

Pascal Bugnion, Arun Manivannan,
Patrick R. Nicolas

Scala: Guide for Data Science Professionals

Learning Path

Scala will be a valuable tool to have on hand during your data science journey for everything from data cleaning to cutting-edge machine learning



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A course in three modules



BIRMINGHAM - MUMBAI

Scala: Guide for Data Science Professionals

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Credits

Authors

Pascal Bugnion
Arun Manivannan
Patrick R. Nicolas

Reviewers

Umanga Bista
Radek Ostrowski
Yuanhang Wang
Amir Hajian
Shams Mahmood Imam
Gerald Loeffler
Subhajit Datta
Rui Gonçalves
Patricia Hoffman, PhD
Md Zahidul Islam

Content Development Editor

Trusha Shriyan

Graphics

Kirk D'Penha

Production Coordinator

Shantanu N. Zagade

Preface

Scala is a popular language for data science. By emphasizing immutability and functional constructs, Scala lends itself well to the construction of robust libraries for concurrency and big data analysis. A rich ecosystem of tools for data science has therefore developed around Scala, including libraries for accessing SQL and NoSQL databases, frameworks for building distributed applications like Apache Spark and libraries for linear algebra and numerical algorithms. We will explore this rich and growing ecosystem in this learning path.

What this learning path covers

Module 1, Scala for Data Science, will introduce you to the libraries for ingesting, storing, manipulating, processing, and visualizing data in Scala. Packed with real-world examples and interesting data sets, this module will teach you to ingest data from flat files and web APIs and store it in a SQL or NoSQL database. It will show you how to design scalable architectures to process and modeling your data, starting from simple concurrency constructs such as parallel collections and futures, through to actor systems and Apache Spark. As well as Scala's emphasis on functional structures and immutability, you will learn how to use the right parallel construct for the job at hand, minimizing development time without compromising scalability. Finally, you will learn how to build beautiful interactive visualizations using web frameworks. This module gives tutorials on some of the most common Scala libraries for data science, allowing you to quickly get up to speed with building data science and data engineering solutions.

Module 2, Scala Data Analysis Cookbook, will introduce you to the most popular Scala tools, libraries, and frameworks through practical recipes around loading, manipulating, and preparing your data. It will also help you explore and make sense of your data using stunning and insightful visualizations, and machine learning toolkits. Starting with introductory recipes on utilizing the Breeze and Spark libraries, get to grips with how to import data from a host of possible sources and how to pre-process numerical, string, and date data. Next, you'll get an understanding of concepts that will help you visualize data using the Apache Zeppelin and Bokeh bindings in Scala, enabling exploratory data analysis. Discover how to program quintessential machine learning algorithms using Spark ML library. Work through steps to scale your machine learning models and deploy them into a standalone cluster, EC2, YARN, and Mesos. Finally dip into the powerful options presented by Spark Streaming, and machine learning for streaming data, as well as utilizing Spark GraphX.

Module 3, Scala for Machine Learning, will introduce you to the functional capabilities of the Scala programming language that are critical to the creation of machine learning algorithms such as dependency injection and implicits. Your learning journey starts with data pre-processing and filtering techniques, then move on to clustering and dimension reduction, Naïve Bayes, regression models, sequential data, regularization and kernelization, support vector machines, Neural networks, generic algorithms and re-enforcement learning. The review of the Akka framework and Apache Spark clusters concludes the tutorial. Techniques throughout the module is applied to the analysis, recommendation, classification, and prediction of financial markets.

This module will guide you through the process of building AI applications with diagrams, formal mathematical notation, source code snippets and useful tips.

What you need for this learning path

The examples provided in this learning path require that you have a working Scala installation and SBT, the Simple Build Tool, a command line utility for compiling and running Scala code. We will walk you through how to install these in the next sections. We do not require a specific IDE. The code examples can be written in your favorite text editor or IDE.

Who this learning path is for

This learning path is perfect for those who are comfortable with Scala programming and now want to enter the field of data science. Some knowledge of statistics is expected.

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Module 1

Scala for Data Science

Leverage the power of Scala to build scalable, robust data science applications

1

Scala and Data Science

The second half of the 20th century was the age of silicon. In fifty years, computing power went from extremely scarce to entirely mundane. The first half of the 21st century is the age of the Internet. The last 20 years have seen the rise of giants such as Google, Twitter, and Facebook – giants that have forever changed the way we view knowledge.

The Internet is a vast nexus of information. Ninety percent of the data generated by humanity has been generated in the last 18 months. The programmers, statisticians, and scientists who can harness this glut of data to derive real understanding will have an ever greater influence on how businesses, governments, and charities make decisions.

This book strives to introduce some of the tools that you will need to synthesize the avalanche of data to produce true insight.

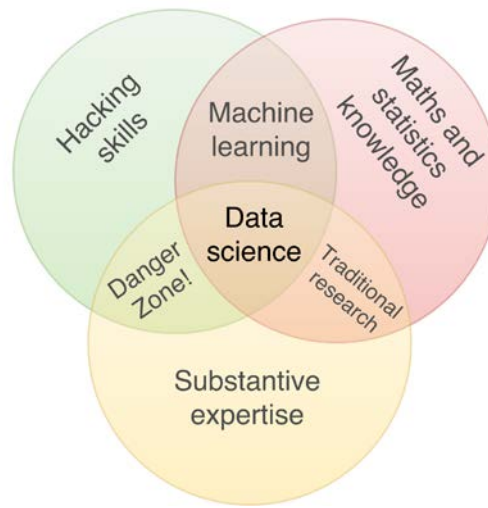
Data science

Data science is the process of extracting useful information from data. As a discipline, it remains somewhat ill-defined, with nearly as many definitions as there are experts. Rather than add yet another definition, I will follow *Drew Conway's* description (<http://drewconway.com/zia/2013/3/26/the-data-science-venn-diagram>). He describes data science as the culmination of three orthogonal sets of skills:

- Data scientists must have *hacking skills*. Data is stored and transmitted through computers. Computers, programming languages, and libraries are the hammers and chisels of data scientists; they must wield them with confidence and accuracy to sculpt the data as they please. This is where Scala comes in: it's a powerful tool to have in your programming toolkit.

- Data scientists must have a sound understanding of *statistics and numerical algorithms*. Good data scientists will understand how machine learning algorithms function and how to interpret results. They will not be fooled by misleading metrics, deceptive statistics, or misinterpreted causal links.
- A good data scientist must have a sound understanding of the *problem domain*. The data science process involves building and discovering knowledge about the problem domain in a scientifically rigorous manner. The data scientist must, therefore, ask the right questions, be aware of previous results, and understand how the data science effort fits in the wider business or research context.

Drew Conway summarizes this elegantly with a Venn diagram showing data science at the intersection of hacking skills, maths and statistics knowledge, and substantive expertise:



It is, of course, rare for people to be experts in more than one of these areas. Data scientists often work in cross-functional teams, with different members providing the expertise for different areas. To function effectively, every member of the team must nevertheless have a general working knowledge of all three areas.

To give a more concrete overview of the workflow in a data science project, let's imagine that we are trying to write an application that analyzes the public perception of a political campaign. This is what the data science pipeline might look like:

- **Obtaining data:** This might involve extracting information from text files, polling a sensor network or querying a web API. We could, for instance, query the Twitter API to obtain lists of tweets with the relevant hashtags.
- **Data ingestion:** Data often comes from many different sources and might be unstructured or semi-structured. Data ingestion involves moving data from the data source, processing it to extract structured information, and storing this information in a database. For tweets, for instance, we might extract the username, the names of other users mentioned in the tweet, the hashtags, text of the tweet, and whether the tweet contains certain keywords.
- **Exploring data:** We often have a clear idea of what information we want to extract from the data but very little idea how. For instance, let's imagine that we have ingested thousands of tweets containing hashtags relevant to our political campaign. There is no clear path to go from our database of tweets to the end goal: insight into the overall public perception of our campaign. Data exploration involves mapping out how we are going to get there. This step will often uncover new questions or sources of data, which requires going back to the first step of the pipeline. For our tweet database, we might, for instance, decide that we need to have a human manually label a thousand or more tweets as expressing "positive" or "negative" sentiments toward the political campaign. We could then use these tweets as a training set to construct a model.
- **Feature building:** A machine learning algorithm is only as good as the features that enter it. A significant fraction of a data scientist's time involves transforming and combining existing features to create new features more closely related to the problem that we are trying to solve. For instance, we might construct a new feature corresponding to the number of "positive" sounding words or pairs of words in a tweet.
- **Model construction and training:** Having built the features that enter the model, the data scientist can now train machine learning algorithms on their datasets. This will often involve trying different algorithms and optimizing model **hyperparameters**. We might, for instance, settle on using a random forest algorithm to decide whether a tweet is "positive" or "negative" about the campaign. Constructing the model involves choosing the right number of trees and how to calculate impurity measures. A sound understanding of statistics and the problem domain will help inform these decisions.

- **Model extrapolation and prediction:** The data scientists can now use their new model to try and infer information about previously unseen data points. They might pass a new tweet through their model to ascertain whether it speaks positively or negatively of the political campaign.
- **Distillation of intelligence and insight from the model:** The data scientists combine the outcome of the data analysis process with knowledge of the business domain to inform business decisions. They might discover that specific messages resonate better with the target audience, or with specific segments of the target audience, leading to more accurate targeting. A key part of informing stakeholders involves data visualization and presentation: data scientists create graphs, visualizations, and reports to help make the insights derived clear and compelling.

