrent.futures Executor for submitting tasks on this Client
`Client.has_what`([workers])	Which keys are held by which workers
`Client.list_datasets`(**kwargs)	List named datasets available on the scheduler
`Client.map`(func, *iterables[, key, workers, . . .])	Map a function on a sequence of arguments
`Client.ncores`([workers])	The number of threads/cores available on each worker node
`Client.persist`(collections[, . . .])	Persist dask collections on cluster
`Client.profile`([key, start, stop, workers, . . .])	Collect statistical profiling information about recent work
`Client.publish_dataset`(*args, **kwargs)	Publish named datasets to scheduler
`Client.rebalance`([futures, workers])	Rebalance data within network
`Client.replicate`(futures[, n, workers, . . .])	Set replication of futures within network
`Client.restart`(**kwargs)	Restart the distributed network
`Client.run`(function, *args, **kwargs)	Run a function on all workers outside of task scheduling system
`Client.run_on_scheduler`(function, *args, . . .)	Run a function on the scheduler process
`Client.scatter`(data[, workers, broadcast, . . .])	Scatter data into distributed memory

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Client.shutdown()	Shut down the connected scheduler and workers
Client.scheduler_info(**kwargs)	Basic information about the workers in the cluster
Client.shutdown()	Shut down the connected scheduler and workers
Client.start_ipython_workers([workers, . . .])	Start IPython kernels on workers
Client.start_ipython_scheduler([magic_name, . . .])	Start IPython kernel on the scheduler
Client.submit(func, *args[, key, workers, . . .])	Submit a function application to the scheduler
Client.unpublish_dataset(name, **kwargs)	Remove named datasets from scheduler
Client.upload_file(filename, **kwargs)	Upload local package to workers
Client.who_has([futures])	The workers storing each future's data

Future

Future(key[, client, inform, state])	A remotely running computation
Future.add_done_callback(fn)	Call callback on future when callback has finished
Future.cancel(**kwargs)	Cancel request to run this future
Future.cancelled()	Returns True if the future has been cancelled
Future.done()	Is the computation complete?
Future.exception([timeout])	Return the exception of a failed task
Future.result([timeout])	Wait until computation completes, gather result to local process.
Future.traceback([timeout])	Return the traceback of a failed task

Functions

as_completed([futures, loop, with_results, . . .])	Return futures in the order in which they complete
fire_and_forget(obj)	Run tasks at least once, even if we release the futures
get_client([address, timeout, resolve_address])	Get a client while within a task.
secede()	Have this task secede from the worker's thread pool
rejoin()	Have this thread rejoin the ThreadPoolExecutor
wait(fs[, timeout, return_when])	Wait until all/any futures are finished

`distributed.`**`as_completed`**(*futures=None*, *loop=None*, *with_results=False*, *raise_errors=True*)

Return futures in the order in which they complete

This returns an iterator that yields the input future objects in the order in which they complete. Calling `next` on the iterator will block until the next future completes, irrespective of order.

Additionally, you can also add more futures to this object during computation with the `.add` method

Parameters

futures: Collection of futures A list of Future objects to be iterated over in the order in which they complete

with_results: bool (False) Whether to wait and include results of futures as well; in this case *as_completed* yields a tuple of (future, result)

raise_errors: bool (True) Whether we should raise when the result of a future raises an exception; only affects behavior when *with_results=True*.

Examples

```
>>> x, y, z = client.map(inc, [1, 2, 3])  # doctest: +SKIP
>>> for future in as_completed([x, y, z]):  # doctest: +SKIP
...     print(future.result())  # doctest: +SKIP
3
2
4
```

Add more futures during computation

```
>>> x, y, z = client.map(inc, [1, 2, 3])  # doctest: +SKIP
>>> ac = as_completed([x, y, z])  # doctest: +SKIP
>>> for future in ac:  # doctest: +SKIP
...     print(future.result())  # doctest: +SKIP
...     if random.random() < 0.5:  # doctest: +SKIP
...         ac.add(c.submit(double, future))  # doctest: +SKIP
4
2
8
3
6
12
24
```

Optionally wait until the result has been gathered as well

```
>>> ac = as_completed([x, y, z], with_results=True)  # doctest: +SKIP
>>> for future, result in ac:  # doctest: +SKIP
...     print(result)  # doctest: +SKIP
2
4
3
```

distributed.**fire_and_forget**(*obj*)

Run tasks at least once, even if we release the futures

Under normal operation Dask will not run any tasks for which there is not an active future (this avoids unnecessary work in many situations). However sometimes you want to just fire off a task, not track its future, and expect it to finish eventually. You can use this function on a future or collection of futures to ask Dask to complete the task even if no active client is tracking it.

The results will not be kept in memory after the task completes (unless there is an active future) so this is only useful for tasks that depend on side effects.

Parameters

obj: Future, list, dict, dask collection The futures that you want to run at least once

Examples

```
>>> fire_and_forget(client.submit(func, *args))  # doctest: +SKIP
```

distributed.**get_client**(*address=None*, *timeout=3*, *resolve_address=True*)

Get a client while within a task.

This client connects to the same scheduler to which the worker is connected

Parameters

address [str, optional] The address of the scheduler to connect to. Defaults to the scheduler the worker is connected to.

timeout [int, default 3] Timeout (in seconds) for getting the Client

resolve_address [bool, default True] Whether to resolve *address* to its canonical form.

Returns

Client

See also:

`get_worker`, `worker_client`, *`secede`*

Examples

```
>>> def f():
...     client = get_client()
...     futures = client.map(lambda x: x + 1, range(10))  # spawn many tasks
...     results = client.gather(futures)
...     return sum(results)
```

```
>>> future = client.submit(f)  # doctest: +SKIP
>>> future.result()  # doctest: +SKIP
55
```

`distributed.`**`secede`**`()`

Have this task secede from the worker's thread pool

This opens up a new scheduling slot and a new thread for a new task. This enables the client to schedule tasks on this node, which is especially useful while waiting for other jobs to finish (e.g., with `client.gather`).

See also:

`get_client`, `get_worker`

Examples

```
>>> def mytask(x):
...     # do some work
...     client = get_client()
...     futures = client.map(...)  # do some remote work
...     secede()  # while that work happens, remove ourself from the pool
...     return client.gather(futures)  # return gathered results
```

`distributed.`**`rejoin`**`()`

Have this thread rejoin the ThreadPoolExecutor

This will block until a new slot opens up in the executor. The next thread to finish a task will leave the pool to allow this one to join.

See also:

`secede` leave the thread pool

`distributed.`**`wait`**(*fs*, *timeout=None*, *return_when='ALL_COMPLETED'*)

Wait until all/any futures are finished

Parameters

fs: list of futures

timeout: number, optional Time in seconds after which to raise a `dask.distributed.TimeoutError`

——-

Named tuple of completed, not completed

class `distributed.`**`Client`**(*address=None, loop=None, timeout='__no_default__', set_as_default=True, scheduler_file=None, security=None, asynchronous=False, name=None, heartbeat_interval=None, serializers=None, deserializers=None, extensions=[<class 'distributed.pubsub.PubSubClientExtension'>], direct_to_workers=None, **kwargs*)

Connect to and submit computation to a Dask cluster

The Client connects users to a Dask cluster. It provides an asynchronous user interface around functions and futures. This class resembles executors in `concurrent.futures` but also allows `Future` objects within `submit/map` calls. When a Client is instantiated it takes over all `dask.compute` and `dask.persist` calls by default.

It is also common to create a Client without specifying the scheduler address , like `Client()`. In this case the Client creates a `LocalCluster` in the background and connects to that. Any extra keywords are passed from Client to LocalCluster in this case. See the LocalCluster documentation for more information.

Parameters

address: string, or Cluster This can be the address of a `Scheduler` server like a string `'127.0.0.1:8786'` or a cluster object like `LocalCluster()`

timeout: int Timeout duration for initial connection to the scheduler

set_as_default: bool (True) Claim this scheduler as the global dask scheduler

scheduler_file: string (optional) Path to a file with scheduler information if available

security: (optional) Optional security information

asynchronous: bool (False by default) Set to True if using this client within async/await functions or within Tornado gen.coroutines. Otherwise this should remain False for normal use.

name: string (optional) Gives the client a name that will be included in logs generated on the scheduler for matters relating to this client

direct_to_workers: bool (optional) Whether or not to connect directly to the workers, or to ask the scheduler to serve as intermediary.

heartbeat_interval: int Time in milliseconds between heartbeats to scheduler

****kwargs:** If you do not pass a scheduler address, Client will create a `LocalCluster` object, passing any extra keyword arguments.

See also:

`distributed.scheduler.Scheduler` Internal scheduler

`distributed.deploy.local.LocalCluster`

Examples

Provide cluster's scheduler node address on initialization:

```
>>> client = Client('127.0.0.1:8786')  # doctest: +SKIP
```

Use `submit` method to send individual computations to the cluster

```
>>> a = client.submit(add, 1, 2)  # doctest: +SKIP
>>> b = client.submit(add, 10, 20)  # doctest: +SKIP
```

Continue using submit or map on results to build up larger computations

```
>>> c = client.submit(add, a, b)  # doctest: +SKIP
```

Gather results with the `gather` method.

```
>>> client.gather(c)  # doctest: +SKIP
33
```

You can also call Client with no arguments in order to create your own local cluster.

```
>>> client = Client()  # makes your own local "cluster" # doctest: +SKIP
```

Extra keywords will be passed directly to LocalCluster

```
>>> client = Client(processes=False, threads_per_worker=1)  # doctest: +SKIP
```

`asynchronous`
Are we running in the event loop?

This is true if the user signaled that we might be when creating the client as in the following:

```
client = Client(asynchronous=True)
```

However, we override this expectation if we can definitively tell that we are running from a thread that is not the event loop. This is common when calling get_client() from within a worker task. Even though the client was originally created in asynchronous mode we may find ourselves in contexts when it is better to operate synchronously.

`call_stack`(*futures=None*, *keys=None*)
The actively running call stack of all relevant keys

You can specify data of interest either by providing futures or collections in the `futures=` keyword or a list of explicit keys in the `keys=` keyword. If neither are provided then all call stacks will be returned.

Parameters

futures: list (optional) List of futures, defaults to all data

keys: list (optional) List of key names, defaults to all data

Examples

```
>>> df = dd.read_parquet(...).persist()  # doctest: +SKIP
>>> client.call_stack(df)  # call on collections
>>> client.call_stack()  # Or call with no arguments for all activity  #␣
↪doctest: +SKIP
```

cancel (*futures*, *asynchronous=None*, *force=False*)
Cancel running futures

This stops future tasks from being scheduled if they have not yet run and deletes them if they have already run. After calling, this result and all dependent results will no longer be accessible

Parameters

futures: list of Futures

force: boolean (False) Cancel this future even if other clients desire it

close (*timeout='__no_default__'*)
Close this client

Clients will also close automatically when your Python session ends

If you started a client without arguments like `Client()` then this will also close the local cluster that was started at the same time.

See also:

`Client.restart`

compute (*collections*, *sync=False*, *optimize_graph=True*, *workers=None*, *allow_other_workers=False*, *resources=None*, *retries=0*, *priority=0*, *fifo_timeout='60s'*, *actors=None*, *traverse=True*, ***kwargs*)
Compute dask collections on cluster

Parameters

collections: iterable of dask objects or single dask object Collections like dask.array or dataframe or dask.value objects

sync: bool (optional) Returns Futures if False (default) or concrete values if True

optimize_graph: bool Whether or not to optimize the underlying graphs

workers: str, list, dict Which workers can run which parts of the computation If a string a list then the output collections will run on the listed workers, but other sub-computations can run anywhere If a dict then keys should be (tuples of) collections and values should be addresses or lists.

allow_other_workers: bool, list If True then all restrictions in workers= are considered loose If a list then only the keys for the listed collections are loose

retries: int (default to 0) Number of allowed automatic retries if computing a result fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: timedelta str (defaults to '60s') Allowed amount of time between calls to consider the same priority

****kwargs:** Options to pass to the graph optimize calls

Returns

List of Futures if input is a sequence, or a single future otherwise

See also:

`Client.get` Normal synchronous dask.get function

Examples

```
>>> from dask import delayed
>>> from operator import add
>>> x = delayed(add)(1, 2)
>>> y = delayed(add)(x, x)
>>> xx, yy = client.compute([x, y])  # doctest: +SKIP
>>> xx  # doctest: +SKIP
<Future: status: finished, key: add-8f6e709446674bad78ea8aeecfee188e>
>>> xx.result()  # doctest: +SKIP
3
>>> yy.result()  # doctest: +SKIP
6
```

Also support single arguments

```
>>> xx = client.compute(x)  # doctest: +SKIP
```

classmethod current()
Return global client if one exists, otherwise raise ValueError

gather(*futures*, *errors='raise'*, *direct=None*, *asynchronous=None*)
Gather futures from distributed memory

Accepts a future, nested container of futures, iterator, or queue. The return type will match the input type.

Parameters

futures: Collection of futures This can be a possibly nested collection of Future objects. Collections can be lists, sets, or dictionaries

errors: string Either 'raise' or 'skip' if we should raise if a future has erred or skip its inclusion in the output collection

direct: boolean Whether or not to connect directly to the workers, or to ask the scheduler to serve as intermediary. This can also be set when creating the Client.

Returns

results: a collection of the same type as the input, but now with

gathered results rather than futures

See also:

`Client.scatter` Send data out to cluster

Examples

```
>>> from operator import add  # doctest: +SKIP
>>> c = Client('127.0.0.1:8787')  # doctest: +SKIP
>>> x = c.submit(add, 1, 2)  # doctest: +SKIP
>>> c.gather(x)  # doctest: +SKIP
3
>>> c.gather([x, [x], x])  # support lists and dicts # doctest: +SKIP
[3, [3], 3]
```

get (*dsk*, *keys*, *restrictions=None*, *loose_restrictions=None*, *resources=None*, *sync=True*, *asynchronous=None*, *direct=None*, *retries=None*, *priority=0*, *fifo_timeout='60s'*, *actors=None*, ***kwargs*)

Compute dask graph

Parameters

dsk: dict

keys: object, or nested lists of objects

restrictions: dict (optional) A mapping of {key: {set of worker hostnames}} that restricts where jobs can take place

retries: int (default to 0) Number of allowed automatic retries if computing a result fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

sync: bool (optional) Returns Futures if False or concrete values if True (default).

direct: bool Whether or not to connect directly to the workers, or to ask the scheduler to serve as intermediary. This can also be set when creating the Client.

See also:

`Client.compute` Compute asynchronous collections

Examples

```
>>> from operator import add  # doctest: +SKIP
>>> c = Client('127.0.0.1:8787')  # doctest: +SKIP
>>> c.get({'x': (add, 1, 2)}, 'x')  # doctest: +SKIP
3
```

get_dataset (*name*, ***kwargs*)

Get named dataset from the scheduler

See also:

`Client.publish_dataset`, `Client.list_datasets`

get_executor (***kwargs*)

Return a concurrent.futures Executor for submitting tasks on this Client

Parameters

****kwargs:** Any submit()- or map()- compatible arguments, such as *workers* or *resources*.

Returns

An Executor object that's fully compatible with the concurrent.futures

API.

get_metadata (*keys*, *default='__no_default__'*)

Get arbitrary metadata from scheduler

See set_metadata for the full docstring with examples

Parameters

keys: key or list Key to access. If a list then gets within a nested collection

default: optional If the key does not exist then return this value instead. If not provided then this raises a KeyError if the key is not present

See also:

`Client.set_metadata`

`classmethod get_restrictions`(*collections*, *workers*, *allow_other_workers*)
Get restrictions from inputs to compute/persist

`get_scheduler_logs`(*n=None*)
Get logs from scheduler

Parameters

n [int] Number of logs to retrive. Maxes out at 10000 by default, confiruable in config.yaml::log-length

Returns

Logs in reversed order (newest first)

`get_task_stream`(*start=None*, *stop=None*, *count=None*, *plot=False*, *filename='task-stream.html'*)
Get task stream data from scheduler

This collects the data present in the diagnostic "Task Stream" plot on the dashboard. It includes the start, stop, transfer, and deserialization time of every task for a particular duration.

Note that the task stream diagnostic does not run by default. You may wish to call this function once before you start work to ensure that things start recording, and then again after you have completed.

Parameters

start: Number or string When you want to start recording If a number it should be the result of calling time() If a string then it should be a time difference before now, like '60s' or '500 ms'

stop: Number or string When you want to stop recording

count: int The number of desired records, ignored if both start and stop are specified

plot: boolean, str If true then also return a Bokeh figure If plot == 'save' then save the figure to a file

filename: str (optional) The filename to save to if you set `plot='save'`

Returns

L: List[Dict]

See also:

`get_task_stream` a context manager version of this method

Examples

```
>>> client.get_task_stream()  # prime plugin if not already connected
>>> x.compute()  # do some work
>>> client.get_task_stream()
[{'task': ...,
  'type': ...,
  'thread': ...,
  ...}]
```

Pass the `plot=True` or `plot='save'` keywords to get back a Bokeh figure

```
>>> data, figure = client.get_task_stream(plot='save', filename='myfile.html
↪')
```

Alternatively consider the context manager

```
>>> from dask.distributed import get_task_stream
>>> with get_task_stream() as ts:
...     x.compute()
>>> ts.data
[...]
```

get_versions(*check=False*, *packages=[]*)
Return version info for the scheduler, all workers and myself

Parameters

check [boolean, default False] raise ValueError if all required & optional packages do not match

packages [List[str]] Extra package names to check

Examples

```
>>> c.get_versions()  # doctest: +SKIP
```

```
>>> c.get_versions(packages=['sklearn', 'geopandas'])  # doctest: +SKIP
```

get_worker_logs(*n=None*, *workers=None*, *nanny=False*)
Get logs from workers

Parameters

n [int] Number of logs to retrive. Maxes out at 10000 by default, confiruable in config.yaml::log-length

workers [iterable] List of worker addresses to retrieve. Gets all workers by default.

nanny [bool, default False] Whether to get the logs from the workers (False) or the nannies (True). If specified, the addresses in *workers* should still be the worker addresses, not the nanny addresses.

Returns

Dictionary mapping worker address to logs.

Logs are returned in reversed order (newest first)

has_what(*workers=None*, ***kwargs*)
Which keys are held by which workers

This returns the keys of the data that are held in each worker's memory.

Parameters

workers: list (optional) A list of worker addresses, defaults to all

See also:

`Client.who_has`, `Client.nthreads`, `Client.processing`

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])  # doctest: +SKIP
>>> wait([x, y, z])  # doctest: +SKIP
>>> c.has_what()  # doctest: +SKIP
{'192.168.1.141:46784': ['inc-1c8dd6be1c21646c71f76c16d09304ea',
                         'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b',
                         'inc-1e297fc27658d7b67b3a758f16bcf47a']}
```

list_datasets(***kwargs*)
List named datasets available on the scheduler

See also:

`Client.publish_dataset`, `Client.get_dataset`

map(*func, *iterables, key=None, workers=None, retries=None, resources=None, priority=0, allow_other_workers=False, fifo_timeout='100 ms', actor=False, actors=False, pure=None, **kwargs*)
Map a function on a sequence of arguments

Arguments can be normal objects or Futures

Parameters

func: callable

iterables: Iterables List-like objects to map over. They should have the same length.

key: str, list Prefix for task names if string. Explicit names if list.

pure: bool (defaults to True) Whether or not the function is pure. Set `pure=False` for impure functions like `np.random.random`.

workers: set, iterable of sets A set of worker hostnames on which computations may be performed. Leave empty to default to all workers (common case)

retries: int (default to 0) Number of allowed automatic retries if a task fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: str timedelta (default '100ms') Allowed amount of time between calls to consider the same priority

****kwargs: dict** Extra keywords to send to the function. Large values will be included explicitly in the task graph.

Returns

List, iterator, or Queue of futures, depending on the type of the

inputs.

See also:

`Client.submit` Submit a single function

Examples

```
>>> L = client.map(func, sequence)  # doctest: +SKIP
```

nbytes(*keys=None*, *summary=True*, ***kwargs*)
The bytes taken up by each key on the cluster

This is as measured by `sys.getsizeof` which may not accurately reflect the true cost.

Parameters

keys: list (optional) A list of keys, defaults to all keys

summary: boolean, (optional) Summarize keys into key types

See also:

Client.who_has

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])  # doctest: +SKIP
>>> c.nbytes(summary=False)  # doctest: +SKIP
{'inc-1c8dd6be1c21646c71f76c16d09304ea': 28,
 'inc-1e297fc27658d7b67b3a758f16bcf47a': 28,
 'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b': 28}
```

```
>>> c.nbytes(summary=True)  # doctest: +SKIP
{'inc': 84}
```

ncores(*workers=None*, ***kwargs*)
The number of threads/cores available on each worker node

Parameters

workers: list (optional) A list of workers that we care about specifically. Leave empty to receive information about all workers.

See also:

Client.who_has, *Client.has_what*

Examples

```
>>> c.threads()  # doctest: +SKIP
{'192.168.1.141:46784': 8,
 '192.167.1.142:47548': 8,
 '192.167.1.143:47329': 8,
 '192.167.1.144:37297': 8}
```

normalize_collection(*collection*)
Replace collection's tasks by already existing futures if they exist

This normalizes the tasks within a collections task graph against the known futures within the scheduler. It returns a copy of the collection with a task graph that includes the overlapping futures.

See also:

Client.persist trigger computation of collection's tasks

Examples

```
>>> len(x.__dask_graph__())  # x is a dask collection with 100 tasks  #␣
↪doctest: +SKIP
100
>>> set(client.futures).intersection(x.__dask_graph__())  # some overlap␣
↪exists  # doctest: +SKIP
10
```

```
>>> x = client.normalize_collection(x)  # doctest: +SKIP
>>> len(x.__dask_graph__())  # smaller computational graph  # doctest: +SKIP
20
```

nthreads(*workers=None*, ***kwargs*)

The number of threads/cores available on each worker node

Parameters

workers: list (optional) A list of workers that we care about specifically. Leave empty to receive information about all workers.

See also:

Client.who_has, *Client.has_what*

Examples

```
>>> c.threads()  # doctest: +SKIP
{'192.168.1.141:46784': 8,
 '192.167.1.142:47548': 8,
 '192.167.1.143:47329': 8,
 '192.167.1.144:37297': 8}
```

persist(*collections*, *optimize_graph=True*, *workers=None*, *allow_other_workers=None*, *resources=None*, *retries=None*, *priority=0*, *fifo_timeout='60s'*, *actors=None*, ***kwargs*)

Persist dask collections on cluster

Starts computation of the collection on the cluster in the background. Provides a new dask collection that is semantically identical to the previous one, but now based off of futures currently in execution.

Parameters

collections: sequence or single dask object Collections like dask.array or dataframe or dask.value objects

optimize_graph: bool Whether or not to optimize the underlying graphs

workers: str, list, dict Which workers can run which parts of the computation If a string a list then the output collections will run on the listed workers, but other sub-computations can run anywhere If a dict then keys should be (tuples of) collections and values should be addresses or lists.

allow_other_workers: bool, list If True then all restrictions in workers= are considered loose If a list then only the keys for the listed collections are loose

retries: int (default to 0) Number of allowed automatic retries if computing a result fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: timedelta str (defaults to '60s') Allowed amount of time between calls to consider the same priority

kwargs: Options to pass to the graph optimize calls

Returns

List of collections, or single collection, depending on type of input.

See also:

`Client.compute`

Examples

```
>>> xx = client.persist(x)  # doctest: +SKIP
>>> xx, yy = client.persist([x, y])  # doctest: +SKIP
```

processing(*workers=None*)
The tasks currently running on each worker

Parameters

workers: list (optional) A list of worker addresses, defaults to all

See also:

`Client.who_has`, `Client.has_what`, `Client.nthreads`

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])  # doctest: +SKIP
>>> c.processing()  # doctest: +SKIP
{'192.168.1.141:46784': ['inc-1c8dd6be1c21646c71f76c16d09304ea',
                         'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b',
                         'inc-1e297fc27658d7b67b3a758f16bcf47a']}
```

profile(*key=None*, *start=None*, *stop=None*, *workers=None*, *merge_workers=True*, *plot=False*, *filename=None*)
Collect statistical profiling information about recent work

Parameters

key: str Key prefix to select, this is typically a function name like 'inc' Leave as None to collect all data

start: time

stop: time

workers: list List of workers to restrict profile information

plot: boolean or string Whether or not to return a plot object

filename: str Filename to save the plot

Examples

```
>>> client.profile()  # call on collections
>>> client.profile(filename='dask-profile.html')  # save to html file
```

publish_dataset(**args*, ***kwargs*)
Publish named datasets to scheduler

This stores a named reference to a dask collection or list of futures on the scheduler. These references are available to other Clients which can download the collection or futures with `get_dataset`.

Datasets are not immediately computed. You may wish to call `Client.persist` prior to publishing a dataset.

Parameters

args [list of objects to publish as name]

name [optional name of the dataset to publish]

kwargs: dict named collections to publish on the scheduler

Returns

None

See also:

`Client.list_datasets`, *`Client.get_dataset`*, *`Client.unpublish_dataset`*, *`Client.persist`*

Examples

Publishing client:

```
>>> df = dd.read_csv('s3://...')  # doctest: +SKIP
>>> df = c.persist(df) # doctest: +SKIP
>>> c.publish_dataset(my_dataset=df)  # doctest: +SKIP
```

Alternative invocation >>> c.publish_dataset(df, name='my_dataset')

Receiving client:

```
>>> c.list_datasets()  # doctest: +SKIP
['my_dataset']
>>> df2 = c.get_dataset('my_dataset')  # doctest: +SKIP
```

rebalance(*futures=None*, *workers=None*, ***kwargs*)
Rebalance data within network

Move data between workers to roughly balance memory burden. This either affects a subset of the keys/workers or the entire network, depending on keyword arguments.

This operation is generally not well tested against normal operation of the scheduler. It it not recommended to use it while waiting on computations.

Parameters

futures: list, optional A list of futures to balance, defaults all data

workers: list, optional A list of workers on which to balance, defaults to all workers

register_worker_callbacks(*setup=None*)
Registers a setup callback function for all current and future workers.

This registers a new setup function for workers in this cluster. The function will run immediately on all currently connected workers. It will also be run upon connection by any workers that are added in the future. Multiple setup functions can be registered - these will be called in the order they were added.

If the function takes an input argument named `dask_worker` then that variable will be populated with the worker itself.

Parameters

setup [callable(dask_worker: Worker) -> None] Function to register and run on all workers

register_worker_plugin(*plugin=None*, *name=None*)

Registers a lifecycle worker plugin for all current and future workers.

This registers a new object to handle setup, task state transitions and teardown for workers in this cluster. The plugin will instantiate itself on all currently connected workers. It will also be run on any worker that connects in the future.

The plugin may include methods `setup`, `teardown`, and `transition`. See the `dask.distributed.WorkerPlugin` class or the examples below for the interface and docstrings. It must be serializable with the pickle or cloudpickle modules.

If the plugin has a `name` attribute, or if the `name=` keyword is used then that will control idempotency. A a plugin with that name has already registered then any future plugins will not run.

For alternatives to plugins, you may also wish to look into preload scripts.

Parameters

plugin: WorkerPlugin The plugin object to pass to the workers

name: str, optional A name for the plugin. Registering a plugin with the same name will have no effect.

See also:

`distributed.WorkerPlugin`

Examples

```
>>> class MyPlugin(WorkerPlugin):
...     def __init__(self, *args, **kwargs):
...         pass  # the constructor is up to you
...     def setup(self, worker: dask.distributed.Worker):
...         pass
...     def teardown(self, worker: dask.distributed.Worker):
...         pass
...     def transition(self, key: str, start: str, finish: str, **kwargs):
...         pass
```

```
>>> plugin = MyPlugin(1, 2, 3)
>>> client.register_worker_plugin(plugin)
```

You can get access to the plugin with the `get_worker` function

```
>>> client.register_worker_plugin(other_plugin, name='my-plugin')
>>> def f():
...    worker = get_worker()
...    plugin = worker.plugins['my-plugin']
...    return plugin.my_state
```

```
>>> future = client.run(f)
```

replicate(*futures*, *n=None*, *workers=None*, *branching_factor=2*, ***kwargs*)
Set replication of futures within network

Copy data onto many workers. This helps to broadcast frequently accessed data and it helps to improve resilience.

This performs a tree copy of the data throughout the network individually on each piece of data. This operation blocks until complete. It does not guarantee replication of data to future workers.

Parameters

futures: list of futures Futures we wish to replicate

n: int, optional Number of processes on the cluster on which to replicate the data. Defaults to all.

workers: list of worker addresses Workers on which we want to restrict the replication. Defaults to all.

branching_factor: int, optional The number of workers that can copy data in each generation

See also:

`Client.rebalance`

Examples

```
>>> x = c.submit(func, *args)  # doctest: +SKIP
>>> c.replicate([x])  # send to all workers  # doctest: +SKIP
>>> c.replicate([x], n=3)  # send to three workers  # doctest: +SKIP
>>> c.replicate([x], workers=['alice', 'bob'])  # send to specific  #␣
↪doctest: +SKIP
>>> c.replicate([x], n=1, workers=['alice', 'bob'])  # send to one of␣
↪specific workers  # doctest: +SKIP
>>> c.replicate([x], n=1)  # reduce replications # doctest: +SKIP
```

restart(***kwargs*)
Restart the distributed network

This kills all active work, deletes all data on the network, and restarts the worker processes.

retire_workers(*workers=None*, *close_workers=True*, ***kwargs*)
Retire certain workers on the scheduler

See dask.distributed.Scheduler.retire_workers for the full docstring.

See also:

`dask.distributed.Scheduler.retire_workers`

Examples

You can get information about active workers using the following: >>> workers = client.scheduler_info()['workers']

From that list you may want to select some workers to close >>> client.retire_workers(workers=['tcp://address:port', . . .])

retry(*futures*, *asynchronous=None*)
Retry failed futures

Parameters

futures: list of Futures

run (*function*, **args*, ***kwargs*)

Run a function on all workers outside of task scheduling system

This calls a function on all currently known workers immediately, blocks until those results come back, and returns the results asynchronously as a dictionary keyed by worker address. This method if generally used for side effects, such and collecting diagnostic information or installing libraries.

If your function takes an input argument named `dask_worker` then that variable will be populated with the worker itself.

Parameters

function: callable

***args: arguments for remote function**

****kwargs: keyword arguments for remote function**

workers: list Workers on which to run the function. Defaults to all known workers.

wait: boolean (optional) If the function is asynchronous whether or not to wait until that function finishes.

nanny [bool, defualt False] Whether to run `function` on the nanny. By default, the function is run on the worker process. If specified, the addresses in `workers` should still be the worker addresses, not the nanny addresses.

Examples

```
>>> c.run(os.getpid)  # doctest: +SKIP
{'192.168.0.100:9000': 1234,
 '192.168.0.101:9000': 4321,
 '192.168.0.102:9000': 5555}
```

Restrict computation to particular workers with the `workers=` keyword argument.

```
>>> c.run(os.getpid, workers=['192.168.0.100:9000',
...                           '192.168.0.101:9000'])  # doctest: +SKIP
{'192.168.0.100:9000': 1234,
 '192.168.0.101:9000': 4321}
```

```
>>> def get_status(dask_worker):
...     return dask_worker.status
```

```
>>> c.run(get_hostname)  # doctest: +SKIP
{'192.168.0.100:9000': 'running',
 '192.168.0.101:9000': 'running}
```

Run asynchronous functions in the background:

```
>>> async def print_state(dask_worker):  # doctest: +SKIP
...    while True:
...        print(dask_worker.status)
...        await gen.sleep(1)
```

```
>>> c.run(print_state, wait=False)  # doctest: +SKIP
```

run_coroutine (*function*, **args*, ***kwargs*)
Spawn a coroutine on all workers.

This spaws a coroutine on all currently known workers and then waits for the coroutine on each worker. The coroutines' results are returned as a dictionary keyed by worker address.

Parameters

function: a coroutine function

(typically a function wrapped in gen.coroutine or a Python 3.5+ async function)

***args: arguments for remote function**

****kwargs: keyword arguments for remote function**

wait: boolean (default True) Whether to wait for coroutines to end.

workers: list Workers on which to run the function. Defaults to all known workers.

run_on_scheduler (*function*, **args*, ***kwargs*)
Run a function on the scheduler process

This is typically used for live debugging. The function should take a keyword argument `dask_scheduler=`, which will be given the scheduler object itself.

See also:

Client.run Run a function on all workers

Client.start_ipython_scheduler Start an IPython session on scheduler

Examples

```
>>> def get_number_of_tasks(dask_scheduler=None):
...     return len(dask_scheduler.tasks)
```

```
>>> client.run_on_scheduler(get_number_of_tasks)  # doctest: +SKIP
100
```

Run asynchronous functions in the background:

```
>>> async def print_state(dask_scheduler):  # doctest: +SKIP
...    while True:
...        print(dask_scheduler.status)
...        await gen.sleep(1)
```

```
>>> c.run(print_state, wait=False)  # doctest: +SKIP
```

scatter (*data*, *workers=None*, *broadcast=False*, *direct=None*, *hash=True*, *timeout='__no_default__'*, *asynchronous=None*)
Scatter data into distributed memory

This moves data from the local client process into the workers of the distributed scheduler. Note that it is often better to submit jobs to your workers to have them load the data rather than loading data locally and then scattering it out to them.

Parameters

data: list, dict, or object Data to scatter out to workers. Output type matches input type.

workers: list of tuples (optional) Optionally constrain locations of data. Specify workers as hostname/port pairs, e.g. `('127.0.0.1', 8787)`.

broadcast: bool (defaults to False) Whether to send each data element to all workers. By default we round-robin based on number of cores.

direct: bool (defaults to automatically check) Whether or not to connect directly to the workers, or to ask the scheduler to serve as intermediary. This can also be set when creating the Client.

hash: bool (optional) Whether or not to hash data to determine key. If False then this uses a random key

Returns

List, dict, iterator, or queue of futures matching the type of input.

See also:

`Client.gather` Gather data back to local process

Examples

```
>>> c = Client('127.0.0.1:8787')  # doctest: +SKIP
>>> c.scatter(1) # doctest: +SKIP
<Future: status: finished, key: c0a8a20f903a4915b94db8de3ea63195>
```

```
>>> c.scatter([1, 2, 3])  # doctest: +SKIP
[<Future: status: finished, key: c0a8a20f903a4915b94db8de3ea63195>,
 <Future: status: finished, key: 58e78e1b34eb49a68c65b54815d1b158>,
 <Future: status: finished, key: d3395e15f605bc35ab1bac6341a285e2>]
```

```
>>> c.scatter({'x': 1, 'y': 2, 'z': 3})  # doctest: +SKIP
{'x': <Future: status: finished, key: x>,
 'y': <Future: status: finished, key: y>,
 'z': <Future: status: finished, key: z>}
```

Constrain location of data to subset of workers

```
>>> c.scatter([1, 2, 3], workers=[('hostname', 8788)])   # doctest: +SKIP
```

Broadcast data to all workers

```
>>> [future] = c.scatter([element], broadcast=True)  # doctest: +SKIP
```

Send scattered data to parallelized function using client futures interface

```
>>> data = c.scatter(data, broadcast=True)  # doctest: +SKIP
>>> res = [c.submit(func, data, i) for i in range(100)]
```

scheduler_info(***kwargs*)
Basic information about the workers in the cluster

Examples

```
>>> c.scheduler_info()  # doctest: +SKIP
{'id': '2de2b6da-69ee-11e6-ab6a-e82aea155996',
 'services': {},
 'type': 'Scheduler',
 'workers': {'127.0.0.1:40575': {'active': 0,
                                 'last-seen': 1472038237.4845693,
                                 'name': '127.0.0.1:40575',
                                 'services': {},
                                 'stored': 0,
                                 'time-delay': 0.0061032772064208984}}}
```

set_metadata (*key*, *value*)

Set arbitrary metadata in the scheduler

This allows you to store small amounts of data on the central scheduler process for administrative purposes. Data should be msgpack serializable (ints, strings, lists, dicts)

If the key corresponds to a task then that key will be cleaned up when the task is forgotten by the scheduler.

If the key is a list then it will be assumed that you want to index into a nested dictionary structure using those keys. For example if you call the following:

```
>>> client.set_metadata(['a', 'b', 'c'], 123)
```

Then this is the same as setting

```
>>> scheduler.task_metadata['a']['b']['c'] = 123
```

The lower level dictionaries will be created on demand.

See also:

get_metadata

Examples

```
>>> client.set_metadata('x', 123)  # doctest: +SKIP
>>> client.get_metadata('x')  # doctest: +SKIP
123
```

```
>>> client.set_metadata(['x', 'y'], 123)  # doctest: +SKIP
>>> client.get_metadata('x')  # doctest: +SKIP
{'y': 123}
```

```
>>> client.set_metadata(['x', 'w', 'z'], 456)  # doctest: +SKIP
>>> client.get_metadata('x')  # doctest: +SKIP
{'y': 123, 'w': {'z': 456}}
```

```
>>> client.get_metadata(['x', 'w'])  # doctest: +SKIP
{'z': 456}
```

shutdown ()

Shut down the connected scheduler and workers

Note, this may disrupt other clients that may be using the same scheudler and workers.

See also:

`Client.close` close only this client

start(***kwargs*)
Start scheduler running in separate thread

start_ipython_scheduler(*magic_name='scheduler_if_ipython'*, *qtconsole=False*, *qtconsole_args=None*)
Start IPython kernel on the scheduler

Parameters

magic_name: str or None (optional) If defined, register IPython magic with this name for executing code on the scheduler. If not defined, register %scheduler magic if IPython is running.

qtconsole: bool (optional) If True, launch a Jupyter QtConsole connected to the worker(s).

qtconsole_args: list(str) (optional) Additional arguments to pass to the qtconsole on startup.

Returns

connection_info: dict connection_info dict containing info necessary to connect Jupyter clients to the scheduler.

See also:

`Client.start_ipython_workers` Start IPython on the workers

Examples

```
>>> c.start_ipython_scheduler() # doctest: +SKIP
>>> %scheduler scheduler.processing  # doctest: +SKIP
{'127.0.0.1:3595': {'inc-1', 'inc-2'},
 '127.0.0.1:53589': {'inc-2', 'add-5'}}
```

```
>>> c.start_ipython_scheduler(qtconsole=True) # doctest: +SKIP
```

start_ipython_workers(*workers=None*, *magic_names=False*, *qtconsole=False*, *qtconsole_args=None*)
Start IPython kernels on workers

Parameters

workers: list (optional) A list of worker addresses, defaults to all

magic_names: str or list(str) (optional) If defined, register IPython magics with these names for executing code on the workers. If string has asterix then expand asterix into 0, 1, ..., n for n workers

qtconsole: bool (optional) If True, launch a Jupyter QtConsole connected to the worker(s).

qtconsole_args: list(str) (optional) Additional arguments to pass to the qtconsole on startup.

Returns

iter_connection_info: list List of connection_info dicts containing info necessary to connect Jupyter clients to the workers.

See also:

`Client.start_ipython_scheduler` start ipython on the scheduler

Examples

```
>>> info = c.start_ipython_workers() # doctest: +SKIP
>>> %remote info['192.168.1.101:5752'] worker.data  # doctest: +SKIP
{'x': 1, 'y': 100}
```

```
>>> c.start_ipython_workers('192.168.1.101:5752', magic_names='w') #␣
↪doctest: +SKIP
>>> %w worker.data  # doctest: +SKIP
{'x': 1, 'y': 100}
```