This is far from a linear pipeline. Often, insights gained at one stage will require the data scientists to backtrack to a previous stage of the pipeline. Indeed, the generation of business insights from raw data is normally an iterative process: the data scientists might do a rapid first pass to verify the premise of the problem and then gradually refine the approach by adding new data sources or new features or trying new machine learning algorithms.

In this book, you will learn how to deal with each step of the pipeline in Scala, leveraging existing libraries to build robust applications.

Programming in data science

This book is not a book about data science. It is a book about how to use Scala, a programming language, for data science. So, where does programming come in when processing data?

Computers are involved at every step of the data science pipeline, but not necessarily in the same manner. The style of programs that we build will be drastically different if we are just writing throwaway scripts to explore data or trying to build a scalable application that pushes data through a well-understood pipeline to continuously deliver business intelligence.

Let's imagine that we work for a company making games for mobile phones in which you can purchase in-game benefits. The majority of users never buy anything, but a small fraction is likely to spend a lot of money. We want to build a model that recognizes big spenders based on their play patterns.

The first step is to explore data, find the right features, and build a model based on a subset of the data. In this exploration phase, we have a clear goal in mind but little idea of how to get there. We want a light, flexible language with strong libraries to get us a working model as soon as possible.

Once we have a working model, we need to deploy it on our gaming platform to analyze the usage patterns of all the current users. This is a very different problem: we have a relatively clear understanding of the goals of the program and of how to get there. The challenge comes in designing software that will scale out to handle all the users and be robust to future changes in usage patterns.

In practice, the type of software that we write typically lies on a spectrum ranging from a single throwaway script to production-level code that must be proof against future expansion and load increases. Before writing any code, the data scientist must understand where their software lies on this spectrum. Let's call this the **permanence spectrum**.

Why Scala?

You want to write a program that handles data. Which language should you choose?

There are a few different options. You might choose a dynamic language such as Python or R or a more traditional object-oriented language such as Java. In this section, we will explore how Scala differs from these languages and when it might make sense to use it.

When choosing a language, the architect's trade-off lies in a balance of provable correctness versus development speed. Which of these aspects you need to emphasize will depend on the application requirements and where on the permanence spectrum your program lies. Is this a short script that will be used by a few people who can easily fix any problems that arise? If so, you can probably permit a certain number of bugs in rarely used code paths: when a developer hits a snag, they can just fix the problem as it arises. By contrast, if you are developing a database engine that you plan on releasing to the wider world, you will, in all likelihood, favor correctness over rapid development. The SQLite database engine, for instance, is famous for its extensive test suite, with 800 times as much testing code as application code (<https://www.sqlite.org/testing.html>).

What matters, when estimating the *correctness* of a program, is not the perceived absence of bugs, it is the degree to which you can prove that certain bugs are absent.

There are several ways of proving the absence of bugs before the code has even run:

- Static type checking occurs at compile time in statically typed languages, but this can also be used in strongly typed dynamic languages that support type annotations or type hints. Type checking helps verify that we are using functions and classes as intended.
- Static analyzers and linters that check for undefined variables or suspicious behavior (such as parts of the code that can never be reached).
- Declaring some attributes as immutable or constant in compiled languages.
- Unit testing to demonstrate the absence of bugs along particular code paths.

There are several more ways of checking for the absence of some bugs at runtime:

- Dynamic type checking in both statically typed and dynamic languages
- Assertions verifying supposed program invariants or expected contracts

In the next sections, we will examine how Scala compares to other languages in data science.

Static typing and type inference

Scala's static typing system is very versatile. A lot of information as to the program's behavior can be encoded in types, allowing the compiler to guarantee a certain level of correctness. This is particularly useful for code paths that are rarely used. A dynamic language cannot catch errors until a particular branch of execution runs, so a bug can persist for a long time until the program runs into it. In a statically typed language, any bug that can be caught by the compiler will be caught at compile time, before the program has even started running.

Statically typed object-oriented languages have often been criticized for being needlessly verbose. Consider the initialization of an instance of the `Example` class in Java:

```
Example myInstance = new Example() ;
```

We have to repeat the class name twice – once to define the compile-time type of the `myInstance` variable and once to construct the instance itself. This feels like unnecessary work: the compiler knows that the type of `myInstance` is `Example` (or a superclass of `Example`) as we are binding a value of the `Example` type.

Scala, like most functional languages, uses type inference to allow the compiler to infer the type of variables from the instances bound to them. We would write the equivalent line in Scala as follows:

```
val myInstance = new Example()
```

The Scala compiler infers that `myInstance` has the `Example` type at compile time. A lot of the time, it is enough to specify the types of the arguments and of the return value of a function. The compiler can then infer types for all the variables defined in the body of the function. Scala code is usually much more concise and readable than the equivalent Java code, without compromising any of the type safety.

Scala encourages immutability

Scala encourages the use of immutable objects. In Scala, it is very easy to define an attribute as immutable:

```
val amountSpent = 200
```

The default collections are immutable:

```
val clientIds = List("123", "456") // List is immutable
clientIds(1) = "589" // Compile-time error
```

Having immutable objects removes a common source of bugs. Knowing that some objects cannot be changed once instantiated reduces the number of places bugs can creep in. Instead of considering the lifetime of the object, we can narrow in on the constructor.

Scala and functional programs

Scala encourages functional code. A lot of Scala code consists of using higher-order functions to transform collections. You, as a programmer, do not have to deal with the details of iterating over the collection. Let's write an `occurrencesOf` function that returns the indices at which an element occurs in a list:

```
def occurrencesOf[A](elem:A, collection:List[A]):List[Int] = {
  for {
    (currentElem, index) <- collection.zipWithIndex
    if (currentElem == elem)
  } yield index
}
```

How does this work? We first declare a new list, `collection.zipWithIndex`, whose elements are `(collection(0), 0)`, `(collection(1), 1)`, and so on: pairs of the collection's elements and their indexes.

We then tell Scala that we want to iterate over this collection, binding the `currentElem` variable to the current element and `index` to the index. We apply a filter on the iteration, selecting only those elements for which `currentElem == elem`. We then tell Scala to just return the `index` variable.

We did not need to deal with the details of the iteration process in Scala. The syntax is very declarative: we tell the compiler that we want the index of every element equal to `elem` in collection and let the compiler worry about how to iterate over collection.

Consider the equivalent in Java:

```
static <T> List<Integer> occurrencesOf(T elem, List<T> collection) {
    List<Integer> occurrences = new ArrayList<Integer>();
    for (int i=0; i<collection.size(); i++) {
        if (collection.get(i).equals(elem)) {
            occurrences.add(i);
        }
    }
    return occurrences;
}
```

In Java, you start by defining a (mutable) list in which to put occurrences as you find them. You then iterate over the collection by defining a counter, considering each element in turn and adding its index to the list of occurrences, if need be. There are many more moving parts that we need to get right for this method to work. These moving parts exist because we must tell Java how to iterate over the collection, and they represent a common source of bugs.

Furthermore, as a lot of code is taken up by the iteration mechanism, the line that defines the logic of the function is harder to find:

```
static <T> List<Integer> occurrencesOf(T elem, List<T> collection) {
    List<Integer> occurrences = new ArrayList<Integer>();
    for (int i=0; i<collection.size(); i++) {
        if (collection.get(i).equals(elem)) {
            occurrences.add(i);
        }
    }
    return occurrences;
}
```

Note that this is not meant as an attack on Java. In fact, Java 8 adds a slew of functional constructs, such as lambda expressions, the `Optional` type that mirrors Scala's `Option`, or stream processing. Rather, it is meant to demonstrate the benefit of functional approaches in minimizing the potential for errors and maximizing clarity.

Null pointer uncertainty

We often need to represent the possible absence of a value. For instance, imagine that we are reading a list of usernames from a CSV file. The CSV file contains name and e-mail information. However, some users have declined to enter their e-mail into the system, so this information is absent. In Java, one would typically represent the e-mail as a string or an `Email` class and represent the absence of e-mail information for a particular user by setting that reference to `null`. Similarly, in Python, we might use `None` to demonstrate the absence of a value.

This approach is dangerous because we are not encoding the possible absence of e-mail information. In any nontrivial program, deciding whether an instance attribute can be `null` requires considering every occasion in which this instance is defined. This quickly becomes impractical, so programmers either assume that a variable is not `null` or code too defensively.

Scala (following the lead of other functional languages) introduces the `Option[T]` type to represent an attribute that might be absent. We might then write the following:

```
class User {  
    ...  
    val email:Option[Email]  
    ...  
}
```

We have now encoded the possible absence of e-mail in the type information. It is obvious to any programmer using the `User` class that e-mail information is possibly absent. Even better, the compiler knows that the `email` field can be absent, forcing us to deal with the problem rather than recklessly ignoring it to have the application burn at runtime in a conflagration of null pointer exceptions.

All this goes back to achieving a certain level of provable correctness. Never using `null`, we know that we will never run into null pointer exceptions. Achieving the same level of correctness in languages without `Option[T]` requires writing unit tests on the client code to verify that it behaves correctly when the e-mail attribute is `null`.

Note that it is possible to achieve this in Java using, for instance, Google's Guava library (<https://code.google.com/p/guava-libraries/wiki/UsingAndAvoidingNullExplained>) or the `Optional` class in Java 8. It is more a matter of convention: using `null` in Java to denote the absence of a value has long been the norm.