```
>>> c.start_ipython_workers('192.168.1.101:5752', qtconsole=True) # doctest:␣
↪+SKIP
```

Add asterix * in magic names to add one magic per worker

```
>>> c.start_ipython_workers(magic_names='w_*') # doctest: +SKIP
>>> %w_0 worker.data  # doctest: +SKIP
{'x': 1, 'y': 100}
>>> %w_1 worker.data  # doctest: +SKIP
{'z': 5}
```

submit (*func*, **args*, *key=None*, *workers=None*, *resources=None*, *retries=None*, *priority=0*, *fifo_timeout='100 ms'*, *allow_other_workers=False*, *actor=False*, *actors=False*, *pure=None*, ***kwargs*)

Submit a function application to the scheduler

Parameters

func: callable

***args:**

****kwargs:**

pure: bool (defaults to True) Whether or not the function is pure. Set `pure=False` for impure functions like `np.random.random`.

workers: set, iterable of sets A set of worker hostnames on which computations may be performed. Leave empty to default to all workers (common case)

key: str Unique identifier for the task. Defaults to function-name and hash

allow_other_workers: bool (defaults to False) Used with *workers*. Indicates whether or not the computations may be performed on workers that are not in the *workers* set(s).

retries: int (default to 0) Number of allowed automatic retries if the task fails

priority: Number Optional prioritization of task. Zero is default. Higher priorities take precedence

fifo_timeout: str timedelta (default '100ms') Allowed amount of time between calls to consider the same priority

Returns

Future

See also:

Client.map Submit on many arguments at once

Examples

```
>>> c = client.submit(add, a, b)  # doctest: +SKIP
```

unpublish_dataset (*name*, ***kwargs*)
Remove named datasets from scheduler

See also:

Client.publish_dataset

Examples

```
>>> c.list_datasets()  # doctest: +SKIP
['my_dataset']
>>> c.unpublish_datasets('my_dataset')  # doctest: +SKIP
>>> c.list_datasets()  # doctest: +SKIP
[]
```

upload_file (*filename*, ***kwargs*)
Upload local package to workers

This sends a local file up to all worker nodes. This file is placed into a temporary directory on Python's system path so any .py, .egg or .zip files will be importable.

Parameters

filename: string Filename of .py, .egg or .zip file to send to workers

Examples

```
>>> client.upload_file('mylibrary.egg')  # doctest: +SKIP
>>> from mylibrary import myfunc  # doctest: +SKIP
>>> L = c.map(myfunc, seq)  # doctest: +SKIP
```

wait_for_workers (*n_workers=0*)
Blocking call to wait for n workers before continuing

who_has (*futures=None*, ***kwargs*)
The workers storing each future's data

Parameters

futures: list (optional) A list of futures, defaults to all data

See also:

Client.has_what, *Client.nthreads*

Examples

```
>>> x, y, z = c.map(inc, [1, 2, 3])  # doctest: +SKIP
>>> wait([x, y, z])  # doctest: +SKIP
>>> c.who_has()  # doctest: +SKIP
{'inc-1c8dd6be1c21646c71f76c16d09304ea': ['192.168.1.141:46784'],
 'inc-1e297fc27658d7b67b3a758f16bcf47a': ['192.168.1.141:46784'],
 'inc-fd65c238a7ea60f6a01bf4c8a5fcf44b': ['192.168.1.141:46784']}
```

```
>>> c.who_has([x, y])  # doctest: +SKIP
{'inc-1c8dd6be1c21646c71f76c16d09304ea': ['192.168.1.141:46784'],
 'inc-1e297fc27658d7b67b3a758f16bcf47a': ['192.168.1.141:46784']}
```

write_scheduler_file(*scheduler_file*)
Write the scheduler information to a json file.

This facilitates easy sharing of scheduler information using a file system. The scheduler file can be used to instantiate a second Client using the same scheduler.

Parameters

scheduler_file: str Path to a write the scheduler file.

Examples

```
>>> client = Client()  # doctest: +SKIP
>>> client.write_scheduler_file('scheduler.json')  # doctest: +SKIP
# connect to previous client's scheduler
>>> client2 = Client(scheduler_file='scheduler.json')  # doctest: +SKIP
```

class distributed.**Future**(*key*, *client=None*, *inform=True*, *state=None*)
A remotely running computation

A Future is a local proxy to a result running on a remote worker. A user manages future objects in the local Python process to determine what happens in the larger cluster.

Parameters

key: str, or tuple Key of remote data to which this future refers

client: Client Client that should own this future. Defaults to _get_global_client()

inform: bool Do we inform the scheduler that we need an update on this future

See also:

`Client` Creates futures

Examples

Futures typically emerge from Client computations

```
>>> my_future = client.submit(add, 1, 2)  # doctest: +SKIP
```

We can track the progress and results of a future

```
>>> my_future  # doctest: +SKIP
<Future: status: finished, key: add-8f6e709446674bad78ea8aeecfee188e>
```

We can get the result or the exception and traceback from the future

```
>>> my_future.result()  # doctest: +SKIP
```

add_done_callback(*fn*)
Call callback on future when callback has finished

The callback `fn` should take the future as its only argument. This will be called regardless of if the future completes successfully, errs, or is cancelled

The callback is executed in a separate thread.

cancel(***kwargs*)
Cancel request to run this future

See also:

Client.cancel

cancelled()
Returns True if the future has been cancelled

done()
Is the computation complete?

exception(*timeout=None*, ***kwargs*)
Return the exception of a failed task

If *timeout* seconds are elapsed before returning, a `dask.distributed.TimeoutError` is raised.

See also:

Future.traceback

result(*timeout=None*)
Wait until computation completes, gather result to local process.

If *timeout* seconds are elapsed before returning, a `dask.distributed.TimeoutError` is raised.

retry(***kwargs*)
Retry this future if it has failed

See also:

Client.retry

traceback(*timeout=None*, ***kwargs*)
Return the traceback of a failed task

This returns a traceback object. You can inspect this object using the `traceback` module. Alternatively if you call `future.result()` this traceback will accompany the raised exception.

If *timeout* seconds are elapsed before returning, a `dask.distributed.TimeoutError` is raised.

See also:

Future.exception

Examples

```
>>> import traceback  # doctest: +SKIP
>>> tb = future.traceback()  # doctest: +SKIP
>>> traceback.format_tb(tb)  # doctest: +SKIP
[...]
```

class distributed.**Queue**(*name=None*, *client=None*, *maxsize=0*)

Distributed Queue

This allows multiple clients to share futures or small bits of data between each other with a multi-producer/multi-consumer queue. All metadata is sequentialized through the scheduler.

Elements of the Queue must be either Futures or msgpack-encodable data (ints, strings, lists, dicts). All data is sent through the scheduler so it is wise not to send large objects. To share large objects scatter the data and share the future instead.

Warning: This object is experimental and has known issues in Python 2

See also:

`Variable` shared variable between clients

Examples

```
>>> from dask.distributed import Client, Queue  # doctest: +SKIP
>>> client = Client()  # doctest: +SKIP
>>> queue = Queue('x')  # doctest: +SKIP
>>> future = client.submit(f, x)  # doctest: +SKIP
>>> queue.put(future)  # doctest: +SKIP
```

get(*timeout=None*, *batch=False*, ***kwargs*)

Get data from the queue

Parameters

timeout: Number (optional) Time in seconds to wait before timing out

batch: boolean, int (optional) If True then return all elements currently waiting in the queue. If an integer than return that many elements from the queue If False (default) then return one item at a time

put(*value*, *timeout=None*, ***kwargs*)

Put data into the queue

qsize(***kwargs*)

Current number of elements in the queue

class distributed.**Variable**(*name=None*, *client=None*, *maxsize=0*)

Distributed Global Variable

This allows multiple clients to share futures and data between each other with a single mutable variable. All metadata is sequentialized through the scheduler. Race conditions can occur.

Values must be either Futures or msgpack-encodable data (ints, lists, strings, etc..) All data will be kept and sent through the scheduler, so it is wise not to send too much. If you want to share a large amount of data then `scatter` it and share the future instead.

Warning: This object is experimental and has known issues in Python 2

See also:

`Queue` shared multi-producer/multi-consumer queue between clients

Examples

```
>>> from dask.distributed import Client, Variable # doctest: +SKIP
>>> client = Client()  # doctest: +SKIP
>>> x = Variable('x')  # doctest: +SKIP
>>> x.set(123)  # docttest: +SKIP
>>> x.get()  # docttest: +SKIP
123
>>> future = client.submit(f, x)  # doctest: +SKIP
>>> x.set(future)  # doctest: +SKIP
```

delete()

Delete this variable

Caution, this affects all clients currently pointing to this variable.

get(*timeout=None*, ***kwargs*)

Get the value of this variable

set(*value*, ***kwargs*)

Set the value of this variable

Parameters

value: Future or object Must be either a Future or a msgpack-encodable value

class distributed.**Lock**(*name=None*, *client=None*)

Distributed Centralized Lock

Parameters

name: string Name of the lock to acquire. Choosing the same name allows two disconnected processes to coordinate a lock.

Examples

```
>>> lock = Lock('x')  # doctest: +SKIP
>>> lock.acquire(timeout=1)  # doctest: +SKIP
>>> # do things with protected resource
>>> lock.release()  # doctest: +SKIP
```

acquire(*blocking=True*, *timeout=None*)

Acquire the lock

Parameters

blocking [bool, optional] If false, don't wait on the lock in the scheduler at all.

timeout [number, optional] Seconds to wait on the lock in the scheduler. This does not include local coroutine time, network transfer time, etc.. It is forbidden to specify a timeout when blocking is false.

Returns

True or False whether or not it sucessfully acquired the lock

Examples

```
>>> lock = Lock('x')  # doctest: +SKIP
>>> lock.acquire(timeout=1)  # doctest: +SKIP
```

release()
Release the lock if already acquired

class distributed.**Pub**(*name*, *worker=None*, *client=None*)
Publish data with Publish-Subscribe pattern

This allows clients and workers to directly communicate data between each other with a typical Publish-Subscribe pattern. This involves two components,

Pub objects, into which we put data:

```
>>> pub = Pub('my-topic')
>>> pub.put(123)
```

And Sub objects, from which we collect data:

```
>>> sub = Sub('my-topic')
>>> sub.get()
123
```

Many Pub and Sub objects can exist for the same topic. All data sent from any Pub will be sent to all Sub objects on that topic that are currently connected. Pub's and Sub's find each other using the scheduler, but they communicate directly with each other without coordination from the scheduler.

Pubs and Subs use the central scheduler to find each other, but not to mediate the communication. This means that there is very little additional latency or overhead, and they are appropriate for very frequent data transfers. For context, most data transfer first checks with the scheduler to find which workers should participate, and then does direct worker-to-worker transfers. This checking in with the scheduler provides some stability guarantees, but also adds in a few extra network hops. PubSub doesn't do this, and so is faster, but also can easily drop messages if Pubs or Subs disappear without notice.

When using a Pub or Sub from a Client all communications will be routed through the scheduler. This can cause some performance degradation. Pubs and Subs only operate at top-speed when they are both on workers.

Parameters

name: object (msgpack serializable) The name of the group of Pubs and Subs on which to participate

See also:

Sub

Examples

```
>>> pub = Pub('my-topic')
>>> sub = Sub('my-topic')
>>> pub.put([1, 2, 3])
>>> sub.get()
[1, 2, 3]
```

You can also use sub within a for loop:

```
>>> for msg in sub:  # doctest: +SKIP
...     print(msg)
```

or an async for loop

```
>>> async for msg in sub:  # doctest: +SKIP
...     print(msg)
```

Similarly the `.get` method will return an awaitable if used by an async client or within the IOLoop thread of a worker

```
>>> await sub.get()  # doctest: +SKIP
```

You can see the set of connected worker subscribers by looking at the `.subscribers` attribute:

```
>>> pub.subscribers
{'tcp://...': {},
 'tcp://...': {}}
```

put (*msg*)
Publish a message to all subscribers of this topic

class distributed.**Sub** (*name*, *worker=None*, *client=None*)
Subscribe to a Publish/Subscribe topic

See also:

Pub for full docstring

get (*timeout=None*)
Get a single message

next (*timeout=None*)
Get a single message

3.12 Best Practices

It is easy to get started with Dask's APIs, but using them *well* requires some experience. This page contains suggestions for best practices, and includes solutions to common problems.

This document specifically focuses on best practices that are shared among all of the Dask APIs. Readers may first want to investigate one of the API-specific Best Practices documents first.

- *Arrays*
- *DataFrames*
- *Delayed*

3.12.1 Start Small

Parallelism brings extra complexity and overhead. Sometimes it's necessary for larger problems, but often it's not. Before adding a parallel computing system like Dask to your workload you may want to first try some alternatives:

- **Use better algorithms or data structures**: NumPy, Pandas, Scikit-Learn may have faster functions for what you're trying to do. It may be worth consulting with an expert or reading through their docs again to find a better pre-built algorithm.
- **Better file formats**: Efficient binary formats that support random access can often help you manage larger-than-memory datasets efficiently and simply. See the *Store Data Efficiently* section below.
- **Compiled code**: Compiling your Python code with Numba or Cython might make parallelism unnecessary. Or you might use the multi-core parallelism available within those libraries.
- **Sampling**: Even if you have a lot of data, there might not be much advantage from using all of it. By sampling intelligently you might be able to derive the same insight from a much more manageable subset.
- **Profile**: If you're trying to speed up slow code it's important that you first understand why it is slow. Modest time investments in profiling your code can help you to identify what is slowing you down. This information can help you make better decisions about if parallelism is likely to help, or if other approaches are likely to be more effective.

3.12.2 Use The Dashboard

Dask's dashboard helps you to understand the state of your workers. This information can help to guide you to efficient solutions. In parallel and distributed computing there are new costs to be aware of and so your old intuition may no longer be true. Working with the dashboard can help you relearn about what is fast and slow and how to deal with it.

See *Documentation on Dask's dashboard* for more information.

3.12.3 Avoid Very Large Partitions

Your chunks of data should be small enough so that many of them fit in a worker's available memory at once. You often control this when you select partition size in Dask DataFrame or chunk size in Dask Array.

Dask will likely manipulate as many chunks in parallel on one machine as you have cores on that machine. So if you have 1 GB chunks and ten cores, then Dask is likely to use *at least* 10 GB of memory. Additionally, it's common for Dask to have 2-3 times as many chunks available to work on so that it always has something to work on.

If you have a machine with 100 GB and 10 cores, then you might want to choose chunks in the 1GB range. You have space for ten chunks per core which gives Dask a healthy margin, without having tasks that are too small

Note that you also want to avoid chunk sizes that are too small. See the next section for details.

3.12.4 Avoid Very Large Graphs

Dask workloads are composed of *tasks*. A task is a Python function, like `np.sum` applied onto a Python object, like a Pandas dataframe or NumPy array. If you are working with Dask collections with many partitions, then every operation you do, like `x + 1` likely generates many tasks, at least as many as partitions in your collection.

Every task comes with some overhead. This is somewhere between 200us and 1ms. If you have a computation with thousands of tasks this is fine, there will be about a second of overhead, and that may not trouble you.

However when you have very large graphs with millions of tasks then this may become troublesome, both because overhead is now in the 10 minutes to hours range, and also because the overhead of dealing with such a large graph can start to overwhelm the scheduler.

There are a few things you can do to address this:

- Build smaller graphs. You can do this by . . .

  - **Increasing your chunk size:** If you have a 1000 GB of data and are using 10 MB chunks, then you have 100,000 partitions. Every operation on such a collection will generate at least 100,000 tasks.

    However if you increase your chunksize to 1 GB or even a few GB then you reduce the overhead by orders of magnitude. This requires that your workers have much more than 1 GB of memory, but that's typical for larger workloads.

  - **Fusing operations together:** Dask will do a bit of this on its own, but you can help it. If you have a very complex operation with dozens of sub-operations, maybe you can pack that into a single Python function and use a function like `da.map_blocks` or `dd.map_partitions`.

    In general, the more administrative work you can move into your functions the better. That way the Dask scheduler doesn't need to think about all of the fine-grained operations.

  - **Breaking up your computation:** For very large workloads you may also want to try sending smaller chunks to Dask at a time. For example if you're processing a petabyte of data but find that Dask is only happy with 100 TB, maybe you can break up your computation into ten pieces and submit them one after the other.

3.12.5 Learn Techniques For Customization

The high level Dask collections (array, dataframe, bag) include common operations that follow standard Python APIs from NumPy and Pandas. However, many Python workloads are complex and may require operations that are not included in these high level APIs.

Fortunately, there are many options to support custom workloads:

- All collections have a `map_partitions` or `map_blocks` function, that applies a user provided function across every Pandas dataframe or NumPy array in the collection. Because Dask collections are made up of normal Python objects, it's often quite easy to map custom functions across partitions of a dataset without much modification.

  ```
  df.map_partitions(my_custom_func)
  ```

- More complex `map_*` functions. Sometimes your custom behavior isn't embarrassingly parallel, but requires more advanced communication. For example maybe you need to communicate a little bit of information from one partition to the next, or maybe you want to build a custom aggregation.

  Dask collections include methods for these as well.

- For even more complex workloads you can convert your collections into individual blocks, and arrange those blocks as you like using Dask Delayed. There is usually a `to_delayed` method on every collection.

map_partitions(func, *args, **kwargs)	Apply Python function on each DataFrame partition.
rolling.map_overlap(func, df, before, after, …)	Apply a function to each partition, sharing rows with adjacent partitions.
groupby.Aggregation(name, chunk, agg[, finalize])	User defined groupby-aggregation.

blockwise(func, out_ind, *args[, name, …])	Tensor operation: Generalized inner and outer products
map_blocks(func, *args[, name, token, …])	Map a function across all blocks of a dask array.
map_overlap(x, func, depth[, boundary, trim])	Map a function over blocks of the array with some overlap
reduction(x, chunk, aggregate[, axis, …])	General version of reductions

3.12.6 Stop Using Dask When No Longer Needed

In many workloads it is common to use Dask to read in a large amount of data, reduce it down, and then iterate on a much smaller amount of data. For this latter stage on smaller data it may make sense to stop using Dask, and start using normal Python again.

```
df = dd.read_parquet("lots-of-data-*.parquet")
df = df.groupby('name').mean()  # reduce data significantly
df = df.compute()               # continue on with Pandas/NumPy
```

3.12.7 Persist When You Can

Accessing data from RAM is often much faster than accessing it from disk. Once you have your dataset in a clean state that both:

1. Fits in memory
2. Is clean enough that you will want to try many different analyses

Then it is a good time to *persist* your data in RAM

```
df = dd.read_parquet("lots-of-data-*.parquet")
df = df.fillna(...)  # clean up things lazily
df = df[df.name == 'Alice']  # get down to a more reasonable size

df = df.persist()  # trigger computation, persist in distributed RAM
```

Note that this is only relevant if you are on a distributed machine (otherwise, as mentioned above, you should probably continue on without Dask).

3.12.8 Store Data Efficiently

As your ability to compute increases you will likely find that data access and I/O take up a larger portion of your total time. Additionally, parallel computing will often add new constraints to how your store your data, particularly around providing random access to blocks of your data that are in line with how you plan to compute on it.

For example ...

- For compression you'll probably find that you drop gzip and bz2, and embrace newer systems like lz4, snappy, and Z-Standard that provide better performance and random access.
- For storage formats you may find that you want self-describing formats that are optimized for random access, metadata storage, and binary encoding like Parquet, ORC, Zarr, HDF5, GeoTIFF and so on
- When working on the cloud you may find that some older formats like HDF5 may not work well
- You may want to partition or chunk your data in ways that align well to common queries. In Dask DataFrame this might mean choosing a column to sort by for fast selection and joins. For Dask dataframe this might mean choosing chunk sizes that are aligned with your access patterns and algorithms.

3.12.9 Processes and Threads

If you're doing mostly numeric work with Numpy, Pandas, Scikit-Learn, Numba, and other libraries that release the GIL, then use mostly threads. If you're doing work on text data or Python collections like lists and dicts then use mostly processes.

If you're on larger machines with a high thread count (greater than 10), then you should probably split things up into at least a few processes regardless. Python can be highly productive with 10 threads per process with numeric work, but not 50 threads.

For more information on threads, processes, and how to configure them in Dask, see *the scheduler documentation*.

3.12.10 Load Data with Dask

If you need to work with large Python objects, then please let Dask create them. A common anti-pattern we see is people creating large Python objects outside of Dask, then giving those objects to Dask and asking it to manage them. This works, but means that Dask needs to move around these very large objects with its metadata, rather than as normal Dask-controlled results.

Here are some common patterns to avoid and nicer alternatives:

DataFrames

```
# Don't

ddf = ... a dask dataframe ...
for fn in filenames:
    df = pandas.read_csv(fn)  # Read locally with Pandas
    ddf = ddf.append(df)            # Give to Dask
```

```
# Do

ddf = dd.read_csv(filenames)
```

Arrays

```
# Don't

f = h5py.File(...)
x = np.asarray(f["x"])  # Get data as a NumPy array locally

x = da.from_array(x)  # Hand NumPy array to Dask
```

```
# Do

f = h5py.File(...)
x = da.from_array(f["x"])  # Let Dask do the reading
```

Delayed

```
# Don't

@dask.delayed
def process(a, b):
    ...

df = pandas.read_csv("some-large-file.csv")  # Create large object locally
```

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```
results = []
for item in L:
    result = process(item, df)  # include df in every delayed call
    results.append(result)
```

```
# Do

@dask.delayed
def process(a, b):
    ...

df = dask.delayed(pandas.read_csv)("some-large-file.csv")  # Let Dask build object
results = []
for item in L:
    result = process(item, df)  # include pointer to df in every delayed call
    results.append(result)
```

3.13 API

Dask APIs generally follow from upstream APIs:

- *Arrays* follows NumPy
- *DataFrames* follows Pandas
- *Bag* follows map/filter/groupby/reduce common in Spark and Python iterators
- Dask-ML follows the Scikit-Learn and others
- *Delayed* wraps general Python code
- *Futures* follows concurrent.futures from the standard library for real-time computation.

Additionally, Dask has its own functions to start computations, persist data in memory, check progress, and so forth that complement the APIs above. These more general Dask functions are described below:

`compute`(*args, **kwargs)	Compute several dask collections at once.
`is_dask_collection`(x)	Returns `True` if `x` is a dask collection
`optimize`(*args, **kwargs)	Optimize several dask collections at once.
`persist`(*args, **kwargs)	Persist multiple Dask collections into memory
`visualize`(*args, **kwargs)	Visualize several dask graphs at once.

These functions work with any scheduler. More advanced operations are available when using the newer scheduler and starting a `dask.distributed.Client` (which, despite its name, runs nicely on a single machine). This API provides the ability to submit, cancel, and track work asynchronously, and includes many functions for complex inter-task workflows. These are not necessary for normal operation, but can be useful for real-time or advanced operation.

This more advanced API is available in the Dask distributed documentation

`dask.`**`compute`**`(`**args*, ***kwargs*`)`

Compute several dask collections at once.

Parameters

args [object] Any number of objects. If it is a dask object, it's computed and the result is returned. By default, python builtin collections are also traversed to look for dask objects (for more information see the `traverse` keyword). Non-dask arguments are passed through unchanged.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `compute`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

optimize_graph [bool, optional] If True [default], the optimizations for each collection are applied before computation. Otherwise the graph is run as is. This can be useful for debugging.

kwargs Extra keywords to forward to the scheduler function.

Examples

```
>>> import dask.array as da
>>> a = da.arange(10, chunks=2).sum()
>>> b = da.arange(10, chunks=2).mean()
>>> compute(a, b)
(45, 4.5)
```

By default, dask objects inside python collections will also be computed:

```
>>> compute({'a': a, 'b': b, 'c': 1})  # doctest: +SKIP
({'a': 45, 'b': 4.5, 'c': 1},)
```

`dask.`**`is_dask_collection`**`(`*x*`)`

Returns `True` if `x` is a dask collection

`dask.`**`optimize`**`(`**args*, ***kwargs*`)`

Optimize several dask collections at once.

Returns equivalent dask collections that all share the same merged and optimized underlying graph. This can be useful if converting multiple collections to delayed objects, or to manually apply the optimizations at strategic points.

Note that in most cases you shouldn't need to call this method directly.

Parameters

***args** [objects] Any number of objects. If a dask object, its graph is optimized and merged with all those of all other dask objects before returning an equivalent dask collection. Non-dask arguments are passed through unchanged.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `optimize`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

optimizations [list of callables, optional] Additional optimization passes to perform.

****kwargs** Extra keyword arguments to forward to the optimization passes.

Examples

```
>>> import dask.array as da
>>> a = da.arange(10, chunks=2).sum()
>>> b = da.arange(10, chunks=2).mean()
>>> a2, b2 = optimize(a, b)
```

```
>>> a2.compute() == a.compute()
True
>>> b2.compute() == b.compute()
True
```

`dask.`**`persist`**`(`**args*, ***kwargs*`)`

Persist multiple Dask collections into memory

This turns lazy Dask collections into Dask collections with the same metadata, but now with their results fully computed or actively computing in the background.

For example a lazy dask.array built up from many lazy calls will now be a dask.array of the same shape, dtype, chunks, etc., but now with all of those previously lazy tasks either computed in memory as many small `numpy.array` (in the single-machine case) or asynchronously running in the background on a cluster (in the distributed case).

This function operates differently if a `dask.distributed.Client` exists and is connected to a distributed scheduler. In this case this function will return as soon as the task graph has been submitted to the cluster, but before the computations have completed. Computations will continue asynchronously in the background. When using this function with the single machine scheduler it blocks until the computations have finished.

When using Dask on a single machine you should ensure that the dataset fits entirely within memory.

Parameters

***args: Dask collections**

scheduler [string, optional] Which scheduler to use like "threads", "synchronous" or "processes". If not provided, the default is to check the global settings first, and then fall back to the collection defaults.

traverse [bool, optional] By default dask traverses builtin python collections looking for dask objects passed to `persist`. For large collections this can be expensive. If none of the arguments contain any dask objects, set `traverse=False` to avoid doing this traversal.

optimize_graph [bool, optional] If True [default], the graph is optimized before computation. Otherwise the graph is run as is. This can be useful for debugging.

****kwargs** Extra keywords to forward to the scheduler function.

Returns

New dask collections backed by in-memory data

Examples

```
>>> df = dd.read_csv('/path/to/*.csv')  # doctest: +SKIP
>>> df = df[df.name == 'Alice']  # doctest: +SKIP
>>> df['in-debt'] = df.balance < 0  # doctest: +SKIP
>>> df = df.persist()  # triggers computation  # doctest: +SKIP
>>> df.value().min()  # future computations are now fast  # doctest: +SKIP
-10
>>> df.value().max()  # doctest: +SKIP
100
```

```
>>> from dask import persist  # use persist function on multiple collections
>>> a, b = persist(a, b)  # doctest: +SKIP
```

`dask.`**`visualize`**`(`**args*, ***kwargs*`)`

Visualize several dask graphs at once.

Requires `graphviz` to be installed. All options that are not the dask graph(s) should be passed as keyword arguments.

Parameters

dsk [dict(s) or collection(s)] The dask graph(s) to visualize.

filename [str or None, optional] The name (without an extension) of the file to write to disk. If *filename* is None, no file will be written, and we communicate with dot using only pipes.

format [{'png', 'pdf', 'dot', 'svg', 'jpeg', 'jpg'}, optional] Format in which to write output file. Default is 'png'.

optimize_graph [bool, optional] If True, the graph is optimized before rendering. Otherwise, the graph is displayed as is. Default is False.

color: {None, 'order'}, optional Options to color nodes. Provide `cmap=` keyword for additional colormap

****kwargs** Additional keyword arguments to forward to `to_graphviz`.

Returns

result [IPython.diplay.Image, IPython.display.SVG, or None] See dask.dot.dot_graph for more information.

See also:

`dask.dot.dot_graph`

Notes

For more information on optimization see here:

https://docs.dask.org/en/latest/optimize.html

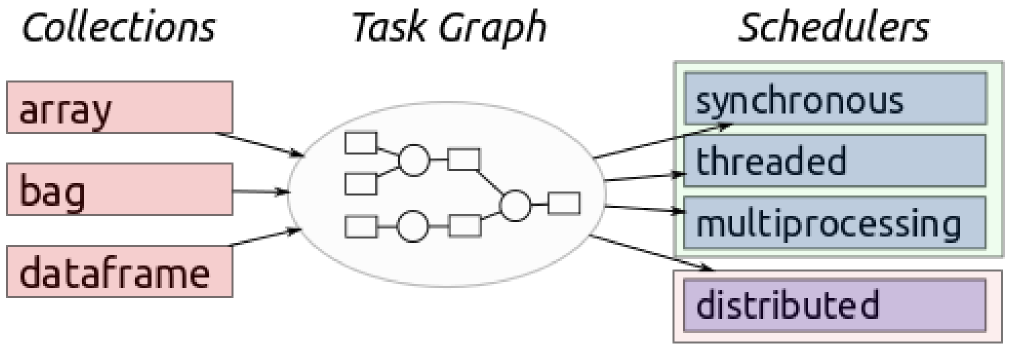
Examples

```
>>> x.visualize(filename='dask.pdf')  # doctest: +SKIP
>>> x.visualize(filename='dask.pdf', color='order')  # doctest: +SKIP
```

Finally, Dask has a few helpers for generating demo datasets

3.14 Scheduling

All of the large-scale Dask collections like *Dask Array*, *Dask DataFrame*, and *Dask Bag* and the fine-grained APIs like *delayed* and *futures* generate task graphs where each node in the graph is a normal Python function and edges between nodes are normal Python objects that are created by one task as outputs and used as inputs in another task. After Dask generates these task graphs, it needs to execute them on parallel hardware. This is the job of a *task scheduler*. Different task schedulers exist, and each will consume a task graph and compute the same result, but with different performance characteristics.



Dask has two families of task schedulers:

1. **Single machine scheduler**: This scheduler provides basic features on a local process or thread pool. This scheduler was made first and is the default. It is simple and cheap to use, although it can only be used on a single machine and does not scale
2. **Distributed scheduler**: This scheduler is more sophisticated, offers more features, but also requires a bit more effort to set up. It can run locally or distributed across a cluster

For different computations you may find better performance with particular scheduler settings. This document helps you understand how to choose between and configure different schedulers, and provides guidelines on when one might be more appropriate.

3.14.1 Local Threads

```python
import dask
dask.config.set(scheduler='threads')  # overwrite default with threaded scheduler
```

The threaded scheduler executes computations with a local `multiprocessing.pool.ThreadPool`. It is lightweight and requires no setup. It introduces very little task overhead (around 50us per task) and, because everything occurs in the same process, it incurs no costs to transfer data between tasks. However, due to Python's Global Interpreter Lock (GIL), this scheduler only provides parallelism when your computation is dominated by non-Python code, such as is the case when operating on numeric data in NumPy arrays, Pandas DataFrames, or using any of the other C/C++/Cython based projects in the ecosystem.

The threaded scheduler is the default choice for *Dask Array*, *Dask DataFrame*, and *Dask Delayed*. However, if your computation is dominated by processing pure Python objects like strings, dicts, or lists, then you may want to try one of the process-based schedulers below (we currently recommend the distributed scheduler on a local machine).

3.14.2 Local Processes

Note: The distributed scheduler described a couple sections below is often a better choice today. We encourage readers to continue reading after this section.

```
import dask.multiprocessing
dask.config.set(scheduler='processes')  # overwrite default with multiprocessing␣
↪scheduler
```

The multiprocessing scheduler executes computations with a local `multiprocessing.Pool`. It is lightweight to use and requires no setup. Every task and all of its dependencies are shipped to a local process, executed, and then their result is shipped back to the main process. This means that it is able to bypass issues with the GIL and provide parallelism even on computations that are dominated by pure Python code, such as those that process strings, dicts, and lists.

However, moving data to remote processes and back can introduce performance penalties, particularly when the data being transferred between processes is large. The multiprocessing scheduler is an excellent choice when workflows are relatively linear, and so does not involve significant inter-task data transfer as well as when inputs and outputs are both small, like filenames and counts.

This is common in basic data ingestion workloads, such as those are common in *Dask Bag*, where the multiprocessing scheduler is the default:

```
>>> import dask.bag as db
>>> db.read_text('*.json').map(json.loads).pluck('name').frequencies().compute()
{'alice': 100, 'bob': 200, 'charlie': 300}
```

For more complex workloads, where large intermediate results may be depended upon by multiple downstream tasks, we generally recommend the use of the distributed scheduler on a local machine. The distributed scheduler is more intelligent about moving around large intermediate results.

3.14.3 Single Thread

```
import dask
dask.config.set(scheduler='synchronous')  # overwrite default with single-threaded␣
↪scheduler
```

The single-threaded synchronous scheduler executes all computations in the local thread with no parallelism at all. This is particularly valuable for debugging and profiling, which are more difficult when using threads or processes.

For example, when using IPython or Jupyter notebooks, the `%debug`, `%pdb`, or `%prun` magics will not work well when using the parallel Dask schedulers (they were not designed to be used in a parallel computing context). However, if you run into an exception and want to step into the debugger, you may wish to rerun your computation under the single-threaded scheduler where these tools will function properly.

3.14.4 Dask Distributed (local)

```
from dask.distributed import Client
client = Client()
# or
client = Client(processes=False)
```

The Dask distributed scheduler can either be *setup on a cluster* or run locally on a personal machine. Despite having the name "distributed", it is often pragmatic on local machines for a few reasons:

1. It provides access to asynchronous API, notably *Futures*
2. It provides a diagnostic dashboard that can provide valuable insight on performance and progress
3. It handles data locality with more sophistication, and so can be more efficient than the multiprocessing scheduler on workloads that require multiple processes

You can read more about using the Dask distributed scheduler on a single machine in *these docs*.

3.14.5 Dask Distributed (Cluster)

You can also run Dask on a distributed cluster. There are a variety of ways to set this up depending on your cluster. We recommend referring to the *setup documentation* for more information.

3.14.6 Configuration

You can configure the global default scheduler by using the `dask.config.set(scheduler...)` command. This can be done globally:

```
dask.config.set(scheduler='threads')

x.compute()
```

or as a context manager:

```
with dask.config.set(scheduler='threads'):
    x.compute()
```

or within a single compute call:

```
x.compute(scheduler='threads')
```

Additionally some of the scheduler support other keyword arguments. For example, the pool-based single-machine scheduler allows you to provide custom pools or specify the desired number of workers:

```
from multiprocessing.pool import ThreadPool
with dask.config.set(pool=ThreadPool(4)):
    ...

with dask.config.set(num_workers=4):
    ...
```

3.15 Understanding Performance

The first step in making computations run quickly is to understand the costs involved. In Python we often rely on tools like the CProfile module, %%prun IPython magic, VMProf, or snakeviz to understand the costs associated with our code. However, few of these tools work well on multi-threaded or multi-process code, and fewer still on computations distributed among many machines. We also have new costs like data transfer, serialization, task scheduling overhead, and more that we may not be accustomed to tracking.

Fortunately, the Dask schedulers come with diagnostics to help you understand the performance characteristics of your computations. By using these diagnostics and with some thought, we can often identify the slow parts of troublesome computations.

The *single-machine and distributed schedulers* come with *different* diagnostic tools. These tools are deeply integrated into each scheduler, so a tool designed for one will not transfer over to the other.

These pages provide four options for profiling parallel code:

1. *Visualize task graphs*
2. *Single threaded scheduler and a normal Python profiler*
3. *Diagnostics for the single-machine scheduler*
4. *Diagnostics for the distributed scheduler and dashboard*

Additionally, if you are interested in understanding the various phases where slowdown can occur, you may wish to read the following:

- Phases of computation

3.16 Visualize task graphs

`visualize(*args, **kwargs)`	Visualize several dask graphs at once.

Before executing your computation you might consider visualizing the underlying task graph. By looking at the inter-connectedness of tasks you can learn more about potential bottlenecks where parallelism may not be possile, or areas where many tasks depend on each other, which may cause a great deal of communication.

The `.visualize` method and `dask.visualize` function work exactly like the `.compute` method and `dask.compute` function, except that rather than computing the result, they produce an image of the task graph.

By default the task graph is rendered from top to bottom. In the case that you prefer to visualize it from left to right, pass `rankdir="LR"` as a keyword argument to `.visualize`.

```python
import dask.array as da
x = da.ones((15, 15), chunks=(5, 5))

y = x + x.T

# y.compute()
y.visualize(filename='transpose.svg')
```

Note that the `visualize` function is powered by the GraphViz system library. This library has a few considerations:

1. You must install both the graphviz system library (with tools like apt-get, yum, or brew) *and* the graphviz Python library. If you use Conda then you need to install `python-graphviz`, which will bring along the `graphviz` system library as a dependency.
2. Graphviz takes a while on graphs larger than about 100 nodes. For large computations you might have to simplify your computation a bit for the visualize method to work well.

3.17 Diagnostics (local)

Profiling parallel code can be challenging, but `dask.diagnostics` provides functionality to aid in profiling and inspecting execution with the *local task scheduler*.

This page describes the following few built-in options:

1. ProgressBar
2. Profiler
3. ResourceProfiler
4. CacheProfiler

Furthermore, this page then provides instructions on how to build your own custom diagnostic.

3.17.1 Progress Bar

ProgressBar([minimum, width, dt, out])	A progress bar for dask.

The `ProgressBar` class builds on the scheduler callbacks described above to display a progress bar in the terminal or notebook during computation. This can give a nice feedback during long running graph execution. It can be used as a context manager around calls to `get` or `compute` to profile the computation:

```
>>> from dask.diagnostics import ProgressBar
>>> a = da.random.normal(size=(10000, 10000), chunks=(1000, 1000))
>>> res = a.dot(a.T).mean(axis=0)

>>> with ProgressBar():
...     out = res.compute()
[########################################] | 100% Completed | 17.1 s
```

or registered globally using the `register` method:

```
>>> pbar = ProgressBar()
>>> pbar.register()
>>> out = res.compute()
[########################################] | 100% Completed | 17.1 s
```

To unregister from the global callbacks, call the `unregister` method:

```
>>> pbar.unregister()
```

3.17.2 Profiler

Profiler()	A profiler for dask execution at the task level.

Dask provides a few tools for profiling execution. As with the `ProgressBar`, they each can be used as context managers or registered globally.

The `Profiler` class is used to profile Dask's execution at the task level. During execution, it records the following information for each task:

1. Key
2. Task
3. Start time in seconds since the epoch
4. Finish time in seconds since the epoch
5. Worker id

3.17.3 ResourceProfiler

`ResourceProfiler`([dt])	A profiler for resource use.

The `ResourceProfiler` class is used to profile Dask's execution at the resource level. During execution, it records the following information for each timestep:

1. Time in seconds since the epoch
2. Memory usage in MB
3. % CPU usage

The default timestep is 1 second, but can be set manually using the `dt` keyword:

```
>>> from dask.diagnostics import ResourceProfiler
>>> rprof = ResourceProfiler(dt=0.5)
```

3.17.4 CacheProfiler

`CacheProfiler`([metric, metric_name])	A profiler for dask execution at the scheduler cache level.