Easier parallelism

Writing programs that take advantage of parallel architectures is challenging. It is nevertheless necessary to tackle all but the simplest data science problems.

Parallel programming is difficult because we, as programmers, tend to think sequentially. Reasoning about the order in which different events can happen in a concurrent program is very challenging.

Scala provides several abstractions that greatly facilitate the writing of parallel code. These abstractions work by imposing constraints on the way parallelism is achieved. For instance, parallel collections force the user to phrase the computation as a sequence of operations (such as **map**, **reduce**, and **filter**) on collections. Actor systems require the developer to think in terms of actors that encapsulate the application state and communicate by passing messages.

It might seem paradoxical that restricting the programmer's freedom to write parallel code as they please avoids many of the problems associated with concurrency. However, limiting the number of ways in which a program behaves facilitates thinking about its behavior. For instance, if an actor is misbehaving, we know that the problem lies either in the code for this actor or in one of the messages that the actor receives.

As an example of the power afforded by having coherent, restrictive abstractions, let's use parallel collections to solve a simple probability problem. We will calculate the probability of getting at least 60 heads out of 100 coin tosses. We can estimate this using Monte Carlo: we simulate 100 coin tosses by drawing 100 random Boolean values and check whether the number of true values is at least 60. We repeat this until results have converged to the required accuracy, or we get bored of waiting.

Let's run through this in a Scala console:

```
scala> val nTosses = 100
nTosses: Int = 100

scala> def trial = (0 until nTosses).count { i =>
  util.Random.nextBoolean() // count the number of heads
}
trial: Int
```

The `trial` function runs a single set of 100 throws, returning the number of heads:

```
scala> trial
Int = 51
```

To get our answer, we just need to repeat `trial` as many times as we can and aggregate the results. Repeating the same set of operations is ideally suited to parallel collections:

```
scala> val nTrials = 100000
nTrials: Int = 100000

scala> (0 until nTrials).par.count { i => trial >= 60 }
Int = 2745
```

The probability is thus approximately 2.5% to 3%. All we had to do to distribute the calculation over every CPU in our computer is use the `par` method to parallelize the range `(0 until nTrials)`. This demonstrates the benefits of having a coherent abstraction: parallel collections let us trivially parallelize any computation that can be phrased in terms of higher-order functions on collections.

Clearly, not every problem is as easy to parallelize as a simple Monte Carlo problem. However, by offering a rich set of intuitive abstractions, Scala makes writing parallel applications manageable.

Interoperability with Java

Scala runs on the Java virtual machine. The Scala compiler compiles programs to Java byte code. Thus, Scala developers have access to Java libraries natively. Given the phenomenal number of applications written in Java, both open source and as part of the legacy code in organizations, the interoperability of Scala and Java helps explain the rapid uptake of Scala.

Interoperability has not just been unidirectional: some Scala libraries, such as the Play framework, are becoming increasingly popular among Java developers.

When not to use Scala

In the previous sections, we described how Scala's strong type system, preference for immutability, functional capabilities, and parallelism abstractions make it easy to write reliable programs and minimize the risk of unexpected behavior.

What reasons might you have to avoid Scala in your next project? One important reason is familiarity. Scala introduces many concepts such as implicits, type classes, and composition using traits that might not be familiar to programmers coming from the object-oriented world. Scala's type system is very expressive, but getting to know it well enough to use its full power takes time and requires adjusting to a new programming paradigm. Finally, dealing with immutable data structures can feel alien to programmers coming from Java or Python.

Nevertheless, these are all drawbacks that can be overcome with time. Scala does fall short of the other data science languages in library availability. The IPython Notebook, coupled with matplotlib, is an unparalleled resource for data exploration. There are ongoing efforts to provide similar functionality in Scala (Spark Notebooks or Apache Zeppelin, for instance), but there are no projects with the same level of maturity. The type system can also be a minor hindrance when one is exploring data or trying out different models.

Thus, in this author's biased opinion, Scala excels for more *permanent* programs. If you are writing a throwaway script or exploring data, you might be better served with Python. If you are writing something that will need to be reused and requires a certain level of provable correctness, you will find Scala extremely powerful.

Summary

Now that the obligatory introduction is over, it is time to write some Scala code. In the next chapter, you will learn about leveraging Breeze for numerical computations with Scala. For our first foray into data science, we will use logistic regression to predict the gender of a person given their height and weight.

References

By far, the best book on Scala is *Programming in Scala* by Martin Odersky, Lex Spoon, and Bill Venners. Besides being authoritative (*Martin Odersky* is the driving force behind Scala), this book is also approachable and readable.

Scala Puzzlers by Andrew Phillips and Nermin Šerifović provides a fun way to learn more advanced Scala.

Scala for Machine Learning by Patrick R. Nicholas provides examples of how to write machine learning algorithms with Scala.

2

Manipulating Data with Breeze

Data science is, by and large, concerned with the manipulation of structured data. A large fraction of structured datasets can be viewed as tabular data: each row represents a particular instance, and columns represent different attributes of that instance. The ubiquity of tabular representations explains the success of spreadsheet programs like Microsoft Excel, or of tools like SQL databases.

To be useful to data scientists, a language must support the manipulation of columns or tables of data. Python does this through NumPy and pandas, for instance. Unfortunately, there is no single, coherent ecosystem for numerical computing in Scala that quite measures up to the SciPy ecosystem in Python.

In this chapter, we will introduce Breeze, a library for fast linear algebra and manipulation of data arrays as well as many other features necessary for scientific computing and data science.

Code examples

The easiest way to access the code examples in this book is to clone the GitHub repository:

```
$ git clone 'https://github.com/pbugnion/s4ds'
```

The code samples for each chapter are in a single, standalone folder. You may also browse the code online on GitHub.

Installing Breeze

If you have downloaded the code examples for this book, the easiest way of using Breeze is to go into the `chap02` directory and type `sbt console` at the command line. This will open a Scala console in which you can import Breeze.

If you want to build a standalone project, the most common way of installing Breeze (and, indeed, any Scala module) is through SBT. To fetch the dependencies required for this chapter, copy the following lines to a file called `build.sbt`, taking care to leave an empty line after `scalaVersion`:

```
scalaVersion := "2.11.7"

libraryDependencies += Seq(
  "org.scalanlp" %% "breeze" % "0.11.2",
  "org.scalanlp" %% "breeze-natives" % "0.11.2"
)
```

Open a Scala console in the same directory as your `build.sbt` file by typing `sbt console` in a terminal. You can check that Breeze is working correctly by importing Breeze from the Scala prompt:

```
scala> import breeze.linalg._
import breeze.linalg._
```

Getting help on Breeze

This chapter gives a reasonably detailed introduction to Breeze, but it does not aim to give a complete API reference.

To get a full list of Breeze's functionality, consult the Breeze Wiki page on GitHub at <https://github.com/scalanlp/breeze/wiki>. This is very complete for some modules and less complete for others. The source code (<https://github.com/scalanlp/breeze/>) is detailed and gives a lot of information. To understand how a particular function is meant to be used, look at the unit tests for that function.

Basic Breeze data types

Breeze is an extensive library providing fast and easy manipulation of arrays of data, routines for optimization, interpolation, linear algebra, signal processing, and numerical integration.

The basic linear algebra operations underlying Breeze rely on the `netlib-java` library, which can use system-optimized **BLAS** and **LAPACK** libraries, if present. Thus, linear algebra operations in Breeze are often extremely fast. Breeze is still undergoing rapid development and can, therefore, be somewhat unstable.

Vectors

Breeze makes manipulating one- and two-dimensional data structures easy. To start, open a Scala console through SBT and import Breeze:

```
$ sbt console
scala> import breeze.linalg._
import breeze.linalg._
```

Let's dive straight in and define a vector:

```
scala> val v = DenseVector(1.0, 2.0, 3.0)
breeze.linalg.DenseVector[Double] = DenseVector(1.0, 2.0, 3.0)
```

We have just defined a three-element vector, `v`. Vectors are just one-dimensional arrays of data exposing methods tailored to numerical uses. They can be indexed like other Scala collections:

```
scala> v(1)
Double = 2.0
```

They support element-wise operations with a scalar:

```
scala> v :* 2.0 // :* is 'element-wise multiplication'
breeze.linalg.DenseVector[Double] = DenseVector(2.0, 4.0, 6.0)
```

They also support element-wise operations with another vector:

```
scala> v :+ DenseVector(4.0, 5.0, 6.0) // :+ is 'element-wise addition'
breeze.linalg.DenseVector[Double] = DenseVector(5.0, 7.0, 9.0)
```

Breeze makes writing vector operations intuitive and considerably more readable than the native Scala equivalent.

Note that Breeze will refuse (at compile time) to coerce operands to the correct type:

```
scala> v :* 2 // element-wise multiplication by integer
<console>:15: error: could not find implicit value for parameter op:
...

```

It will also refuse (at runtime) to add vectors together if they have different lengths:

```
scala> v :+: DenseVector(8.0, 9.0)
java.lang.IllegalArgumentException: requirement failed: Vectors must have
same length: 3 != 2
...

```

Basic manipulation of vectors in Breeze will feel natural to anyone used to working with NumPy, MATLAB, or R.