The `CacheProfiler` class is used to profile Dask's execution at the scheduler cache level. During execution, it records the following information for each task:

1. Key
2. Task
3. Size metric
4. Cache entry time in seconds since the epoch
5. Cache exit time in seconds since the epoch

Here the size metric is the output of a function called on the result of each task. The default metric is to count each task (`metric` is 1 for all tasks). Other functions may be used as a metric instead through the `metric` keyword. For example, the `nbytes` function found in `cachey` can be used to measure the number of bytes in the scheduler cache:

```
>>> from dask.diagnostics import CacheProfiler
>>> from cachey import nbytes
>>> cprof = CacheProfiler(metric=nbytes)
```

3.17.5 Example

As an example to demonstrate using the diagnostics, we'll profile some linear algebra done with Dask Array. We'll create a random array, take its QR decomposition, and then reconstruct the initial array by multiplying the Q and R components together. Note that since the profilers (and all diagnostics) are just context managers, multiple profilers can be used in a with block:

```
>>> import dask.array as da
>>> from dask.diagnostics import Profiler, ResourceProfiler, CacheProfiler
>>> a = da.random.random(size=(10000, 1000), chunks=(1000, 1000))
>>> q, r = da.linalg.qr(a)
```

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```
>>> a2 = q.dot(r)

>>> with Profiler() as prof, ResourceProfiler(dt=0.25) as rprof,
...         CacheProfiler() as cprof:
...     out = a2.compute()
```

The results of each profiler are stored in their `results` attribute as a list of `namedtuple` objects:

```
>>> prof.results[0]
TaskData(key=('tsqr-8d16e396b237bf7a731333130d310cb9_QR_st1', 5, 0),
         task=(qr, (_apply_random, 'random_sample', 1060164455, (1000, 1000), (), {}
↪)),
         start_time=1454368444.493292,
         end_time=1454368444.902987,
         worker_id=4466937856)

>>> rprof.results[0]
ResourceData(time=1454368444.078748, mem=74.100736, cpu=0.0)

>>> cprof.results[0]
CacheData(key=('tsqr-8d16e396b237bf7a731333130d310cb9_QR_st1', 7, 0),
          task=(qr, (_apply_random, 'random_sample', 1310656009, (1000, 1000), (), {}
↪)),
          metric=1,
          cache_time=1454368444.49662,
          free_time=1454368446.769452)
```

These can be analyzed separately or viewed in a bokeh plot using the provided `visualize` method on each profiler:

```
>>> prof.visualize()
```

To view multiple profilers at the same time, the `dask.diagnostics.visualize` function can be used. This takes a list of profilers and creates a vertical stack of plots aligned along the x-axis:

```
>>> from dask.diagnostics import visualize
>>> visualize([prof, rprof, cprof])
```

Looking at the above figure, from top to bottom:

1. The results from the `Profiler` object: This shows the execution time for each task as a rectangle, organized along the y-axis by worker (in this case threads). Similar tasks are grouped by color and, by hovering over each task, one can see the key and task that each block represents.

2. The results from the `ResourceProfiler` object: This shows two lines, one for total CPU percentage used by all the workers, and one for total memory usage.

3. The results from the `CacheProfiler` object: This shows a line for each task group, plotting the sum of the current `metric` in the cache against time. In this case it's the default metric (count) and the lines represent the number of each object in the cache at time. Note that the grouping and coloring is the same as for the `Profiler` plot, and that the task represented by each line can be found by hovering over the line.

From these plots we can see that the initial tasks (calls to `numpy.random.random` and `numpy.linalg.qr` for each chunk) are run concurrently, but only use slightly more than 100% CPU. This is because the call to `numpy.linalg.qr` currently doesn't release the Global Interpreter Lock (GIL), so those calls can't truly be done in parallel. Next, there's a reduction step where all the blocks are combined. This requires all the results from the first step to be held in memory, as shown by the increased number of results in the cache, and increase in memory usage. Immediately after this task ends, the number of elements in the cache decreases, showing that they were only needed for this step.

Finally, there's an interleaved set of calls to `dot` and `sum`. Looking at the CPU plot, it shows that these run both concurrently and in parallel, as the CPU percentage spikes up to around 350%.

3.17.6 Custom Callbacks

`Callback`([start, start_state, pretask, . . .])	Base class for using the callback mechanism

Schedulers based on `dask.local.get_async` (currently `dask.get`, `dask.threaded.get`, and `dask.multiprocessing.get`) accept five callbacks, allowing for inspection of scheduler execution.

The callbacks are:

1. `start(dsk)`: Run at the beginning of execution, right before the state is initialized. Receives the Dask graph

2. `start_state(dsk, state)`: Run at the beginning of execution, right after the state is initialized. Receives the Dask graph and scheduler state

3. `pretask(key, dsk, state)`: Run every time a new task is started. Receives the key of the task to be run, the Dask graph, and the scheduler state

4. `posttask(key, result, dsk, state, id)`: Run every time a task is finished. Receives the key of the task that just completed, the result, the Dask graph, the scheduler state, and the id of the worker that ran the task

5. `finish(dsk, state, errored)`: Run at the end of execution, right before the result is returned. Receives the Dask graph, the scheduler state, and a boolean indicating whether or not the exit was due to an error

Custom diagnostics can be created either by instantiating the `Callback` class with the some of the above methods as keywords or by subclassing the `Callback` class. Here we create a class that prints the name of every key as it's computed:

```
from dask.callbacks import Callback
class PrintKeys(Callback):
    def _pretask(self, key, dask, state):
        """Print the key of every task as it's started"""
        print("Computing: {0}!".format(repr(key)))
```

This can now be used as a context manager during computation:

```
>>> from operator import add, mul
>>> dsk = {'a': (add, 1, 2), 'b': (add, 3, 'a'), 'c': (mul, 'a', 'b')}

>>> with PrintKeys():
...     get(dsk, 'c')
Computing 'a'!
Computing 'b'!
Computing 'c'!
```

Alternatively, functions may be passed in as keyword arguments to `Callback`:

```
>>> def printkeys(key, dask, state):
...    print("Computing: {0}!".format(repr(key)))

>>> with Callback(pretask=printkeys):
...     get(dsk, 'c')
Computing 'a'!
Computing 'b'!
Computing 'c'!
```

3.17.7 API

`CacheProfiler`([metric, metric_name])	A profiler for dask execution at the scheduler cache level.
`Callback`([start, start_state, pretask, . . .])	Base class for using the callback mechanism
`Profiler`()	A profiler for dask execution at the task level.
`ProgressBar`([minimum, width, dt, out])	A progress bar for dask.
`ResourceProfiler`([dt])	A profiler for resource use.
`visualize`(profilers[, file_path, show, save])	Visualize the results of profiling in a bokeh plot.

`dask.diagnostics.`**`ProgressBar`**`(`*minimum=0*, *width=40*, *dt=0.1*, *out=None*`)`

A progress bar for dask.

Parameters

minimum [int, optional] Minimum time threshold in seconds before displaying a progress bar. Default is 0 (always display)

width [int, optional] Width of the bar

dt [float, optional] Update resolution in seconds, default is 0.1 seconds

Examples

Below we create a progress bar with a minimum threshold of 1 second before displaying. For cheap computations nothing is shown:

```
>>> with ProgressBar(minimum=1.0):      # doctest: +SKIP
...     out = some_fast_computation.compute()
```

But for expensive computations a full progress bar is displayed:

```
>>> with ProgressBar(minimum=1.0):      # doctest: +SKIP
...     out = some_slow_computation.compute()
[########################################] | 100% Completed | 10.4 s
```

The duration of the last computation is available as an attribute

```
>>> pbar = ProgressBar()
>>> with pbar:                          # doctest: +SKIP
...     out = some_computation.compute()
[########################################] | 100% Completed | 10.4 s
>>> pbar.last_duration                  # doctest: +SKIP
10.4
```

You can also register a progress bar so that it displays for all computations:

```
>>> pbar = ProgressBar()                # doctest: +SKIP
>>> pbar.register()                     # doctest: +SKIP
>>> some_slow_computation.compute()     # doctest: +SKIP
[########################################] | 100% Completed | 10.4 s
```

`dask.diagnostics.`**`Profiler`**`()`

A profiler for dask execution at the task level.

Records the following information for each task:

1. Key
2. Task
3. Start time in seconds since the epoch
4. Finish time in seconds since the epoch
5. Worker id

Examples

```
>>> from operator import add, mul
>>> from dask.threaded import get
>>> dsk = {'x': 1, 'y': (add, 'x', 10), 'z': (mul, 'y', 2)}
>>> with Profiler() as prof:
...     get(dsk, 'z')
22
```

```
>>> prof.results  # doctest: +SKIP
[('y', (add, 'x', 10), 1435352238.48039, 1435352238.480655, 140285575100160),
 ('z', (mul, 'y', 2), 1435352238.480657, 1435352238.480803, 140285566707456)]
```

These results can be visualized in a bokeh plot using the `visualize` method. Note that this requires bokeh to be installed.

```
>>> prof.visualize() # doctest: +SKIP
```

You can activate the profiler globally

```
>>> prof.register()  # doctest: +SKIP
```

If you use the profiler globally you will need to clear out old results manually.

```
>>> prof.clear()
```

`dask.diagnostics.`**`ResourceProfiler`**`(`*dt=1*`)`

A profiler for resource use.

Records the following each timestep

1. Time in seconds since the epoch
2. Memory usage in MB
3. % CPU usage

Examples

```
>>> from operator import add, mul
>>> from dask.threaded import get
>>> dsk = {'x': 1, 'y': (add, 'x', 10), 'z': (mul, 'y', 2)}
>>> with ResourceProfiler() as prof:  # doctest: +SKIP
...     get(dsk, 'z')
22
```

These results can be visualized in a bokeh plot using the `visualize` method. Note that this requires bokeh to be installed.

```
>>> prof.visualize() # doctest: +SKIP
```

You can activate the profiler globally

```
>>> prof.register()  # doctest: +SKIP
```

If you use the profiler globally you will need to clear out old results manually.

```
>>> prof.clear()  # doctest: +SKIP
```

Note that when used as a context manager data will be collected throughout the duration of the enclosed block. In contrast, when registered globally data will only be collected while a dask scheduler is active.

`dask.diagnostics.`**`CacheProfiler`**`(`*metric=None*, *metric_name=None*`)`

A profiler for dask execution at the scheduler cache level.

Records the following information for each task:

1. Key
2. Task
3. Size metric
4. Cache entry time in seconds since the epoch
5. Cache exit time in seconds since the epoch

Examples

```
>>> from operator import add, mul
>>> from dask.threaded import get
>>> dsk = {'x': 1, 'y': (add, 'x', 10), 'z': (mul, 'y', 2)}
>>> with CacheProfiler() as prof:
...     get(dsk, 'z')
22
```

```
>>> prof.results    # doctest: +SKIP
[CacheData('y', (add, 'x', 10), 1, 1435352238.48039, 1435352238.480655),
 CacheData('z', (mul, 'y', 2), 1, 1435352238.480657, 1435352238.480803)]
```

The default is to count each task (`metric` is 1 for all tasks). Other functions may used as a metric instead through the `metric` keyword. For example, the `nbytes` function found in `cachey` can be used to measure the number of bytes in the cache.

```
>>> from cachey import nbytes    # doctest: +SKIP
>>> with CacheProfiler(metric=nbytes) as prof:  # doctest: +SKIP
...     get(dsk, 'z')
```

The profiling results can be visualized in a bokeh plot using the `visualize` method. Note that this requires bokeh to be installed.

```
>>> prof.visualize() # doctest: +SKIP
```

You can activate the profiler globally

```
>>> prof.register()  # doctest: +SKIP
```

If you use the profiler globally you will need to clear out old results manually.

```
>>> prof.clear()
```

`dask.diagnostics.`**`Callback`**(*start=None*, *start_state=None*, *pretask=None*, *posttask=None*, *finish=None*)

Base class for using the callback mechanism

Create a callback with functions of the following signatures:

```
>>> def start(dsk):
...     pass
>>> def start_state(dsk, state):
...     pass
>>> def pretask(key, dsk, state):
...     pass
>>> def posttask(key, result, dsk, state, worker_id):
...     pass
>>> def finish(dsk, state, failed):
...     pass
```

You may then construct a callback object with any number of them

```
>>> cb = Callback(pretask=pretask, finish=finish)   # doctest: +SKIP
```

And use it either as a context manager over a compute/get call

```
>>> with cb:   # doctest: +SKIP
...     x.compute()   # doctest: +SKIP
```

Or globally with the `register` method

```
>>> cb.register()   # doctest: +SKIP
>>> cb.unregister()   # doctest: +SKIP
```

Alternatively subclass the `Callback` class with your own methods.

```
>>> class PrintKeys(Callback):
...     def _pretask(self, key, dask, state):
...         print("Computing: {0}!".format(repr(key)))
```

```
>>> with PrintKeys():   # doctest: +SKIP
...     x.compute()   # doctest: +SKIP
```

`dask.diagnostics.`**`visualize`**(*profilers*, *file_path=None*, *show=True*, *save=True*, ***kwargs*)

Visualize the results of profiling in a bokeh plot.

If multiple profilers are passed in, the plots are stacked vertically.

Parameters

profilers [profiler or list] Profiler or list of profilers.

file_path [string, optional] Name of the plot output file.

show [boolean, optional] If True (default), the plot is opened in a browser.

save [boolean, optional] If True (default), the plot is saved to disk.

****kwargs** Other keyword arguments, passed to bokeh.figure. These will override all defaults set by visualize.

Returns

The completed bokeh plot object.

3.18 Diagnostics (distributed)

The *Dask distributed scheduler* provides live feedback in two forms:

1. An interactive dashboard containing many plots and tables with live information
2. A progress bar suitable for interactive use in consoles or notebooks

3.18.1 Dashboard

If Bokeh is installed then the dashboard will start up automatically whenever the scheduler is created. For local use this happens when you create a client with no arguments:

```
from dask.distributed import Client
client = Client()  # start distributed scheduler locally.  Launch dashboard
```

It is typically served at http://localhost:8787/status , but may be served elsewhere if this port is taken. The address of the dashboard will be displayed if you are in a Jupyter Notebook, or can be queriesd from `client.scheduler_info()['services']`.

There are numerous pages with information about task runtimes, communication, statistical profiling, load balancing, memory use, and much more. For more information we recommend the video guide above.

`Client`([address, loop, timeout, …])	Connect to and submit computation to a Dask cluster

3.18.2 Capture diagnostics

`get_task_stream`([client, plot, filename])	Collect task stream within a context block
`Client.profile`([key, start, stop, workers, …])	Collect statistical profiling information about recent work

You can capture some of the same information that the dashboard presents for offline processing using the `get_task_stream` and `Client.profile` functions. These capture the start and stop time of every task and transfer, as well as the results of a statistical profiler.

```
with get_task_stream(plot='save', filename="task-stream.html") as ts:
    x.compute()

client.profile(filename="dask-profile.html")

history = ts.data
```

3.18.3 Progress bar

progress(*futures[, notebook, multi, complete])	Track progress of futures

The `dask.distributed` progress bar differs from the `ProgressBar` used for *local diagnostics*. The `progress` function takes a Dask object that is executing in the background:

```
# Single machine progress bar
from dask.diagnostics import ProgressBar

with ProgressBar():
    x.compute()

# Distributed scheduler ProgressBar

from dask.distributed import Client, progress

client = Client()  # use dask.distributed by default

x = x.persist()  # start computation in the background
progress(x)      # watch progress

x.compute()      # convert to final result when done if desired
```

3.18.4 External Documentation

More in-depth technical documentation about Dask's distributed scheduler is available at https://distributed.dask.org/en/latest

3.18.5 API

`dask.distributed.`**`progress`**`(`**futures*, *notebook=None*, *multi=True*, *complete=True*, ***kwargs*`)`

Track progress of futures

This operates differently in the notebook and the console

- Notebook: This returns immediately, leaving an IPython widget on screen
- Console: This blocks until the computation completes

Parameters

futures: Futures A list of futures or keys to track

notebook: bool (optional) Running in the notebook or not (defaults to guess)

multi: bool (optional) Track different functions independently (defaults to True)

complete: bool (optional) Track all keys (True) or only keys that have not yet run (False) (defaults to True)

Notes

In the notebook, the output of *progress* must be the last statement in the cell. Typically, this means calling *progress* at the end of a cell.

Examples

```
>>> progress(futures)  # doctest: +SKIP
[########################################] | 100% Completed |  1.7s
```

dask.distributed.**get_task_stream**(*client=None*, *plot=False*, *filename='task-stream.html'*)
Collect task stream within a context block

This provides diagnostic information about every task that was run during the time when this block was active.

This must be used as a context manager.

Parameters

plot: boolean, str If true then also return a Bokeh figure If plot == 'save' then save the figure to a file

filename: str (optional) The filename to save to if you set `plot='save'`

See also:

`Client.get_task_stream` Function version of this context manager

Examples

```
>>> with get_task_stream() as ts:
...     x.compute()
>>> ts.data
[...]
```

Get back a Bokeh figure and optionally save to a file

```
>>> with get_task_stream(plot='save', filename='task-stream.html') as ts:
...    x.compute()
>>> ts.figure
<Bokeh Figure>
```

To share this file with others you may wish to upload and serve it online. A common way to do this is to upload the file as a gist, and then serve it on https://raw.githack.com

```
$ pip install gist
$ gist task-stream.html
https://gist.github.com/8a5b3c74b10b413f612bb5e250856ceb
```

You can then navigate to that site, click the "Raw" button to the right of the `task-stream.html` file, and then provide that URL to https://raw.githack.com . This process should provide a sharable link that others can use to see your task stream plot.

3.19 Debugging

Debugging parallel programs is hard. Normal debugging tools like logging and using `pdb` to interact with tracebacks stop working normally when exceptions occur in far-away machines, different processes, or threads.

Dask has a variety of mechanisms to make this process easier. Depending on your situation, some of these approaches may be more appropriate than others.

These approaches are ordered from lightweight or easy solutions to more involved solutions.

3.19.1 Exceptions

When a task in your computation fails, the standard way of understanding what went wrong is to look at the exception and traceback. Often people do this with the `pdb` module, IPython `%debug` or `%pdb` magics, or by just looking at the traceback and investigating where in their code the exception occurred.

Normally when a computation executes in a separate thread or a different machine, these approaches break down. To address this, Dask provides a few mechanisms to recreate the normal Python debugging experience.

Inspect Exceptions and Tracebacks

By default, Dask already copies the exception and traceback wherever they occur and reraises that exception locally. If your task failed with a `ZeroDivisionError` remotely, then you'll get a `ZeroDivisionError` in your interactive session. Similarly you'll see a full traceback of where this error occurred, which, just like in normal Python, can help you to identify the troublesome spot in your code.

However, you cannot use the `pdb` module or `%debug` IPython magics with these tracebacks to look at the value of variables during failure. You can only inspect things visually. Additionally, the top of the traceback may be filled with functions that are Dask-specific and not relevant to your problem, so you can safely ignore these.

Both the single-machine and distributed schedulers do this.

Use the Single-Threaded Scheduler

Dask ships with a simple single-threaded scheduler. This doesn't offer any parallel performance improvements but does run your Dask computation faithfully in your local thread, allowing you to use normal tools like `pdb`, `%debug` IPython magics, the profiling tools like the `cProfile` module, and snakeviz. This allows you to use all of your normal Python debugging tricks in Dask computations, as long as you don't need parallelism.

The single-threaded scheduler can be used, for example, by setting `scheduler='single-threaded'` in a compute call:

```
>>> x.compute(scheduler='single-threaded')
```

For more ways to configure schedulers, see the *scheduler configuration documentation*.

This only works for single-machine schedulers. It does not work with `dask.distributed` unless you are comfortable using the Tornado API (look at the testing infrastructure docs, which accomplish this). Also, because this operates on a single machine, it assumes that your computation can run on a single machine without exceeding memory limits. It may be wise to use this approach on smaller versions of your problem if possible.

Rerun Failed Task Locally

If a remote task fails, we can collect the function and all inputs, bring them to the local thread, and then rerun the function in hopes of triggering the same exception locally where normal debugging tools can be used.

With the single machine schedulers, use the `rerun_exceptions_locally=True` keyword:

```
>>> x.compute(rerun_exceptions_locally=True)
```

On the distributed scheduler use the `recreate_error_locally` method on anything that contains `Futures`:

```
>>> x.compute()
ZeroDivisionError(...)

```

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```
>>> %pdb
>>> future = client.compute(x)
>>> client.recreate_error_locally(future)
```

Remove Failed Futures Manually

Sometimes only parts of your computations fail, for example, if some rows of a CSV dataset are faulty in some way. When running with the distributed scheduler, you can remove chunks of your data that have produced bad results if you switch to dealing with Futures:

```
>>> import dask.dataframe as dd
>>> df = ...           # create dataframe
>>> df = df.persist()  # start computing on the cluster

>>> from distributed.client import futures_of
>>> futures = futures_of(df)  # get futures behind dataframe
>>> futures
[<Future: status: finished, type: pd.DataFrame, key: load-1>
 <Future: status: finished, type: pd.DataFrame, key: load-2>
 <Future: status: error, key: load-3>
 <Future: status: pending, key: load-4>
 <Future: status: error, key: load-5>]

>>> # wait until computation is done
>>> while any(f.status == 'pending' for f in futures):
...     sleep(0.1)

>>> # pick out only the successful futures and reconstruct the dataframe
>>> good_futures = [f for f in futures if f.status == 'finished']
>>> df = dd.from_delayed(good_futures, meta=df._meta)
```

This is a bit of a hack, but often practical when first exploring messy data. If you are using the concurrent.futures API (map, submit, gather), then this approach is more natural.

3.19.2 Inspect Scheduling State

Not all errors present themselves as exceptions. For example, in a distributed system workers may die unexpectedly, your computation may be unreasonably slow due to inter-worker communication or scheduler overhead, or one of several other issues. Getting feedback about what's going on can help to identify both failures and general performance bottlenecks.

For the single-machine scheduler, see *diagnostics* documentation. The rest of the section will assume that you are using the distributed scheduler where these issues arise more commonly.

Web Diagnostics

First, the distributed scheduler has a number of diagnostic web pages showing dozens of recorded metrics like CPU, memory, network, and disk use, a history of previous tasks, allocation of tasks to workers, worker memory pressure, work stealing, open file handle limits, etc. *Many* problems can be correctly diagnosed by inspecting these pages. By default, these are available at `http://scheduler:8787/`, `http://scheduler:8788/`, and `http://worker:8789/`, where `scheduler` and `worker` should be replaced by the addresses of the scheduler and each of the workers. See web diagnostic docs for more information.

Logs

The scheduler, workers, and client all emits logs using Python's standard logging module. By default, these emit to standard error. When Dask is launched by a cluster job scheduler (SGE/SLURM/YARN/Mesos/Marathon/Kubernetes/whatever), that system will track these logs and will have an interface to help you access them. If you are launching Dask on your own, they will probably dump to the screen unless you redirect stderr to a file .

You can control the logging verbosity in the `~/.dask/config.yaml` file. Defaults currently look like the following:

```
logging:
  distributed: info
  distributed.client: warning
  bokeh: error
```

So, for example, you could add a line like `distributed.worker:  debug` to get *very* verbose output from the workers.

3.19.3 LocalCluster

If you are using the distributed scheduler from a single machine, you may be setting up workers manually using the command line interface or you may be using LocalCluster which is what runs when you just call `Client()`:

```
>>> from dask.distributed import Client, LocalCluster
>>> client = Client()  # This is actually the following two commands

>>> cluster = LocalCluster()
>>> client = Client(cluster.scheduler.address)
```

LocalCluster is useful because the scheduler and workers are in the same process with you, so you can easily inspect their state while they run (they are running in a separate thread):

```
>>> cluster.scheduler.processing
{'worker-one:59858': {'inc-123', 'add-443'},
 'worker-two:48248': {'inc-456'}}
```

You can also do this for the workers *if* you run them without nanny processes:

```
>>> cluster = LocalCluster(nanny=False)
>>> client = Client(cluster)
```

This can be very helpful if you want to use the Dask distributed API and still want to investigate what is going on directly within the workers. Information is not distilled for you like it is in the web diagnostics, but you have full low-level access.

3.19.4 Inspect state with IPython

Sometimes you want to inspect the state of your cluster but you don't have the luxury of operating on a single machine. In these cases you can launch an IPython kernel on the scheduler and on every worker, which lets you inspect state on the scheduler and workers as computations are completing.

This does not give you the ability to run `%pdb` or `%debug` on remote machines. The tasks are still running in separate threads, and so are not easily accessible from an interactive IPython session.

For more details, see the Dask distributed IPython docs.

3.20 Development Guidelines

Dask is a community maintained project. We welcome contributions in the form of bug reports, documentation, code, design proposals, and more. This page provides resources on how best to contribute.

3.20.1 Where to ask for help

Dask conversation happens in the following places:

1. Stack Overflow #dask tag: for usage questions
2. GitHub Issue Tracker: for discussions around new features or established bugs
3. Gitter chat: for real-time discussion

For usage questions and bug reports we strongly prefer the use of Stack Overflow and GitHub issues over gitter chat. GitHub and Stack Overflow are more easily searchable by future users and so is more efficient for everyone's time. Gitter chat is generally reserved for community discussion.

3.20.2 Separate Code Repositories

Dask maintains code and documentation in a few git repositories hosted on the GitHub `dask` organization, https://github.com/dask. This includes the primary repository and several other repositories for different components. A non-exhaustive list follows:

- https://github.com/dask/dask: The main code repository holding parallel algorithms, the single-machine scheduler, and most documentation
- https://github.com/dask/distributed: The distributed memory scheduler
- https://github.com/dask/dask-ml: Machine learning algorithms
- https://github.com/dask/s3fs: S3 Filesystem interface
- https://github.com/dask/gcsfs: GCS Filesystem interface
- https://github.com/dask/hdfs3: Hadoop Filesystem interface
- . . .

Git and GitHub can be challenging at first. Fortunately good materials exist on the internet. Rather than repeat these materials here, we refer you to Pandas' documentation and links on this subject at https://pandas.pydata.org/pandas-docs/stable/contributing.html

3.20.3 Issues

The community discusses and tracks known bugs and potential features in the GitHub Issue Tracker. If you have a new idea or have identified a bug, then you should raise it there to start public discussion.

If you are looking for an introductory issue to get started with development, then check out the "good first issue" label, which contains issues that are good for starting developers. Generally, familiarity with Python, NumPy, Pandas, and some parallel computing are assumed.

3.20.4 Development Environment

Download code

Make a fork of the main Dask repository and clone the fork:

```
git clone https://github.com/<your-github-username>/dask
```

Contributions to Dask can then be made by submitting pull requests on GitHub.

Install

You may want to install larger dependencies like NumPy and Pandas using a binary package manager like conda. You can skip this step if you already have these libraries, don't care to use them, or have sufficient build environment on your computer to compile them when installing with `pip`:

```
conda install -y numpy pandas scipy bokeh psutil
```

Install Dask and dependencies:

```
cd dask
pip install -e ".[complete]"
```

For development, Dask uses the following additional dependencies:

```
pip install pytest moto
```

Run Tests

Dask uses py.test for testing. You can run tests from the main dask directory as follows:

```
py.test dask --verbose --doctest-modules
```

3.20.5 Contributing to Code

Dask maintains development standards that are similar to most PyData projects. These standards include language support, testing, documentation, and style.

Python Versions

Dask supports Python versions 3.5, 3.6, and 3.7. Name changes are handled by the `dask/compatibility.py` file.

Test

Dask employs extensive unit tests to ensure correctness of code both for today and for the future. Test coverage is expected for all code contributions.

Tests are written in a py.test style with bare functions:

```python
def test_fibonacci():
    assert fib(0) == 0
    assert fib(1) == 0
    assert fib(10) == 55
    assert fib(8) == fib(7) + fib(6)

    for x in [-3, 'cat', 1.5]:
        with pytest.raises(ValueError):
            fib(x)
```

These tests should compromise well between covering all branches and fail cases and running quickly (slow test suites get run less often).

You can run tests locally by running `py.test` in the local dask directory:

```
py.test dask --verbose
```

You can also test certain modules or individual tests for faster response:

```
py.test dask/dataframe --verbose

py.test dask/dataframe/tests/test_dataframe_core.py::test_set_index
```

Tests run automatically on the Travis.ci and Appveyor continuous testing frameworks on every push to every pull request on GitHub.

Tests are organized within the various modules' subdirectories:

```
dask/array/tests/test_*.py
dask/bag/tests/test_*.py
dask/dataframe/tests/test_*.py
dask/diagnostics/tests/test_*.py
```

For the Dask collections like Dask Array and Dask DataFrame, behavior is typically tested directly against the NumPy or Pandas libraries using the `assert_eq` functions:

```python
import numpy as np
import dask.array as da
from dask.array.utils import assert_eq

def test_aggregations():
    nx = np.random.random(100)
    dx = da.from_array(nx, chunks=(10,))

    assert_eq(nx.sum(), dx.sum())
    assert_eq(nx.min(), dx.min())
    assert_eq(nx.max(), dx.max())
    ...
```

This technique helps to ensure compatibility with upstream libraries and tends to be simpler than testing correctness directly. Additionally, by passing Dask collections directly to the `assert_eq` function rather than call compute manually, the testing suite is able to run a number of checks on the lazy collections themselves.

Docstrings

User facing functions should roughly follow the numpydoc standard, including sections for `Parameters`, `Examples`, and general explanatory prose.

By default, examples will be doc-tested. Reproducible examples in documentation is valuable both for testing and, more importantly, for communication of common usage to the user. Documentation trumps testing in this case and clear examples should take precedence over using the docstring as testing space. To skip a test in the examples add the comment `# doctest: +SKIP` directly after the line.

```
def fib(i):
    """ A single line with a brief explanation

    A more thorough description of the function, consisting of multiple
    lines or paragraphs.

    Parameters
    ----------
    i: int
         A short description of the argument if not immediately clear

    Examples
    --------
    >>> fib(4)
    3
    >>> fib(5)
    5
    >>> fib(6)
    8
    >>> fib(-1)  # Robust to bad inputs
    ValueError(...)
    """
```

Docstrings are currently tested under Python 3.6 on Travis.ci. You can test docstrings with pytest as follows:

```
py.test dask --doctest-modules
```

Docstring testing requires `graphviz` to be installed. This can be done via:

```
conda install -y graphviz
```

Code Formatting

Dask uses Black and Flake8 to ensure a consistent code format throughout the project. `black` and `flake8` can be installed with `pip`:

```
pip install black flake8
```

and then run from the root of the Dask repository:

```
black dask
flake8 dask
```

to auto-format your code. Additionally, many editors have plugins that will apply `black` as you edit files.

Optionally, you may wish to setup pre-commit hooks to automatically run `black` and `flake8` when you make a git commit. This can be done by installing `pre-commit`:

```
pip install pre-commit
```

and then running:

```
pre-commit install
```

from the root of the Dask repository. Now `black` and `flake8` will be run each time you commit changes. You can skip these checks with `git commit --no-verify`.

3.20.6 Contributing to Documentation

Dask uses Sphinx for documentation, hosted on https://readthedocs.org . Documentation is maintained in the RestructuredText markup language (`.rst` files) in `dask/docs/source`. The documentation consists both of prose and API documentation.

To build the documentation locally, first install the necessary requirements:

```
cd docs/
pip install -r requirements-docs.txt
```

Then build the documentation with `make`:

```
make html
```

The resulting HTML files end up in the `build/html` directory.

You can now make edits to rst files and run `make html` again to update the affected pages.

3.21 Changelog

3.21.1 2.6.0 / 2019-10-15

Core

- Call `ensure_dict` on graphs before entering `toolz.merge` (GH#5486) Matthew Rocklin
- Consolidating hash dispatch functions (GH#5476) Richard J Zamora

DataFrame

- Support Python 3.5 in Parquet code (GH#5491) Ben Zaitlen
- Avoid identity check in `warn_dtype_mismatch` (GH#5489) Tom Augspurger
- Enable unused groupby tests (GH#3480) Jörg Dietrich
- Remove old parquet and bcolz dataframe optimizations (GH#5484) Matthew Rocklin
- Add getitem optimization for `read_parquet` (GH#5453) Tom Augspurger
- Use `_constructor_sliced` method to determine Series type (GH#5480) Richard J Zamora
- Fix map(series) for unsorted base series index (GH#5459) Justin Waugh
- Fix `KeyError` with Groupby label (GH#5467) Ryan Nazareth

Documentation

- Use Zoom meeting instead of appear.in (GH#5494) Matthew Rocklin
- Added curated list of resources (GH#5460) Javad
- Update SSH docs to include `SSHCluster` (GH#5482) Matthew Rocklin
- Update "Why Dask?" page (GH#5473) Matthew Rocklin
- Fix typos in docstrings (GH#5469) garanews

3.21.2 2.5.2 / 2019-10-04

Array

- Correct chunk size logic for asymmetric overlaps (GH#5449) Ben Jeffery
- Make da.unify_chunks public API (GH#5443) Matthew Rocklin

DataFrame

- Fix dask.dataframe.fillna handling of Scalar object (GH#5463) Zhenqing Li

Documentation

- Remove boxes in Spark comparison page (GH#5445) Matthew Rocklin
- Add latest presentations (GH#5446) Javad
- Update cloud documentation (GH#5444) Matthew Rocklin

3.21.3 2.5.0 / 2019-09-27

Core

- Add sentinel no_default to get_dependencies task (GH#5420) James Bourbeau
- Update fsspec version (GH#5415) Matthew Rocklin
- Remove PY2 checks (GH#5400) Jim Crist

DataFrame

- Add option to not check meta in dd.from_delayed (GH#5436) Christopher J. Wright
- Fix test_timeseries_nulls_in_schema failures with pyarrow master (GH#5421) Richard J Zamora
- Reduce read_metadata output size in pyarrow/parquet (GH#5391) Richard J Zamora
- Test numeric edge case for repartition with npartitions. (GH#5433) amerkel2
- Unxfail pandas-datareader test (GH#5430) Tom Augspurger
- Add DataFrame.pop implementation (GH#5422) Matthew Rocklin
- Enable merge/set_index for cudf-based dataframes with cupy `values` (GH#5322) Richard J Zamora

- drop_duplicates support for positional subset parameter (GH#5410) Wes Roach

Documentation

- Add screencasts to array, bag, dataframe, delayed, futures and setup (GH#5429) (GH#5424) Matthew Rocklin
- Fix delimeter parsing documentation (GH#5428) Mahmut Bulut
- Update overview image (GH#5404) James Bourbeau

3.21.4 2.4.0 / 2019-09-13

Array

- Adds explicit `h5py.File` mode (GH#5390) James Bourbeau
- Provides method to compute unknown array chunks sizes (GH#5312) Scott Sievert
- Ignore runtime warning in Array `compute_meta` (GH#5356) estebanag
- Add `_meta` to `Array.__dask_postpersist__` (GH#5353) Benoit Bovy
- Fixup `da.asarray` and `da.asanyarray` for datetime64 dtype and xarray objects (GH#5334) Stephan Hoyer
- Add shape implementation (GH#5293) Tom Augspurger
- Add chunktype to array text repr (GH#5289) James Bourbeau
- Array.random.choice: handle array-like non-arrays (GH#5283) Gabe Joseph

Core

- Remove deprecated code (GH#5401) Jim Crist
- Fix `funcname` when vectorized func has no `__name__` (GH#5399) James Bourbeau
- Truncate `funcname` to avoid long key names (GH#5383) Matthew Rocklin
- Add support for `numpy.vectorize` in `funcname` (GH#5396) James Bourbeau
- Fixed HDFS upstream test (GH#5395) Tom Augspurger
- Support numbers and None in `parse_bytes/timedelta` (GH#5384) Matthew Rocklin
- Fix tokenizing of subindexes on memmapped numpy arrays (GH#5351) Henry Pinkard
- Upstream fixups (GH#5300) Tom Augspurger

DataFrame

- Allow pandas to cast type of statistics (GH#5402) Richard J Zamora
- Preserve index dtype after applying `dd.pivot_table` (GH#5385) therhaag
- Implement explode for Series and DataFrame (GH#5381) Arpit Solanki
- `set_index` on categorical fails with less categories than partitions (GH#5354) Oliver Hofkens
- Support output to a single CSV file (GH#5304) Hongjiu Zhang

- Add `groupby().transform()` (GH#5327) Oliver Hofkens
- Adding filter kwarg to pyarrow dataset call (GH#5348) Richard J Zamora
- Implement and check compression defaults for parquet (GH#5335) Sarah Bird
- Pass sqlalchemy params to delayed objects (GH#5332) Arpit Solanki
- Fixing schema handling in arrow-parquet (GH#5307) Richard J Zamora
- Add support for DF and Series `groupby().idxmin/max()` (GH#5273) Oliver Hofkens
- Add correlation calculation and add test (GH#5296) Ben Zaitlen

Documentation

- Numpy docstring standard has moved (GH#5405) Wes Roach
- Reference correct NumPy array name (GH#5403) Wes Roach
- Minor edits to Array chunk documentation (GH#5372) Scott Sievert
- Add methods to API docs (GH#5387) Tom Augspurger
- Add namespacing to configuration example (GH#5374) Matthew Rocklin
- Add get_task_stream and profile to the diagnostics page (GH#5375) Matthew Rocklin
- Add best practice to load data with Dask (GH#5369) Matthew Rocklin
- Update `institutional-faq.rst` (GH#5345) DomHudson
- Add threads and processes note to the best practices (GH#5340) Matthew Rocklin
- Update cuDF links (GH#5328) James Bourbeau
- Fixed small typo with parentheses placement (GH#5311) Eugene Huang
- Update link in reshape docstring (GH#5297) James Bourbeau

3.21.5 2.3.0 / 2019-08-16

Array

- Raise exception when `from_array` is given a dask array (GH#5280) David Hoese
- Avoid adjusting gufunc's meta dtype twice (GH#5274) Peter Andreas Entschev
- Add `meta=` keyword to map_blocks and add test with sparse (GH#5269) Matthew Rocklin
- Add rollaxis and moveaxis (GH#4822) Tobias de Jong
- Always increment old chunk index (GH#5256) James Bourbeau
- Shuffle dask array (GH#3901) Tom Augspurger
- Fix ordering when indexing a dask array with a bool dask array (GH#5151) James Bourbeau

Bag

- Add workaround for memory leaks in bag generators (GH#5208) Marco Neumann

Core

- Set strict xfail option (GH#5220) James Bourbeau
- test-upstream (GH#5267) Tom Augspurger
- Fixed HDFS CI failure (GH#5234) Tom Augspurger
- Error nicely if no file size inferred (GH#5231) Jim Crist
- A few changes to `config.set` (GH#5226) Jim Crist
- Fixup black string normalization (GH#5227) Jim Crist
- Pin NumPy in windows tests (GH#5228) Jim Crist
- Ensure parquet tests are skipped if fastparquet and pyarrow not installed (GH#5217) James Bourbeau
- Add fsspec to readthedocs (GH#5207) Matthew Rocklin
- Bump NumPy and Pandas to 1.17 and 0.25 in CI test (GH#5179) John A Kirkham

DataFrame

- Fix `DataFrame.query` docstring (incorrect numexpr API) (GH#5271) Doug Davis
- Parquet metadata-handling improvements (GH#5218) Richard J Zamora
- Improve messaging around sorted parquet columns for index (GH#5265) Martin Durant
- Add `rearrange_by_divisions` and `set_index` support for cudf (GH#5205) Richard J Zamora
- Fix `groupby.std()` with integer colum names (GH#5096) Nicolas Hug
- Add `Series.__iter__` (GH#5071) Blane
- Generalize `hash_pandas_object` to work for non-pandas backends (GH#5184) GALI PREM SAGAR
- Add rolling cov (GH#5154) Ivars Geidans
- Add columns argument in drop function (GH#5223) Henrique Ribeiro