So far, we have only looked at *element-wise* operators. These are all prefixed with a colon. All the usual suspects are present: `:+`, `:*`, `:-`, `:/`, `:%` (remainder), and `:^` (power) as well as Boolean operators. To see the full list of operators, have a look at the API documentation for `DenseVector` or `DenseMatrix` (<https://github.com/scalanlp/breeze/wiki/Linear-Algebra-Cheat-Sheet>).

Besides element-wise operations, Breeze vectors support the operations you might expect of mathematical vectors, such as the dot product:

```
scala> val v2 = DenseVector(4.0, 5.0, 6.0)
breeze.linalg.DenseVector[Double] = DenseVector(4.0, 5.0, 6.0)

scala> v dot v2
Double = 32.0

```

Pitfalls of element-wise operators

Besides the `:+` and `:-` operators for element-wise addition and subtraction that we have seen so far, we can also use the more traditional `+` and `-` operators:

```
scala> v + v2
breeze.linalg.DenseVector[Double] = DenseVector(5.0,
7.0, 9.0)
```

One must, however, be very careful with operator precedence rules when mixing `:+` or `:*` with `+` operators. The `:+` and `:*` operators have very low operator precedence, so they will be evaluated last. This can lead to some counter-intuitive behavior:



```
scala> 2.0 :* v + v2 // !! equivalent to 2.0 :* (v + v2)
breeze.linalg.DenseVector[Double] = DenseVector(10.0,
14.0, 18.0)
```

By contrast, if we use `:+` instead of `+`, the mathematical precedence of operators is respected:

```
scala> 2.0 :* v :+ v2 // equivalent to (2.0 :* v) :+ v2
breeze.linalg.DenseVector[Double] = DenseVector(6.0,
9.0, 12.0)
```

In summary, one should avoid mixing the `:+` style operators with the `+` style operators as much as possible.

Dense and sparse vectors and the vector trait

All the vectors we have looked at thus far have been dense vectors. Breeze also supports sparse vectors. When dealing with arrays of numbers that are mostly zero, it may be more computationally efficient to use sparse vectors. The point at which a vector has enough zeros to warrant switching to a sparse representation depends strongly on the type of operations, so you should run your own benchmarks to determine which type to use. Nevertheless, a good heuristic is that, if your vector is about 90% zero, you may benefit from using a sparse representation.

Sparse vectors are available in Breeze as the `SparseVector` and `HashVector` classes. Both these types support many of the same operations as `DenseVector` but use a different internal implementation. The `SparseVector` instances are very memory-efficient, but adding non-zero elements is slow. `HashVector` is more versatile, at the cost of an increase in memory footprint and computational time for iterating over non-zero elements. Unless you need to squeeze the last bits of memory out of your application, I recommend using `HashVector`. We will not discuss these further in this book, but the reader should find them straightforward to use if needed. `DenseVector`, `SparseVector`, and `HashVector` all implement the `Vector` trait, giving them a common interface.



Breeze remains very experimental and, as of this writing, somewhat unstable. I have found dealing with specific implementations of the `Vector` trait, such as `DenseVector` or `SparseVector`, to be more reliable than dealing with the `Vector` trait directly. In this chapter, we will explicitly type every vector as `DenseVector`.

Matrices

Breeze allows the construction and manipulation of two-dimensional arrays in a similar manner:

```
scala> val m = DenseMatrix((1.0, 2.0, 3.0), (4.0, 5.0, 6.0))
breeze.linalg.DenseMatrix[Double] =
1.0  2.0  3.0
4.0  5.0  6.0

scala> 2.0 :* m
breeze.linalg.DenseMatrix[Double] =
2.0  4.0  6.0
8.0 10.0 12.0
```

Building vectors and matrices

We have seen how to explicitly build vectors and matrices by passing their values to the constructor (or rather, to the companion object's `apply` method): `DenseVector(1.0, 2.0, 3.0)`. Breeze offers several other powerful ways of building vectors and matrices:

```
scala> DenseVector.ones[Double](5)
breeze.linalg.DenseVector[Double] = DenseVector(1.0, 1.0, 1.0, 1.0, 1.0)

scala> DenseVector.zeros[Int](3)
breeze.linalg.DenseVector[Int] = DenseVector(0, 0, 0)
```

The `linspace` method (available in the `breeze.linalg` package object) creates a `Double` vector of equally spaced values. For instance, to create a vector of 10 values distributed uniformly between 0 and 1, perform the following:

```
scala> linspace(0.0, 1.0, 10)
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 0.11111111111111111,
..., 1.0)
```

The `tabulate` method lets us construct vectors and matrices from functions:

```
scala> DenseVector.tabulate(4) { i => 5.0 * i }
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 5.0, 10.0, 15.0)
```

```
scala> DenseMatrix.tabulate[Int](2, 3) {
  (irow, icol) => irow*2 + icol
}
breeze.linalg.DenseMatrix[Int] =
0  1  2
2  3  4
```

The first argument to `DenseVector.tabulate` is the size of the vector, and the second is a function returning the value of the vector at a particular position. This is useful for creating ranges of data, among other things.

The `rand` function lets us create random vectors and matrices:

```
scala> DenseVector.rand(2)
breeze.linalg.DenseVector[Double] = DenseVector(0.8072865137359484,
0.5566507203838562)
```

```
scala> DenseMatrix.rand(2, 3)
breeze.linalg.DenseMatrix[Double] =
0.5755491874682879  0.8142161471517582  0.9043780212739738
0.31530195124023974  0.2095094278911871  0.22069103504148346
```

Finally, we can construct vectors from Scala arrays:

```
scala> DenseVector(Array(2, 3, 4))
breeze.linalg.DenseVector[Int] = DenseVector(2, 3, 4)
```

To construct vectors from other Scala collections, you must use the `splat` operator,

```
:_ *
```

```
scala> val l = Seq(2, 3, 4)
l: Seq[Int] = List(2, 3, 4)
```

```
scala> DenseVector(l :_ *)
breeze.linalg.DenseVector[Int] = DenseVector(2, 3, 4)
```


Advanced indexing and slicing

We have already seen how to select a particular element in a vector v by its index with, for instance, $v(2)$. Breeze also offers several powerful methods for selecting parts of a vector.

Let's start by creating a vector to play around with:

```
scala> val v = DenseVector.tabulate(5) { _, _ => Double }
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 1.0, 2.0, 3.0, 4.0)
```

Unlike native Scala collections, Breeze vectors support negative indexing:

```
scala> v(-1) // last element
Double = 4.0
```

Breeze lets us slice the vector using a range:

```
scala> v(1 to 3)
breeze.linalg.DenseVector[Double] = DenseVector(1.0, 2.0, 3.0)
```

```
scala> v(1 until 3) // equivalent to Python v[1:3]
breeze.linalg.DenseVector[Double] = DenseVector(1.0, 2.0)
```

```
scala> v(v.length-1 to 0 by -1) // reverse view of v
breeze.linalg.DenseVector[Double] = DenseVector(4.0, 3.0, 2.0, 1.0, 0.0)
```



Indexing by a range returns a *view* of the original vector: when running `val v2 = v(1 to 3)`, no data is copied. This means that slicing is extremely efficient. Taking a slice of a huge vector does not increase the memory footprint at all. It also means that one should be careful updating a slice, since it will also update the original vector. We will discuss mutating vectors and matrices in a subsequent section in this chapter.

Breeze also lets us select an arbitrary set of elements from a vector:

```
scala> val vSlice = v(2, 4) // Select elements at index 2 and 4
breeze.linalg.SliceVector[Int,Double] = breeze.linalg.SliceVector@9c04d22
```

This creates a `SliceVector`, which behaves like a `DenseVector` (both implement the `Vector` interface), but does not actually have memory allocated for values: it just knows how to map from its indices to values in its parent vector. One should think of `vSlice` as a specific view of `v`. We can materialize the view (give it its own data rather than acting as a lens through which `v` is viewed) by converting it to `DenseVector`:

```
scala> vSlice.toDenseVector
breeze.linalg.DenseVector[Double] = DenseVector(2.0, 4.0)
```

Note that if an element of a slice is out of bounds, an exception will only be thrown when that element is accessed:

```
scala> val vSlice = v(2, 7) // there is no v(7)
breeze.linalg.SliceVector[Int,Double] = breeze.linalg.
SliceVector@2a83f9d1
```

```
scala> vSlice(0) // valid since v(2) is still valid
Double = 2.0
```

```
scala> vSlice(1) // invalid since v(7) is out of bounds
java.lang.IndexOutOfBoundsException: 7 not in [-5,5)
...
```

Finally, one can index vectors using Boolean arrays. Let's start by defining an array:

```
scala> val mask = DenseVector(true, false, false, true, true)
breeze.linalg.DenseVector[Boolean] = DenseVector(true, false, false,
true, true)
```

Then, `v(mask)` results in a view containing the elements of `v` for which `mask` is `true`:

```
scala> v(mask).toDenseVector
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 3.0, 4.0)
```

This can be used as a way of filtering certain elements in a vector. For instance, to select the elements of `v` which are less than 3.0:

```
scala> val filtered = v(v :< 3.0) // :< is element-wise "less than"
breeze.linalg.SliceVector[Int,Double] = breeze.linalg.
SliceVector@2b1edef3
```

```
scala> filtered.toDenseVector
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 1.0, 2.0)
```