Documentation

- Update institutional FAQ doc (GH#5277) Matthew Rocklin
- Add draft of institutional FAQ (GH#5214) Matthew Rocklin
- Make boxes for dask-spark page (GH#5249) Martin Durant
- Add motivation for shuffle docs (GH#5213) Matthew Rocklin
- Fix links and API entries for best-practices (GH#5246) Martin Durant
- Remove "bytes" (internal data ingestion) doc page (GH#5242) Martin Durant
- Redirect from our local distributed page to distributed.dask.org (GH#5248) Matthew Rocklin
- Cleanup API page (GH#5247) Matthew Rocklin
- Remove excess endlines from install docs (GH#5243) Matthew Rocklin
- Remove item list in phases of computation doc (GH#5245) Martin Durant
- Remove custom graphs from the TOC sidebar (GH#5241) Matthew Rocklin

- Remove experimental status of custom collections (GH#5236) James Bourbeau
- Adds table of contents to Why Dask? (GH#5244) James Bourbeau
- Moves bag overview to top-level bag page (GH#5240) James Bourbeau
- Remove use-cases in favor of stories.dask.org (GH#5238) Matthew Rocklin
- Removes redundant TOC information in index.rst (GH#5235) James Bourbeau
- Elevate dashboard in distributed diagnostics documentation (GH#5239) Martin Durant
- Updates "add" layer in HLG docs example (GH#5237) James Bourbeau
- Update GUFunc documentation (GH#5232) Matthew Rocklin

3.21.6 2.2.0 / 2019-08-01

Array

- Use da.from_array(..., asarray=False) if input follows NEP-18 (GH#5074) Matthew Rocklin
- Add missing attributes to from_array documentation (GH#5108) Peter Andreas Entschev
- Fix meta computation for some reduction functions (GH#5035) Peter Andreas Entschev
- Raise informative error in to_zarr if unknown chunks (GH#5148) James Bourbeau
- Remove invalid pad tests (GH#5122) Tom Augspurger
- Ignore NumPy warnings in compute_meta (GH#5103) Peter Andreas Entschev
- Fix kurtosis calc for single dimension input array (GH#5177) @andrethrill
- Support Numpy 1.17 in tests (GH#5192) Matthew Rocklin

Bag

- Supply pool to bag test to resolve intermittent failure (GH#5172) Tom Augspurger

Core

- Base dask on fsspec (GH#5064) (GH#5121) Martin Durant
- Various upstream compatibility fixes (GH#5056) Tom Augspurger
- Make distributed tests optional again. (GH#5128) Elliott Sales de Andrade
- Fix HDFS in dask (GH#5130) Martin Durant
- Ignore some more invalid value warnings. (GH#5140) Elliott Sales de Andrade

DataFrame

- Fix pd.MultiIndex size estimate (GH#5066) Brett Naul
- Generalizing has_known_categories (GH#5090) GALI PREM SAGAR
- Refactor Parquet engine (GH#4995) Richard J Zamora
- Add divide method to series and dataframe (GH#5094) msbrown47

- fix flaky partd test (GH#5111) Tom Augspurger
- Adjust is_dataframe_like to adjust for value_counts change (GH#5143) Tom Augspurger
- Generalize rolling windows to support non-Pandas dataframes (GH#5149) Nick Becker
- Avoid unnecessary aggregation in pivot_table (GH#5173) Daniel Saxton
- Add column names to apply_and_enforce error message (GH#5180) Matthew Rocklin
- Add schema keyword argument to to_parquet (GH#5150) Sarah Bird
- Remove recursion error in accessors (GH#5182) Jim Crist
- Allow fastparquet to handle gather_statistics=False for file lists (GH#5157) Richard J Zamora

Documentation

- Adds NumFOCUS badge to the README (GH#5086) James Bourbeau
- Update developer docs [ci skip] (GH#5093) Jim Crist
- Document DataFrame.set_index computataion behavior Natalya Rapstine
- Use pip install . instead of calling setup.py (GH#5139) Matthias Bussonier
- Close user survey (GH#5147) Tom Augspurger
- Fix Google Calendar meeting link (GH#5155) Loïc Estève
- Add docker image customization example (GH#5171) James Bourbeau
- Update remote-data-services after fsspec (GH#5170) Martin Durant
- Fix typo in spark.rst (GH#5164) Xavier Holt
- Update setup/python docs for async/await API (GH#5163) Matthew Rocklin
- Update Local Storage HPC documentation (GH#5165) Matthew Rocklin

3.21.7 2.1.0 / 2019-07-08

Array

- Add `recompute=` keyword to `svd_compressed` for lower-memory use (GH#5041) Matthew Rocklin
- Change `__array_function__` implementation for backwards compatibility (GH#5043) Ralf Gommers
- Added `dtype` and `shape` kwargs to `apply_along_axis` (GH#3742) Davis Bennett
- Fix reduction with empty tuple axis (GH#5025) Peter Andreas Entschev
- Drop size 0 arrays in `stack` (GH#4978) John A Kirkham

Core

- Removes index keyword from pandas `to_parquet` call (GH#5075) James Bourbeau
- Fixes upstream dev CI build installation (GH#5072) James Bourbeau
- Ensure scalar arrays are not rendered to SVG (GH#5058) Willi Rath
- Environment creation overhaul (GH#5038) Tom Augspurger

- s3fs, moto compatibility (GH#5033) Tom Augspurger
- pytest 5.0 compat (GH#5027) Tom Augspurger

DataFrame

- Fix `compute_meta` recursion in blockwise (GH#5048) Peter Andreas Entschev
- Remove hard dependency on pandas in `get_dummies` (GH#5057) GALI PREM SAGAR
- Check dtypes unchanged when using `DataFrame.assign` (GH#5047) asmith26
- Fix cumulative functions on tables with more than 1 partition (GH#5034) tshatrov
- Handle non-divisible sizes in repartition (GH#5013) George Sakkis
- Handles timestamp and `preserve_index` changes in pyarrow (GH#5018) Richard J Zamora
- Fix undefined `meta` for `str.split(expand=False)` (GH#5022) Brett Naul
- Removed checks used for debugging `merge_asof` (GH#5011) Cody Johnson
- Don't use type when getting accessor in dataframes (GH#4992) Matthew Rocklin
- Add `melt` as a method of Dask DataFrame (GH#4984) Dustin Tindall
- Adds path-like support to `to_hdf` (GH#5003) James Bourbeau

Documentation

- Point to latest K8s setup article in JupyterHub docs (GH#5065) Sean McKenna
- Changes vizualize to visualize (GH#5061) David Brochart
- Fix `from_sequence` typo in delayed best practices (GH#5045) James Bourbeau
- Add user survey link to docs (GH#5026) James Bourbeau
- Fixes typo in optimization docs (GH#5015) James Bourbeau
- Update community meeting information (GH#5006) Tom Augspurger

3.21.8 2.0.0 / 2019-06-25

Array

- Support automatic chunking in da.indices (GH#4981) James Bourbeau
- Err if there are no arrays to stack (GH#4975) John A Kirkham
- Asymmetrical Array Overlap (GH#4863) Michael Eaton
- Dispatch concatenate where possible within dask array (GH#4669) Hameer Abbasi
- Fix tokenization of memmapped numpy arrays on different part of same file (GH#4931) Henry Pinkard
- Preserve NumPy condition in da.asarray to preserve output shape (GH#4945) Alistair Miles
- Expand foo_like_safe usage (GH#4946) Peter Andreas Entschev
- Defer order/casting einsum parameters to NumPy implementation (GH#4914) Peter Andreas Entschev
- Remove numpy warning in moment calculation (GH#4921) Matthew Rocklin

- Fix meta_from_array to support Xarray test suite (GH#4938) Matthew Rocklin
- Cache chunk boundaries for integer slicing (GH#4923) Bruce Merry
- Drop size 0 arrays in concatenate (GH#4167) John A Kirkham
- Raise ValueError if concatenate is given no arrays (GH#4927) John A Kirkham
- Promote types in *concatenate* using *_meta* (GH#4925) John A Kirkham
- Add chunk type to html repr in Dask array (GH#4895) Matthew Rocklin
- **Add Dask Array._meta attribute (GH#4543) Peter Andreas Entschev**
  - Fix _meta slicing of flexible types (GH#4912) Peter Andreas Entschev
  - Minor meta construction cleanup in concatenate (GH#4937) Peter Andreas Entschev
  - Further relax Array meta checks for Xarray (GH#4944) Matthew Rocklin
  - Support meta= keyword in da.from_delayed (GH#4972) Matthew Rocklin
  - Concatenate meta along axis (GH#4977) John A Kirkham
  - Use meta in stack (GH#4976) John A Kirkham
  - Move blockwise_meta to more general compute_meta function (GH#4954) Matthew Rocklin
- Alias .partitions to .blocks attribute of dask arrays (GH#4853) Genevieve Buckley
- Drop outdated *numpy_compat* functions (GH#4850) John A Kirkham
- Allow da.eye to support arbitrary chunking sizes with chunks='auto' (GH#4834) Anderson Banihirwe
- Fix CI warnings in dask.array tests (GH#4805) Tom Augspurger
- Make map_blocks work with drop_axis + block_info (GH#4831) Bruce Merry
- Add SVG image and table in Array._repr_html_ (GH#4794) Matthew Rocklin
- ufunc: avoid __array_wrap__ in favor of __array_function__ (GH#4708) Peter Andreas Entschev
- Ensure trivial padding returns the original array (GH#4990) John A Kirkham
- Test `da.block` with 0-size arrays (GH#4991) John A Kirkham

Core

- **Drop Python 2.7** (GH#4919) Jim Crist
- Quiet dependency installs in CI (GH#4960) Tom Augspurger
- Raise on warnings in tests (GH#4916) Tom Augspurger
- Add a diagnostics extra to setup.py (includes bokeh) (GH#4924) John A Kirkham
- Add newline delimter keyword to OpenFile (GH#4935) btw08
- Overload HighLevelGraphs values method (GH#4918) James Bourbeau
- Add __await__ method to Dask collections (GH#4901) Matthew Rocklin
- Also ignore AttributeErrors which may occur if snappy (not python-snappy) is installed (GH#4908) Mark Bell
- Canonicalize key names in config.rename (GH#4903) Ian Bolliger
- Bump minimum partd to 0.3.10 (GH#4890) Tom Augspurger
- Catch async def SyntaxError (GH#4836) James Bourbeau

- catch IOError in ensure_file (GH#4806) Justin Poehnelt
- Cleanup CI warnings (GH#4798) Tom Augspurger
- Move distributed's parse and format functions to dask.utils (GH#4793) Matthew Rocklin
- Apply black formatting (GH#4983) James Bourbeau
- Package license file in wheels (GH#4988) John A Kirkham

DataFrame

- Add an optional partition_size parameter to repartition (GH#4416) George Sakkis
- merge_asof and prefix_reduction (GH#4877) Cody Johnson
- Allow dataframes to be indexed by dask arrays (GH#4882) Endre Mark Borza
- Avoid deprecated message parameter in pytest.raises (GH#4962) James Bourbeau
- Update test_to_records to test with lengths argument(GH#4515) asmith26
- Remove pandas pinning in Dataframe accessors (GH#4955) Matthew Rocklin
- Fix correlation of series with same names (GH#4934) Philipp S. Sommer
- Map Dask Series to Dask Series (GH#4872) Justin Waugh
- Warn in dd.merge on dtype warning (GH#4917) mcsoini
- Add groupby Covariance/Correlation (GH#4889) Ben Zaitlen
- keep index name with to_datetime (GH#4905) Ian Bolliger
- Add Parallel variance computation for dataframes (GH#4865) Ksenia Bobrova
- Add divmod implementation to arrays and dataframes (GH#4884) Henrique Ribeiro
- Add documentation for dataframe reshape methods (GH#4896) tpanza
- Avoid use of pandas.compat (GH#4881) Tom Augspurger
- Added accessor registration for Series, DataFrame, and Index (GH#4829) Tom Augspurger
- Add read_function keyword to read_json (GH#4810) Richard J Zamora
- Provide full type name in check_meta (GH#4819) Matthew Rocklin
- Correctly estimate bytes per row in read_sql_table (GH#4807) Lijo Jose
- Adding support of non-numeric data to describe() (GH#4791) Ksenia Bobrova
- Scalars for extension dtypes. (GH#4459) Tom Augspurger
- Call head before compute in dd.from_delayed (GH#4802) Matthew Rocklin
- Add support for rolling operations with larger window that partition size in DataFrames with Time-based index (GH#4796) Jorge Pessoa
- Update groupby-apply doc with warning (GH#4800) Tom Augspurger
- Change groupby-ness tests in *_maybe_slice* (GH#4786) Ben Zaitlen
- Add master best practices document (GH#4745) Matthew Rocklin
- Add document for how Dask works with GPUs (GH#4792) Matthew Rocklin
- Add cli API docs (GH#4788) James Bourbeau

- Ensure concat output has coherent dtypes (GH#4692) Guillaume Lemaitre
- Fixes pandas_datareader dependencies installation (GH#4989) James Bourbeau
- Accept pathlib.Path as pattern in read_hdf (GH#3335) Jörg Dietrich

Documentation

- Move CLI API docs to relavant pages (GH#4980) James Bourbeau
- Add to_datetime function to dataframe API docs Matthew Rocklin
- Add documentation entry for dask.array.ma.average (GH#4970) Bouwe Andela
- Add bag.read_avro to bag API docs (GH#4969) James Bourbeau
- Fix typo (GH#4968) mbarkhau
- Docs: Drop support for Python 2.7 (GH#4932) Hugo
- Remove requirement to modify changelog (GH#4915) Matthew Rocklin
- Add documentation about meta column order (GH#4887) Tom Augspurger
- Add documentation note in DataFrame.shift (GH#4886) Tom Augspurger
- Docs: Fix typo (GH#4868) Paweł Kordek
- Put do/don't into boxes for delayed best practice docs (GH#3821) Martin Durant
- Doc fixups (GH#2528) Tom Augspurger
- Add quansight to paid support doc section (GH#4838) Martin Durant
- Add document for custom startup (GH#4833) Matthew Rocklin
- Allow *utils.derive_from* to accept functions, apply across array (GH#4804) Martin Durant
- Add "Avoid Large Partitions" section to best practices (GH#4808) Matthew Rocklin
- Update URL for joblib to new website hosting their doc (GH#4816) Christian Hudon

3.21.9 1.2.2 / 2019-05-08

Array

- Clarify regions kwarg to array.store (GH#4759) Martin Durant
- Add dtype= parameter to da.random.randint (GH#4753) Matthew Rocklin
- Use "row major" rather than "C order" in docstring (GH#4452) @asmith26
- Normalize Xarray datasets to Dask arrays (GH#4756) Matthew Rocklin
- Remove normed keyword in da.histogram (GH#4755) Matthew Rocklin

Bag

- Add key argument to Bag.distinct (GH#4423) Daniel Severo

Core

- Add core dask config file (GH#4774) Matthew Rocklin
- Add core dask config file to MANIFEST.in (GH#4780) James Bourbeau
- Enabling glob with HTTP file-system (GH#3926) Martin Durant
- HTTPFile.seek with whence=1 (GH#4751) Martin Durant
- Remove config key normalization (GH#4742) Jim Crist

DataFrame

- Remove explicit references to Pandas in dask.dataframe.groupby (GH#4778) Matthew Rocklin
- Add support for group_keys kwarg in DataFrame.groupby() (GH#4771) Brian Chu
- Describe doc (GH#4762) Martin Durant
- Remove explicit pandas check in cumulative aggregations (GH#4765) Nick Becker
- Added meta for read_json and test (GH#4588) Abhinav Ralhan
- Add test for dtype casting (GH#4760) Martin Durant
- Document alignment in map_partitions (GH#4757) Jim Crist
- Implement Series.str.split(expand=True) (GH#4744) Matthew Rocklin

Documentation

- Tweaks to develop.rst from trying to run tests (GH#4772) Christian Hudon
- Add document describing phases of computation (GH#4766) Matthew Rocklin
- Point users to Dask-Yarn from spark documentation (GH#4770) Matthew Rocklin
- Update images in delayed doc to remove labels (GH#4768) Martin Durant
- Explain intermediate storage for dask arrays (GH#4025) John A Kirkham
- Specify bash code-block in array best practices (GH#4764) James Bourbeau
- Add array best practices doc (GH#4705) Matthew Rocklin
- Update optimization docs now that cull is not automatic (GH#4752) Matthew Rocklin

3.21.10 1.2.1 / 2019-04-29

Array

- Fix map_blocks with block_info and broadcasting (GH#4737) Bruce Merry
- Make ‘minlength’ keyword argument optional in da.bincount (GH#4684) Genevieve Buckley
- Add support for map_blocks with no array arguments (GH#4713) Bruce Merry
- Add dask.array.trace (GH#4717) Danilo Horta
- Add sizeof support for cupy.ndarray (GH#4715) Peter Andreas Entschev
- Add name kwarg to from_zarr (GH#4663) Michael Eaton

- Add chunks='auto' to from_array (GH#4704) Matthew Rocklin
- Raise TypeError if dask array is given as shape for da.ones, zeros, empty or full (GH#4707) Genevieve Buckley
- Add TileDB backend (GH#4679) Isaiah Norton

Core

- Delay long list arguments (GH#4735) Matthew Rocklin
- Bump to numpy >= 1.13, pandas >= 0.21.0 (GH#4720) Jim Crist
- Remove file "test" (GH#4710) James Bourbeau
- Reenable development build, uses upstream libraries (GH#4696) Peter Andreas Entschev
- Remove assertion in HighLevelGraph constructor (GH#4699) Matthew Rocklin

DataFrame

- Change cum-aggregation last-nonnull-value algorithm (GH#4736) Nick Becker
- Fixup series-groupby-apply (GH#4738) Jim Crist
- Refactor array.percentile and dataframe.quantile to use t-digest (GH#4677) Janne Vuorela
- Allow naive concatenation of sorted dataframes (GH#4725) Matthew Rocklin
- Fix perf issue in dd.Series.isin (GH#4727) Jim Crist
- Remove hard pandas dependency for melt by using methodcaller (GH#4719) Nick Becker
- A few dataframe metadata fixes (GH#4695) Jim Crist
- Add Dataframe.replace (GH#4714) Matthew Rocklin
- Add 'threshold' parameter to pd.DataFrame.dropna (GH#4625) Nathan Matare

Documentation

- Add warning about derived docstrings early in the docstring (GH#4716) Matthew Rocklin
- Create dataframe best practices doc (GH#4703) Matthew Rocklin
- Uncomment dask_sphinx_theme (GH#4728) James Bourbeau
- Fix minor typo fix in a Queue/fire_and_forget example (GH#4709) Matthew Rocklin
- Update from_pandas docstring to match signature (GH#4698) James Bourbeau

3.21.11 1.2.0 / 2019-04-12

Array

- Fixed mean() and moment() on sparse arrays (GH#4525) Peter Andreas Entschev
- Add test for NEP-18. (GH#4675) Hameer Abbasi
- Allow None to say "no chunking" in normalize_chunks (GH#4656) Matthew Rocklin
- Fix limit value in auto_chunks (GH#4645) Matthew Rocklin

Core

- Updated diagnostic bokeh test for compatibility with bokeh>=1.1.0 (GH#4680) Philipp Rudiger
- Adjusts codecov's target/threshold, disable patch (GH#4671) Peter Andreas Entschev
- Always start with empty http buffer, not None (GH#4673) Martin Durant

DataFrame

- Propagate index dtype and name when create dask dataframe from array (GH#4686) Henrique Ribeiro
- Fix ordering of quantiles in describe (GH#4647) gregrf
- Clean up and document rearrange_column_by_tasks (GH#4674) Matthew Rocklin
- Mark some parquet tests xfail (GH#4667) Peter Andreas Entschev
- Fix parquet breakages with arrow 0.13.0 (GH#4668) Martin Durant
- Allow sample to be False when reading CSV from a remote URL (GH#4634) Ian Rose
- Fix timezone metadata inference on parquet load (GH#4655) Martin Durant
- Use is_dataframe/index_like in dd.utils (GH#4657) Matthew Rocklin
- Add min_count parameter to groupby sum method (GH#4648) Henrique Ribeiro
- Correct quantile to handle unsorted quantiles (GH#4650) gregrf

Documentation

- Add delayed extra dependencies to install docs (GH#4660) James Bourbeau

3.21.12 1.1.5 / 2019-03-29

Array

- Ensure that we use the dtype keyword in normalize_chunks (GH#4646) Matthew Rocklin

Core

- Use recursive glob in LocalFileSystem (GH#4186) Brett Naul
- Avoid YAML deprecation (GH#4603)
- Fix CI and add set -e (GH#4605) James Bourbeau
- Support builtin sequence types in dask.visualize (GH#4602)
- unpack/repack orderedDict (GH#4623) Justin Poehnelt
- Add da.random.randint to API docs (GH#4628) James Bourbeau
- Add zarr to CI environment (GH#4604) James Bourbeau
- Enable codecov (GH#4631) Peter Andreas Entschev

DataFrame

- Support setting the index (GH#4565)
- DataFrame.itertuples accepts index, name kwargs (GH#4593) Dan O'Donovan
- Support non-Pandas series in dd.Series.unique (GH#4599) Ben Zaitlen
- Replace use of explicit type check with ._is_partition_type predicate (GH#4533)
- Remove additional pandas warnings in tests (GH#4576)
- Check object for name/dtype attributes rather than type (GH#4606)
- Fix comparison against pd.Series (GH#4613) amerkel2
- Fixing warning from setting categorical codes to floats (GH#4624) Julia Signell
- Fix renaming on index to_frame method (GH#4498) Henrique Ribeiro
- Fix divisions when joining two single-partition dataframes (GH#4636) Justin Waugh
- Warn if partitions overlap in compute_divisions (GH#4600) Brian Chu
- Give informative meta= warning (GH#4637) Matthew Rocklin
- Add informative error message to Series.__getitem__ (GH#4638) Matthew Rocklin
- Add clear exception message when using index or index_col in read_csv (GH#4651) Álvaro Abella Bascarán

Documentation

- Add documentation for custom groupby aggregations (GH#4571)
- Docs dataframe joins (GH#4569)
- Specify fork-based contributions (GH#4619) James Bourbeau
- correct to_parquet example in docs (GH#4641) Aaron Fowles
- Update and secure several references (GH#4649) Søren Fuglede Jørgensen

3.21.13 1.1.4 / 2019-03-08

Array

- Use mask selection in compress (GH#4548) John A Kirkham
- Use *asarray* in *extract* (GH#4549) John A Kirkham
- Use correct dtype when test concatenation. (GH#4539) Elliott Sales de Andrade
- Fix CuPy tests or properly marks as xfail (GH#4564) Peter Andreas Entschev

Core

- Fix local scheduler callback to deal with custom caching (GH#4542) Yu Feng
- Use parse_bytes in read_bytes(sample=. . .) (GH#4554) Matthew Rocklin

DataFrame

- Fix up groupby-standard deviation again on object dtype keys (GH#4541) Matthew Rocklin
- TST/CI: Updates for pandas 0.24.1 (GH#4551) Tom Augspurger
- Add ability to control number of unique elements in timeseries (GH#4557) Matthew Rocklin
- Add support in read_csv for parameter skiprows for other iterables (GH#4560) @JulianWgs

Documentation

- DataFrame to Array conversion and unknown chunks (GH#4516) Scott Sievert
- Add docs for random array creation (GH#4566) Matthew Rocklin
- Fix typo in docstring (GH#4572) Shyam Saladi

3.21.14 1.1.3 / 2019-03-01

Array

- Modify mean chunk functions to return dicts rather than arrays (GH#4513) Matthew Rocklin
- Change sparse installation in CI for NumPy/Python2 compatibility (GH#4537) Matthew Rocklin

DataFrame

- Make merge dispatchable on pandas/other dataframe types (GH#4522) Matthew Rocklin
- read_sql_table - datetime index fix and index type checking (GH#4474) Joe Corbett
- Use generalized form of index checking (is_index_like) (GH#4531) Ben Zaitlen
- Add tests for groupby reductions with object dtypes (GH#4535) Matthew Rocklin
- Fixes #4467 : Updates time_series for pandas deprecation (GH#4530) @HSR05

Documentation

- Add missing method to documentation index (GH#4528) Bart Broere

3.21.15 1.1.2 / 2019-02-25

Array

- Fix another unicode/mixed-type edge case in normalize_array (GH#4489) Marco Neumann
- Add dask.array.diagonal (GH#4431) Danilo Horta
- Call asanyarray in unify_chunks (GH#4506) Jim Crist
- Modify moment chunk functions to return dicts (GH#4519) Peter Andreas Entschev

Bag

- Don't inline output keys in dask.bag (GH#4464) Jim Crist
- Ensure that bag.from_sequence always includes at least one partition (GH#4475) Anderson Banihirwe
- Implement out_type for bag.fold (GH#4502) Matthew Rocklin
- Remove map from bag keynames (GH#4500) Matthew Rocklin
- Avoid itertools.repeat in map_partitions (GH#4507) Matthew Rocklin

DataFrame

- Fix relative path parsing on windows when using fastparquet (GH#4445) Janne Vuorela
- Fix bug in pyarrow and hdfs (GH#4453) (GH#4455) Michał Jastrzębski
- df getitem with integer slices is not implemented (GH#4466) Jim Crist
- Replace cudf-specific code with dask-cudf import (GH#4470) Matthew Rocklin
- Avoid groupby.agg(callable) in groupby-var (GH#4482) Matthew Rocklin
- Consider uint types as numerical in check_meta (GH#4485) Marco Neumann
- Fix some typos in groupby comments (GH#4494) Daniel Saxton
- Add error message around set_index(inplace=True) (GH#4501) Matthew Rocklin
- meta_nonempty works with categorical index (GH#4505) Jim Crist
- Add module name to expected meta error message (GH#4499) Matthew Rocklin
- groupby-nunique works on empty chunk (GH#4504) Jim Crist
- Propogate index metadata if not specified (GH#4509) Jim Crist

Documentation

- Update docs to use `from_zarr` (GH#4472) John A Kirkham
- DOC: add section of *Using Other S3-Compatible Services* for remote-data-services (GH#4405) Aploium
- Fix header level of section in changelog (GH#4483) Bruce Merry
- Add quotes to pip install [skip-ci] (GH#4508) James Bourbeau

Core

- Extend started_cbs AFTER state is initialized (GH#4460) Marco Neumann
- Fix bug in HTTPFile._fetch_range with headers (GH#4479) (GH#4480) Ross Petchler
- Repeat optimize_blockwise for diamond fusion (GH#4492) Matthew Rocklin

3.21.16 1.1.1 / 2019-01-31

Array

- Add support for cupy.einsum (GH#4402) Johnnie Gray
- Provide byte size in chunks keyword (GH#4434) Adam Beberg
- Raise more informative error for histogram bins and range (GH#4430) James Bourbeau

DataFrame

- Lazily register more cudf functions and move to backends file (GH#4396) Matthew Rocklin
- Fix ORC tests for pyarrow 0.12.0 (GH#4413) Jim Crist
- rearrange_by_column: ensure that shuffle arg defaults to 'disk' if it's None in dask.config (GH#4414) George Sakkis
- Implement filters for _read_pyarrow (GH#4415) George Sakkis
- Avoid checking against types in is_dataframe_like (GH#4418) Matthew Rocklin
- Pass username as 'user' when using pyarrow (GH#4438) Roma Sokolov

Delayed

- Fix DelayedAttr return value (GH#4440) Matthew Rocklin

Documentation

- Use SVG for pipeline graphic (GH#4406) John A Kirkham
- Add doctest-modules to py.test documentation (GH#4427) Daniel Severo

Core

- Work around psutil 5.5.0 not allowing pickling Process objects Janne Vuorela

3.21.17 1.1.0 / 2019-01-18

Array

- Fix the average function when there is a masked array (GH#4236) Damien Garaud
- Add allow_unknown_chunksizes to hstack and vstack (GH#4287) Paul Vecchio
- Fix tensordot for 27+ dimensions (GH#4304) Johnnie Gray
- Fixed block_info with axes. (GH#4301) Tom Augspurger
- Use safe_wraps for matmul (GH#4346) Mark Harfouche
- Use chunks="auto" in array creation routines (GH#4354) Matthew Rocklin
- Fix np.matmul in dask.array.Array.__array_ufunc__ (GH#4363) Stephan Hoyer

- COMPAT: Re-enable multifield copy->view change (GH#4357) Diane Trout
- Calling np.dtype on a delayed object works (GH#4387) Jim Crist
- Rework normalize_array for numpy data (GH#4312) Marco Neumann

DataFrame

- Add fill_value support for series comparisons (GH#4250) James Bourbeau
- Add schema name in read_sql_table for empty tables (GH#4268) Mina Farid
- Adjust check for bad chunks in map_blocks (GH#4308) Tom Augspurger
- Add dask.dataframe.read_fwf (GH#4316) @slnguyen
- Use atop fusion in dask dataframe (GH#4229) Matthew Rocklin
- Use parallel_types() in from_pandas (GH#4331) Matthew Rocklin
- Change DataFrame._repr_data to method (GH#4330) Matthew Rocklin
- Install pyarrow fastparquet for Appveyor (GH#4338) Gábor Lipták
- Remove explicit pandas checks and provide cudf lazy registration (GH#4359) Matthew Rocklin
- Replace isinstance(. . . , pandas) with is_dataframe_like (GH#4375) Matthew Rocklin
- ENH: Support 3rd-party ExtensionArrays (GH#4379) Tom Augspurger
- Pandas 0.24.0 compat (GH#4374) Tom Augspurger

Documentation

- Fix link to ‘map_blocks’ function in array api docs (GH#4258) David Hoese
- Add a paragraph on Dask-Yarn in the cloud docs (GH#4260) Jim Crist
- Copy edit documentation (GH#4267), (GH#4263), (GH#4262), (GH#4277), (GH#4271), (GH#4279), (GH#4265), (GH#4295), (GH#4293), (GH#4296), (GH#4302), (GH#4306), (GH#4318), (GH#4314), (GH#4309), (GH#4317), (GH#4326), (GH#4325), (GH#4322), (GH#4332), (GH#4333), Miguel Farrajota
- Fix typo in code example (GH#4272) Daniel Li
- Doc: Update array-api.rst (GH#4259) (GH#4282) Prabakaran Kumaresshan
- Update hpc doc (GH#4266) Guillaume Eynard-Bontemps
- Doc: Replace from_avro with read_avro in documents (GH#4313) Prabakaran Kumaresshan
- Remove reference to “get” scheduler functions in docs (GH#4350) Matthew Rocklin
- Fix typo in docstring (GH#4376) Daniel Saxton
- Added documentation for dask.dataframe.merge (GH#4382) Jendrik Jördening

Core

- Avoid recursion in dask.core.get (GH#4219) Matthew Rocklin
- Remove verbose flag from pytest setup.cfg (GH#4281) Matthew Rocklin
- Support Pytest 4.0 by specifying marks explicitly (GH#4280) Takahiro Kojima

- Add High Level Graphs (GH#4092) Matthew Rocklin
- Fix SerializableLock locked and acquire methods (GH#4294) Stephan Hoyer
- Pin boto3 to earlier version in tests to avoid moto conflict (GH#4276) Martin Durant
- Treat None as missing in config when updating (GH#4324) Matthew Rocklin
- Update Appveyor to Python 3.6 (GH#4337) Gábor Lipták
- Use parse_bytes more liberally in dask.dataframe/bytes/bag (GH#4339) Matthew Rocklin
- Add a better error message when cloudpickle is missing (GH#4342) Mark Harfouche
- Support pool= keyword argument in threaded/multiprocessing get functions (GH#4351) Matthew Rocklin
- Allow updates from arbitrary Mappings in config.update, not only dicts. (GH#4356) Stuart Berg
- Move dask/array/top.py code to dask/blockwise.py (GH#4348) Matthew Rocklin
- Add has_parallel_type (GH#4395) Matthew Rocklin
- CI: Update Appveyor (GH#4381) Tom Augspurger
- Ignore non-readable config files (GH#4388) Jim Crist

3.21.18 1.0.0 / 2018-11-28

Array

- Add nancumsum/nancumprod unit tests (GH#4215) Guido Imperiale

DataFrame

- Add index to to_dask_dataframe docstring (GH#4232) James Bourbeau
- Text and fix when appending categoricals with fastparquet (GH#4245) Martin Durant
- Don’t reread metadata when passing ParquetFile to read_parquet (GH#4247) Martin Durant

Documentation

- Copy edit documentation (GH#4222) (GH#4224) (GH#4228) (GH#4231) (GH#4230) (GH#4234) (GH#4235) (GH#4254) Miguel Farrajota
- Updated doc for the new scheduler keyword (GH#4251) @milesial

Core

- Avoid a few warnings (GH#4223) Matthew Rocklin
- Remove dask.store module (GH#4221) Matthew Rocklin
- Remove AUTHORS.md Jim Crist

3.21.19 0.20.2 / 2018-11-15

Array

- Avoid fusing dependencies of atop reductions (GH#4207) Matthew Rocklin

Dataframe

- Improve memory footprint for dataframe correlation (GH#4193) Damien Garaud
- Add empty DataFrame check to boundary_slice (GH#4212) James Bourbeau

Documentation

- Copy edit documentation (GH#4197) (GH#4204) (GH#4198) (GH#4199) (GH#4200) (GH#4202) (GH#4209) Miguel Farrajota
- Add stats module namespace (GH#4206) James Bourbeau
- Fix link in dataframe documentation (GH#4208) James Bourbeau

3.21.20 0.20.1 / 2018-11-09

Array

- Only allocate the result space in wrapped_pad_func (GH#4153) John A Kirkham
- Generalize expand_pad_width to expand_pad_value (GH#4150) John A Kirkham
- Test da.pad with 2D linear_ramp case (GH#4162) John A Kirkham
- Fix import for broadcast_to. (GH#4168) samc0de
- Rewrite Dask Array's *pad* to add only new chunks (GH#4152) John A Kirkham
- Validate index inputs to atop (GH#4182) Matthew Rocklin

Core

- Dask.config set and get normalize underscores and hyphens (GH#4143) James Bourbeau
- Only subs on core collections, not subclasses (GH#4159) Matthew Rocklin
- Add block_size=0 option to HTTPFileSystem. (GH#4171) Martin Durant
- Add traverse support for dataclasses (GH#4165) Armin Berres
- Avoid optimization on sharedicts without dependencies (GH#4181) Matthew Rocklin
- Update the pytest version for TravisCI (GH#4189) Damien Garaud
- Use key_split rather than funcname in visualize names (GH#4160) Matthew Rocklin

Dataframe

- Add fix for DataFrame.__setitem__ for index (GH#4151) Anderson Banihirwe
- Fix column choice when passing list of files to fastparquet (GH#4174) Martin Durant
- Pass engine_kwargs from read_sql_table to sqlalchemy (GH#4187) Damien Garaud

Documentation

- Fix documentation in Delayed best practices example that returned an empty list (GH#4147) Jonathan Fraine
- Copy edit documentation (GH#4164) (GH#4175) (GH#4185) (GH#4192) (GH#4191) (GH#4190) (GH#4180) Miguel Farrajota
- Fix typo in docstring (GH#4183) Carlos Valiente

3.21.21 0.20.0 / 2018-10-26

Array

- Fuse Atop operations (GH#3998), (GH#4081) Matthew Rocklin
- Support da.asanyarray on dask dataframes (GH#4080) Matthew Rocklin
- Remove unnecessary endianness check in datetime test (GH#4113) Elliott Sales de Andrade
- Set name=False in array foo_like functions (GH#4116) Matthew Rocklin
- Remove dask.array.ghost module (GH#4121) Matthew Rocklin
- Fix use of getargspec in dask array (GH#4125) Stephan Hoyer
- Adds dask.array.invert (GH#4127), (GH#4131) Anderson Banihirwe
- Raise informative error on arg-reduction on unknown chunksize (GH#4128), (GH#4135) Matthew Rocklin
- Normalize reversed slices in dask array (GH#4126) Matthew Rocklin

Bag

- Add bag.to_avro (GH#4076) Martin Durant

Core

- Pull num_workers from config.get (GH#4086), (GH#4093) James Bourbeau
- Fix invalid escape sequences with raw strings (GH#4112) Elliott Sales de Andrade
- Raise an error on the use of the get= keyword and set_options (GH#4077) Matthew Rocklin
- Add import for Azure DataLake storage, and add docs (GH#4132) Martin Durant
- Avoid collections.Mapping/Sequence (GH#4138) Matthew Rocklin

Dataframe

- Include index keyword in to_dask_dataframe (GH#4071) Matthew Rocklin
- add support for duplicate column names (GH#4087) Jan Koch
- Implement min_count for the DataFrame methods sum and prod (GH#4090) Bart Broere
- Remove pandas warnings in concat (GH#4095) Matthew Rocklin
- DataFrame.to_csv header option to only output headers in the first chunk (GH#3909) Rahul Vaidya
- Remove Series.to_parquet (GH#4104) Justin Dennison
- Avoid warnings and deprecated pandas methods (GH#4115) Matthew Rocklin
- Swap 'old' and 'previous' when reporting append error (GH#4130) Martin Durant

Documentation

- Copy edit documentation (GH#4073), (GH#4074), (GH#4094), (GH#4097), (GH#4107), (GH#4124), (GH#4133), (GH#4139) Miguel Farrajota
- Fix typo in code example (GH#4089) Antonino Ingargiola
- Add pycon 2018 presentation (GH#4102) Javad
- Quick description for gcsfs (GH#4109) Martin Durant
- Fixed typo in docstrings of read_sql_table method (GH#4114) TakaakiFuruse
- Make target directories in redirects if they don't exist (GH#4136) Matthew Rocklin

3.21.22 0.19.4 / 2018-10-09

Array

- Implement `apply_gufunc(..., axes=..., keepdims=...)` (GH#3985) Markus Gonser

Bag

- Fix typo in datasets.make_people (GH#4069) Matthew Rocklin

Dataframe

- Added *percentiles* options for *dask.dataframe.describe* method (GH#4067) Zhenqing Li
- Add DataFrame.partitions accessor similar to Array.blocks (GH#4066) Matthew Rocklin

Core

- Pass get functions and Clients through scheduler keyword (GH#4062) Matthew Rocklin

Documentation

- Fix Typo on hpc example. (missing = in kwarg). (GH#4068) Matthias Bussonier
- Extensive copy-editing: (GH#4065), (GH#4064), (GH#4063) Miguel Farrajota

3.21.23 0.19.3 / 2018-10-05

Array

- Make da.RandomState extensible to other modules (GH#4041) Matthew Rocklin
- Support unknown dims in ravel no-op case (GH#4055) Jim Crist
- Add basic infrastructure for cupy (GH#4019) Matthew Rocklin
- Avoid asarray and lock arguments for from_array(getitem) (GH#4044) Matthew Rocklin
- Move local imports in *corrcoef* to global imports (GH#4030) John A Kirkham
- Move local *indices* import to global import (GH#4029) John A Kirkham
- Fix-up Dask Array's fromfunction w.r.t. dtype and kwargs (GH#4028) John A Kirkham
- Don't use dummy expansion for trim_internal in overlapped (GH#3964) Mark Harfouche
- Add unravel_index (GH#3958) John A Kirkham

Bag

- Sort result in Bag.frequencies (GH#4033) Matthew Rocklin
- Add support for npartitions=1 edge case in groupby (GH#4050) James Bourbeau
- Add new random dataset for people (GH#4018) Matthew Rocklin
- Improve performance of bag.read_text on small files (GH#4013) Eric Wolak
- Add bag.read_avro (GH#4000) (GH#4007) Martin Durant

Dataframe

- Added an `index` parameter to `dask.dataframe.from_dask_array()` for creating a dask DataFrame from a dask Array with a given index. (GH#3991) Tom Augspurger
- Improve sub-classability of dask dataframe (GH#4015) Matthew Rocklin
- Fix failing hdfs test [test-hdfs] (GH#4046) Jim Crist
- fuse_subgraphs works without normal fuse (GH#4042) Jim Crist
- Make path for reading many parquet files without prescan (GH#3978) Martin Durant
- Index in dd.from_dask_array (GH#3991) Tom Augspurger
- Making skiprows accept lists (GH#3975) Julia Signell
- Fail early in fastparquet read for nonexistent column (GH#3989) Martin Durant

Core

- Add support for npartitions=1 edge case in groupby (GH#4050) James Bourbeau
- Automatically wrap large arguments with dask.delayed in map_blocks/partitions (GH#4002) Matthew Rocklin
- Fuse linear chains of subgraphs (GH#3979) Jim Crist
- Make multiprocessing context configurable (GH#3763) Itamar Turner-Trauring

Documentation

- Extensive copy-editing (GH#4049), (GH#4034), (GH#4031), (GH#4020), (GH#4021), (GH#4022), (GH#4023), (GH#4016), (GH#4017), (GH#4010), (GH#3997), (GH#3996), Miguel Farrajota
- Update shuffle method selection docs (GH#4048) James Bourbeau
- Remove docs/source/examples, point to examples.dask.org (GH#4014) Matthew Rocklin
- Replace readthedocs links with dask.org (GH#4008) Matthew Rocklin
- Updates DataFrame.to_hdf docstring for returned values (GH#3992) James Bourbeau

3.21.24 0.19.2 / 2018-09-17

Array

- `apply_gufunc` implements automatic infer of functions output dtypes (GH#3936) Markus Gonser
- Fix array histogram range error when array has nans (GH#3980) James Bourbeau
- Issue 3937 follow up, int type checks. (GH#3956) Yu Feng
- from_array: add @martindurant's explaining of how hashing is done for an array. (GH#3965) Mark Harfouche
- Support gradient with coordinate (GH#3949) Keisuke Fujii

Core

- Fix use of has_keyword with partial in Python 2.7 (GH#3966) Mark Harfouche
- Set pyarrow as default for HDFS (GH#3957) Matthew Rocklin

Documentation

- Use dask_sphinx_theme (GH#3963) Matthew Rocklin
- Use JupyterLab in Binder links from main page Matthew Rocklin
- DOC: fixed sphinx syntax (GH#3960) Tom Augspurger

3.21.25 0.19.1 / 2018-09-06

Array

- Don't enforce dtype if result has no dtype (GH#3928) Matthew Rocklin

- Fix NumPy issubtype deprecation warning (GH#3939) Bruce Merry
- Fix arg reduction tokens to be unique with different arguments (GH#3955) Tobias de Jong
- Coerce numpy integers to ints in slicing code (GH#3944) Yu Feng
- Linalg.norm ndim along axis partial fix (GH#3933) Tobias de Jong

Dataframe

- Deterministic DataFrame.set_index (GH#3867) George Sakkis
- Fix divisions in read_parquet when dealing with filters #3831 #3930 (GH#3923) (GH#3931) @andrethrill
- Fixing returning type in categorical.as_known (GH#3888) Sriharsha Hatwar
- Fix DataFrame.assign for callables (GH#3919) Tom Augspurger
- Include partitions with no width in repartition (GH#3941) Matthew Rocklin
- Don't constrict stage/k dtype in dataframe shuffle (GH#3942) Matthew Rocklin

Documentation

- DOC: Add hint on how to render task graphs horizontally (GH#3922) Uwe Korn
- Add try-now button to main landing page (GH#3924) Matthew Rocklin

3.21.26 0.19.0 / 2018-08-29

Array

- Support coordinate in gradient (GH#3949) Keisuke Fujii
- Fix argtopk split_every bug (GH#3810) Guido Imperiale
- Ensure result computing dask.array.isnull() always gives a numpy array (GH#3825) Stephan Hoyer
- Support concatenate for scipy.sparse in dask array (GH#3836) Matthew Rocklin
- Fix argtopk on 32-bit systems. (GH#3823) Elliott Sales de Andrade
- Normalize keys in rechunk (GH#3820) Matthew Rocklin
- Allow shape of dask.array to be a numpy array (GH#3844) Mark Harfouche
- Fix numpy deprecation warning on tuple indexing (GH#3851) Tobias de Jong
- Rename ghost module to overlap (GH#3830) Robert Sare
- Re-add the ghost import to da __init__ (GH#3861) Jim Crist
- Ensure copy preserves masked arrays (GH#3852) Tobias de Jong

DataFrame

- Added `dtype` and `sparse` keywords to `dask.dataframe.get_dummies()` (GH#3792) Tom Augspurger
- Added `dask.dataframe.to_dask_array()` for converting a Dask Series or DataFrame to a Dask Array, possibly with known chunk sizes (GH#3884) *Tom Augspurger*

- Changed the behavior for `dask.array.asarray()` for dask dataframe and series inputs. Previously, the series was eagerly converted to an in-memory NumPy array before creating a dask array with known chunks sizes. This caused unexpectedly high memory usage. Now, no intermediate NumPy array is created, and a Dask array with unknown chunk sizes is returned (GH#3884) *Tom Augspurger*
- DataFrame.iloc (GH#3805) Tom Augspurger
- When reading multiple paths, expand globs. (GH#3828) Irina Truong
- Added index column name after resample (GH#3833) Eric Bonfadini
- Add (lazy) shape property to dataframe and series (GH#3212) Henrique Ribeiro
- Fix failing hdfs test [test-hdfs] (GH#3858) Jim Crist
- Fixes for pyarrow 0.10.0 release (GH#3860) Jim Crist
- Rename to_csv keys for diagnostics (GH#3890) Matthew Rocklin
- Match pandas warnings for concat sort (GH#3897) Tom Augspurger
- Include filename in read_csv (GH#3908) Julia Signell

Core

- Better error message on import when missing common dependencies (GH#3771) Danilo Horta
- Drop Python 3.4 support (GH#3840) Jim Crist
- Remove expired deprecation warnings (GH#3841) Jim Crist
- Add DASK_ROOT_CONFIG environment variable (GH#3849) Joe Hamman
- Don't cull in local scheduler, do cull in delayed (GH#3856) Jim Crist
- Increase conda download retries (GH#3857) Jim Crist
- Add python_requires and Trove classifiers (GH#3855) @hugovk
- Fix collections.abc deprecation warnings in Python 3.7.0 (GH#3876) Jan Margeta
- Allow dot jpeg to xfail in visualize tests (GH#3896) Matthew Rocklin
- Add Python 3.7 to travis.yml (GH#3894) Matthew Rocklin
- Add expand_environment_variables to dask.config (GH#3893) Joe Hamman

Docs

- Fix typo in import statement of diagnostics (GH#3826) John Mrziglod
- Add link to YARN docs (GH#3838) Jim Crist
- fix of minor typos in landing page index.html (GH#3746) Christoph Moehl
- Update delayed-custom.rst (GH#3850) Anderson Banihirwe
- DOC: clarify delayed docstring (GH#3709) Scott Sievert
- Add new presentations (GH#3880) Javad
- Add dask array normalize_chunks to documentation (GH#3878) Daniel Rothenberg
- Docs: Fix link to snakeviz (GH#3900) Hans Moritz Günther
- Add missing ' to docstring (GH#3915) @rtobar

3.21.27 0.18.2 / 2018-07-23

Array

- Reimplemented `argtopk` to make it release the GIL (GH#3610) Guido Imperiale
- Don't overlap on non-overlapped dimensions in `map_overlap` (GH#3653) Matthew Rocklin
- Fix `linalg.tsqr` for dimensions of uncertain length (GH#3662) Jeremy Chen
- Break apart uneven array-of-int slicing to separate chunks (GH#3648) Matthew Rocklin
- Align auto chunks to provided chunks, rather than shape (GH#3679) Matthew Rocklin
- Adds endpoint and retstep support for linspace (GH#3675) James Bourbeau
- Implement `.blocks` accessor (GH#3689) Matthew Rocklin
- Add `block_info` keyword to `map_blocks` functions (GH#3686) Matthew Rocklin
- Slice by dask array of ints (GH#3407) Guido Imperiale
- Support `dtype` in `arange` (GH#3722) Guido Imperiale
- Fix `argtopk` with uneven chunks (GH#3720) Guido Imperiale
- Raise error when `replace=False` in `da.choice` (GH#3765) James Bourbeau
- Update chunks in `Array.__setitem__` (GH#3767) Itamar Turner-Trauring
- Add a `chunksize` convenience property (GH#3777) Jacob Tomlinson
- Fix and simplify array slicing behavior when `step < 0` (GH#3702) Ziyao Wei
- Ensure `to_zarr` with `return_stored` `True` returns a Dask Array (GH#3786) John A Kirkham

Bag

- Add `last_endline` optional parameter in `to_textfiles` (GH#3745) George Sakkis

Dataframe

- Add aggregate function for rolling objects (GH#3772) Gerome Pistre
- Properly tokenize cumulative groupby aggregations (GH#3799) Cloves Almeida

Delayed

- Add the `@` operator to the delayed objects (GH#3691) Mark Harfouche
- Add delayed best practices to documentation (GH#3737) Matthew Rocklin
- Fix `@delayed` decorator for methods and add tests (GH#3757) Ziyao Wei

Core

- Fix extra progressbar (GH#3669) Mike Neish
- Allow tasks back onto ordering stack if they have one dependency (GH#3652) Matthew Rocklin
- Prefer end-tasks with low numbers of dependencies when ordering (GH#3588) Tom Augspurger

- Add `assert_eq` to top-level modules (GH#3726) Matthew Rocklin
- Test that dask collections can hold `scipy.sparse` arrays (GH#3738) Matthew Rocklin
- Fix setup of lz4 decompression functions (GH#3782) Elliott Sales de Andrade
- Add datasets module (GH#3780) Matthew Rocklin

3.21.28 0.18.1 / 2018-06-22

Array

- `from_array` now supports scalar types and nested lists/tuples in input, just like all numpy functions do; it also produces a simpler graph when the input is a plain ndarray (GH#3568) Guido Imperiale
- Fix slicing of big arrays due to cumsum dtype bug (GH#3620) Marco Rossi
- Add Dask Array implementation of pad (GH#3578) John A Kirkham
- Fix array random API examples (GH#3625) James Bourbeau
- Add average function to dask array (GH#3640) James Bourbeau
- Tokenize ghost_internal with axes (GH#3643) Matthew Rocklin
- Add outer for Dask Arrays (GH#3658) John A Kirkham

DataFrame

- Add Index.to_series method (GH#3613) Henrique Ribeiro
- Fix missing partition columns in pyarrow-parquet (GH#3636) Martin Durant

Core

- Minor tweaks to CI (GH#3629) Guido Imperiale
- Add back dask.utils.effective_get (GH#3642) Matthew Rocklin
- DASK_CONFIG dictates config write location (GH#3621) Jim Crist
- Replace 'collections' key in unpack_collections with unique key (GH#3632) Yu Feng
- Avoid deepcopy in dask.config.set (GH#3649) Matthew Rocklin

3.21.29 0.18.0 / 2018-06-14

Array

- Add to/from_zarr for Zarr-format datasets and arrays (GH#3460) Martin Durant
- Experimental addition of generalized ufunc support, `apply_gufunc`, `gufunc`, and `as_gufunc` (GH#3109) (GH#3526) (GH#3539) Markus Gonser
- Avoid unnecessary rechunking tasks (GH#3529) Matthew Rocklin
- Compute dtypes at runtime for fft (GH#3511) Matthew Rocklin
- Generate UUIDs for all da.store operations (GH#3540) Martin Durant

- Correct internal dimension of Dask's SVD (GH#3517) John A Kirkham
- BUG: do not raise IndexError for identity slice in array.vindex (GH#3559) Scott Sievert
- Adds *isneginf* and *isposinf* (GH#3581) John A Kirkham
- Drop Dask Array's *learn* module (GH#3580) John A Kirkham
- added sfqr (short-and-fat) as a counterpart to tsqr… (GH#3575) Jeremy Chen
- Allow 0-width chunks in dask.array.rechunk (GH#3591) Marc Pfister
- Document Dask Array's *nan_to_num* in public API (GH#3599) John A Kirkham
- Show block example (GH#3601) John A Kirkham
- Replace token= keyword with name= in map_blocks (GH#3597) Matthew Rocklin
- Disable locking in to_zarr (needed for using to_zarr in a distributed context) (GH#3607) John A Kirkham
- Support Zarr Arrays in *to_zarr*/*from_zarr* (GH#3561) John A Kirkham
- Added recursion to array/linalg/tsqr to better manage the single core bottleneck (GH#3586) Jeremy Chan (GH#3396) Guido Imperiale

Dataframe

- Add to/read_json (GH#3494) Martin Durant
- Adds `index` to unsupported arguments for `DataFrame.rename` method (GH#3522) James Bourbeau
- Adds support to subset Dask DataFrame columns using `numpy.ndarray`, `pandas.Series`, and `pandas.Index` objects (GH#3536) James Bourbeau
- Raise error if meta columns do not match dataframe (GH#3485) Christopher Ren
- Add index to unsupprted argument for DataFrame.rename (GH#3522) James Bourbeau
- Adds support for subsetting DataFrames with pandas Index/Series and numpy ndarrays (GH#3536) James Bourbeau
- Dataframe sample method docstring fix (GH#3566) James Bourbeau
- fixes dd.read_json to infer file compression (GH#3594) Matt Lee
- Adds n to sample method (GH#3606) James Bourbeau
- Add fastparquet ParquetFile object support (GH#3573) @andrethrill

Bag

- Rename method= keyword to shuffle= in bag.groupby (GH#3470) Matthew Rocklin

Core

- Replace get= keyword with scheduler= keyword (GH#3448) Matthew Rocklin
- Add centralized dask.config module to handle configuration for all Dask subprojects (GH#3432) (GH#3513) (GH#3520) Matthew Rocklin
- Add *dask-ssh* CLI Options and Description. (GH#3476) @beomi
- Read whole files fix regardless of header for HTTP (GH#3496) Martin Durant

- Adds synchronous scheduler syntax to debugging docs (GH#3509) James Bourbeau
- Replace dask.set_options with dask.config.set (GH#3502) Matthew Rocklin
- Update sphinx readthedocs-theme (GH#3516) Matthew Rocklin
- Introduce "auto" value for normalize_chunks (GH#3507) Matthew Rocklin
- Fix check in configuration with env=None (GH#3562) Simon Perkins
- Update sizeof definitions (GH#3582) Matthew Rocklin
- Remove –verbose flag from travis-ci (GH#3477) Matthew Rocklin
- Remove "da.random" from random array keys (GH#3604) Matthew Rocklin

3.21.30 0.17.5 / 2018-05-16

Array

- Fix `rechunk` with chunksize of -1 in a dict (GH#3469) Stephan Hoyer
- `einsum` now accepts the `split_every` parameter (GH#3471) Guido Imperiale
- Improved slicing performance (GH#3479) Yu Feng

DataFrame

- Compatibility with pandas 0.23.0 (GH#3499) Tom Augspurger

3.21.31 0.17.4 / 2018-05-03

Dataframe

- Add support for indexing Dask DataFrames with string subclasses (GH#3461) James Bourbeau
- Allow using both sorted_index and chunksize in read_hdf (GH#3463) Pierre Bartet
- Pass filesystem to arrow piece reader (GH#3466) Martin Durant
- Switches to using dask.compat string_types (GH#3462) James Bourbeau

3.21.32 0.17.3 / 2018-05-02

Array

- Add `einsum` for Dask Arrays (GH#3412) Simon Perkins
- Add `piecewise` for Dask Arrays (GH#3350) John A Kirkham
- Fix handling of `nan` in `broadcast_shapes` (GH#3356) John A Kirkham
- Add `isin` for dask arrays (GH#3363). Stephan Hoyer
- Overhauled `topk` for Dask Arrays: faster algorithm, particularly for large k's; added support for multiple axes, recursive aggregation, and an option to pick the bottom k elements instead. (GH#3395) Guido Imperiale
- The `topk` API has changed from topk(k, array) to the more conventional topk(array, k). The legacy API still works but is now deprecated. (GH#2965) Guido Imperiale

- New function `argtopk` for Dask Arrays (GH#3396) Guido Imperiale
- Fix handling partial depth and boundary in `map_overlap` (GH#3445) John A Kirkham
- Add `gradient` for Dask Arrays (GH#3434) John A Kirkham

DataFrame

- Allow *t* as shorthand for *table* in *to_hdf* for pandas compatibility (GH#3330) Jörg Dietrich
- Added top level *isna* method for Dask DataFrames (GH#3294) Christopher Ren
- Fix selection on partition column on `read_parquet` for `engine="pyarrow"` (GH#3207) Uwe Korn
- Added DataFrame.squeeze method (GH#3366) Christopher Ren
- Added *infer_divisions* option to `read_parquet` to specify whether read engines should compute divisions (GH#3387) Jon Mease
- Added support for inferring division for `engine="pyarrow"` (GH#3387) Jon Mease
- Provide more informative error message for meta= errors (GH#3343) Matthew Rocklin
- add orc reader (GH#3284) Martin Durant
- Default compression for parquet now always Snappy, in line with pandas (GH#3373) Martin Durant
- Fixed bug in Dask DataFrame and Series comparisons with NumPy scalars (GH#3436) James Bourbeau
- Remove outdated requirement from repartition docstring (GH#3440) Jörg Dietrich
- Fixed bug in aggregation when only a Series is selected (GH#3446) Jörg Dietrich
- Add default values to make_timeseries (GH#3421) Matthew Rocklin

Core

- Support traversing collections in persist, visualize, and optimize (GH#3410) Jim Crist
- Add schedule= keyword to compute and persist. This replaces common use of the get= keyword (GH#3448) Matthew Rocklin

3.21.33 0.17.2 / 2018-03-21

Array

- Add `broadcast_arrays` for Dask Arrays (GH#3217) John A Kirkham
- Add `bitwise_*` ufuncs (GH#3219) John A Kirkham
- Add optional `axis` argument to `squeeze` (GH#3261) John A Kirkham
- Validate inputs to atop (GH#3307) Matthew Rocklin
- Avoid calls to astype in concatenate if all parts have the same dtype (GH#3301) Martin Durant

DataFrame

- Fixed bug in shuffle due to aggressive truncation (GH#3201) Matthew Rocklin
- Support specifying categorical columns on `read_parquet` with `categories=[...]` for `engine="pyarrow"` (GH#3177) Uwe Korn
- Add `dd.tseries.Resampler.agg` (GH#3202) Richard Postelnik
- Support operations that mix dataframes and arrays (GH#3230) Matthew Rocklin
- Support extra Scalar and Delayed args in `dd.groupby._Groupby.apply` (GH#3256) Gabriele Lanaro

Bag

- Support joining against single-partitioned bags and delayed objects (GH#3254) Matthew Rocklin

Core

- Fixed bug when using unexpected but hashable types for keys (GH#3238) Daniel Collins
- Fix bug in task ordering so that we break ties consistently with the key name (GH#3271) Matthew Rocklin
- Avoid sorting tasks in order when the number of tasks is very large (GH#3298) Matthew Rocklin

3.21.34 0.17.1 / 2018-02-22

Array

- Corrected dimension chunking in indices (GH#3166, GH#3167) Simon Perkins
- Inline `store_chunk` calls for `store`'s `return_stored` option (GH#3153) John A Kirkham
- Compatibility with struct dtypes for NumPy 1.14.1 release (GH#3187) Matthew Rocklin

DataFrame

- Bugfix to allow column assignment of pandas datetimes(GH#3164) Max Epstein

Core

- New file-system for HTTP(S), allowing direct loading from specific URLs (GH#3160) Martin Durant
- Fix bug when tokenizing partials with no keywords (GH#3191) Matthew Rocklin
- Use more recent LZ4 API (GH#3157) Thrasibule
- Introduce output stream parameter for progress bar (GH#3185) Dieter Weber

3.21.35 0.17.0 / 2018-02-09

Array

- Added a support object-type arrays for nansum, nanmin, and nanmax (GH#3133) Keisuke Fujii
- Update error handling when len is called with empty chunks (GH#3058) Xander Johnson
- Fixes a metadata bug with `store`'s `return_stored` option (GH#3064) John A Kirkham
- Fix a bug in `optimization.fuse_slice` to properly handle when first input is `None` (GH#3076) James Bourbeau
- Support arrays with unknown chunk sizes in percentile (GH#3107) Matthew Rocklin
- Tokenize scipy.sparse arrays and np.matrix (GH#3060) Roman Yurchak

DataFrame

- Support month timedeltas in repartition(freq=. . .) (GH#3110) Matthew Rocklin
- Avoid mutation in dataframe groupby tests (GH#3118) Matthew Rocklin
- `read_csv`, `read_table`, and `read_parquet` accept iterables of paths (GH#3124) Jim Crist
- Deprecates the `dd.to_delayed` *function* in favor of the existing method (GH#3126) Jim Crist
- Return dask.arrays from df.map_partitions calls when the UDF returns a numpy array (GH#3147) Matthew Rocklin
- Change handling of `columns` and `index` in `dd.read_parquet` to be more consistent, especially in handling of multi-indices (GH#3149) Jim Crist
- fastparquet append=True allowed to create new dataset (GH#3097) Martin Durant
- dtype rationalization for sql queries (GH#3100) Martin Durant

Bag

- Document `bag.map_paritions` function may receive either a list or generator. (GH#3150) Nir

Core

- Change default task ordering to prefer nodes with few dependents and then many downstream dependencies (GH#3056) Matthew Rocklin
- Add color= option to visualize to color by task order (GH#3057) (GH#3122) Matthew Rocklin
- Deprecate `dask.bytes.open_text_files` (GH#3077) Jim Crist
- Remove short-circuit hdfs reads handling due to maintenance costs. May be re-added in a more robust manner later (GH#3079) Jim Crist
- Add `dask.base.optimize` for optimizing multiple collections without computing. (GH#3071) Jim Crist
- Rename `dask.optimize` module to `dask.optimization` (GH#3071) Jim Crist
- Change task ordering to do a full traversal (GH#3066) Matthew Rocklin
- Adds an `optimize_graph` keyword to all `to_delayed` methods to allow controlling whether optimizations occur on conversion. (GH#3126) Jim Crist

- Support using `pyarrow` for hdfs integration (GH#3123) Jim Crist
- Move HDFS integration and tests into dask repo (GH#3083) Jim Crist
- Remove write_bytes (GH#3116) Jim Crist

3.21.36 0.16.1 / 2018-01-09

Array

- Fix handling of scalar percentile values in `percentile` (GH#3021) James Bourbeau
- Prevent `bool()` coercion from calling compute (GH#2958) Albert DeFusco
- Add `matmul` (GH#2904) John A Kirkham
- Support N-D arrays with `matmul` (GH#2909) John A Kirkham
- Add `vdot` (GH#2910) John A Kirkham
- Explicit `chunks` argument for `broadcast_to` (GH#2943) Stephan Hoyer
- Add `meshgrid` (GH#2938) John A Kirkham and (GH#3001) Markus Gonser
- Preserve singleton chunks in `fftshift/ifftshift` (GH#2733) John A Kirkham
- Fix handling of negative indexes in `vindex` and raise errors for out of bounds indexes (GH#2967) Stephan Hoyer
- Add `flip`, `flipud`, `fliplr` (GH#2954) John A Kirkham
- Add `float_power` ufunc (GH#2962) (GH#2969) John A Kirkham
- Compatability for changes to structured arrays in the upcoming NumPy 1.14 release (GH#2964) Tom Augspurger
- Add `block` (GH#2650) John A Kirkham
- Add `frompyfunc` (GH#3030) Jim Crist
- Add the `return_stored` option to `store` for chaining stored results (GH#2980) John A Kirkham

DataFrame

- Fixed naming bug in cumulative aggregations (GH#3037) Martijn Arts
- Fixed `dd.read_csv` when `names` is given but `header` is not set to `None` (GH#2976) Martijn Arts
- Fixed `dd.read_csv` so that passing instances of `CategoricalDtype` in `dtype` will result in known categoricals (GH#2997) Tom Augspurger
- Prevent `bool()` coercion from calling compute (GH#2958) Albert DeFusco
- `DataFrame.read_sql()` (GH#2928) to an empty database tables returns an empty dask dataframe Apostolos Vlachopoulos
- Compatability for reading Parquet files written by PyArrow 0.8.0 (GH#2973) Tom Augspurger
- Correctly handle the column name (*df.columns.name*) when reading in `dd.read_parquet` (GH#2973) Tom Augspurger
- Fixed `dd.concat` losing the index dtype when the data contained a categorical (GH#2932) Tom Augspurger
- Add `dd.Series.rename` (GH#3027) Jim Crist

- `DataFrame.merge()` now supports merging on a combination of columns and the index (GH#2960) Jon Mease
- Removed the deprecated `dd.rolling*` methods, in preparation for their removal in the next pandas release (GH#2995) Tom Augspurger
- Fix metadata inference bug in which single-partition series were mistakenly special cased (GH#3035) Jim Crist
- Add support for `Series.str.cat` (GH#3028) Jim Crist

Core

- Improve 32-bit compatibility (GH#2937) Matthew Rocklin
- Change task prioritization to avoid upwards branching (GH#3017) Matthew Rocklin

3.21.37 0.16.0 / 2017-11-17

This is a major release. It includes breaking changes, new protocols, and a large number of bug fixes.

Array

- Add `atleast_1d`, `atleast_2d`, and `atleast_3d` (GH#2760) (GH#2765) John A Kirkham
- Add `allclose` (GH#2771) by John A Kirkham
- Remove `random.different_seeds` from Dask Array API docs (GH#2772) John A Kirkham
- Deprecate `vnorm` in favor of `dask.array.linalg.norm` (GH#2773) John A Kirkham
- Reimplement `unique` to be lazy (GH#2775) John A Kirkham
- Support broadcasting of Dask Arrays with 0-length dimensions (GH#2784) John A Kirkham
- Add `asarray` and `asanyarray` to Dask Array API docs (GH#2787) James Bourbeau
- Support `unique`'s `return_*` arguments (GH#2779) John A Kirkham
- Simplify `_unique_internal` (GH#2850) (GH#2855) John A Kirkham
- Avoid removing some getter calls in array optimizations (GH#2826) Jim Crist

DataFrame

- Support `pyarrow` in `dd.to_parquet` (GH#2868) Jim Crist
- Fixed `DataFrame.quantile` and `Series.quantile` returning `nan` when missing values are present (GH#2791) Tom Augspurger
- Fixed `DataFrame.quantile` losing the result `.name` when `q` is a scalar (GH#2791) Tom Augspurger
- Fixed `dd.concat` return a `dask.Dataframe` when concatenating a single series along the columns, matching pandas' behavior (GH#2800) James Munroe
- Fixed default inplace parameter for `DataFrame.eval` to match the pandas defualt for pandas >= 0.21.0 (GH#2838) Tom Augspurger
- Fix exception when calling `DataFrame.set_index` on text column where one of the partitions was empty (GH#2831) Jesse Vogt

- Do not raise exception when calling `DataFrame.set_index` on empty dataframe (GH#2827) Jesse Vogt
- Fixed bug in `Dataframe.fillna` when filling with a `Series` value (GH#2810) Tom Augspurger
- Deprecate old argument ordering in `dd.to_parquet` to better match convention of putting the dataframe first (GH#2867) Jim Crist
- df.astype(categorical_dtype -> known categoricals (GH#2835) Jim Crist
- Test against Pandas release candidate (GH#2814) Tom Augspurger
- Add more tests for read_parquet(engine='pyarrow') (GH#2822) Uwe Korn
- Remove unnecessary map_partitions in aggregate (GH#2712) Christopher Prohm
- Fix bug calling sample on empty partitions (GH#2818) @xwang777
- Error nicely when parsing dates in read_csv (GH#2863) Jim Crist
- Cleanup handling of passing filesystem objects to PyArrow readers (GH#2527) @fjetter
- Support repartitioning even if there are no divisions (GH#2873) @Ced4
- Support reading/writing to hdfs using `pyarrow` in `dd.to_parquet` (GH#2894, GH#2881) Jim Crist

Core

- Allow tuples as sharedict keys (GH#2763) Matthew Rocklin
- Calling compute within a dask.distributed task defaults to distributed scheduler (GH#2762) Matthew Rocklin
- Auto-import gcsfs when gcs:// protocol is used (GH#2776) Matthew Rocklin
- Fully remove dask.async module, use dask.local instead (GH#2828) Thomas Caswell
- Compatability with bokeh 0.12.10 (GH#2844) Tom Augspurger
- Reduce test memory usage (GH#2782) Jim Crist
- Add Dask collection interface (GH#2748) Jim Crist
- Update Dask collection interface during XArray integration (GH#2847) Matthew Rocklin
- Close resource profiler process on __exit__ (GH#2871) Jim Crist
- Fix S3 tests (GH#2875) Jim Crist
- Fix port for bokeh dashboard in docs (GH#2889) Ian Hopkinson
- Wrap Dask filesystems for PyArrow compatibility (GH#2881) Jim Crist

3.21.38 0.15.4 / 2017-10-06

Array

- `da.random.choice` now works with array arguments (GH#2781)
- Support indexing in arrays with np.int (fixes regression) (GH#2719)
- Handle zero dimension with rechunking (GH#2747)
- Support -1 as an alias for "size of the dimension" in `chunks` (GH#2749)
- Call mkdir in array.to_npy_stack (GH#2709)

DataFrame

- Added the *.str* accessor to Categoricals with string categories (GH#2743)
- Support int96 (spark) datetimes in parquet writer (GH#2711)
- Pass on file scheme to fastparquet (GH#2714)
- Support Pandas 0.21 (GH#2737)

Bag

- Add tree reduction support for foldby (GH#2710)

Core

- Drop s3fs from `pip install dask[complete]` (GH#2750)

3.21.39 0.15.3 / 2017-09-24

Array

- Add masked arrays (GH#2301)
- Add `*_like array creation functions` (GH#2640)
- Indexing with unsigned integer array (GH#2647)
- Improved slicing with boolean arrays of different dimensions (GH#2658)
- Support literals in `top` and `atop` (GH#2661)
- Optional axis argument in cumulative functions (GH#2664)
- Improve tests on scalars with `assert_eq` (GH#2681)
- Fix norm keepdims (GH#2683)
- Add `ptp` (GH#2691)
- Add apply_along_axis (GH#2690) and apply_over_axes (GH#2702)

DataFrame

- Added `Series.str[index]` (GH#2634)
- Allow the groupby by param to handle columns and index levels (GH#2636)
- **`DataFrame.to_csv` and `Bag.to_textfiles` now return the filenames to** which they have written (GH#2655)
- Fix combination of `partition_on` and `append` in `to_parquet` (GH#2645)
- Fix for parquet file schemes (GH#2667)
- Repartition works with mixed categoricals (GH#2676)

Core

- `python setup.py test` now runs tests (GH#2641)
- Added new cheatsheet (GH#2649)
- Remove resize tool in Bokeh plots (GH#2688)

3.21.40 0.15.2 / 2017-08-25

Array

- Remove spurious keys from map_overlap graph (GH#2520)
- where works with non-bool condition and scalar values (GH#2543) (GH#2549)
- Improve compress (GH#2541) (GH#2545) (GH#2555)
- Add argwhere, _nonzero, and where(cond) (GH#2539)
- Generalize vindex in dask.array to handle multi-dimensional indices (GH#2573)
- Add choose method (GH#2584)
- Split code into reorganized files (GH#2595)
- Add linalg.norm (GH#2597)
- Add diff, ediff1d (GH#2607), (GH#2609)
- Improve dtype inference and reflection (GH#2571)

Bag

- Remove deprecated Bag behaviors (GH#2525)

DataFrame

- Support callables in assign (GH#2513)
- better error messages for read_csv (GH#2522)
- Add dd.to_timedelta (GH#2523)
- Verify metadata in from_delayed (GH#2534) (GH#2591)
- Add DataFrame.isin (GH#2558)
- Read_hdf supports iterables of files (GH#2547)

Core

- Remove bare `except:` blocks everywhere (GH#2590)

3.21.41 0.15.1 / 2017-07-08

- Add storage_options to to_textfiles and to_csv (GH#2466)
- Rechunk and simplify rfftfreq (GH#2473), (GH#2475)
- Better support ndarray subclasses (GH#2486)
- Import star in dask.distributed (GH#2503)
- Threadsafe cache handling with tokenization (GH#2511)

3.21.42 0.15.0 / 2017-06-09

Array

- Add dask.array.stats submodule (GH#2269)
- Support `ufunc.outer` (GH#2345)
- Optimize fancy indexing by reducing graph overhead (GH#2333) (GH#2394)
- Faster array tokenization using alternative hashes (GH#2377)
- Added the matmul `@` operator (GH#2349)
- Improved coverage of the `numpy.fft` module (GH#2320) (GH#2322) (GH#2327) (GH#2323)
- Support NumPy's `__array_ufunc__` protocol (GH#2438)

Bag

- Fix bug where reductions on bags with no partitions would fail (GH#2324)
- Add broadcasting and variadic `db.map` top-level function. Also remove auto-expansion of tuples as map arguments (GH#2339)
- Rename `Bag.concat` to `Bag.flatten` (GH#2402)

DataFrame

- Parquet improvements (GH#2277) (GH#2422)

Core

- Move dask.async module to dask.local (GH#2318)
- Support callbacks with nested scheduler calls (GH#2397)
- Support pathlib.Path objects as uris (GH#2310)

3.21.43 0.14.3 / 2017-05-05

DataFrame

- Pandas 0.20.0 support

3.21.44 0.14.2 / 2017-05-03

Array

- Add da.indices (GH#2268), da.tile (GH#2153), da.roll (GH#2135)
- Simultaneously support drop_axis and new_axis in da.map_blocks (GH#2264)
- Rechunk and concatenate work with unknown chunksizes (GH#2235) and (GH#2251)
- Support non-numpy container arrays, notably sparse arrays (GH#2234)
- Tensordot contracts over multiple axes (GH#2186)
- Allow delayed targets in da.store (GH#2181)
- Support interactions against lists and tuples (GH#2148)
- Constructor plugins for debugging (GH#2142)
- Multi-dimensional FFTs (single chunk) (GH#2116)

Bag

- to_dataframe enforces consistent types (GH#2199)

DataFrame

- Set_index always fully sorts the index (GH#2290)
- Support compatibility with pandas 0.20.0 (GH#2249), (GH#2248), and (GH#2246)
- Support Arrow Parquet reader (GH#2223)
- Time-based rolling windows (GH#2198)
- Repartition can now create more partitions, not just less (GH#2168)

Core

- Always use absolute paths when on POSIX file system (GH#2263)
- Support user provided graph optimizations (GH#2219)
- Refactor path handling (GH#2207)
- Improve fusion performance (GH#2129), (GH#2131), and (GH#2112)

3.21.45 0.14.1 / 2017-03-22

Array

- Micro-optimize optimizations (GH#2058)
- Change slicing optimizations to avoid fusing raw numpy arrays (GH#2075) (GH#2080)
- Dask.array operations now work on numpy arrays (GH#2079)
- Reshape now works in a much broader set of cases (GH#2089)

- Support deepcopy python protocol (GH#2090)
- Allow user-provided FFT implementations in `da.fft` (GH#2093)

DataFrame

- Fix to_parquet with empty partitions (GH#2020)
- Optional `npartitions='auto'` mode in `set_index` (GH#2025)
- Optimize shuffle performance (GH#2032)
- Support efficient repartitioning along time windows like `repartition(freq='12h')` (GH#2059)
- Improve speed of categorize (GH#2010)
- Support single-row dataframe arithmetic (GH#2085)
- Automatically avoid shuffle when setting index with a sorted column (GH#2091)
- Improve handling of integer-na handling in read_csv (GH#2098)

Delayed

- Repeated attribute access on delayed objects uses the same key (GH#2084)

Core

- Improve naming of nodes in dot visuals to avoid generic `apply` (GH#2070)
- Ensure that worker processes have different random seeds (GH#2094)

3.21.46 0.14.0 / 2017-02-24

Array

- Fix corner cases with zero shape and misaligned values in `arange` (GH#1902), (GH#1904), (GH#1935), (GH#1955), (GH#1956)
- Improve concatenation efficiency (GH#1923)
- Avoid hashing in `from_array` if name is provided (GH#1972)

Bag

- Repartition can now increase number of partitions (GH#1934)
- Fix bugs in some reductions with empty partitions (GH#1939), (GH#1950), (GH#1953)

DataFrame

- Support non-uniform categoricals (GH#1877), (GH#1930)
- Groupby cumulative reductions (GH#1909)
- DataFrame.loc indexing now supports lists (GH#1913)

- Improve multi-level groupbys (GH#1914)
- Improved HTML and string repr for DataFrames (GH#1637)
- Parquet append (GH#1940)
- Add `dd.demo.daily_stock` function for teaching (GH#1992)

Delayed

- Add `traverse=` keyword to delayed to optionally avoid traversing nested data structures (GH#1899)
- Support Futures in from_delayed functions (GH#1961)
- Improve serialization of decorated delayed functions (GH#1969)

Core

- Improve windows path parsing in corner cases (GH#1910)
- Rename tasks when fusing (GH#1919)
- Add top level `persist` function (GH#1927)
- Propagate `errors=` keyword in byte handling (GH#1954)
- Dask.compute traverses Python collections (GH#1975)
- Structural sharing between graphs in dask.array and dask.delayed (GH#1985)

3.21.47 0.13.0 / 2017-01-02

Array

- Mandatory dtypes on dask.array. All operations maintain dtype information and UDF functions like map_blocks now require a dtype= keyword if it can not be inferred. (GH#1755)
- Support arrays without known shapes, such as arises when slicing arrays with arrays or converting dataframes to arrays (GH#1838)
- Support mutation by setting one array with another (GH#1840)
- Tree reductions for covariance and correlations. (GH#1758)
- Add SerializableLock for better use with distributed scheduling (GH#1766)
- Improved atop support (GH#1800)
- Rechunk optimization (GH#1737), (GH#1827)

Bag

- Avoid wrong results when recomputing the same groupby twice (GH#1867)

DataFrame

- Add `map_overlap` for custom rolling operations (GH#1769)
- Add `shift` (GH#1773)
- Add Parquet support (GH#1782) (GH#1792) (GH#1810), (GH#1843), (GH#1859), (GH#1863)
- Add missing methods combine, abs, autocorr, sem, nsmallest, first, last, prod, (GH#1787)
- Approximate nunique (GH#1807), (GH#1824)
- Reductions with multiple output partitions (for operations like drop_duplicates) (GH#1808), (GH#1823) (GH#1828)
- Add delitem and copy to DataFrames, increasing mutation support (GH#1858)

Delayed

- Changed behaviour for `delayed(nout=0)` and `delayed(nout=1)`: `delayed(nout=1)` does not default to `out=None` anymore, and `delayed(nout=0)` is also enabled. I.e. functions with return tuples of length 1 or 0 can be handled correctly. This is especially handy, if functions with a variable amount of outputs are wrapped by `delayed`. E.g. a trivial example: `delayed(lambda *args: args, nout=len(vals))(*vals)`

Core

- Refactor core byte ingest (GH#1768), (GH#1774)
- Improve import time (GH#1833)

3.21.48 0.12.0 / 2016-11-03

DataFrame

- Return a series when functions given to `dataframe.map_partitions` return scalars (GH#1515)
- Fix type size inference for series (GH#1513)
- `dataframe.DataFrame.categorize` no longer includes missing values in the `categories`. This is for compatibility with a pandas change (GH#1565)
- Fix head parser error in `dataframe.read_csv` when some lines have quotes (GH#1495)
- Add `dataframe.reduction` and `series.reduction` methods to apply generic row-wise reduction to dataframes and series (GH#1483)
- Add `dataframe.select_dtypes`, which mirrors the pandas method (GH#1556)
- `dataframe.read_hdf` now supports reading `Series` (GH#1564)
- Support Pandas 0.19.0 (GH#1540)
- Implement `select_dtypes` (GH#1556)
- String accessor works with indexes (GH#1561)
- Add pipe method to dask.dataframe (GH#1567)
- Add `indicator` keyword to merge (GH#1575)

- Support Series in `read_hdf` (GH#1575)
- Support Categories with missing values (GH#1578)
- Support inplace operators like `df.x += 1` (GH#1585)
- Str accessor passes through args and kwargs (GH#1621)
- Improved groupby support for single-machine multiprocessing scheduler (GH#1625)
- Tree reductions (GH#1663)
- Pivot tables (GH#1665)
- Add clip (GH#1667), align (GH#1668), combine_first (GH#1725), and any/all (GH#1724)
- Improved handling of divisions on dask-pandas merges (GH#1666)
- Add `groupby.aggregate` method (GH#1678)
- Add `dd.read_table` function (GH#1682)
- Improve support for multi-level columns (GH#1697) (GH#1712)
- Support 2d indexing in `loc` (GH#1726)
- Extend `resample` to include DataFrames (GH#1741)
- Support dask.array ufuncs on dask.dataframe objects (GH#1669)

Array

- Add information about how `dask.array` `chunks` argument work (GH#1504)
- Fix field access with non-scalar fields in `dask.array` (GH#1484)
- Add concatenate= keyword to atop to concatenate chunks of contracted dimensions
- Optimized slicing performance (GH#1539) (GH#1731)
- Extend `atop` with a `concatenate=` (GH#1609) `new_axes=` (GH#1612) and `adjust_chunks=` (GH#1716) keywords
- Add clip (GH#1610) swapaxes (GH#1611) round (GH#1708) repeat
- Automatically align chunks in `atop`-backed operations (GH#1644)
- Cull dask.arrays on slicing (GH#1709)

Bag

- Fix issue with callables in `bag.from_sequence` being interpreted as tasks (GH#1491)
- Avoid non-lazy memory use in reductions (GH#1747)

Administration

- Added changelog (GH#1526)
- Create new threadpool when operating from thread (GH#1487)
- Unify example documentation pages into one (GH#1520)
- Add versioneer for git-commit based versions (GH#1569)

- Pass through node_attr and edge_attr keywords in dot visualization (GH#1614)
- Add continuous testing for Windows with Appveyor (GH#1648)
- Remove use of multiprocessing.Manager (GH#1653)
- Add global optimizations keyword to compute (GH#1675)
- Micro-optimize get_dependencies (GH#1722)

3.21.49 0.11.0 / 2016-08-24

Major Points

DataFrames now enforce knowing full metadata (columns, dtypes) everywhere. Previously we would operate in an ambiguous state when functions lost dtype information (such as `apply`). Now all dataframes always know their dtypes and raise errors asking for information if they are unable to infer (which they usually can). Some internal attributes like `_pd` and `_pd_nonempty` have been moved.