Matrices can be indexed in much the same way as vectors. Matrix indexing functions take two arguments – the first argument selects the row(s) and the second one slices the column(s):

```
scala> val m = DenseMatrix((1.0, 2.0, 3.0), (5.0, 6.0, 7.0))
m: breeze.linalg.DenseMatrix[Double] =
1.0  2.0  3.0
5.0  6.0  7.0
```

```
scala> m(1, 2)
Double = 7.0
```

```
scala> m(1, -1)
Double = 7.0
```

```
scala> m(0 until 2, 0 until 2)
breeze.linalg.DenseMatrix[Double] =
1.0  2.0
5.0  6.0
```

You can also mix different slicing types for rows and columns:

```
scala> m(0 until 2, 0)
breeze.linalg.DenseVector[Double] = DenseVector(1.0, 5.0)
```

Note how, in this case, Breeze returns a vector. In general, slicing returns the following objects:

- A scalar when single indices are passed as the row and column arguments
- A vector when the row argument is a range and the column argument is a single index
- A vector transpose when the column argument is a range and the row argument is a single index
- A matrix otherwise

The symbol `::` can be used to indicate *every element along a particular direction*. For instance, we can select the second column of `m`:

```
scala> m(:, 1)
breeze.linalg.DenseVector[Double] = DenseVector(2.0, 6.0)
```

Mutating vectors and matrices

Breeze vectors and matrices are mutable. Most of the slicing operations described above can also be used to set elements of a vector or matrix:

```
scala> val v = DenseVector(1.0, 2.0, 3.0)
v: breeze.linalg.DenseVector[Double] = DenseVector(1.0, 2.0, 3.0)
```

```
scala> v(1) = 22.0 // v is now DenseVector(1.0, 22.0, 3.0)
```

We are not limited to mutating single elements. In fact, all the indexing operations outlined above can be used to set the elements of vectors or matrices. When mutating slices of vectors or matrices, use the element-wise assignment operator, `:=`:

```
scala> v(0 until 2) := DenseVector(50.0, 51.0) // set elements at
position 0 and 1
breeze.linalg.DenseVector[Double] = DenseVector(50.0, 51.0)
```

```
scala> v
breeze.linalg.DenseVector[Double] = DenseVector(50.0, 51.0, 3.0)
```

The assignment operator, `:=`, works like other element-wise operators in Breeze. If the right-hand side is a scalar, it will automatically be broadcast to a vector of the given shape:

```
scala> v(0 until 2) := 0.0 // equivalent to v(0 until 2) :=
DenseVector(0.0, 0.0)
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 0.0)
```

```
scala> v
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 0.0, 3.0)
```

All element-wise operators have an update counterpart. For instance, the `+=` operator acts like the element-wise addition operator `:+`, but also updates its left-hand operand:

```
scala> val v = DenseVector(1.0, 2.0, 3.0)
v: breeze.linalg.DenseVector[Double] = DenseVector(1.0, 2.0, 3.0)
```

```
scala> v += 4.0
breeze.linalg.DenseVector[Double] = DenseVector(5.0, 6.0, 7.0)
```

```
scala> v
breeze.linalg.DenseVector[Double] = DenseVector(5.0, 6.0, 7.0)
```

Notice how the update operator updates the vector in place and returns it.

We have learnt how to slice vectors and matrices in Breeze to create new views of the original data. These views are not independent of the vector they were created from – updating the view will update the underlying vector and vice-versa. This is best illustrated with an example:

```
scala> val v = DenseVector.tabulate(6) { _._toDouble }
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 1.0, 2.0, 3.0, 4.0, 5.0)

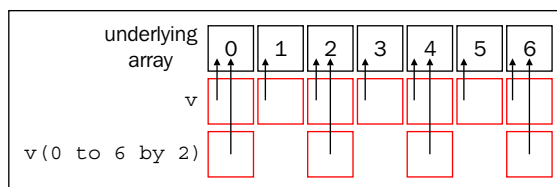
scala> val viewEvens = v(0 until v.length by 2)
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 2.0, 4.0)

scala> viewEvens := 10.0 // mutate viewEvens
breeze.linalg.DenseVector[Double] = DenseVector(10.0, 10.0, 10.0)

scala> viewEvens
breeze.linalg.DenseVector[Double] = DenseVector(10.0, 10.0, 10.0)

scala> v // v has also been mutated!
breeze.linalg.DenseVector[Double] = DenseVector(10.0, 1.0, 10.0, 3.0, 10.0, 5.0)
```

This quickly becomes intuitive if we remember that, when we create a vector or matrix, we are creating a view of an underlying data array rather than creating the data itself:



A vector slice `v(0 to 6 by 2)` of the `v` vector is just a different view of the array underlying `v`. The view itself contains no data. It just contains pointers to the data in the original array. Internally, the view is just stored as a pointer to the underlying data and a recipe for iterating over that data: in the case of this slice, the recipe is just "start at the first element of the underlying data and go to the seventh element of the underlying data in steps of two".

Breeze offers a `copy` function for when we want to create independent copies of data. In the previous example, we can construct a copy of `viewEvens` as:

```
scala> val copyEvens = v(0 until v.length by 2).copy
breeze.linalg.DenseVector[Double] = DenseVector(10.0, 10.0, 10.0)
```

We can now update `copyEvens` independently of `v`.

Matrix multiplication, transposition, and the orientation of vectors

So far, we have mostly looked at element-wise operations on vectors and matrices. Let's now look at matrix multiplication and related operations.

The matrix multiplication operator is `*`:

```
scala> val m1 = DenseMatrix((2.0, 3.0), (5.0, 6.0), (8.0, 9.0))
breeze.linalg.DenseMatrix[Double] =
2.0  3.0
5.0  6.0
8.0  9.0
```

```
scala> val m2 = DenseMatrix((10.0, 11.0), (12.0, 13.0))
breeze.linalg.DenseMatrix[Double]
10.0  11.0
12.0  13.0
```

```
scala> m1 * m2
56.0   61.0
122.0  133.0
188.0  205.0
```

Besides matrix-matrix multiplication, we can use the matrix multiplication operator between matrices and vectors. All vectors in Breeze are column vectors. This means that, when multiplying matrices and vectors together, a vector should be viewed as an $(n * 1)$ matrix. Let's walk through an example of matrix-vector multiplication. We want the following operation:

$$\begin{pmatrix} 2 & 3 \\ 5 & 6 \\ 8 & 9 \end{pmatrix} \begin{pmatrix} 1 \\ 2 \end{pmatrix}$$

```
scala> val v = DenseVector(1.0, 2.0)
breeze.linalg.DenseVector[Double] = DenseVector(1.0, 2.0)

scala> m1 * v
breeze.linalg.DenseVector[Double] = DenseVector(8.0, 17.0, 26.0)
```

By contrast, if we wanted:

$$(1 \ 2) \begin{pmatrix} 10 & 11 \\ 12 & 13 \end{pmatrix}$$

We must convert v to a row vector. We can do this using the transpose operation:

```
scala> val vt = v.t
breeze.linalg.Transpose[breeze.linalg.DenseVector[Double]] =
Transpose(DenseVector(1.0, 2.0))

scala> vt * m2
breeze.linalg.Transpose[breeze.linalg.DenseVector[Double]] =
Transpose(DenseVector(34.0, 37.0))
```

Note that the type of $v.t$ is `Transpose [DenseVector [_]]`. A `Transpose [DenseVector [_]]` behaves in much the same way as a `DenseVector` as far as element-wise operations are concerned, but it does not support mutation or slicing.

Data preprocessing and feature engineering

We have now discovered the basic components of Breeze. In the next few sections, we will apply them to real examples to understand how they fit together to form a robust base for data science.

An important part of data science involves preprocessing datasets to construct useful features. Let's walk through an example of this. To follow this example and access the data, you will need to download the code examples for the book (www.github.com/pbugnion/s4ds).

You will find, in directory `chap02/data/` of the code attached to this book, a CSV file with true heights and weights as well as self-reported heights and weights for 181 men and women. The original dataset was collected as part of a study on body image. Refer to the following link for more information: <http://vincentarelbundock.github.io/Rdatasets/doc/car/Davis.html>.

There is a helper function in the package provided with the book to load the data into Breeze arrays:

```
scala> val data = HWDData.load
HWDData [ 181 rows ]

scala> data.genders
breeze.linalg.Vector[Char] = DenseVector(M, F, F, M, ... )
```

The data object contains five vectors, each 181 element long:

- `data.genders`: A Char vector describing the gender of the participants
- `data.heights`: A Double vector of the true height of the participants
- `data.weights`: A Double vector of the true weight of the participants
- `data.reportedHeights`: A Double vector of the self-reported height of the participants
- `data.reportedWeights`: A Double vector of the self-reported weight of the participants

Let's start by counting the number of men and women in the study. We will define an array that contains just 'M' and do an element-wise comparison with `data.genders`:

```
scala> val maleVector = DenseVector.fill(data.genders.length)('M')
breeze.linalg.DenseVector[Char] = DenseVector(M, M, M, M, M, M, ... )

scala> val isMale = (data.genders == maleVector)
breeze.linalg.DenseVector[Boolean] = DenseVector(true, false, false, true ...)
```


The `isMale` vector is the same length as `data.genders`. It is `true` where the participant is male, and `false` otherwise. We can use this Boolean array as a mask for the other arrays in the dataset (remember that `vector(mask)` selects the elements of `vector` where `mask` is `true`). Let's get the height of the men in our dataset:

```
scala> val maleHeights = data.heights(isMale)
breeze.linalg.SliceVector[Int,Double] = breeze.linalg.SliceVector@61717d42

scala> maleHeights.toDenseVector
breeze.linalg.DenseVector[Double] = DenseVector(182.0, 177.0, 170.0, ...
```

To count the number of men in our dataset, we can use the indicator function. This transforms a Boolean array into an array of doubles, mapping `false` to `0.0` and `true` to `1.0`:

```
scala> import breeze.numerics._
import breeze.numerics._
```

```
scala> sum(I(isMale))
Double: 82.0
```

Let's calculate the mean height of men and women in the experiment. We can calculate the mean of a vector using `mean(v)`, which we can access by importing `breeze.stats._`:

```
scala> import breeze.stats._
import breeze.stats._
```

```
scala> mean(data.heights)
Double = 170.75690607734808
```

To calculate the mean height of the men, we can use our `isMale` array to slice `data.heights`; `data.heights(isMale)` is a view of the `data.heights` array with all the height values for the men:

```
scala> mean(data.heights(isMale)) // mean male height
Double = 178.0121951219512
```

```
scala> mean(data.heights(!isMale)) // mean female height
Double = 164.74747474747474
```

As a somewhat more involved example, let's look at the discrepancy between real and reported weight for both men and women in this experiment. We can get an array of the percentage difference between the reported weight and the true weight:

```
scala> val discrepancy =
  (data.weights - data.reportedWeights) / data.weights
 breeze.linalg.Vector[Double] = DenseVector(0.0, 0.1206896551724138,
 -0.018867924528301886, -0.029411764705882353, ... )
```

Notice how Breeze's overloading of mathematical operators allows us to manipulate data arrays easily and elegantly.

We can now calculate the mean and standard deviation of this array for men:

```
scala> mean(discrepancy(isMale))
res6: Double = -0.008451852933123775
```

```
scala> stddev(discrepancy(isMale))
res8: Double = 0.031901519634244195
```

We can also calculate the fraction of men who overestimated their height:

```
scala> val overReportMask =
  (data.reportedHeights :> data.heights).toDenseVector
 breeze.linalg.DenseVector[Boolean] = DenseVector(false, false, false,
 false...

scala> sum(I(overReportMask :& isMale))
Double: 10.0
```

There are thus ten men who believe they are taller than they actually are. The element-wise AND operator `:&` returns a vector that is true for all indices for which both its arguments are true. The vector `overReportMask :& isMale` is thus true for all participants that are male and over-reported their height.

Breeze – function optimization

Having studied feature engineering, let's now look at the other end of the data science pipeline. Typically, a machine learning algorithm defines a loss function that is a function of a set of parameters. The value of the loss function represents how well the model fits the data. The parameters are then optimized to minimize (or maximize) the loss function.

In *Chapter 12, Distributed Machine Learning with MLlib*, we will look at **MLlib**, a machine learning library that contains many well-known algorithms. Often, we don't need to worry about optimizing loss functions directly since we can rely on the machine learning algorithms provided by MLlib. It is nevertheless useful to have a basic knowledge of optimization.

Breeze has an `optimize` module that contains functions for finding a local minimum:

```
scala> import breeze.optimize._
import breeze.optimize._
```

Let's create a toy function that we want to optimize:

$$f(x) = \sum_i x_i^2$$

We can represent this function in Scala as follows:

```
scala> def f(xs:DenseVector[Double]) = sum(xs :^ 2.0)
f: (xs:breeze.linalg.DenseVector[Double])Double
```

Most local optimizers also require the gradient of the function being optimized. The gradient is a vector of the same dimension as the arguments to the function. In our case, the gradient is:

$$\nabla f = 2\bar{x}$$

We can represent the gradient in Breeze with a function that takes a vector argument and returns a vector of the same length:

```
scala> def gradf(xs:DenseVector[Double]) = 2.0 :* xs
gradf: (xs:breeze.linalg.DenseVector[Double])breeze.linalg.
DenseVector[Double]
```

For instance, at the point $(1, 1, 1)$, we have:

```
scala> val xs = DenseVector.ones[Double](3)
breeze.linalg.DenseVector[Double] = DenseVector(1.0, 1.0, 1.0)

scala> f(xs)
Double = 3.0

scala> gradf(xs)
breeze.linalg.DenseVector[Double] = DenseVector(2.0, 2.0, 2.0)
```

Let's set up the optimization problem. Breeze's optimization methods require that we pass in an implementation of the `DiffFunction` trait with a single method, `calculate`. This method must return a tuple of the function and its gradient:

```
scala> val optTrait = new DiffFunction[DenseVector[Double]] {
  def calculate(xs:DenseVector[Double]) = (f(xs), gradf(xs))
}
breeze.optimize.DiffFunction[breeze.linalg.DenseVector[Double]] =
<function1>
```

We are now ready to run the optimization. The `optimize` module provides a `minimize` function that does just what we want. We pass it `optTrait` and a starting point for the optimization:

```
scala> val minimum = minimize(optTrait, DenseVector(1.0, 1.0, 1.0))
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 0.0, 0.0)
```

The true minimum is at $(0.0, 0.0, 0.0)$. The optimizer therefore correctly finds the minimum.

The `minimize` function uses the **L-BFGS** method to run the optimization by default. It takes several additional arguments to control the optimization. We will explore these in the next sections.

Numerical derivatives

In the previous example, we specified the gradient of f explicitly. While this is generally good practice, calculating the gradient of a function can often be tedious. Breeze provides a gradient approximation function using finite differences. Reusing the same objective function `def f(xs:DenseVector[Double]) = sum(xs :^ 2.0)` as in the previous section:

```
scala> val approxOptTrait = new ApproximateGradientFunction(f)
breeze.optimize.ApproximateGradientFunction[Int,breeze.linalg.
DenseVector[Double]] = <function1>
```

The trait `approxOptTrait` has a `gradientAt` method that returns an approximation to the gradient at a point:

```
scala> approxOptTrait.gradientAt(DenseVector.ones(3))
breeze.linalg.DenseVector[Double] = DenseVector(2.00001000001393,
2.00001000001393, 2.00001000001393)
```

Note that this can be quite inaccurate. The `ApproximateGradientFunction` constructor takes an `epsilon` optional argument that controls the size of the step taken when calculating the finite differences. Changing the value of `epsilon` can improve the accuracy of the finite difference algorithm.

The `ApproximateGradientFunction` instance implements the `DiffFunction` trait. It can therefore be passed to `minimize` directly:

```
scala> minimize(approxOptTrait, DenseVector.ones[Double](3))
breeze.linalg.DenseVector[Double] = DenseVector(-5.000001063126813E-6,
-5.000001063126813E-6, -5.000001063126813E-6)
```

This, again, gives a result close to zero, but somewhat further away than when we specified the gradient explicitly. In general, it will be significantly more efficient and more accurate to calculate the gradient of a function analytically than to rely on Breeze's numerical gradient. It is probably best to only use the numerical gradient during data exploration or to check analytical gradients.

Regularization

The `minimize` function takes many optional arguments relevant to machine learning algorithms. In particular, we can instruct the optimizer to use a regularization parameter when performing the optimization. Regularization introduces a penalty in the loss function to prevent the parameters from growing arbitrarily. This is useful to avoid overfitting. We will discuss regularization in greater detail in *Chapter 12, Distributed Machine Learning with MLlib*.

For instance, to use `L2Regularization` with a hyperparameter of 0.5:

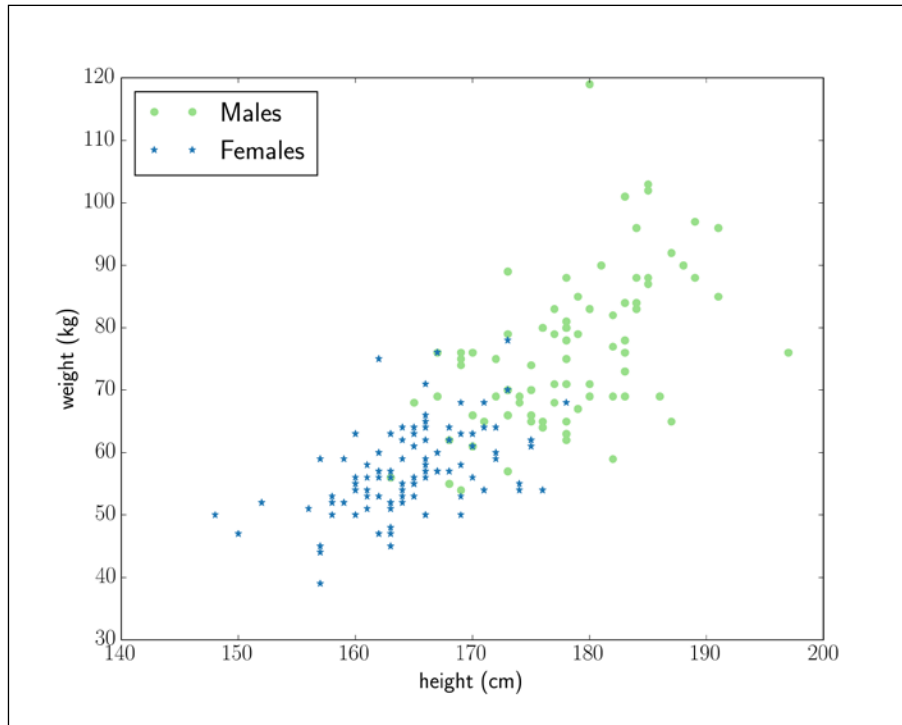
```
scala> minimize(optTrait,
  DenseVector(1.0, 1.0, 1.0), L2Regularization(0.5))
breeze.linalg.DenseVector[Double] = DenseVector(0.0, 0.0, 0.0)
```

The regularization makes no difference in this case, since the parameters are zero at the minimum.