The internals of the distributed scheduler have been refactored to transition tasks between explicit states. This improves resilience, reasoning about scheduling, plugin operation, and logging. It also makes the scheduler code easier to understand for newcomers.

Breaking Changes

- The `distributed.s3` and `distributed.hdfs` namespaces are gone. Use protocols in normal methods like `read_text('s3://...'` instead.
- `Dask.array.reshape` now errs in some cases where previously it would have create a very large number of tasks

3.21.50 0.10.2 / 2016-07-27

- More Dataframe shuffles now work in distributed settings, ranging from setting-index to hash joins, to sorted joins and groupbys.
- Dask passes the full test suite when run when under in Python's optimized-OO mode.
- On-disk shuffles were found to produce wrong results in some highly-concurrent situations, especially on Windows. This has been resolved by a fix to the partd library.
- Fixed a growth of open file descriptors that occurred under large data communications
- Support ports in the `--bokeh-whitelist` option ot dask-scheduler to better routing of web interface messages behind non-trivial network settings
- Some improvements to resilience to worker failure (though other known failures persist)
- You can now start an IPython kernel on any worker for improved debugging and analysis
- Improvements to `dask.dataframe.read_hdf`, especially when reading from multiple files and docs

3.21.51 0.10.0 / 2016-06-13

Major Changes

- This version drops support for Python 2.6

- Conda packages are built and served from conda-forge
- The `dask.distributed` executables have been renamed from dfoo to dask-foo. For example dscheduler is renamed to dask-scheduler
- Both Bag and DataFrame include a preliminary distributed shuffle.

Bag

- Add task-based shuffle for distributed groupbys
- Add accumulate for cumulative reductions

DataFrame

- Add a task-based shuffle suitable for distributed joins, groupby-applys, and set_index operations. The single-machine shuffle remains untouched (and much more efficient.)
- Add support for new Pandas rolling API with improved communication performance on distributed systems.
- Add `groupby.std/var`
- Pass through S3/HDFS storage options in `read_csv`
- Improve categorical partitioning
- Add eval, info, isnull, notnull for dataframes

Distributed

- Rename executables like dscheduler to dask-scheduler
- Improve scheduler performance in the many-fast-tasks case (important for shuffling)
- Improve work stealing to be aware of expected function run-times and data sizes. The drastically increases the breadth of algorithms that can be efficiently run on the distributed scheduler without significant user expertise.
- Support maximum buffer sizes in streaming queues
- Improve Windows support when using the Bokeh diagnostic web interface
- Support compression of very-large-bytestrings in protocol
- Support clean cancellation of submitted futures in Joblib interface

Other

- All dask-related projects (dask, distributed, s3fs, hdfs, partd) are now building conda packages on conda-forge.
- Change credential handling in s3fs to only pass around delegated credentials if explicitly given secret/key. The default now is to rely on managed environments. This can be changed back by explicitly providing a keyword argument. Anonymous mode must be explicitly declared if desired.

3.21.52 0.9.0 / 2016-05-11

API Changes

- `dask.do` and `dask.value` have been renamed to `dask.delayed`
- `dask.bag.from_filenames` has been renamed to `dask.bag.read_text`
- All S3/HDFS data ingest functions like `db.from_s3` or `distributed.s3.read_csv` have been moved into the plain `read_text`, `read_csv functions`, which now support protocols, like `dd.read_csv('s3://bucket/keys*.csv')`

Array

- Add support for `scipy.LinearOperator`
- Improve optional locking to on-disk data structures
- Change rechunk to expose the intermediate chunks

Bag

- Rename `from_filenames` to `read_text`
- Remove `from_s3` in favor of `read_text('s3://...')`

DataFrame

- Fixed numerical stability issue for correlation and covariance
- Allow no-hash `from_pandas` for speedy round-trips to and from-pandas objects
- Generally reengineered `read_csv` to be more in line with Pandas behavior
- Support fast `set_index` operations for sorted columns

Delayed

- Rename `do/value` to `delayed`
- Rename `to/from_imperative` to `to/from_delayed`

Distributed

- Move s3 and hdfs functionality into the dask repository
- Adaptively oversubscribe workers for very fast tasks
- Improve PyPy support
- Improve work stealing for unbalanced workers
- Scatter data efficiently with tree-scatters

Other

- Add lzma/xz compression support
- Raise a warning when trying to split unsplittable compression types, like gzip or bz2
- Improve hashing for single-machine shuffle operations
- Add new callback method for start state
- General performance tuning

3.21.53 0.8.1 / 2016-03-11

Array

- Bugfix for range slicing that could periodically lead to incorrect results.
- Improved support and resiliency of `arg` reductions (`argmin`, `argmax`, etc.)

Bag

- Add `zip` function

DataFrame

- Add `corr` and `cov` functions
- Add `melt` function
- Bugfixes for io to bcolz and hdf5

3.21.54 0.8.0 / 2016-02-20

Array

- Changed default array reduction split from 32 to 4
- Linear algebra, `tril`, `triu`, `LU`, `inv`, `cholesky`, `solve`, `solve_triangular`, `eye`, `lstsq`, `diag`, `corrcoef`.

Bag

- Add tree reductions
- Add range function
- drop `from_hdfs` function (better functionality now exists in hdfs3 and distributed projects)

DataFrame

- Refactor `dask.dataframe` to include a full empty pandas dataframe as metadata. Drop the `.columns` attribute on Series
- Add Series categorical accessor, series.nunique, drop the `.columns` attribute for series.
- `read_csv` fixes (multi-column parse_dates, integer column names, etc.)
- Internal changes to improve graph serialization

Other

- Documentation updates
- Add from_imperative and to_imperative functions for all collections
- Aesthetic changes to profiler plots
- Moved the dask project to a new dask organization

3.21.55 0.7.6 / 2016-01-05

Array

- Improve thread safety
- Tree reductions
- Add `view`, `compress`, `hstack`, `dstack`, `vstack` methods
- `map_blocks` can now remove and add dimensions

DataFrame

- Improve thread safety
- Extend sampling to include replacement options

Imperative

- Removed optimization passes that fused results.

Core

- Removed `dask.distributed`
- Improved performance of blocked file reading
- Serialization improvements
- Test Python 3.5

3.21.56 0.7.4 / 2015-10-23

This was mostly a bugfix release. Some notable changes:

- Fix minor bugs associated with the release of numpy 1.10 and pandas 0.17
- Fixed a bug with random number generation that would cause repeated blocks due to the birthday paradox
- Use locks in `dask.dataframe.read_hdf` by default to avoid concurrency issues
- Change `dask.get` to point to `dask.async.get_sync` by default
- Allow visualization functions to accept general graphviz graph options like rankdir='LR'
- Add reshape and ravel to `dask.array`
- Support the creation of `dask.arrays` from `dask.imperative` objects

Deprecation

This release also includes a deprecation warning for `dask.distributed`, which will be removed in the next version.

Future development in distributed computing for dask is happening here: https://distributed.dask.org . General feedback on that project is most welcome from this community.

3.21.57 0.7.3 / 2015-09-25

Diagnostics

- A utility for profiling memory and cpu usage has been added to the `dask.diagnostics` module.

DataFrame

This release improves coverage of the pandas API. Among other things it includes `nunique`, `nlargest`, `quantile`. Fixes encoding issues with reading non-ascii csv files. Performance improvements and bug fixes with resample. More flexible read_hdf with globbing. And many more. Various bug fixes in `dask.imperative` and `dask.bag`.

3.21.58 0.7.0 / 2015-08-15

DataFrame

This release includes significant bugfixes and alignment with the Pandas API. This has resulted both from use and from recent involvement by Pandas core developers.

- New operations: query, rolling operations, drop
- Improved operations: quantiles, arithmetic on full dataframes, dropna, constructor logic, merge/join, elemwise operations, groupby aggregations

Bag

- Fixed a bug in fold where with a null default argument

Array

- New operations: da.fft module, da.image.imread

Infrastructure

- The array and dataframe collections create graphs with deterministic keys. These tend to be longer (hash strings) but should be consistent between computations. This will be useful for caching in the future.
- All collections (Array, Bag, DataFrame) inherit from common subclass

3.21.59 0.6.1 / 2015-07-23

Distributed

- Improved (though not yet sufficient) resiliency for `dask.distributed` when workers die

DataFrame

- Improved writing to various formats, including to_hdf, to_castra, and to_csv
- Improved creation of dask DataFrames from dask Arrays and Bags
- Improved support for categoricals and various other methods

Array

- Various bug fixes
- Histogram function

Scheduling

- Added tie-breaking ordering of tasks within parallel workloads to better handle and clear intermediate results

Other

- Added the dask.do function for explicit construction of graphs with normal python code
- Traded pydot for graphviz library for graph printing to support Python3
- There is also a gitter chat room and a stackoverflow tag

3.22 Configuration

Taking full advantage of Dask sometimes requires user configuration. This might be to control logging verbosity, specify cluster configuration, provide credentials for security, or any of several other options that arise in production.

Configuration is specified in one of the following ways:

1. YAML files in `~/.config/dask/` or `/etc/dask/`

2. Environment variables like `DASK_DISTRIBUTED__SCHEDULER__WORK_STEALING=True`
3. Default settings within sub-libraries

This combination makes it easy to specify configuration in a variety of settings ranging from personal workstations, to IT-mandated configuration, to docker images.

3.22.1 Access Configuration

dask.config.get(key[, default, config])	Get elements from global config

Configuration is usually read by using the `dask.config` module, either with the `config` dictionary or the `get` function:

```
>>> import dask
>>> import dask.distributed  # populate config with distributed defaults
>>> dask.config.config
{
    "array": {
        "chunk-size": "128 MiB",
    }
    "distributed": {
        "logging": {
            "distributed": "info",
            "bokeh": "critical",
            "tornado": "critical"
         },
         "admin": {
             "log-format": "%(name)s - %(levelname)s - %(message)s"
         }
    }
}

>>> dask.config.get("distributed.logging")
{
    'distributed': 'info',
    'bokeh': 'critical',
    'tornado': 'critical'
}

>>> dask.config.get('distributed.logging.bokeh')  # use `.` for nested access
'critical'
```

You may wish to inspect the `dask.config.config` dictionary to get a sense for what configuration is being used by your current system.

Note that the `get` function treats underscores and hyphens identically. For example, `dask.config.get('num_workers')` is equivalent to `dask.config.get('num-workers')`.

3.22.2 Specify Configuration

YAML files

You can specify configuration values in YAML files like the following:

```
array:
   chunk-size: 128 MiB

distributed:
  logging:
    distributed: info
    bokeh: critical
    tornado: critical

  scheduler:
    work-stealing: True
    allowed-failures: 5

   admin:
     log-format: '%(name)s - %(levelname)s - %(message)s'
```

These files can live in any of the following locations:

1. The `~/.config/dask` directory in the user's home directory
2. The `{sys.prefix}/etc/dask` directory local to Python
3. The root directory (specified by the `DASK_ROOT_CONFIG` environment variable or `/etc/dask/` by default)

Dask searches for *all* YAML files within each of these directories and merges them together, preferring configuration files closer to the user over system configuration files (preference follows the order in the list above). Additionally, users can specify a path with the `DASK_CONFIG` environment variable, which takes precedence at the top of the list above.

The contents of these YAML files are merged together, allowing different Dask subprojects like `dask-kubernetes` or `dask-ml` to manage configuration files separately, but have them merge into the same global configuration.

Note: for historical reasons we also look in the ''~/.dask'' directory for config files. This is deprecated and will soon be removed.

Environment Variables

You can also specify configuration values with environment variables like the following:

```
export DASK_DISTRIBUTED__SCHEDULER__WORK_STEALING=True
export DASK_DISTRIBUTED__SCHEDULER__ALLOWED_FAILURES=5
```

resulting in configuration values like the following:

```
{
    'distributed': {
        'scheduler': {
            'work-stealing': True,
            'allowed-failures': 5
        }
    }
}
```

Dask searches for all environment variables that start with `DASK_`, then transforms keys by converting to lower case and changing double-underscores to nested structures.

Dask tries to parse all values with ast.literal_eval, letting users pass numeric and boolean values (such as `True` in the example above) as well as lists, dictionaries, and so on with normal Python syntax.

Environment variables take precedence over configuration values found in YAML files.

Defaults

Additionally, individual subprojects may add their own default values when they are imported. These are always added with lower priority than the YAML files or environment variables mentioned above:

```
>>> import dask.config
>>> dask.config.config  # no configuration by default
{}

>>> import dask.distributed
>>> dask.config.config  # New values have been added
{
    'scheduler': ...,
    'worker': ...,
    'tls': ...
}
```

Directly within Python

dask.config.set([arg, config, lock])	Temporarily set configuration values within a context manager

Configuration is stored within a normal Python dictionary in `dask.config.config` and can be modified using normal Python operations.

Additionally, you can temporarily set a configuration value using the `dask.config.set` function. This function accepts a dictionary as an input and interprets `"."` as nested access:

```
>>> dask.config.set({'scheduler.work-stealing': True})
```

This function can also be used as a context manager for consistent cleanup:

```
with dask.config.set({'scheduler.work-stealing': True}):
    ...
```

Note that the `set` function treats underscores and hyphens identically. For example, `dask.config.set({'scheduler.work-stealing': True})` is equivalent to `dask.config.set({'scheduler.work_stealing': True})`.

3.22.3 Updating Configuration

Manipulating configuration dictionaries

dask.config.merge(*dicts)	Update a sequence of nested dictionaries
dask.config.update(old, new[, priority])	Update a nested dictionary with values from another
dask.config.expand_environment_variables(config)	Expand environment variables in a nested config dictionary

As described above, configuration can come from many places, including several YAML files, environment variables, and project defaults. Each of these provides a configuration that is possibly nested like the following:

```
x = {'a': 0, 'c': {'d': 4}}
y = {'a': 1, 'b': 2, 'c': {'e': 5}}
```

Dask will merge these configurations respecting nested data structures, and respecting order:

```
>>> dask.config.merge(x, y)
{'a': 1, 'b': 2, 'c': {'d': 4, 'e': 5}}
```

You can also use the `update` function to update the existing configuration in place with a new configuration. This can be done with priority being given to either config. This is often used to update the global configuration in `dask.config.config`:

```
dask.config.update(dask.config, new, priority='new')  # Give priority to new values
dask.config.update(dask.config, new, priority='old')  # Give priority to old values
```

Sometimes it is useful to expand environment variables stored within a configuration. This can be done with the `expand_environment_variables` function:

```
dask.config.config = dask.config.expand_environment_variables(dask.config.config)
```

Refreshing Configuration

dask.config.collect([paths, env])	Collect configuration from paths and environment variables
dask.config.refresh([config, defaults])	Update configuration by re-reading yaml files and env variables

If you change your environment variables or YAML files, Dask will not immediately see the changes. Instead, you can call `refresh` to go through the configuration collection process and update the default configuration:

```
>>> dask.config.config
{}

>>> # make some changes to yaml files

>>> dask.config.refresh()
>>> dask.config.config
{...}
```

This function uses `dask.config.collect`, which returns the configuration without modifying the global configuration. You might use this to determine the configuration of particular paths not yet on the config path:

```
>>> dask.config.collect(paths=[...])
{...}
```

3.22.4 Downstream Libraries

dask.config.ensure_file(source[, ...])	Copy file to default location if it does not already exist

Continued on next page

Table 86 – continued from previous page

`dask.config.update(old, new[, priority])`	Update a nested dictionary with values from another
`dask.config.update_defaults(new[, config, ...])`	Add a new set of defaults to the configuration

Downstream Dask libraries often follow a standard convention to use the central Dask configuration. This section provides recommendations for integration using a fictional project, `dask-foo`, as an example.

Downstream projects typically follow the following convention:

1. Maintain default configuration in a YAML file within their source directory:

```
setup.py
dask_foo/__init__.py
dask_foo/config.py
dask_foo/core.py
dask_foo/foo.yaml  # <---
```

2. Place configuration in that file within a namespace for the project:

```
# dask_foo/foo.yaml

foo:
  color: red
  admin:
    a: 1
    b: 2
```

3. Within a config.py file (or anywhere) load that default config file and update it into the global configuration:

```
# dask_foo/config.py
import os
import yaml

import dask.config

fn = os.path.join(os.path.dirname(__file__), 'foo.yaml')

with open(fn) as f:
    defaults = yaml.load(f)

dask.config.update_defaults(defaults)
```

4. Within that same config.py file, copy the `'foo.yaml'` file to the user's configuration directory if it doesn't already exist.

   We also comment the file to make it easier for us to change defaults in the future.

```
# ... continued from above

dask.config.ensure_file(source=fn, comment=True)
```

   The user can investigate `~/.config/dask/*.yaml` to see all of the commented out configuration files to which they have access.

5. Ensure that this file is run on import by including it in `__init__.py`:

```
# dask_foo/__init__.py

from . import config
```

6. Within `dask_foo` code, use the `dask.config.get` function to access configuration values:

```
# dask_foo/core.py

def process(fn, color=dask.config.get('foo.color')):
    ...
```

7. You may also want to ensure that your yaml configuration files are included in your package. This can be accomplished by including the following line in your MANIFEST.in:

```
recursive-include <PACKAGE_NAME> *.yaml
```

and the following in your setup.py `setup` call:

```
from setuptools import setup

setup(...,
      include_package_data=True,
      ...)
```

This process keeps configuration in a central place, but also keeps it safe within namespaces. It places config files in an easy to access location by default (`~/.config/dask/\*.yaml`), so that users can easily discover what they can change, but maintains the actual defaults within the source code, so that they more closely track changes in the library.

However, downstream libraries may choose alternative solutions, such as isolating their configuration within their library, rather than using the global dask.config system. All functions in the `dask.config` module also work with parameters, and do not need to mutate global state.

3.22.5 API

`dask.config.`**`get`**(*key*, *default='__no_default__'*, *config={'array': {'chunk-size': '128MiB', 'rechunk-threshold': 4, 'svg': {'size': 120}}, 'temporary-directory': None}*)

Get elements from global config

Use '.' for nested access

See also:

dask.config.set

Examples

```
>>> from dask import config
>>> config.get('foo')   # doctest: +SKIP
{'x': 1, 'y': 2}
```

```
>>> config.get('foo.x')   # doctest: +SKIP
1
```

```
>>> config.get('foo.x.y', default=123)  # doctest: +SKIP
123
```

`dask.config.`**`set`**(*arg=None, config={'array': {'chunk-size': '128MiB', 'rechunk-threshold': 4, 'svg': {'size': 120}}, 'temporary-directory': None}, lock=<unlocked _thread.lock object>, **kwargs*)

Temporarily set configuration values within a context manager

Parameters

arg [mapping or None, optional] A mapping of configuration key-value pairs to set.

****kwargs :** Additional key-value pairs to set. If `arg` is provided, values set in `arg` will be applied before those in `kwargs`. Double-underscores (__) in keyword arguments will be replaced with `.`, allowing nested values to be easily set.

See also:

dask.config.get

Examples

```
>>> import dask
```

Set `'foo.bar'` in a context, by providing a mapping.

```
>>> with dask.config.set({'foo.bar': 123}):
...     pass
```

Set `'foo.bar'` in a context, by providing a keyword argument.

```
>>> with dask.config.set(foo__bar=123):
...     pass
```

Set `'foo.bar'` globally.

```
>>> dask.config.set(foo__bar=123)  # doctest: +SKIP
```

`dask.config.`**`merge`**(**dicts*)

Update a sequence of nested dictionaries

This prefers the values in the latter dictionaries to those in the former

See also:

dask.config.update

Examples

```
>>> a = {'x': 1, 'y': {'a': 2}}
>>> b = {'y': {'b': 3}}
>>> merge(a, b)  # doctest: +SKIP
{'x': 1, 'y': {'a': 2, 'b': 3}}
```

`dask.config.`**`update`**(*old, new, priority='new'*)

Update a nested dictionary with values from another

This is like dict.update except that it smoothly merges nested values

This operates in-place and modifies old

Parameters

priority: string {'old', 'new'} If new (default) then the new dictionary has preference. Otherwise the old dictionary does.

See also:

`dask.config.merge`

Examples

```
>>> a = {'x': 1, 'y': {'a': 2}}
>>> b = {'x': 2, 'y': {'b': 3}}
>>> update(a, b)  # doctest: +SKIP
{'x': 2, 'y': {'a': 2, 'b': 3}}
```

```
>>> a = {'x': 1, 'y': {'a': 2}}
>>> b = {'x': 2, 'y': {'b': 3}}
>>> update(a, b, priority='old')  # doctest: +SKIP
{'x': 1, 'y': {'a': 2, 'b': 3}}
```

`dask.config.`**`collect`**(*paths=['/etc/dask', '/home/docs/checkouts/readthedocs.org/user_builds/dask/envs/latest/etc/dask', '/home/docs/.config/dask', '/home/docs/.dask'], env=None*)

Collect configuration from paths and environment variables

Parameters

paths [List[str]] A list of paths to search for yaml config files

env [dict] The system environment variables

Returns

config: dict

See also:

`dask.config.refresh` collect configuration and update into primary config

`dask.config.`**`refresh`**(*config={'array': {'chunk-size': '128MiB', 'rechunk-threshold': 4, 'svg': {'size': 120}}, 'temporary-directory': None}, defaults=[{'temporary-directory': None, 'array': {'svg': {'size': 120}}}, {'array': {'chunk-size': '128MiB', 'rechunk-threshold': 4}}], **kwargs*)

Update configuration by re-reading yaml files and env variables

This mutates the global dask.config.config, or the config parameter if passed in.

This goes through the following stages:

1. Clearing out all old configuration
2. Updating from the stored defaults from downstream libraries (see update_defaults)
3. Updating from yaml files and environment variables

Note that some functionality only checks configuration once at startup and may not change behavior, even if configuration changes. It is recommended to restart your python process if convenient to ensure that new configuration changes take place.

See also:

dask.config.collect for parameters

`dask.config.update_defaults`

`dask.config.`**`ensure_file`**`(`*source*, *destination=None*, *comment=True*`)`

Copy file to default location if it does not already exist

This tries to move a default configuration file to a default location if if does not already exist. It also comments out that file by default.

This is to be used by downstream modules (like dask.distributed) that may have default configuration files that they wish to include in the default configuration path.

Parameters

source [string, filename] Source configuration file, typically within a source directory.

destination [string, directory] Destination directory. Configurable by `DASK_CONFIG` environment variable, falling back to ~/.config/dask.

comment [bool, True by default] Whether or not to comment out the config file when copying.

`dask.config.`**`expand_environment_variables`**`(`*config*`)`

Expand environment variables in a nested config dictionary

This function will recursively search through any nested dictionaries and/or lists.

Parameters

config [dict, iterable, or str] Input object to search for environment variables

Returns

config [same type as input]

Examples

```
>>> expand_environment_variables({'x': [1, 2, '$USER']})  # doctest: +SKIP
{'x': [1, 2, 'my-username']}
```

3.23 Educational Resources

This is the curated list of resources for learning Dask:

- Tutorials
- Examples
- Presentations

3.24 Presentations On Dask

- PyCon Korea 2019, August 2019
  - Adapting from Spark to Dask: what to expect (18 minutes)
- SciPy 2019, July 2019

  - Refactoring the SciPy Ecosystem for Heterogeneous Computing (29 minutes)
  - Renewable Power Forecast Generation with Dask & Visualization with Bokeh (31 minutes)
  - Efficient Atmospheric Analogue Selection with Xarray and Dask (18 minutes)
  - Better and Faster Hyper Parameter Optimization with Dask (27 minutes)
  - Dask image:A Library for Distributed Image Processing (22 minutes)
- EuroPython 2019, July 2019
  - Distributed Multi-GPU Computing with Dask, CuPy and RAPIDS (29 minutes)
- SciPy 2018, July 2018
  - Scalable Machine Learning with Dask (30 minutes)
- PyCon 2018, May 2018
  - Democratizing Distributed Computing with Dask and JupyterHub (32 minutes)
- AMS & ESIP, January 2018
  - Pangeo quick demo: Dask, XArray, Zarr on the cloud with JupyterHub (3 minutes)
  - Pangeo talk: An open-source big data science platform with Dask, XArray, Zarr on the cloud with JupyterHub (43 minutes)
- PYCON.DE 2017, November 2017
  - Dask: Parallelism in Python (1 hour, 2 minutes)
- PYCON 2017, May 2017
  - Dask: A Pythonic Distributed Data Science Framework (46 minutes)
- PLOTCON 2016, December 2016
  - Visualizing Distributed Computations with Dask and Bokeh (33 minutes)
- PyData DC, October 2016
  - Using Dask for Parallel Computing in Python (44 minutes)
- SciPy 2016, July 2016
  - Dask Parallel and Distributed Computing (28 minutes)
- PyData NYC, December 2015
  - Dask Parallelizing NumPy and Pandas through Task Scheduling (33 minutes)
- PyData Seattle, August 2015
  - Dask: out of core arrays with task scheduling (1 hour, 50 minutes)
- SciPy 2015, July 2015
  - Dask Out of core NumPy:Pandas through Task Scheduling (16 minutes)

3.25 Dask Cheat Sheet

The 300KB pdf `Dask cheat sheet` is a single page summary about using Dask. It is commonly distributed at conferences and trade shows.

3.26 Comparison to Spark

Apache Spark is a popular distributed computing tool for tabular datasets that is growing to become a dominant name in Big Data analysis today. Dask has several elements that appear to intersect this space and we are often asked, "How does Dask compare with Spark?"

Answering such comparison questions in an unbiased and informed way is hard, particularly when the differences can be somewhat technical. This document tries to do this; we welcome any corrections.

3.26.1 Summary

Generally Dask is smaller and lighter weight than Spark. This means that it has fewer features and, instead, is used in conjunction with other libraries, particularly those in the numeric Python ecosystem. It couples with libraries like Pandas or Scikit-Learn to achieve high-level functionality.

Language

- Spark is written in Scala with some support for Python and R. It interoperates well with other JVM code.
- Dask is written in Python and only really supports Python. It interoperates well with C/C++/Fortran/LLVM or other natively compiled code linked through Python.

Ecosystem

- Spark is an all-in-one project that has inspired its own ecosystem. It integrates well with many other Apache projects.
- Dask is a component of the larger Python ecosystem. It couples with and enhances other libraries like NumPy, Pandas, and Scikit-Learn.

Age and Trust

- Spark is older (since 2010) and has become a dominant and well-trusted tool in the Big Data enterprise world.
- Dask is younger (since 2014) and is an extension of the well trusted NumPy/Pandas/Scikit-learn/Jupyter stack.

Scope

- Spark is more focused on traditional business intelligence operations like SQL and lightweight machine learning.
- Dask is applied more generally both to business intelligence applications, as well as a number of scientific and custom situations.

Internal Design

- Spark's internal model is higher level, providing good high level optimizations on uniformly applied computations, but lacking flexibility for more complex algorithms or ad-hoc systems. It is fundamentally an extension of the Map-Shuffle-Reduce paradigm.
- Dask's internal model is lower level, and so lacks high level optimizations, but is able to implement more sophisticated algorithms and build more complex bespoke systems. It is fundamentally based on generic task scheduling.

Scale

- Spark scales from a single node to thousand-node clusters.
- Dask scales from a single node to thousand-node clusters.

APIs

DataFrames

- Spark DataFrame has its own API and memory model. It also implements a large subset of the SQL language. Spark includes a high-level query optimizer for complex queries.
- Dask DataFrame reuses the Pandas API and memory model. It implements neither SQL nor a query optimizer. It is able to do random access, efficient time series operations, and other Pandas-style indexed operations.

Machine Learning

- Spark MLLib is a cohesive project with support for common operations that are easy to implement with Spark's Map-Shuffle-Reduce style system. People considering MLLib might also want to consider *other* JVM-based machine learning libraries like H2O, which may have better performance.
- Dask relies on and interoperates with existing libraries like Scikit-Learn and XGBoost. These can be more familiar or higher performance, but generally results in a less-cohesive whole. See the dask-ml project for integrations.

Arrays

- Spark does not include support for multi-dimensional arrays natively (this would be challenging given their computation model), although some support for two-dimensional matrices may be found in MLLib. People may also want to look at the Thunder project, which combines Apache Spark with NumPy arrays.
- Dask fully supports the NumPy model for *scalable multi-dimensional arrays*.

Streaming

- Spark's support for streaming data is first-class and integrates well into their other APIs. It follows a mini-batch approach. This provides decent performance on large uniform streaming operations.
- Dask provides a *real-time futures interface* that is lower-level than Spark streaming. This enables more creative and complex use-cases, but requires more work than Spark streaming.

Graphs / complex networks

- Spark provides GraphX, a library for graph processing.
- Dask provides no such library.

Custom parallelism

- Spark generally expects users to compose computations out of their high-level primitives (map, reduce, groupby, join, . . .). It is also possible to extend Spark through subclassing RDDs, although this is rarely done.
- Dask allows you to specify arbitrary task graphs for more complex and custom systems that are not part of the standard set of collections.

3.26.2 Reasons you might choose Spark

- You prefer Scala or the SQL language
- You have mostly JVM infrastructure and legacy systems
- You want an established and trusted solution for business
- You are mostly doing business analytics with some lightweight machine learning
- You want an all-in-one solution

3.26.3 Reasons you might choose Dask

- You prefer Python or native code, or have large legacy code bases that you do not want to entirely rewrite
- Your use case is complex or does not cleanly fit the Spark computing model
- You want a lighter-weight transition from local computing to cluster computing
- You want to interoperate with other technologies and don't mind installing multiple packages

3.26.4 Reasons to choose both

It is easy to use both Dask and Spark on the same data and on the same cluster.

They can both read and write common formats, like CSV, JSON, ORC, and Parquet, making it easy to hand results off between Dask and Spark workflows.

They can both deploy on the same clusters. Most clusters are designed to support many different distributed systems at the same time, using resource managers like Kubernetes and YARN. If you already have a cluster on which you run Spark workloads, it's likely easy to also run Dask workloads on your current infrastructure and vice versa.

In particular, for users coming from traditional Hadoop/Spark clusters (such as those sold by Cloudera/Hortonworks) you are using the Yarn resource manager. You can deploy Dask on these systems using the Dask Yarn project, as well as other projects, like JupyterHub on Hadoop.

3.26.5 Developer-Facing Differences

Graph Granularity

Both Spark and Dask represent computations with directed acyclic graphs. These graphs however represent computations at very different granularities.

One operation on a Spark RDD might add a node like `Map` and `Filter` to the graph. These are high-level operations that convey meaning and will eventually be turned into many little tasks to execute on individual workers. This many-little-tasks state is only available internally to the Spark scheduler.

Dask graphs skip this high-level representation and go directly to the many-little-tasks stage. As such, one `map` operation on a Dask collection will immediately generate and add possibly thousands of tiny tasks to the Dask graph.

This difference in the scale of the underlying graph has implications on the kinds of analysis and optimizations one can do and also on the generality that one exposes to users. Dask is unable to perform some optimizations that Spark can because Dask schedulers do not have a top-down picture of the computation they were asked to perform. However, Dask is able to easily represent far more complex algorithms and expose the creation of these algorithms to normal users.

3.26.6 Conclusion

- Spark is mature and all-inclusive. If you want a single project that does everything and you're already on Big Data hardware, then Spark is a safe bet, especially if your use cases are typical ETL + SQL and you're already using Scala.
- Dask is lighter weight and is easier to integrate into existing code and hardware. If your problems vary beyond typical ETL + SQL and you want to add flexible parallelism to existing solutions, then Dask may be a good fit, especially if you are already using Python and associated libraries like NumPy and Pandas.

If you are looking to manage a terabyte or less of tabular CSV or JSON data, then you should forget both Spark and Dask and use Postgres or MongoDB.

3.27 Opportunistic Caching

EXPERIMENTAL FEATURE added to Version 0.6.2 and above - see *disclaimer*.

Dask usually removes intermediate values as quickly as possible in order to make space for more data to flow through your computation. However, in some cases, we may want to hold onto intermediate values, because they might be useful for future computations in an interactive session.

We need to balance the following concerns:

1. Intermediate results might be useful in future unknown computations
2. Intermediate results also fill up memory, reducing space for the rest of our current computation

Negotiating between these two concerns helps us to leverage the memory that we have available to speed up future, unanticipated computations. Which intermediate results should we keep?

This document explains an experimental, opportunistic caching mechanism that automatically picks out and stores useful tasks.

3.27.1 Motivating Example

Consider computing the maximum value of a column in a CSV file:

```
>>> import dask.dataframe as dd
>>> df = dd.read_csv('myfile.csv')
>>> df.columns
['first-name', 'last-name', 'amount', 'id', 'timestamp']

>>> df.amount.max().compute()
1000
```

Even though our full dataset may be too large to fit in memory, the single `df.amount` column may be small enough to hold in memory just in case it might be useful in the future. This is often the case during data exploration, because we investigate the same subset of our data repeatedly before moving on.

For example, we may now want to find the minimum of the amount column:

```
>>> df.amount.min().compute()
-1000
```

Under normal operations, this would need to read through the entire CSV file over again. This is somewhat wasteful and stymies interactive data exploration.

3.27.2 Two Simple Solutions

If we know ahead of time that we want both the maximum and minimum, we can compute them simultaneously. Dask will share intermediates intelligently, reading through the dataset only once:

```
>>> dd.compute(df.amount.max(), df.amount.min())
(1000, -1000)
```

If we know that this column fits in memory, then we can also explicitly compute the column and then continue forward with straight Pandas:

```
>>> amount = df.amount.compute()
>>> amount.max()
1000
>>> amount.min()
-1000
```

If either of these solutions work for you, great. Otherwise, continue on for a third approach.

3.27.3 Automatic Opportunistic Caching

Another approach is to watch *all* intermediate computations, and *guess* which ones might be valuable to keep for the future. Dask has an *opportunistic caching mechanism* that stores intermediate tasks that show the following characteristics:

1. Expensive to compute
2. Cheap to store
3. Frequently used

We can activate a fixed sized cache as a callback:

```
>>> from dask.cache import Cache
>>> cache = Cache(2e9)  # Leverage two gigabytes of memory
>>> cache.register()    # Turn cache on globally
```

Now the cache will watch every small part of the computation and judge the value of that part based on the three characteristics listed above (expensive to compute, cheap to store, and frequently used).

Dask will hold on to 2GB of the best intermediate results it can find, evicting older results as better results come in. If the `df.amount` column fits in 2GB, then probably all of it will be stored while we keep working on it.

If we start work on something else, then the `df.amount` column will likely be evicted to make space for other more timely results:

```
>>> df.amount.max().compute()  # slow the first time
1000
>>> df.amount.min().compute()  # fast because df.amount is in the cache
-1000
>>> df.id.nunique().compute()  # starts to push out df.amount from cache
```

3.27.4 Cache tasks, not expressions

This caching happens at the low-level scheduling layer, not the high-level Dask DataFrame or Dask Array layer. We don't explicitly cache the column `df.amount`. Instead, we cache the hundreds of small pieces of that column that form the dask graph. It could be that we end up caching only a fraction of the column.

This means that the opportunistic caching mechanism described above works for *all* Dask computations, as long as those computations employ a consistent naming scheme (as all of Dask DataFrame, Dask Array, and Dask Delayed do).

You can see which tasks are held by the cache by inspecting the following attributes of the cache object:

```
>>> cache.cache.data
<stored values>
>>> cache.cache.heap.heap
<scores of items in cache>
>>> cache.cache.nbytes
<number of bytes per item in cache>
```

The cache object is powered by cachey, a tiny library for opportunistic caching.

3.27.5 Disclaimer

This feature is still experimental, and can cause your computation to fill up RAM.

Restricting your cache to a fixed size like 2GB requires Dask to accurately count the size of each of our objects in memory. This can be tricky, particularly for Pythonic objects like lists and tuples, and for DataFrames that contain object dtypes.

It is entirely possible that the caching mechanism will *undercount* the size of objects, causing it to use up more memory than anticipated, which can lead to blowing up RAM and crashing your session.