To see a list of optional arguments that can be passed to `minimize`, consult the Breeze documentation online.

An example – logistic regression

Let's now imagine we want to build a classifier that takes a person's **height** and **weight** and assigns a probability to their being **Male** or **Female**. We will reuse the height and weight data introduced earlier in this chapter. Let's start by plotting the dataset:



Height versus weight data for 181 men and women

There are many different algorithms for classification. A first glance at the data shows that we can, approximately, separate men from women by drawing a straight line across the plot. A linear method is therefore a reasonable initial attempt at classification. In this section, we will use logistic regression to build a classifier.

A detailed explanation of logistic regression is beyond the scope of this book. The reader unfamiliar with logistic regression is referred to *The Elements of Statistical Learning* by Hastie, Tibshirani, and Friedman. We will just give a brief summary here.

Logistic regression estimates the probability of a given *height* and *weight* belonging to a *male* with the following sigmoid function:

$$P(\text{male} \mid \text{height}, \text{weight}) = \frac{1}{1 + \exp(-f(\text{height}, \text{weight}; \text{params}))}$$

Here, f is a linear function:

$$f(\text{height}, \text{weight}; \text{params}) = \text{params}(0) + \text{height} \cdot \text{params}(1) + \text{weight} \cdot \text{params}(2)$$

Here, *params* is an array of parameters that we need to determine using the training set. If we consider the height and weight as a *features* = (*height*, *weight*) matrix, we can re-write the sigmoid kernel f as a matrix multiplication of the *features* matrix with the *params* vector:

$$f(\text{features}; \text{params}) = \text{params}(0) + \text{features} \cdot \text{params}(1:)$$

To simplify this expression further, it is common to add a dummy feature whose value is always 1 to the *features* matrix. We can then multiply *params*(0) by this feature, allowing us to write the entire sigmoid kernel f as a single matrix-vector multiplication:

$$f(\text{features}; \text{params}) = \text{params} \cdot \text{features}$$

The feature matrix, *features*, is now a (181 * 3) matrix, where each row is (1, *height*, *weight*) for a particular participant.

To find the optimal values of the parameters, we can maximize the likelihood function, $L(\text{params} \mid \text{features})$. The likelihood takes a given set of parameter values as input and returns the probability that these particular parameters gave rise to the training set. For a set of parameters and associated probability function $P(\text{male} \mid \text{features}_i)$, the likelihood is:

$$L(\text{params} \mid \text{features}) = \prod_{\substack{i \\ \text{target}_i \text{ is male}}} P(\text{male} \mid \text{features}_i) \times \prod_{\substack{i \\ \text{target}_i \text{ not male}}} 1 - P(\text{male} \mid \text{features}_i)$$

If we magically know, ahead of time, the gender of everyone in the population, we can assign $P(\text{male})=1$ for the men and $P(\text{male})=0$ for the women. The likelihood function would then be **1**. Conversely, any uncertainty leads to a reduction in the likelihood function. If we choose a set of parameters that consistently lead to classification errors (low $P(\text{male})$ for men or high $P(\text{male})$ for women), the likelihood function drops to **0**.

The maximum likelihood corresponds to those values of the parameters most likely to describe the observed data. Thus, to find the parameters that best describe our training set, we just need to find parameters that maximize $L(\text{params} \mid \text{features})$. However, maximizing the likelihood function itself is very rarely done, since it involves multiplying many small values together, which quickly leads to floating point underflow. It is best to maximize the log of the likelihood, which has the same maximum as the likelihood. Finally, since most optimization algorithms are geared to minimize a function rather than maximize it, we will minimize $-\log(L(\text{params} \mid \text{features}))$.

For logistic regression, this is equivalent to minimizing:

$$\text{Cost}(\text{params}) = \sum_i \text{target}_i \times (\text{params} \cdot \text{features}_i) - \log(\exp(\text{params} \cdot \text{features}_i) + 1)$$

Here, the sum runs over all participants in the training data, features_i is a vector $(1, \text{height}_i, \text{weight}_i)$ of the i -th observation in the training set, and target_i is 1 if the person is male, and 0 if the participant is female.

To minimize the *Cost* function, we must also know its gradient with respect to the parameters. This is:

$$\nabla_{\text{params}} \text{Cost} = \sum_i \text{features}_i \cdot [P(\text{male} \mid \text{features}_i) - \text{target}_i]$$

We will start by rescaling the height and weight by their mean and standard deviation. While this is not strictly necessary for logistic regression, it is generally good practice. It facilitates the optimization and would become necessary if we wanted to use regularization methods or build superlinear features (features that allow the boundary separating men from women to be curved rather than a straight line).

For this example, we will move away from the Scala shell and write a standalone Scala script. Here's the full code listing. Don't worry if this looks daunting. We will break it up into manageable chunks in a minute:

```
import breeze.linalg._
import breeze.numerics._
import breeze.optimize._
import breeze.stats._

object LogisticRegressionHWDData extends App {

  val data = HWDData.load

  // Rescale the features to have mean of 0.0 and s.d. of 1.0
  def rescaled(v:DenseVector[Double]) =
    (v - mean(v)) / stddev(v)

  val rescaledHeights = rescaled(data.heights)
  val rescaledWeights = rescaled(data.weights)

  // Build the feature matrix as a matrix with
  //181 rows and 3 columns.
  val rescaledHeightsAsMatrix = rescaledHeights.toDenseMatrix.t
  val rescaledWeightsAsMatrix = rescaledWeights.toDenseMatrix.t

  val featureMatrix = DenseMatrix.horzcat(
    DenseMatrix.ones[Double](rescaledHeightsAsMatrix.rows, 1),
    rescaledHeightsAsMatrix,
    rescaledWeightsAsMatrix
  )

  println(s"Feature matrix size: ${featureMatrix.rows} x " +
    s"${featureMatrix.cols}")

  // Build the target variable to be 1.0 where a participant
  // is male, and 0.0 where the participant is female.
  val target = data.genders.values.map {
```

```

    gender => if(gender == 'M') 1.0 else 0.0
  }

  // Build the loss function ready for optimization.
  // We will worry about refactoring this to be more
  // efficient later.
  def costFunction(parameters:DenseVector[Double]):Double = {
    val xBeta = featureMatrix * parameters
    val expXBeta = exp(xBeta)
    - sum((target :* xBeta) - log1p(expXBeta))
  }

  def costFunctionGradient(parameters:DenseVector[Double])
  :DenseVector[Double] = {
    val xBeta = featureMatrix * parameters
    val probs = sigmoid(xBeta)
    featureMatrix.t * (probs - target)
  }

  val f = new DiffFunction[DenseVector[Double]] {
    def calculate(parameters:DenseVector[Double]) =
      (costFunction(parameters), costFunctionGradient(parameters))
  }

  val optimalParameters = minimize(f, DenseVector(0.0, 0.0, 0.0))

  println(optimalParameters)
  // => DenseVector(-0.0751454743, 2.476293647, 2.23054540)
}

```

That was a mouthful! Let's take this one step at a time. After the obvious imports, we start with:

```
object LogisticRegressionHWDData extends App {
```

By extending the built-in `App` trait, we tell Scala to treat the entire object as a main function. This just cuts out `def main(args:Array[String])` boilerplate. We then load the data and rescale the height and weight to have a mean of zero and a standard deviation of one:

```

def rescaled(v:DenseVector[Double]) =
  (v - mean(v)) / stddev(v)

val rescaledHeights = rescaled(data.heights)
val rescaledWeights = rescaled(data.weights)

```

The `rescaledHeights` and `rescaledWeights` vectors will be the features of our model. We can now build the training set matrix for this model. This is a $(181 * 3)$ matrix, for which the i -th row is $(1, \text{height}(i), \text{weight}(i))$, corresponding to the values of the height and weight for the i th participant. We start by transforming both `rescaledHeights` and `rescaledWeights` from vectors to $(181 * 1)$ matrices

```
val rescaledHeightsAsMatrix = rescaledHeights.toDenseMatrix.t
val rescaledWeightsAsMatrix = rescaledWeights.toDenseMatrix.t
```

We must also create a $(181 * 1)$ matrix containing just `1` to act as the dummy feature. We can do this using:

```
DenseMatrix.ones[Double](rescaledHeightsAsMatrix.rows, 1)
```

We now need to combine our three $(181 * 1)$ matrices together into a single feature matrix of shape $(181 * 3)$. We can use the `horzcat` method to concatenate the three matrices together:

```
val featureMatrix = DenseMatrix.horzcat(
  DenseMatrix.ones[Double](rescaledHeightsAsMatrix.rows, 1),
  rescaledHeightsAsMatrix,
  rescaledWeightsAsMatrix
)
```

The final step in the data preprocessing stage is to create the target variable. We need to convert the `data.genders` vector to a vector of ones and zeros. We assign a value of one for men and zero for women. Thus, our classifier will predict the probability that any given person is male. We will use the `.values.map` method, a method equivalent to the `.map` method on Scala collections:

```
val target = data.genders.values.map {
  gender => if(gender == 'M') 1.0 else 0.0
}
```

Note that we could also have used the indicator function which we discovered earlier:

```
val maleVector = DenseVector.fill(data.genders.size)('M')
val target = I(data.genders := maleVector)
```

This results in the allocation of a temporary array, `maleVector`, and might therefore increase the program's memory footprint if there were many participants in the experiment.