3.28 Task Graphs

Internally, Dask encodes algorithms in a simple format involving Python dicts, tuples, and functions. This graph format can be used in isolation from the dask collections. Working directly with dask graphs is rare, unless you intend to develop new modules with Dask. Even then, *dask.delayed* is often a better choice. If you are a *core developer*, then you should start here.

3.28.1 Specification

Dask is a specification to encode a graph – specifically, a directed acyclic graph of tasks with data dependencies – using ordinary Python data structures, namely dicts, tuples, functions, and arbitrary Python values.

Definitions

A **Dask graph** is a dictionary mapping **keys** to **computations**:

```
{'x': 1,
 'y': 2,
 'z': (add, 'x', 'y'),
 'w': (sum, ['x', 'y', 'z']),
 'v': [(sum, ['w', 'z']), 2]}
```

A **key** is any hashable value that is not a **task**:

```
'x'
('x', 2, 3)
```

A **task** is a tuple with a callable first element. Tasks represent atomic units of work meant to be run by a single worker. Example:

```
(add, 'x', 'y')
```

We represent a task as a tuple such that the *first element is a callable function* (like `add`), and the succeeding elements are *arguments* for that function. An *argument* may be any valid **computation**.

A **computation** may be one of the following:

1. Any **key** present in the Dask graph like `'x'`
2. Any other value like `1`, to be interpreted literally
3. A **task** like `(inc, 'x')` (see below)
4. A list of **computations**, like `[1, 'x', (inc, 'x')]`

So all of the following are valid **computations**:

```
np.array([...])
(add, 1, 2)
(add, 'x', 2)
(add, (inc, 'x'), 2)
(sum, [1, 2])
(sum, ['x', (inc, 'x')])
(np.dot, np.array([...]), np.array([...]))
[(sum, ['x', 'y']), 'z']
```

To encode keyword arguments, we recommend the use of `functools.partial` or `toolz.curry`.

What functions should expect

In cases like `(add, 'x', 'y')`, functions like `add` receive concrete values instead of keys. A Dask scheduler replaces keys (like `'x'` and `'y'`) with their computed values (like `1`, and `2`) *before* calling the `add` function.

Entry Point - The `get` function

The `get` function serves as entry point to computation for all schedulers. This function gets the value associated to the given key. That key may refer to stored data, as is the case with `'x'`, or to a task, as is the case with `'z'`. In the latter case, `get` should perform all necessary computation to retrieve the computed value.

```
>>> from dask.threaded import get

>>> from operator import add

>>> dsk = {'x': 1,
...        'y': 2,
...        'z': (add, 'x', 'y'),
...        'w': (sum, ['x', 'y', 'z'])}
```

```
>>> get(dsk, 'x')
1

>>> get(dsk, 'z')
3

>>> get(dsk, 'w')
6
```

Additionally, if given a `list`, get should simultaneously acquire values for multiple keys:

```
>>> get(dsk, ['x', 'y', 'z'])
[1, 2, 3]
```

Because we accept lists of keys as keys, we support nested lists:

```
>>> get(dsk, [['x', 'y'], ['z', 'w']])
[[1, 2], [3, 6]]
```

Internally `get` can be arbitrarily complex, calling out to distributed computing, using caches, and so on.

Why use tuples

With `(add, 'x', 'y')`, we wish to encode the result of calling `add` on the values corresponding to the keys `'x'` and `'y'`.

We intend the following meaning:

```
add('x', 'y')  # after x and y have been replaced
```

But this will err because Python executes the function immediately before we know values for `'x'` and `'y'`.

We delay the execution by moving the opening parenthesis one term to the left, creating a tuple:

```
Before: add( 'x', 'y')
After: (add, 'x', 'y')
```

This lets us store the desired computation as data that we can analyze using other Python code, rather than cause immediate execution.

LISP users will identify this as an s-expression, or as a rudimentary form of quoting.

3.28.2 Custom Graphs

There may be times when you want to do parallel computing but your application doesn't fit neatly into something like Dask Array or Dask Bag. In these cases, you can interact directly with the Dask schedulers. These schedulers operate well as standalone modules.

This separation provides a release valve for complex situations and allows advanced projects to have additional opportunities for parallel execution, even if those projects have an internal representation for their computations. As Dask schedulers improve or expand to distributed memory, code written to use Dask schedulers will advance as well.

Example

As discussed in the *motivation* and *specification* sections, the schedulers take a task graph (which is a dict of tuples of functions) and a list of desired keys from that graph.

Here is a mocked out example building a graph for a traditional clean and analyze pipeline:

```
def load(filename):
    ...

def clean(data):
    ...

def analyze(sequence_of_data):
    ...

def store(result):
    with open(..., 'w') as f:
        f.write(result)

dsk = {'load-1': (load, 'myfile.a.data'),
       'load-2': (load, 'myfile.b.data'),
       'load-3': (load, 'myfile.c.data'),
       'clean-1': (clean, 'load-1'),
       'clean-2': (clean, 'load-2'),
       'clean-3': (clean, 'load-3'),
       'analyze': (analyze, ['clean-%d' % i for i in [1, 2, 3]]),
       'store': (store, 'analyze')}

from dask.multiprocessing import get
get(dsk, 'store')  # executes in parallel
```

Related Projects

The following excellent projects also provide parallel execution:

- Joblib
- Multiprocessing
- IPython Parallel
- Concurrent.futures
- Luigi

Each library lets you dictate how your tasks relate to each other with various levels of sophistication. Each library executes those tasks with some internal logic.

Dask schedulers differ in the following ways:

1. You specify the entire graph as a Python dict rather than using a specialized API
2. You get a variety of schedulers ranging from single machine, single core to threaded, multiprocessing, distributed, and

3. The Dask single-machine schedulers have logic to execute the graph in a way that minimizes memory footprint

But the other projects offer different advantages and different programming paradigms. One should inspect all such projects before selecting one.

3.28.3 Optimization

Performance can be significantly improved in different contexts by making small optimizations on the Dask graph before calling the scheduler.

The `dask.optimization` module contains several functions to transform graphs in a variety of useful ways. In most cases, users won't need to interact with these functions directly, as specialized subsets of these transforms are done automatically in the Dask collections (`dask.array`, `dask.bag`, and `dask.dataframe`). However, users working with custom graphs or computations may find that applying these methods results in substantial speedups.

In general, there are two goals when doing graph optimizations:

1. Simplify computation
2. Improve parallelism

Simplifying computation can be done on a graph level by removing unnecessary tasks (`cull`), or on a task level by replacing expensive operations with cheaper ones (`RewriteRule`).

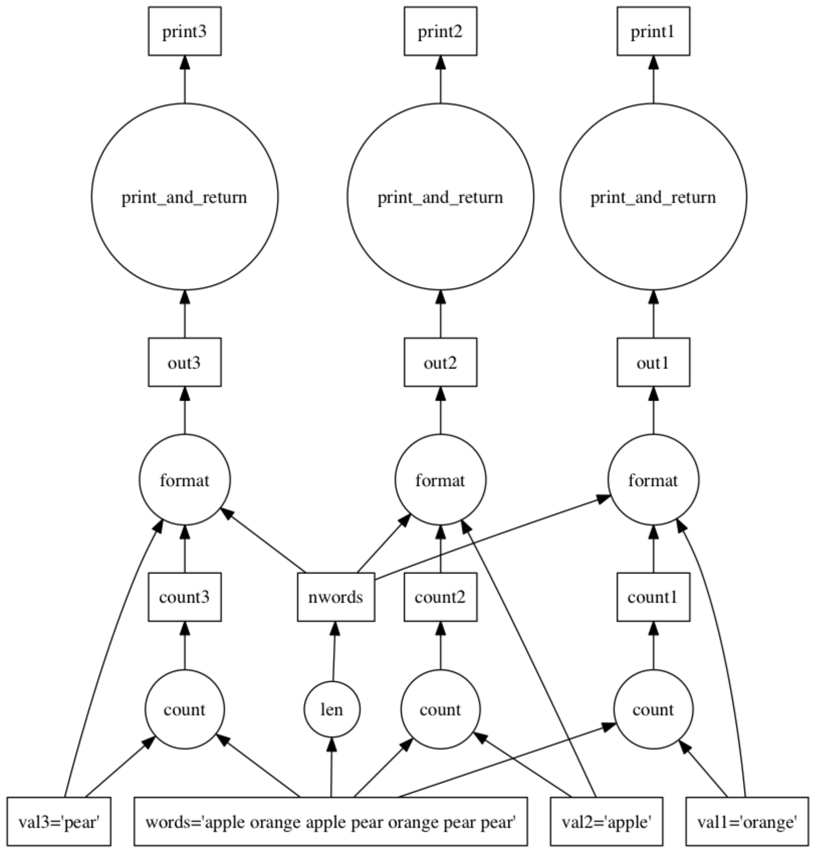
Parallelism can be improved by reducing inter-task communication, whether by fusing many tasks into one (`fuse`), or by inlining cheap operations (`inline`, `inline_functions`).

Below, we show an example walking through the use of some of these to optimize a task graph.

Example

Suppose you had a custom Dask graph for doing a word counting task:

```
>>> from __future__ import print_function

>>> def print_and_return(string):
...     print(string)
...     return string

>>> def format_str(count, val, nwords):
...     return ('word list has {0} occurrences of {1}, '
...             'out of {2} words').format(count, val, nwords)

>>> dsk = {'words': 'apple orange apple pear orange pear pear',
...        'nwords': (len, (str.split, 'words')),
...        'val1': 'orange',
...        'val2': 'apple',
...        'val3': 'pear',
...        'count1': (str.count, 'words', 'val1'),
...        'count2': (str.count, 'words', 'val2'),
...        'count3': (str.count, 'words', 'val3'),
...        'out1': (format_str, 'count1', 'val1', 'nwords'),
...        'out2': (format_str, 'count2', 'val2', 'nwords'),
...        'out3': (format_str, 'count3', 'val3', 'nwords'),
...        'print1': (print_and_return, 'out1'),
...        'print2': (print_and_return, 'out2'),
...        'print3': (print_and_return, 'out3')}
```



Here we are counting the occurrence of the words `'orange`, `'apple'`, and `'pear'` in the list of words, formatting an output string reporting the results, printing the output, and then returning the output string.

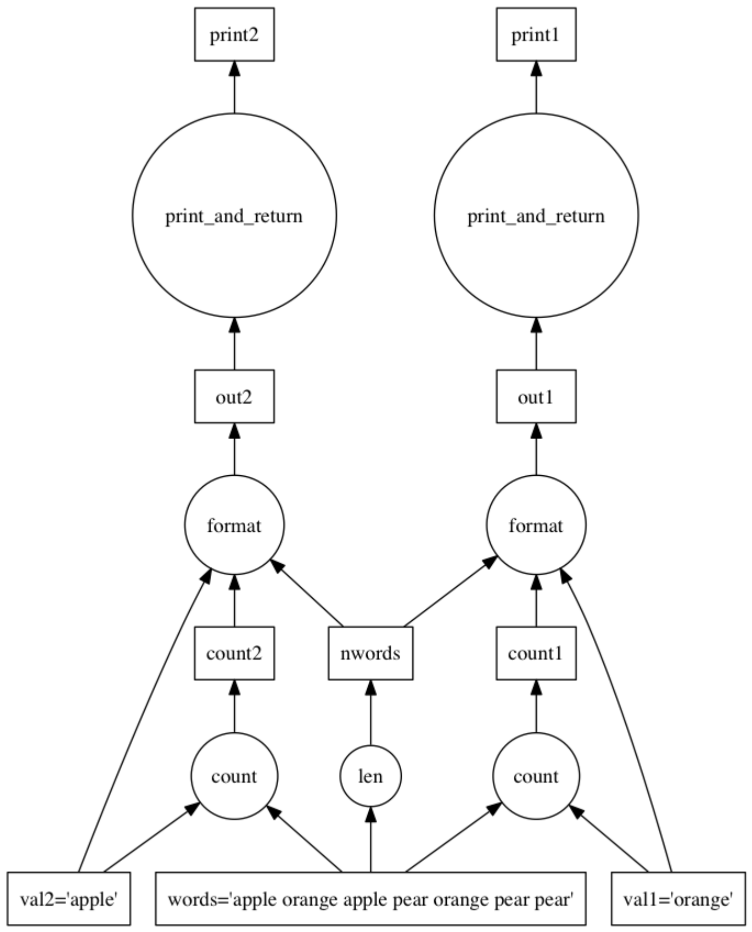
To perform the computation, we first remove unnecessary components from the graph using the `cull` function and then pass the Dask graph and the desired output keys to a scheduler `get` function:

```
>>> from dask.threaded import get
>>> from dask.optimization import cull

>>> outputs = ['print1', 'print2']
>>> dsk2, _ = cull(dsk, outputs)   # remove unnecessary tasks from the graph

>>> results = get(dsk2, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words

>>> results
('word list has 2 occurrences of orange, out of 7 words',
 'word list has 2 occurrences of apple, out of 7 words')
```

As can be seen above, the scheduler computed only the requested outputs (`'print3'` was never computed). This is because we called the `dask.optimization.cull` function, which removes the unnecessary tasks from the graph.

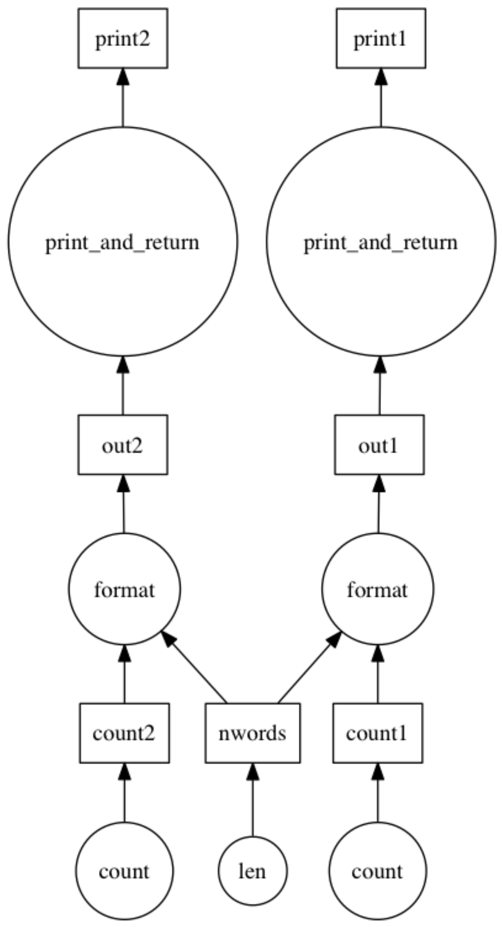
Culling is part of the default optimization pass of almost all collections. Often you want to call it somewhat early to reduce the amount of work done in later steps:

```
>>> from dask.optimization import cull
>>> dsk1, dependencies = cull(dsk, outputs)
```



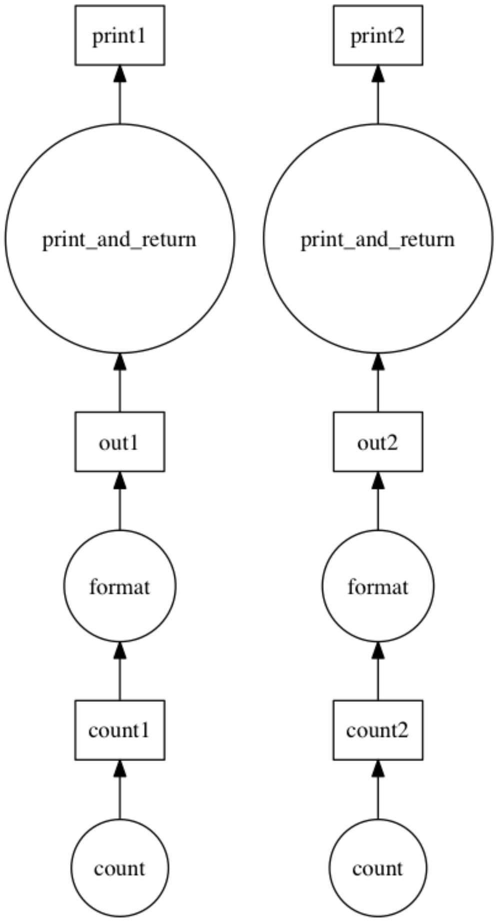
Looking at the task graph above, there are multiple accesses to constants such as `'val1'` or `'val2'` in the Dask graph. These can be inlined into the tasks to improve efficiency using the `inline` function. For example:

```
>>> from dask.optimization import inline
>>> dsk2 = inline(dsk1, dependencies=dependencies)
>>> results = get(dsk2, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```



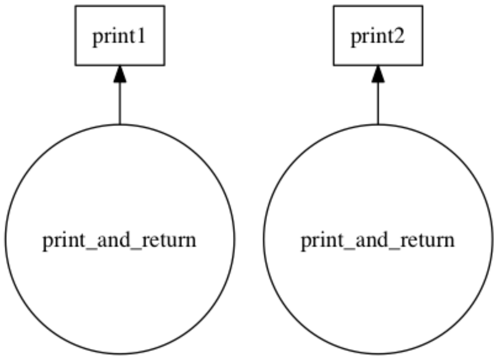
Now we have two sets of *almost* linear task chains. The only link between them is the word counting function. For cheap operations like this, the serialization cost may be larger than the actual computation, so it may be faster to do the computation more than once, rather than passing the results to all nodes. To perform this function inlining, the `inline_functions` function can be used:

```
>>> from dask.optimization import inline_functions
>>> dsk3 = inline_functions(dsk2, outputs, [len, str.split],
...                         dependencies=dependencies)
>>> results = get(dsk3, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```



Now we have a set of purely linear tasks. We'd like to have the scheduler run all of these on the same worker to reduce data serialization between workers. One option is just to merge these linear chains into one big task using the `fuse` function:

```
>>> from dask.optimization import fuse
>>> dsk4, dependencies = fuse(dsk3)
>>> results = get(dsk4, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```



Putting it all together:

```
>>> def optimize_and_get(dsk, keys):
...     dsk1, deps = cull(dsk, keys)
...     dsk2 = inline(dsk1, dependencies=deps)
...     dsk3 = inline_functions(dsk2, keys, [len, str.split],
...                                  dependencies=deps)
...     dsk4, deps = fuse(dsk3)
...     return get(dsk4, keys)

>>> optimize_and_get(dsk, outputs)
word list has 2 occurrences of apple, out of 7 words
word list has 2 occurrences of orange, out of 7 words
```

In summary, the above operations accomplish the following:

1. Removed tasks unnecessary for the desired output using `cull`
2. Inlined constants using `inline`
3. Inlined cheap computations using `inline_functions`, improving parallelism
4. Fused linear tasks together to ensure they run on the same worker using `fuse`

As stated previously, these optimizations are already performed automatically in the Dask collections. Users not working with custom graphs or computations should rarely need to directly interact with them.

These are just a few of the optimizations provided in `dask.optimization`. For more information, see the API below.

Rewrite Rules

For context based optimizations, `dask.rewrite` provides functionality for pattern matching and term rewriting. This is useful for replacing expensive computations with equivalent, cheaper computations. For example, Dask Array uses the rewrite functionality to replace series of array slicing operations with a more efficient single slice.

The interface to the rewrite system consists of two classes:

1. `RewriteRule(lhs, rhs, vars)`

   Given a left-hand-side (`lhs`), a right-hand-side (`rhs`), and a set of variables (`vars`), a rewrite rule declaratively encodes the following operation:

   `lhs -> rhs if task matches lhs over variables`

2. `RuleSet(*rules)`

   A collection of rewrite rules. The design of `RuleSet` class allows for efficient "many-to-one" pattern matching, meaning that there is minimal overhead for rewriting with multiple rules in a rule set.

Example

Here we create two rewrite rules expressing the following mathematical transformations:

1. `a + a -> 2*a`
2. `a * a -> a**2`

where `'a'` is a variable:

```
>>> from dask.rewrite import RewriteRule, RuleSet
>>> from operator import add, mul, pow

>>> variables = ('a',)

>>> rule1 = RewriteRule((add, 'a', 'a'), (mul, 'a', 2), variables)

>>> rule2 = RewriteRule((mul, 'a', 'a'), (pow, 'a', 2), variables)

>>> rs = RuleSet(rule1, rule2)
```

The `RewriteRule` objects describe the desired transformations in a declarative way, and the `RuleSet` builds an efficient automata for applying that transformation. Rewriting can then be done using the `rewrite` method:

```
>>> rs.rewrite((add, 5, 5))
(mul, 5, 2)

>>> rs.rewrite((mul, 5, 5))
(pow, 5, 2)

>>> rs.rewrite((mul, (add, 3, 3), (add, 3, 3)))
(pow, (mul, 3, 2), 2)
```

The whole task is traversed by default. If you only want to apply a transform to the top-level of the task, you can pass in `strategy='top_level'` as shown:

```
# Transforms whole task
>>> rs.rewrite((sum, [(add, 3, 3), (mul, 3, 3)]))
(sum, [(mul, 3, 2), (pow, 3, 2)])

# Only applies to top level, no transform occurs
>>> rs.rewrite((sum, [(add, 3, 3), (mul, 3, 3)]), strategy='top_level')
(sum, [(add, 3, 3), (mul, 3, 3)])
```

The rewriting system provides a powerful abstraction for transforming computations at a task level. Again, for many users, directly interacting with these transformations will be unnecessary.

Keyword Arguments

Some optimizations take optional keyword arguments. To pass keywords from the compute call down to the right optimization, prepend the keyword with the name of the optimization. For example, to send a `keys=` keyword argument to the `fuse` optimization from a compute call, use the `fuse_keys=` keyword:

```
def fuse(dsk, keys=None):
    ...

x.compute(fuse_keys=['x', 'y', 'z'])
```

Customizing Optimization

Dask defines a default optimization strategy for each collection type (Array, Bag, DataFrame, Delayed). However, different applications may have different needs. To address this variability of needs, you can construct your own custom optimization function and use it instead of the default. An optimization function takes in a task graph and list of desired keys and returns a new task graph:

```python
def my_optimize_function(dsk, keys):
    new_dsk = {...}
    return new_dsk
```

You can then register this optimization class against whichever collection type you prefer and it will be used instead of the default scheme:

```python
with dask.config.set(array_optimize=my_optimize_function):
    x, y = dask.compute(x, y)
```

You can register separate optimization functions for different collections, or you can register `None` if you do not want particular types of collections to be optimized:

```python
with dask.config.set(array_optimize=my_optimize_function,
                     dataframe_optimize=None,
                     delayed_optimize=my_other_optimize_function):
    ...
```

You do not need to specify all collections. Collections will default to their standard optimization scheme (which is usually a good choice).

API

Top level optimizations

cull(dsk, keys)	Return new dask with only the tasks required to calculate keys.
fuse(dsk[, keys, dependencies, ave_width, . . .])	Fuse tasks that form reductions; more advanced than `fuse_linear`
inline(dsk[, keys, inline_constants, . . .])	Return new dask with the given keys inlined with their values.
inline_functions(dsk, output[, . . .])	Inline cheap functions into larger operations

Utility functions

functions_of(task)	Set of functions contained within nested task

Rewrite Rules

RewriteRule(lhs, rhs[, vars])	A rewrite rule.
RuleSet(*rules)	A set of rewrite rules.

Definitions

`dask.optimization.`**`cull`**(*dsk*, *keys*)

Return new dask with only the tasks required to calculate keys.

In other words, remove unnecessary tasks from dask. `keys` may be a single key or list of keys.

Returns

dsk: culled dask graph

dependencies: Dict mapping {key: [deps]}. Useful side effect to accelerate other optimizations, notably fuse.

Examples

```
>>> d = {'x': 1, 'y': (inc, 'x'), 'out': (add, 'x', 10)}
>>> dsk, dependencies = cull(d, 'out')  # doctest: +SKIP
>>> dsk  # doctest: +SKIP
{'x': 1, 'out': (add, 'x', 10)}
>>> dependencies  # doctest: +SKIP
{'x': set(), 'out': set(['x'])}
```

`dask.optimization.`**`fuse`**(*dsk*, *keys=None*, *dependencies=None*, *ave_width=None*, *max_width=None*, *max_height=None*, *max_depth_new_edges=None*, *rename_keys=None*, *fuse_subgraphs=None*)

Fuse tasks that form reductions; more advanced than `fuse_linear`

This trades parallelism opportunities for faster scheduling by making tasks less granular. It can replace `fuse_linear` in optimization passes.

This optimization applies to all reductions–tasks that have at most one dependent–so it may be viewed as fusing "multiple input, single output" groups of tasks into a single task. There are many parameters to fine tune the behavior, which are described below. `ave_width` is the natural parameter with which to compare parallelism to granularity, so it should always be specified. Reasonable values for other parameters will be determined using `ave_width` if necessary.

Parameters

dsk: dict dask graph

keys: list or set, optional Keys that must remain in the returned dask graph

dependencies: dict, optional {key: [list-of-keys]}. Must be a list to provide count of each key This optional input often comes from `cull`

ave_width: float (default 2) Upper limit for `width = num_nodes / height`, a good measure of parallelizability

max_width: int Don't fuse if total width is greater than this

max_height: int Don't fuse more than this many levels

max_depth_new_edges: int Don't fuse if new dependencies are added after this many levels

rename_keys: bool or func, optional Whether to rename the fused keys with `default_fused_keys_renamer` or not. Renaming fused keys can keep the graph more understandable and comprehensive, but it comes at the cost of additional processing. If False, then the top-most key will be used. For advanced usage, a function to create the new name is also accepted.

fuse_subgraphs [bool, optional] Whether to fuse multiple tasks into `SubgraphCallable` objects.

Returns

dsk: output graph with keys fused

dependencies: dict mapping dependencies after fusion. Useful side effect to accelerate other downstream optimizations.

`dask.optimization.`**`inline`**(*dsk*, *keys=None*, *inline_constants=True*, *dependencies=None*)

Return new dask with the given keys inlined with their values.

Inlines all constants if `inline_constants` keyword is True. Note that the constant keys will remain in the graph, to remove them follow `inline` with `cull`.

Examples

```
>>> d = {'x': 1, 'y': (inc, 'x'), 'z': (add, 'x', 'y')}
>>> inline(d)  # doctest: +SKIP
{'x': 1, 'y': (inc, 1), 'z': (add, 1, 'y')}
```

```
>>> inline(d, keys='y')  # doctest: +SKIP
{'x': 1, 'y': (inc, 1), 'z': (add, 1, (inc, 1))}
```

```
>>> inline(d, keys='y', inline_constants=False)  # doctest: +SKIP
{'x': 1, 'y': (inc, 1), 'z': (add, 'x', (inc, 'x'))}
```

`dask.optimization.`**`inline_functions`**(*dsk*, *output*, *fast_functions=None*, *inline_constants=False*, *dependencies=None*)

Inline cheap functions into larger operations

Examples

```
>>> dsk = {'out': (add, 'i', 'd'),  # doctest: +SKIP
...        'i': (inc, 'x'),
...        'd': (double, 'y'),
...        'x': 1, 'y': 1}
>>> inline_functions(dsk, [], [inc])  # doctest: +SKIP
{'out': (add, (inc, 'x'), 'd'),
 'd': (double, 'y'),
 'x': 1, 'y': 1}
```

Protect output keys. In the example below `i` is not inlined because it is marked as an output key.

```
>>> inline_functions(dsk, ['i', 'out'], [inc, double])  # doctest: +SKIP
{'out': (add, 'i', (double, 'y')),
 'i': (inc, 'x'),
 'x': 1, 'y': 1}
```

`dask.optimization.`**`functions_of`**(*task*)

Set of functions contained within nested task

Examples

```
>>> task = (add, (mul, 1, 2), (inc, 3))  # doctest: +SKIP
>>> functions_of(task)  # doctest: +SKIP
set([add, mul, inc])
```

`dask.rewrite.`**`RewriteRule`**(*lhs*, *rhs*, *vars=()*)

A rewrite rule.

Expresses *lhs* -> *rhs*, for variables *vars*.

Parameters

lhs [task] The left-hand-side of the rewrite rule.

rhs [task or function] The right-hand-side of the rewrite rule. If it's a task, variables in *rhs* will be replaced by terms in the subject that match the variables in *lhs*. If it's a function, the function will be called with a dict of such matches.

vars: tuple, optional Tuple of variables found in the lhs. Variables can be represented as any hashable object; a good convention is to use strings. If there are no variables, this can be omitted.

Examples

Here's a *RewriteRule* to replace all nested calls to *list*, so that *(list, (list, 'x'))* is replaced with *(list, 'x')*, where *'x'* is a variable.

```
>>> lhs = (list, (list, 'x'))
>>> rhs = (list, 'x')
>>> variables = ('x',)
>>> rule = RewriteRule(lhs, rhs, variables)
```

Here's a more complicated rule that uses a callable right-hand-side. A callable *rhs* takes in a dictionary mapping variables to their matching values. This rule replaces all occurrences of *(list, 'x')* with *'x'* if *'x'* is a list itself.

```
>>> lhs = (list, 'x')
>>> def repl_list(sd):
...     x = sd['x']
...     if isinstance(x, list):
...         return x
...     else:
...         return (list, x)
>>> rule = RewriteRule(lhs, repl_list, variables)
```

`dask.rewrite.`**`RuleSet`**`(*rules)`

A set of rewrite rules.

Forms a structure for fast rewriting over a set of rewrite rules. This allows for syntactic matching of terms to patterns for many patterns at the same time.

Examples

```
>>> def f(*args): pass
>>> def g(*args): pass
>>> def h(*args): pass
>>> from operator import add
```

```
>>> rs = RuleSet(                 # Make RuleSet with two Rules
...         RewriteRule((add, 'x', 0), 'x', ('x',)),
...         RewriteRule((f, (g, 'x'), 'y'),
...                     (h, 'x', 'y'),
...                     ('x', 'y')))
```

```
>>> rs.rewrite((add, 2, 0))       # Apply ruleset to single task
2
```

```
>>> rs.rewrite((f, (g, 'a', 3)))  # doctest: +SKIP
(h, 'a', 3)
```

```
>>> dsk = {'a': (add, 2, 0),       # Apply ruleset to full dask graph
...        'b': (f, (g, 'a', 3))}
```

```
>>> from toolz import valmap
>>> valmap(rs.rewrite, dsk)  # doctest: +SKIP
{'a': 2,
 'b': (h, 'a', 3)}
```

Attributes

rules [list] A list of *RewriteRule's included in the 'RuleSet*.

3.28.4 Custom Collections

For many problems, the built-in Dask collections (`dask.array`, `dask.dataframe`, `dask.bag`, and `dask.delayed`) are sufficient. For cases where they aren't, it's possible to create your own Dask collections. Here we describe the required methods to fulfill the Dask collection interface.

Note: This is considered an advanced feature. For most cases the built-in collections are probably sufficient.

Before reading this you should read and underestand:

- *overview*
- *graph specification*
- *custom graphs*

Contents

The Dask Collection Interface

To create your own Dask collection, you need to fulfill the following interface. Note that there is no required base class.

It is recommended to also read *Internals of the Core Dask Methods* to see how this interface is used inside Dask.

`__dask_graph__`(*self*)
The Dask graph.

dsk [MutableMapping, None] The Dask graph. If `None`, this instance will not be interpreted as a Dask collection, and none of the remaining interface methods will be called.

`__dask_keys__`(*self*)

The output keys for the Dask graph.

keys [list] A possibly nested list of keys that represent the outputs of the graph. After computation, the results will be returned in the same layout, with the keys replaced with their corresponding outputs.

`static __dask_optimize__`(*dsk*, *keys*, ***kwargs*)

Given a graph and keys, return a new optimized graph.

This method can be either a `staticmethod` or a `classmethod`, but not an `instancemethod`.

Note that graphs and keys are merged before calling `__dask_optimize__`; as such, the graph and keys passed to this method may represent more than one collection sharing the same optimize method.

If not implemented, defaults to returning the graph unchanged.

dsk [MutableMapping] The merged graphs from all collections sharing the same `__dask_optimize__` method.

keys [list] A list of the outputs from `__dask_keys__` from all collections sharing the same `__dask_optimize__` method.

****kwargs** Extra keyword arguments forwarded from the call to `compute` or `persist`. Can be used or ignored as needed.

optimized_dsk [MutableMapping] The optimized Dask graph.

`static __dask_scheduler__`(*dsk*, *keys*, ***kwargs*)

The default scheduler `get` to use for this object.

Usually attached to the class as a staticmethod, e.g.:

```
>>> import dask.threaded
>>> class MyCollection(object):
...     # Use the threaded scheduler by default
...     __dask_scheduler__ = staticmethod(dask.threaded.get)
```

`__dask_postcompute__`(*self*)

Return the finalizer and (optional) extra arguments to convert the computed results into their in-memory representation.

Used to implement `dask.compute`.

finalize [callable] A function with the signature `finalize(results, *extra_args)`. Called with the computed results in the same structure as the corresponding keys from `__dask_keys__`, as well as any extra arguments as specified in `extra_args`. Should perform any necessary finalization before returning the corresponding in-memory collection from `compute`. For example, the `finalize` function for `dask.array.Array` concatenates all the individual array chunks into one large numpy array, which is then the result of `compute`.

extra_args [tuple] Any extra arguments to pass to `finalize` after `results`. If no extra arguments should be an empty tuple.

`__dask_postpersist__`(*self*)

Return the rebuilder and (optional) extra arguments to rebuild an equivalent Dask collection from a persisted graph.

Used to implement `dask.persist`.

rebuild [callable] A function with the signature `rebuild(dsk, *extra_args)`. Called with a persisted graph containing only the keys and results from `__dask_keys__`, as well as any extra arguments as specified in `extra_args`. Should return an equivalent Dask collection with the same keys as `self`, but with the results already computed. For example, the `rebuild` function for `dask.array.Array` is just the `__init__` method called with the new graph but the same metadata.

extra_args [tuple] Any extra arguments to pass to `rebuild` after `dsk`. If no extra arguments should be an empty tuple.

Note: It's also recommended to define `__dask_tokenize__`, see *Implementing Deterministic Hashing*.

Internals of the Core Dask Methods

Dask has a few *core* functions (and corresponding methods) that implement common operations:

- `compute`: Convert one or more Dask collections into their in-memory counterparts
- `persist`: Convert one or more Dask collections into equivalent Dask collections with their results already computed and cached in memory
- `optimize`: Convert one or more Dask collections into equivalent Dask collections sharing one large optimized graph
- `visualize`: Given one or more Dask collections, draw out the graph that would be passed to the scheduler during a call to `compute` or `persist`

Here we briefly describe the internals of these functions to illustrate how they relate to the above interface.

Compute

The operation of `compute` can be broken into three stages:

1. **Graph Merging & Optimization**

   First, the individual collections are converted to a single large graph and nested list of keys. How this happens depends on the value of the `optimize_graph` keyword, which each function takes:

   - If `optimize_graph` is `True` (default), then the collections are first grouped by their `__dask_optimize__` methods. All collections with the same `__dask_optimize__` method have their graphs merged and keys concatenated, and then a single call to each respective `__dask_optimize__` is made with the merged graphs and keys. The resulting graphs are then merged.
   - If `optimize_graph` is `False`, then all the graphs are merged and all the keys concatenated.

   After this stage there is a single large graph and nested list of keys which represents all the collections.

2. **Computation**

   After the graphs are merged and any optimizations performed, the resulting large graph and nested list of keys are passed on to the scheduler. The scheduler to use is chosen as follows:

   - If a `get` function is specified directly as a keyword, use that
   - Otherwise, if a global scheduler is set, use that
   - Otherwise fall back to the default scheduler for the given collections. Note that if all collections don't share the same `__dask_scheduler__` then an error will be raised.

   Once the appropriate scheduler `get` function is determined, it is called with the merged graph, keys, and extra keyword arguments. After this stage, `results` is a nested list of values. The structure of this list mirrors that of `keys`, with each key substituted with its corresponding result.

3. **Postcompute**

   After the results are generated, the output values of `compute` need to be built. This is what the `__dask_postcompute__` method is for. `__dask_postcompute__` returns two things:

   - A `finalize` function, which takes in the results for the corresponding keys
   - A tuple of extra arguments to pass to `finalize` after the results

   To build the outputs, the list of collections and results is iterated over, and the finalizer for each collection is called on its respective results.

In pseudocode, this process looks like the following:

```
def compute(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    if kwargs.pop('optimize_graph', True):
        # If optimization is turned on, group the collections by
        # optimization method, and apply each method only once to the merged
        # sub-graphs.
        optimization_groups = groupby_optimization_methods(collections)
        graphs = []
        for optimize_method, cols in optimization_groups:
            # Merge the graphs and keys for the subset of collections that
            # share this optimization method
            sub_graph = merge_graphs([x.__dask_graph__() for x in cols])
            sub_keys = [x.__dask_keys__() for x in cols]
            # kwargs are forwarded to ``__dask_optimize__`` from compute
            optimized_graph = optimize_method(sub_graph, sub_keys, **kwargs)
            graphs.append(optimized_graph)
        graph = merge_graphs(graphs)
    else:
        graph = merge_graphs([x.__dask_graph__() for x in collections])
    # Keys are always the same
    keys = [x.__dask_keys__() for x in collections]

    # 2. Computation
    # --------------
    # Determine appropriate get function based on collections, global
    # settings, and keyword arguments
    get = determine_get_function(collections, **kwargs)
    # Pass the merged graph, keys, and kwargs to ``get``
    results = get(graph, keys, **kwargs)

    # 3. Postcompute
    # --------------
    output = []
    # Iterate over the results and collections
    for res, collection in zip(results, collections):
        finalize, extra_args = collection.__dask_postcompute__()
        out = finalize(res, **extra_args)
        output.append(out)

    # `dask.compute` always returns tuples
    return tuple(output)
```

Persist

Persist is very similar to `compute`, except for how the return values are created. It too has three stages:

1. **Graph Merging & Optimization**

   Same as in `compute`.

2. **Computation**

   Same as in `compute`, except in the case of the distributed scheduler, where the values in `results` are futures instead of values.

3. **Postpersist**

   Similar to `__dask_postcompute__`, `__dask_postpersist__` is used to rebuild values in a call to `persist`. `__dask_postpersist__` returns two things:

   - A `rebuild` function, which takes in a persisted graph. The keys of this graph are the same as `__dask_keys__` for the corresponding collection, and the values are computed results (for the single machine scheduler) or futures (for the distributed scheduler).
   - A tuple of extra arguments to pass to `rebuild` after the graph

   To build the outputs of `persist`, the list of collections and results is iterated over, and the rebuilder for each collection is called on the graph for its respective results.

In pseudocode, this looks like the following:

```
def persist(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    # **Same as in compute**
    graph = ...
    keys = ...

    # 2. Computation
    # --------------
    # **Same as in compute**
    results = ...

    # 3. Postpersist
    # --------------
    output = []
    # Iterate over the results and collections
    for res, collection in zip(results, collections):
        # res has the same structure as keys
        keys = collection.__dask_keys__()
        # Get the computed graph for this collection.
        # Here flatten converts a nested list into a single list
        subgraph = {k: r for (k, r) in zip(flatten(keys), flatten(res))}

        # Rebuild the output dask collection with the computed graph
        rebuild, extra_args = collection.__dask_postpersist__()
        out = rebuild(subgraph, *extra_args)

        output.append(out)

    # dask.persist always returns tuples
    return tuple(output)
```

Optimize

The operation of `optimize` can be broken into two stages:

1. **Graph Merging & Optimization**

   Same as in `compute`.

2. **Rebuilding**

   Similar to `persist`, the `rebuild` function and arguments from `__dask_postpersist__` are used to reconstruct equivalent collections from the optimized graph.

In pseudocode, this looks like the following:

```
def optimize(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    # **Same as in compute**
    graph = ...

    # 2. Rebuilding
    # -------------
    # Rebuild each dask collection using the same large optimized graph
    output = []
    for collection in collections:
        rebuild, extra_args = collection.__dask_postpersist__()
        out = rebuild(graph, *extra_args)
        output.append(out)

    # dask.optimize always returns tuples
    return tuple(output)
```

Visualize

Visualize is the simplest of the 4 core functions. It only has two stages:

1. **Graph Merging & Optimization**

   Same as in `compute`.

2. **Graph Drawing**

   The resulting merged graph is drawn using `graphviz` and outputs to the specified file.

In pseudocode, this looks like the following:

```
def visualize(*collections, **kwargs):
    # 1. Graph Merging & Optimization
    # -------------------------------
    # **Same as in compute**
    graph = ...

    # 2. Graph Drawing
    # ----------------
    # Draw the graph with graphviz's `dot` tool and return the result.
    return dot_graph(graph, **kwargs)
```

Adding the Core Dask Methods to Your Class

Defining the above interface will allow your object to used by the core Dask functions (`dask.compute`, `dask.persist`, `dask.visualize`, etc.). To add corresponding method versions of these, you can subclass from `dask.base.DaskMethodsMixin` which adds implementations of `compute`, `persist`, and `visualize` based on the interface above.

Example Dask Collection

Here we create a Dask collection representing a tuple. Every element in the tuple is represented as a task in the graph. Note that this is for illustration purposes only - the same user experience could be done using normal tuples with elements of `dask.delayed`:

```python
# Saved as dask_tuple.py
from dask.base import DaskMethodsMixin
from dask.optimization import cull

# We subclass from DaskMethodsMixin to add common dask methods to our
# class. This is nice but not necessary for creating a dask collection.
class Tuple(DaskMethodsMixin):
    def __init__(self, dsk, keys):
        # The init method takes in a dask graph and a set of keys to use
        # as outputs.
        self._dsk = dsk
        self._keys = keys

    def __dask_graph__(self):
        return self._dsk

    def __dask_keys__(self):
        return self._keys

    @staticmethod
    def __dask_optimize__(dsk, keys, **kwargs):
        # We cull unnecessary tasks here. Note that this isn't necessary,
        # dask will do this automatically, this just shows one optimization
        # you could do.
        dsk2, _ = cull(dsk, keys)
        return dsk2

    # Use the threaded scheduler by default.
    __dask_scheduler__ = staticmethod(dask.threaded.get)

    def __dask_postcompute__(self):
        # We want to return the results as a tuple, so our finalize
        # function is `tuple`. There are no extra arguments, so we also
        # return an empty tuple.
        return tuple, ()

    def __dask_postpersist__(self):
        # Since our __init__ takes a graph as its first argument, our
        # rebuild function can just be the class itself. For extra
        # arguments we also return a tuple containing just the keys.
        return Tuple, (self._keys,)

    def __dask_tokenize__(self):
```

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```
        # For tokenize to work we want to return a value that fully
        # represents this object. In this case it's the list of keys
        # to be computed.
        return tuple(self._keys)
```

Demonstrating this class:

```
>>> from dask_tuple import Tuple
>>> from operator import add, mul

# Define a dask graph
>>> dsk = {'a': 1,
...        'b': 2,
...        'c': (add, 'a', 'b'),
...        'd': (mul, 'b', 2),
...        'e': (add, 'b', 'c')}

# The output keys for this graph
>>> keys = ['b', 'c', 'd', 'e']

>>> x = Tuple(dsk, keys)

# Compute turns Tuple into a tuple
>>> x.compute()
(2, 3, 4, 5)

# Persist turns Tuple into a Tuple, with each task already computed
>>> x2 = x.persist()
>>> isinstance(x2, Tuple)
True
>>> x2.__dask_graph__()
{'b': 2,
 'c': 3,
 'd': 4,
 'e': 5}
>>> x2.compute()
(2, 3, 4, 5)
```

Checking if an object is a Dask collection

To check if an object is a Dask collection, use `dask.base.is_dask_collection`:

```
>>> from dask.base import is_dask_collection
>>> from dask import delayed

>>> x = delayed(sum)([1, 2, 3])
>>> is_dask_collection(x)
True
>>> is_dask_collection(1)
False
```

Implementing Deterministic Hashing

Dask implements its own deterministic hash function to generate keys based on the value of arguments. This function is available as `dask.base.tokenize`. Many common types already have implementations of `tokenize`, which can be found in `dask/base.py`.

When creating your own custom classes, you may need to register a `tokenize` implementation. There are two ways to do this:

1. The `__dask_tokenize__` method

   Where possible, it is recommended to define the `__dask_tokenize__` method. This method takes no arguments and should return a value fully representative of the object.

2. Register a function with `dask.base.normalize_token`

   If defining a method on the class isn't possible, you can register a tokenize function with the `normalize_token` dispatch. The function should have the same signature as described above.

In both cases the implementation should be the same, where only the location of the definition is different.

Note: Both Dask collections and normal Python objects can have implementations of `tokenize` using either of the methods described above.

Example

```
>>> from dask.base import tokenize, normalize_token

# Define a tokenize implementation using a method.
>>> class Foo(object):
...     def __init__(self, a, b):
...         self.a = a
...         self.b = b
...
...     def __dask_tokenize__(self):
...         # This tuple fully represents self
...         return (Foo, self.a, self.b)

>>> x = Foo(1, 2)
>>> tokenize(x)
'5988362b6e07087db2bc8e7c1c8cc560'
>>> tokenize(x) == tokenize(x)   # token is deterministic
True

# Register an implementation with normalize_token
>>> class Bar(object):
...     def __init__(self, x, y):
...         self.x = x
...         self.y = y

>>> @normalize_token.register(Bar)
... def tokenize_bar(x):
...     return (Bar, x.x, x.x)

>>> y = Bar(1, 2)
>>> tokenize(y)
```

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```
'5a7e9c3645aa44cf13d021c14452152e'
>>> tokenize(y) == tokenize(y)
True
>>> tokenize(y) == tokenize(x)  # tokens for different objects aren't equal
False
```

For more examples, see `dask/base.py` or any of the built-in Dask collections.

3.28.5 High Level Graphs

Dask graphs produced by collections like Arrays, Bags, and DataFrames have high-level structure that can be useful for visualization and high-level optimization. The task graphs produced by these collections encode this structure explicitly as `HighLevelGraph` objects. This document describes how to work with these in more detail.

Motivation and Example

In full generality, Dask schedulers expect arbitrary task graphs where each node is a single Python function call and each edge is a dependency between two function calls. These are usually stored in flat dictionaries. Here is some simple Dask DataFrame code and the task graph that it might generate:

```
import dask.dataframe as dd

df = dd.read_csv('myfile.*.csv')
df = df + 100
df = df[df.name == 'Alice']
```

```
{
 ('read-csv', 0): (pandas.read_csv, 'myfile.0.csv'),
 ('read-csv', 1): (pandas.read_csv, 'myfile.1.csv'),
 ('read-csv', 2): (pandas.read_csv, 'myfile.2.csv'),
 ('read-csv', 3): (pandas.read_csv, 'myfile.3.csv'),
 ('add', 0): (operator.add, ('read-csv', 0), 100),
 ('add', 1): (operator.add, ('read-csv', 1), 100),
 ('add', 2): (operator.add, ('read-csv', 2), 100),
 ('add', 3): (operator.add, ('read-csv', 3), 100),
 ('filter', 0): (lambda part: part[part.name == 'Alice'], ('add', 0)),
 ('filter', 1): (lambda part: part[part.name == 'Alice'], ('add', 1)),
 ('filter', 2): (lambda part: part[part.name == 'Alice'], ('add', 2)),
 ('filter', 3): (lambda part: part[part.name == 'Alice'], ('add', 3)),
}
```

The task graph is a dictionary that stores every Pandas-level function call necessary to compute the final result. We can see that there is some structure to this dictionary if we separate out the tasks that were associated to each high-level Dask DataFrame operation:

```
{
 # From the dask.dataframe.read_csv call
 ('read-csv', 0): (pandas.read_csv, 'myfile.0.csv'),
 ('read-csv', 1): (pandas.read_csv, 'myfile.1.csv'),
 ('read-csv', 2): (pandas.read_csv, 'myfile.2.csv'),
 ('read-csv', 3): (pandas.read_csv, 'myfile.3.csv'),

 # From the df + 100 call
```

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```
 ('add', 0): (operator.add, ('read-csv', 0), 100),
 ('add', 1): (operator.add, ('read-csv', 1), 100),
 ('add', 2): (operator.add, ('read-csv', 2), 100),
 ('add', 3): (operator.add, ('read-csv', 3), 100),

 # From the df[df.name == 'Alice'] call
 ('filter', 0): (lambda part: part[part.name == 'Alice'], ('add', 0)),
 ('filter', 1): (lambda part: part[part.name == 'Alice'], ('add', 1)),
 ('filter', 2): (lambda part: part[part.name == 'Alice'], ('add', 2)),
 ('filter', 3): (lambda part: part[part.name == 'Alice'], ('add', 3)),
}
```

By understanding this high-level structure we are able to understand our task graphs more easily (this is more important for larger datasets when there are thousands of tasks per layer) and how to perform high-level optimizations. For example, in the case above we may want to automatically rewrite our code to filter our datasets before adding 100:

```
# Before
df = dd.read_csv('myfile.*.csv')
df = df + 100
df = df[df.name == 'Alice']

# After
df = dd.read_csv('myfile.*.csv')
df = df[df.name == 'Alice']
df = df + 100
```

Dask's high level graphs help us to explicitly encode this structure by storing our task graphs in layers with dependencies between layers:

```
>>> import dask.dataframe as dd

>>> df = dd.read_csv('myfile.*.csv')
>>> df = df + 100
>>> df = df[df.name == 'Alice']

>>> graph = df.__dask_graph__()
>>> graph.layers
{
 'read-csv': {('read-csv', 0): (pandas.read_csv, 'myfile.0.csv'),
              ('read-csv', 1): (pandas.read_csv, 'myfile.1.csv'),
              ('read-csv', 2): (pandas.read_csv, 'myfile.2.csv'),
              ('read-csv', 3): (pandas.read_csv, 'myfile.3.csv')},

 'add': {('add', 0): (operator.add, ('read-csv', 0), 100),
         ('add', 1): (operator.add, ('read-csv', 1), 100),
         ('add', 2): (operator.add, ('read-csv', 2), 100),
         ('add', 3): (operator.add, ('read-csv', 3), 100)}

 'filter': {('filter', 0): (lambda part: part[part.name == 'Alice'], ('add', 0)),
            ('filter', 1): (lambda part: part[part.name == 'Alice'], ('add', 1)),
            ('filter', 2): (lambda part: part[part.name == 'Alice'], ('add', 2)),
            ('filter', 3): (lambda part: part[part.name == 'Alice'], ('add', 3))}
}

>>> graph.dependencies
{
```

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```
 'read-csv': set(),
 'add': {'read-csv'},
 'filter': {'add'}
}
```

While the DataFrame points to the output layers on which it depends directly:

```
>>> df.__dask_layers__()
{'filter'}
```

HighLevelGraphs

The `HighLevelGraph` object is a `Mapping` object composed of other sub-`Mappings`, along with a high-level dependency mapping between them:

```
class HighLevelGraph(Mapping):
    layers: Dict[str, Mapping]
    dependencies: Dict[str, Set[str]]
```

You can construct a HighLevelGraph explicitly by providing both to the constructor:

```
layers = {
   'read-csv': {('read-csv', 0): (pandas.read_csv, 'myfile.0.csv'),
                ('read-csv', 1): (pandas.read_csv, 'myfile.1.csv'),
                ('read-csv', 2): (pandas.read_csv, 'myfile.2.csv'),
                ('read-csv', 3): (pandas.read_csv, 'myfile.3.csv')},

   'add': {('add', 0): (operator.add, ('read-csv', 0), 100),
           ('add', 1): (operator.add, ('read-csv', 1), 100),
           ('add', 2): (operator.add, ('read-csv', 2), 100),
           ('add', 3): (operator.add, ('read-csv', 3), 100)}

   'filter': {('filter', 0): (lambda part: part[part.name == 'Alice'], ('add', 0)),
              ('filter', 1): (lambda part: part[part.name == 'Alice'], ('add', 1)),
              ('filter', 2): (lambda part: part[part.name == 'Alice'], ('add', 2)),
              ('filter', 3): (lambda part: part[part.name == 'Alice'], ('add', 3))}
}

dependencies = {'read-csv': set(),
                'add': {'read-csv'},
                'filter': {'add'}}

graph = HighLevelGraph(layers, dependencies)
```

This object satisfies the `Mapping` interface, and so operates as a normal Python dictionary that is the semantic merger of the underlying layers:

```
>>> len(graph)
12
>>> graph[('read-csv', 0)]
('read-csv', 0): (pandas.read_csv, 'myfile.0.csv'),
```

API

class dask.highlevelgraph.**HighLevelGraph**(*layers*, *dependencies*)

Task graph composed of layers of dependent subgraphs

This object encodes a Dask task graph that is composed of layers of dependent subgraphs, such as commonly occurs when building task graphs using high level collections like Dask array, bag, or dataframe.

Typically each high level array, bag, or dataframe operation takes the task graphs of the input collections, merges them, and then adds one or more new layers of tasks for the new operation. These layers typically have at least as many tasks as there are partitions or chunks in the collection. The HighLevelGraph object stores the subgraphs for each operation separately in sub-graphs, and also stores the dependency structure between them.

Parameters

layers [Dict[str, Mapping]] The subgraph layers, keyed by a unique name

dependencies [Dict[str, Set[str]]] The set of layers on which each layer depends

See also:

HighLevelGraph.from_collections typically used by developers to make new HighLevelGraphs

Examples

Here is an idealized example that shows the internal state of a HighLevelGraph

```
>>> import dask.dataframe as dd
```

```
>>> df = dd.read_csv('myfile.*.csv')  # doctest: +SKIP
>>> df = df + 100  # doctest: +SKIP
>>> df = df[df.name == 'Alice']  # doctest: +SKIP
```

```
>>> graph = df.__dask_graph__()  # doctest: +SKIP
>>> graph.layers  # doctest: +SKIP
{
 'read-csv': {('read-csv', 0): (pandas.read_csv, 'myfile.0.csv'),
              ('read-csv', 1): (pandas.read_csv, 'myfile.1.csv'),
              ('read-csv', 2): (pandas.read_csv, 'myfile.2.csv'),
              ('read-csv', 3): (pandas.read_csv, 'myfile.3.csv')},
 'add': {('add', 0): (operator.add, ('read-csv', 0), 100),
         ('add', 1): (operator.add, ('read-csv', 1), 100),
         ('add', 2): (operator.add, ('read-csv', 2), 100),
         ('add', 3): (operator.add, ('read-csv', 3), 100)}
 'filter': {('filter', 0): (lambda part: part[part.name == 'Alice'], ('add', 0)),
            ('filter', 1): (lambda part: part[part.name == 'Alice'], ('add', 1)),
            ('filter', 2): (lambda part: part[part.name == 'Alice'], ('add', 2)),
            ('filter', 3): (lambda part: part[part.name == 'Alice'], ('add', 3))}
}
```

```
>>> graph.dependencies  # doctest: +SKIP
{
 'read-csv': set(),
 'add': {'read-csv'},
 'filter': {'add'}
}
```

classmethod from_collections (*name*, *layer*, *dependencies=()*)

Construct a HighLevelGraph from a new layer and a set of collections

This constructs a HighLevelGraph in the common case where we have a single new layer and a set of old collections on which we want to depend.

This pulls out the `__dask_layers__()` method of the collections if they exist, and adds them to the dependencies for this new layer. It also merges all of the layers from all of the dependent collections together into the new layers for this graph.

Parameters

name [str] The name of the new layer

layer [Mapping] The graph layer itself

dependencies [List of Dask collections] A lit of other dask collections (like arrays or dataframes) that have graphs themselves

Examples

In typical usage we make a new task layer, and then pass that layer along with all dependent collections to this method.

```
>>> def add(self, other):
...     name = 'add-' + tokenize(self, other)
...     layer = {(name, i): (add, input_key, other)
...              for i, input_key in enumerate(self.__dask_keys__())}
...     graph = HighLevelGraph.from_collections(name, layer,␣
↪dependencies=[self])
...     return new_collection(name, graph)
```

get (*k*[, *d*]) → D[k] if k in D, else d. d defaults to None.

items () → a set-like object providing a view on D's items

keys () → a set-like object providing a view on D's keys

values () → an object providing a view on D's values

3.28.6 Motivation

Normally, humans write programs and then compilers/interpreters interpret them (for example, `python`, `javac`, `clang`). Sometimes humans disagree with how these compilers/interpreters choose to interpret and execute their programs. In these cases, humans often bring the analysis, optimization, and execution of code into the code itself.

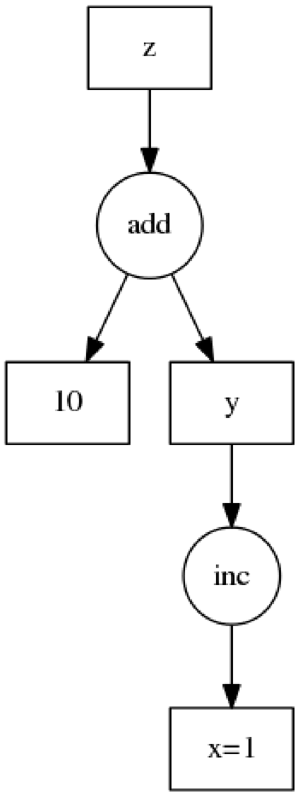
Commonly a desire for parallel execution causes this shift of responsibility from compiler to human developer. In these cases, we often represent the structure of our program explicitly as data within the program itself.

A common approach to parallel execution in user-space is *task scheduling*. In task scheduling we break our program into many medium-sized tasks or units of computation, often a function call on a non-trivial amount of data. We represent these tasks as nodes in a graph with edges between nodes if one task depends on data produced by another. We call upon a *task scheduler* to execute this graph in a way that respects these data dependencies and leverages parallelism where possible, multiple independent tasks can be run simultaneously.

Many solutions exist. This is a common approach in parallel execution frameworks. Often task scheduling logic hides within other larger frameworks (Luigi, Storm, Spark, IPython Parallel, and so on) and so is often reinvented.

Dask is a specification that encodes task schedules with minimal incidental complexity using terms common to all Python projects, namely dicts, tuples, and callables. Ideally this minimum solution is easy to adopt and understand by a broad community.

3.28.7 Example



Consider the following simple program:

```
def inc(i):
    return i + 1

def add(a, b):
    return a + b

x = 1
y = inc(x)
z = add(y, 10)
```

We encode this as a dictionary in the following way:

```
d = {'x': 1,
     'y': (inc, 'x'),
     'z': (add, 'y', 10)}
```

While less pleasant than our original code, this representation can be analyzed and executed by other Python code, not just the CPython interpreter. We don't recommend that users write code in this way, but rather that it is an appropriate target for automated systems. Also, in non-toy examples, the execution times are likely much larger than for `inc` and `add`, warranting the extra complexity.

3.28.8 Schedulers

The Dask library currently contains a few schedulers to execute these graphs. Each scheduler works differently, providing different performance guarantees and operating in different contexts. These implementations are not special and others can write different schedulers better suited to other applications or architectures easily. Systems that emit dask graphs (like Dask Array, Dask Bag, and so on) may leverage the appropriate scheduler for the application and hardware.

3.29 Remote Data

Dask can read data from a variety of data stores including local file systems, network file systems, cloud object stores, and Hadoop. Typically this is done by prepending a protocol like `"s3://"` to paths used in common data access functions like `dd.read_csv`:

```
import dask.dataframe as dd
df = dd.read_csv('s3://bucket/path/to/data-*.csv')
df = dd.read_parquet('gcs://bucket/path/to/data-*.parq')

import dask.bag as db
b = db.read_text('hdfs://path/to/*.json').map(json.loads)
```

Dask uses fsspec for local, cluster and remote data IO. Other file interaction, such as loading of configuration, is done using ordinary python method.

The following remote services are well supported and tested against the main codebase:

- **Local or Network File System**: `file://` - the local file system, default in the absence of any protocol
- **Hadoop File System**: `hdfs://` - Hadoop Distributed File System, for resilient, replicated files within a cluster. This uses PyArrow as the backend.
- **Amazon S3**: `s3://` - Amazon S3 remote binary store, often used with Amazon EC2, using the library s3fs
- **Google Cloud Storage**: `gcs://` or `gs:` - Google Cloud Storage, typically used with Google Compute resource using gcsfs (in development)
- **HTTP(s)**: `http://` or `https://` for reading data directly from HTTP web servers
- **Azure Datalake Storage**: `adl://`, for use with the Microsoft Azure platform, using azure-data-lake-store-python, is unavailable in the current release of `fsspec`, but a new version using Microsoft's "protocol 2" should come soon.

`fsspec` also provides other file sytstems that may be of interest to Dask users, such as ssh, ftp and webhdfs. See the documentation for more information.

When specifying a storage location, a URL should be provided using the general form `protocol://path/to/data`. If no protocol is provided, the local file system is assumed (same as `file://`).

Lower-level details on how Dask handles remote data is described is described below in the Internals section

3.29.1 Optional Parameters

Two methods exist for passing parameters to the backend file system driver: extending the URL to include username, password, server, port, etc.; and providing `storage_options`, a dictionary of parameters to pass on. The second form is more general, as any number of file system-specific options can be passed.

Examples:

```
df = dd.read_csv('hdfs://user@server:port/path/*.csv')

df = dd.read_parquet('s3://bucket/path',
                     storage_options={'anon': True, 'use_ssl': False})
```

Details on how to provide configuration for the main back-ends are listed next, but further details can be found in the documentation pages of the relevant back-end.

Each back-end has additional installation requirements and may not be available at runtime. The dictionary `fsspec.registry` contains the currently imported file systems. To see which backends `fsspec` knows how to import, you can do

```
from fsspec.registry import known_implementations
known_implementations
```

Note that some backends appear twice, if they can be referenced with multiple protocol strings, like "http" and "https".

3.29.2 Local File System

Local files are always accessible, and all parameters passed as part of the URL (beyond the path itself) or with the `storage_options` dictionary will be ignored.

This is the default back-end, and the one used if no protocol is passed at all.

We assume here that each worker has access to the same file system - either the workers are co-located on the same machine, or a network file system is mounted and referenced at the same path location for every worker node.

Locations specified relative to the current working directory will, in general, be respected (as they would be with the built-in python `open`), but this may fail in the case that the client and worker processes do not necessarily have the same working directory.

3.29.3 Hadoop File System

The Hadoop File System (HDFS) is a widely deployed, distributed, data-local file system written in Java. This file system backs many clusters running Hadoop and Spark. HDFS support can be provided by PyArrow.

By default, the back-end attempts to read the default server and port from local Hadoop configuration files on each node, so it may be that no configuration is required. However, the server, port, and user can be passed as part of the url: `hdfs://user:pass@server:port/path/to/data`, or using the `storage_options=` kwarg.

Extra Configuration for PyArrow

The following additional options may be passed to the `PyArrow` driver via `storage_options`:

- `host`, `port`, `user`: Basic authentication
- `kerb_ticket`: Path to kerberos ticket cache

PyArrow's `libhdfs` driver can also be affected by a few environment variables. For more information on these, see the PyArrow documentation.

3.29.4 Amazon S3

Amazon S3 (Simple Storage Service) is a web service offered by Amazon Web Services.

The S3 back-end available to Dask is s3fs, and is importable when Dask is imported.

Authentication for S3 is provided by the underlying library boto3. As described in the auth docs, this could be achieved by placing credentials files in one of several locations on each node: `~/.aws/credentials`, `~/.aws/config`, `/etc/boto.cfg`, and `~/.boto`. Alternatively, for nodes located within Amazon EC2, IAM roles can be set up for each node, and then no further configuration is required. The final authentication option for user credentials can be passed directly in the URL (`s3://keyID:keySecret/bucket/key/name`) or using `storage_options`. In this case, however, the key/secret will be passed to all workers in-the-clear, so this method is only recommended on well-secured networks.

The following parameters may be passed to s3fs using `storage_options`:

- anon: Whether access should be anonymous (default False)
- key, secret: For user authentication
- token: If authentication has been done with some other S3 client
- use_ssl: Whether connections are encrypted and secure (default True)
- client_kwargs: Dict passed to the boto3 client, with keys such as *region_name* or *endpoint_url*. Notice: do not pass the *config* option here, please pass it's content to *config_kwargs* instead.
- config_kwargs: Dict passed to the s3fs.S3FileSystem, which passes it to the boto3 client's config option.
- requester_pays: Set True if the authenticated user will assume transfer costs, which is required by some providers of bulk data
- default_block_size, default_fill_cache: These are not of particular interest to Dask users, as they concern the behaviour of the buffer between successive reads
- kwargs: Other parameters are passed to the boto3 Session object, such as *profile_name*, to pick one of the authentication sections from the configuration files referred to above (see here)

Using Other S3-Compatible Services

By using the *endpoint_url* option, you may use other s3-compatible services, for example, using *AlibabaCloud OSS*:

```
dask_function(...,
    storage_options={
        "key": ...,
        "secret": ...,
        "client_kwargs": {
            "endpoint_url": "http://some-region.some-s3-compatible.com",
        },
        # this dict goes to boto3 client's `config`
        #   `addressing_style` is required by AlibabaCloud, other services may not
        "config_kwargs": {"s3": {"addressing_style": "virtual"}},
    })
```

3.29.5 Google Cloud Storage

Google Cloud Storage is a RESTful online file storage web service for storing and accessing data on Google's infrastructure.

The GCS back-end is identified by the protocol identifiers `gcs` and `gs`, which are identical in their effect.

Multiple modes of authentication are supported. These options should be included in the `storage_options` dictionary as `{'token': ..}` submitted with your call to a storage-based Dask function/method. See the gcsfs documentation for further details.

General recommendations for distributed clusters, in order:

- use `anon` for public data
- use `cloud` if this is available
- use gcloud to generate a JSON file, and distribute this to all workers, and supply the path to the file
- use gcsfs directly with the `browser` method to generate a token cache file (`~/.gcs_tokens`) and distribute this to all workers, thereafter using method `cache`

A final suggestion is shown below, which may be the fastest and simplest for authenticated access (as opposed to anonymous), since it will not require re-authentication. However, this method is not secure since credentials will be passed directly around the cluster. This is fine if you are certain that the cluster is itself secured. You need to create a `GCSFileSystem` object using any method that works for you and then pass its credentials directly:

```
gcs = GCSFileSystem(...)
dask_function(..., storage_options={'token': gcs.session.credentials})
```

3.29.6 Azure

Warning: Support for AzureDLFileSystem (ADL) is not currently offered. We hope to provide both datalake and blob support using Protocol 2 soon.

authentication in `storage_options=`, and all other parameters will be passed on to the AzureDLFileSystem constructor (follow the link for further information). The auth parameters are passed directly to workers, so this should only be used within a secure cluster.

3.29.7 HTTP(S)

Direct file-like access to arbitrary URLs is available over HTTP and HTTPS. However, there is no such thing as `glob` functionality over HTTP, so only explicit lists of files can be used.

Server implementations differ in the information they provide - they may or may not specify the size of a file via a HEAD request or at the start of a download - and some servers may not respect byte range requests. The HTTPFileSystem therefore offers best-effort behaviour: the download is streamed but, if more data is seen than the configured block-size, an error will be raised. To be able to access such data you must read the whole file in one shot (and it must fit in memory).

Using a block size of 0 will return normal `requests` streaming file-like objects, which are stable, but provide no random access.

3.29.8 Developer API

The prototype for any file system back-end can be found in `fsspec.spec.AbstractFileSystem`. Any new implementation should provide the same API, or directly subclass, and make itself available as a protocol to Dask. For example, the following would register the protocol "myproto", described by the implementation class `MyProtoFileSystem`. URLs of the form `myproto://` would thereafter be dispatched to the methods of this class:

```
fsspec.registry['myproto'] = MyProtoFileSystem
```

However, it would be better to submit a PR to `fsspec` to include the class in the `known_implementations`.

3.29.9 Internals

Dask contains internal tools for extensible data ingestion in the `dask.bytes` package and using fsspec. . *These functions are developer-focused rather than for direct consumption by users. These functions power user facing functions like* `dd.read_csv` *and* `db.read_text` *which are probably more useful for most users.*

`read_bytes`(urlpath[, delimiter, not_zero, . . .])	Given a path or paths, return delayed objects that read from those paths.
`open_files`(urlpath[, mode, compression, . . .])	Given a path or paths, return a list of `OpenFile` objects.

These functions are extensible in their output formats (bytes, file objects), their input locations (file system, S3, HDFS), line delimiters, and compression formats.

Both functions are *lazy*, returning either point to blocks of bytes (`read_bytes`) or open file objects (`open_files`). They can handle different storage backends by prepending protocols like `s3://` or `hdfs://` (see below). They handle compression formats listed in `fsspec.compression`, some of which may require additional packages to be installed.

These functions are not used for all data sources. Some data sources like HDF5 are quite particular and receive custom treatment.

Delimiters

The `read_bytes` function takes a path (or globstring of paths) and produces a sample of the first file and a list of delayed objects for each of the other files. If passed a delimiter such as `delimiter=b'\n'`, it will ensure that the blocks of bytes start directly after a delimiter and end directly before a delimiter. This allows other functions, like `pd.read_csv`, to operate on these delayed values with expected behavior.

These delimiters are useful both for typical line-based formats (log files, CSV, JSON) as well as other delimited formats like Avro, which may separate logical chunks by a complex sentinel string. Note that the delimiter finding algorithm is simple, and will not account for characters that are escaped, part of a UTF-8 code sequence or within the quote marks of a string.

Compression

These functions support widely available compression technologies like `gzip`, `bz2`, `xz`, `snappy`, and `lz4`. More compressions can be easily added by inserting functions into dictionaries available in the `fsspec.compression` module. This can be done at runtime and need not be added directly to the codebase.

However, most compression technologies like `gzip` do not support efficient random access, and so are useful for streaming `open_files` but not useful for `read_bytes` which splits files at various points.

API

`dask.bytes.`**`read_bytes`**(*urlpath*, *delimiter=None*, *not_zero=False*, *blocksize='128 MiB'*, *sample='10 kiB'*, *compression=None*, *include_path=False*, ***kwargs*)

Given a path or paths, return delayed objects that read from those paths.

The path may be a filename like `'2015-01-01.csv'` or a globstring like `'2015-*-*.csv'`.

The path may be preceded by a protocol, like `s3://` or `hdfs://` if those libraries are installed.

This cleanly breaks data by a delimiter if given, so that block boundaries start directly after a delimiter and end on the delimiter.

Parameters

urlpath [string or list] Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

delimiter [bytes] An optional delimiter, like `b'\n'` on which to split blocks of bytes.

not_zero [bool] Force seek of start-of-file delimiter, discarding header.

blocksize [int, str] Chunk size in bytes, defaults to "128 MiB"

compression [string or None] String like 'gzip' or 'xz'. Must support efficient random access.

sample [int, string, or boolean] Whether or not to return a header sample. Values can be `False` for "no sample requested" Or an integer or string value like `2**20` or `"1 MiB"`

include_path [bool] Whether or not to include the path with the bytes representing a particular file. Default is False.

****kwargs** [dict] Extra options that make sense to a particular storage connection, e.g. host, port, username, password, etc.

Returns

sample [bytes] The sample header

blocks [list of lists of `dask.Delayed`] Each list corresponds to a file, and each delayed object computes to a block of bytes from that file.

paths [list of strings, only included if include_path is True] List of same length as blocks, where each item is the path to the file represented in the corresponding block.

Examples

```
>>> sample, blocks = read_bytes('2015-*-*.csv', delimiter=b'\n')  # doctest: +SKIP
>>> sample, blocks = read_bytes('s3://bucket/2015-*-*.csv', delimiter=b'\n')  #␣
↪doctest: +SKIP
>>> sample, paths, blocks = read_bytes('2015-*-*.csv', include_path=True)  #␣
↪doctest: +SKIP
```

`dask.bytes.open_files`(*urlpath*, *mode='rb'*, *compression=None*, *encoding='utf8'*, *errors=None*, *name_function=None*, *num=1*, *protocol=None*, *newline=None*, ***kwargs*)

Given a path or paths, return a list of `OpenFile` objects.

For writing, a str path must contain the "*" character, which will be filled in by increasing numbers, e.g., "part*" -> "part1", "part2" if num=2.

For either reading or writing, can instead provide explicit list of paths.

Parameters

urlpath: string or list Absolute or relative filepath(s). Prefix with a protocol like `s3://` to read from alternative filesystems. To read from multiple files you can pass a globstring or a list of paths, with the caveat that they must all have the same protocol.

mode: 'rb', 'wt', etc.

compression: string Compression to use. See `dask.bytes.compression.files` for options.

encoding: str For text mode only

errors: None or str Passed to TextIOWrapper in text mode

name_function: function or None if opening a set of files for writing, those files do not yet exist, so we need to generate their names by formatting the urlpath for each sequence number

num: int [1] if writing mode, number of files we expect to create (passed to name+function)

protocol: str or None If given, overrides the protocol found in the URL.

newline: bytes or None Used for line terminator in text mode. If None, uses system default; if blank, uses no translation.

****kwargs: dict** Extra options that make sense to a particular storage connection, e.g. host, port, username, password, etc.

Returns

List of ‘‘OpenFile‘‘ objects.

Examples

```
>>> files = open_files('2015-*-*.csv')  # doctest: +SKIP
>>> files = open_files('s3://bucket/2015-*-*.csv.gz', compression='gzip')  #␣
↪doctest: +SKIP
```

3.30 GPUs

Dask works with GPUs in a few ways.

3.30.1 Custom Computations

Many people use Dask alongside GPU-accelerated libraries like PyTorch and TensorFlow to manage workloads across several machines. They typically use Dask's custom APIs, notably *Delayed* and *Futures*.

Dask doesn't need to know that these functions use GPUs. It just runs Python functions. Whether or not those Python functions use a GPU is orthogonal to Dask. It will work regardless.

As a worked example, you may want to view this talk:

3.30.2 High Level Collections

Dask can also help to scale out large array and dataframe computations by combining the Dask Array and DataFrame collections with a GPU-accelerated array or dataframe library.

Recall that *Dask Array* creates a large array out of many NumPy arrays and *Dask DataFrame* creates a large dataframe out of many Pandas dataframes. We can use these same systems with GPUs if we swap out the NumPy/Pandas components with GPU-accelerated versions of those same libraries, as long as the GPU accelerated version looks enough like NumPy/Pandas in order to interoperate with Dask.

Fortunately, libraries that mimic NumPy, Pandas, and Scikit-Learn on the GPU do exist.

DataFrames

The RAPIDS libraries provide a GPU accelerated Pandas-like library, cuDF, which interoperates well and is tested against Dask DataFrame.

If you have cuDF installed then you should be able to convert a Pandas-backed Dask DataFrame to a cuDF-backed Dask DataFrame as follows:

```
import cudf

df = df.map_partitions(cudf.from_pandas)  # convert pandas partitions into cudf␣
↪partitions
```

However, cuDF does not support the entire Pandas interface, and so a variety of Dask DataFrame operations will not function properly. Check the cuDF API Reference for currently supported interface.

Arrays

Note: Dask's integration with CuPy relies on features recently added to NumPy and CuPy, particularly in version `numpy>=1.17` and `cupy>=6`

Chainer's CuPy library provides a GPU accelerated NumPy-like library that interoperates nicely with Dask Array.

If you have CuPy installed then you should be able to convert a NumPy-backed Dask Array into a CuPy backed Dask Array as follows:

```
import cupy

x = x.map_blocks(cupy.asarray)
```

CuPy is fairly mature and adheres closely to the NumPy API. However, small differences do exist and these can cause Dask Array operations to function improperly. Check the CuPy Reference Manual for API compatibility.

Scikit-Learn

There are a variety of GPU accelerated machine learning libraries that follow the Scikit-Learn Estimator API of fit, transform, and predict. These can generally be used within Dask-ML's meta estimators, such as hyper parameter optimization.

Some of these include:

- Skorch
- cuML
- LightGBM
- XGBoost
- Thunder SVM
- Thunder GBM

3.30.3 Setup

From the examples above we can see that the user experience of using Dask with GPU-backed libraries isn't very different from using it with CPU-backed libraries. However, there are some changes you might consider making when setting up your cluster.

Restricting Work

By default Dask allows as many tasks as you have CPU cores to run concurrently. However if your tasks primarily use a GPU then you probably want far fewer tasks running at once. There are a few ways to limit parallelism here:

- Limit the number of threads explicitly on your workers using the `--nthreads` keyword in the CLI or the `ncores=` keyword the Cluster constructor.
- Use worker resources and tag certain tasks as GPU tasks so that the scheduler will limit them, while leaving the rest of your CPU cores for other work

Specifying GPUs per Machine

Some configurations may have many GPU devices per node. Dask is often used to balance and coordinate work between these devices.

In these situations it is common to start one Dask worker per device, and use the CUDA environment varible `CUDA_VISIBLE_DEVICES` to pin each worker to prefer one device.

```
# If we have four GPUs on one machine
CUDA_VISIBLE_DEVICES=0 dask-worker ...
CUDA_VISIBLE_DEVICES=1 dask-worker ...
CUDA_VISIBLE_DEVICES=2 dask-worker ...
CUDA_VISIBLE_DEVICES=3 dask-worker ...
```

The Dask CUDA project contains some convenience CLI and Python utilities to automate this process.

3.30.4 Work in Progress

GPU computing is a quickly moving field today and as a result the information in this page is likely to go out of date quickly. We encourage interested readers to check out Dask's Blog which has more timely updates on ongoing work.

3.31 Citations

Dask is developed by many people from many institutions. Some of these developers are academics who depend on academic citations to justify their efforts. Unfortunately, no single citation can do all of these developers (and the developers to come) sufficient justice. Instead, we choose to use a single blanket citation for all developers past and present.

To cite Dask in publications, please use the following:

```
Dask Development Team (2016). Dask: Library for dynamic task scheduling
URL https://dask.org
```

A BibTeX entry for LaTeX users follows:

```
@Manual{,
  title = {Dask: Library for dynamic task scheduling},
  author = {{Dask Development Team}},
  year = {2016},
  url = {https://dask.org},
}
```

The full author list is available using `git` (e.g. `git shortlog -ns`).

3.31.1 Papers about parts of Dask

Rocklin, Matthew. "Dask: Parallel Computation with Blocked algorithms and Task Scheduling." (2015). PDF.

```
@InProceedings{ matthew_rocklin-proc-scipy-2015,
  author     = { Matthew Rocklin },
  title      = { Dask: Parallel Computation with Blocked algorithms and Task␣
↪Scheduling },
  booktitle = { Proceedings of the 14th Python in Science Conference },
  pages      = { 130 - 136 },
  year       = { 2015 },
  editor     = { Kathryn Huff and James Bergstra }
}
```

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Dask receives generous funding and support from the following sources:

1. The time and effort of numerous open source contributors
2. The DARPA XData program
3. The Moore Foundation's Data Driven Discovery program
4. Anaconda Inc
5. A variety of private companies who sponsor the development of particular open source features

We encourage monetary donations to NumFOCUS to support open source scientific computing software.

3.33 Images and Logos

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[1] Pebay, Philippe (2008), "Formulas for Robust, One-Pass Parallel

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