We now have a matrix representing the training set and a vector denoting the target variable. We can write the loss function that we want to minimize. As mentioned previously, we will minimize $-\log(L(\text{parameters} | \text{training}))$. The loss function takes as input a set of values for the linear coefficients and returns a number indicating how well those values of the linear coefficients fit the training data:

```
def costFunction(parameters:DenseVector[Double]):Double = {
  val xBeta = featureMatrix * parameters
  val expXBeta = exp(xBeta)
  - sum((target :* xBeta) - log1p(expXBeta))
}
```

Note that we use `log1p(x)` to calculate $\log(1+x)$. This is robust to underflow for small values of x .

Let's explore the cost function:

```
costFunction(DenseVector(0.0, 0.0, 0.0)) // 125.45963968135031
costFunction(DenseVector(0.0, 0.1, 0.1)) // 113.33336518036882
costFunction(DenseVector(0.0, -0.1, -0.1)) // 139.17134594294433
```

We can see that the cost function is somewhat lower for slightly positive values of the height and weight parameters. This indicates that the likelihood function is larger for slightly positive values of the height and weight. This, in turn, implies (as we expect from the plot) that people who are taller and heavier than average are more likely to be male.

We also need a function that calculates the gradient of the loss function, since that will help with the optimization:

```
def costFunctionGradient(parameters:DenseVector[Double])
:DenseVector[Double] = {
  val xBeta = featureMatrix * parameters
  val probs = sigmoid(xBeta)
  featureMatrix.t * (probs - target)
}
```

Having defined the loss function and gradient, we are now in a position to set up the optimization:

```
val f = new DiffFunction[DenseVector[Double]] {
  def calculate(parameters:DenseVector[Double]) =
    (costFunction(parameters), costFunctionGradient(parameters))
}
```

All that is left now is to run the optimization. The cost function for logistic regression is convex (it has a single minimum), so the starting point for optimization is irrelevant in principle. In practice, it is common to start with a coefficient vector that is zero everywhere (equating to assigning a 0.5 probability of being male to every participant):

```
val optimalParameters = minimize(f, DenseVector(0.0, 0.0, 0.0))
```

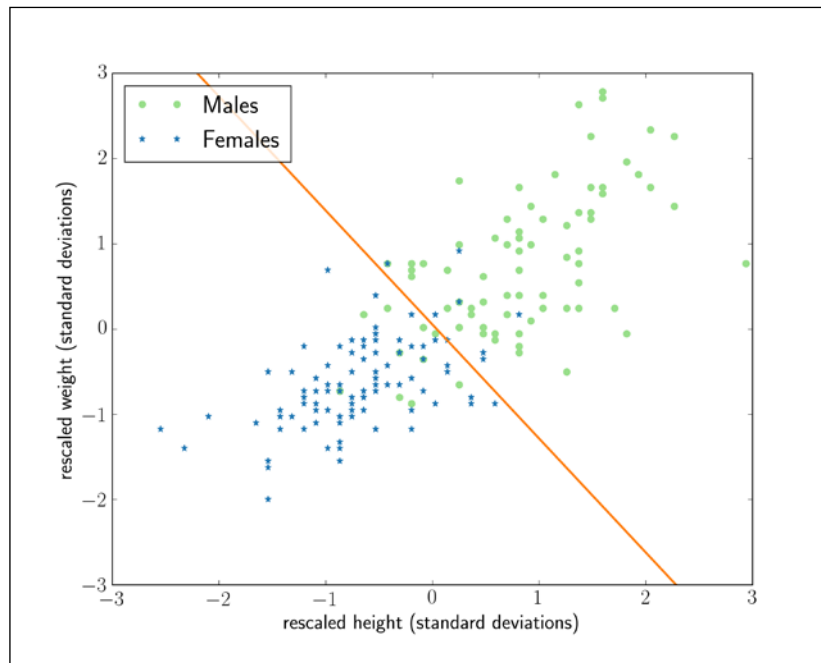
This returns the vector of optimal parameters:

```
DenseVector(-0.0751454743, 2.476293647, 2.23054540)
```

How can we interpret the values of the optimal parameters? The coefficients for the height and weight are both positive, indicating that people who are taller and heavier are more likely to be male.

We can also get the decision boundary (the line separating (height, weight) pairs more likely to belong to a woman from (height, weight) pairs more likely to belong to a man) directly from the coefficients. The decision boundary is:

$$-0.075 + 2.48 \text{ rescaledHeight} + 2.23 \text{ rescaledWeight} = 0$$



Height and weight data (shifted by the mean and rescaled by the standard deviation). The orange line is the logistic regression decision boundary. Logistic regression predicts that individuals above the boundary are male.

Towards re-usable code

In the previous section, we performed all of the computation in a single script. While this is fine for data exploration, it means that we cannot reuse the logistic regression code that we have built. In this section, we will start the construction of a machine learning library that you can reuse across different projects.

We will factor the logistic regression algorithm out into its own class. We construct a `LogisticRegression` class:

```
import breeze.linalg._
import breeze.numerics._
import breeze.optimize._

class LogisticRegression(
  val training:DenseMatrix[Double],
  val target:DenseVector[Double])
{
```

The class takes, as input, a matrix representing the training set and a vector denoting the target variable. Notice how we assign these to `vals`, meaning that they are set on class creation and will remain the same until the class is destroyed. Of course, the `DenseMatrix` and `DenseVector` objects are mutable, so the values that `training` and `target` point to might change. Since programming best practice dictates that mutable state makes reasoning about program behavior difficult, we will avoid taking advantage of this mutability.

Let's add a method that calculates the cost function and its gradient:

```
def costFunctionAndGradient(coefficients:DenseVector[Double])
:(Double, DenseVector[Double]) = {
  val xBeta = training * coefficients
  val expXBeta = exp(xBeta)
  val cost = - sum((target :* xBeta) - log1p(expXBeta))
  val probs = sigmoid(xBeta)
  val grad = training.t * (probs - target)
  (cost, grad)
}
```

We are now all set up to run the optimization to calculate the coefficients that best reproduce the training set. In traditional object-oriented languages, we might define a `getOptimalCoefficients` method that returns a `DenseVector` of the coefficients. Scala, however, is more elegant. Since we have defined the `training` and `target` attributes as `vals`, there is only one possible set of values of the optimal coefficients. We could, therefore, define a `val optimalCoefficients = ???` class attribute that holds the optimal coefficients. The problem with this is that it forces all the computation to happen when the instance is constructed. This will be unexpected for the user and might be wasteful: if the user is only interested in accessing the cost function, for instance, the time spent minimizing it will be wasted. The solution is to use a `lazy val`. This value will only be evaluated when the client code requests it:

```
lazy val optimalCoefficients = ???
```

To help with the calculation of the coefficients, we will define a private helper method:

```
private def calculateOptimalCoefficients
:DenseVector[Double] = {
  val f = new DiffFunction[DenseVector[Double]] {
    def calculate(parameters:DenseVector[Double]) =
      costFunctionAndGradient(parameters)
  }

  minimize(f, DenseVector.zeros[Double](training.cols))
}

lazy val optimalCoefficients = calculateOptimalCoefficients
```

We have refactored the logistic regression into its own class, that we can reuse across different projects.

If we were planning on reusing the height-weight data, we could, similarly, refactor it into a class of its own that facilitates data loading, feature scaling, and any other functionality that we find ourselves reusing often.

Alternatives to Breeze

Breeze is the most feature-rich and approachable Scala framework for linear algebra and numeric computation. However, do not take my word for it: experiment with other libraries for tabular data. In particular, I recommend trying *Saddle*, which provides a `Frame` object similar to data frames in pandas or R. In the Java world, the *Apache Commons Maths library* provides a very rich toolkit for numerical computation. In *Chapter 10, Distributed Batch Processing with Spark*, *Chapter 11, Spark SQL and DataFrames*, and *Chapter 12, Distributed Machine Learning with MLlib*, we will explore *Spark* and *MLlib*, which allow the user to run distributed machine learning algorithms.

Summary

This concludes our brief overview of Breeze. We have learned how to manipulate basic Breeze data types, how to use them for linear algebra, and how to perform convex optimization. We then used our knowledge to clean a real dataset and performed logistic regression on it.

In the next chapter, we will discuss *breeze-viz*, a plotting library for Scala.

References

The Elements of Statistical Learning, by Hastie, Tibshirani, and Friedman, gives a lucid, practical description of the mathematical underpinnings of machine learning. Anyone aspiring to do more than mindlessly apply machine learning algorithms as black boxes ought to have a well-thumbed copy of this book.

Scala for Machine Learning, by Patrick R. Nicholas, describes practical implementations of many useful machine learning algorithms in Scala.

The Breeze documentation (<https://github.com/scalanlp/breeze/wiki/Quickstart>), API docs (<http://www.scalanlp.org/api/breeze/#package>), and source code (<https://github.com/scalanlp/breeze>) provide the most up-to-date sources of documentation on Breeze.

3

Plotting with breeze-viz

Data visualization is an integral part of data science. Visualization needs fall into two broad categories: during the development and validation of new models and, at the end of the pipeline, to distill meaning from the data and the models to provide insight to external stakeholders.

The two types of visualizations are quite different. At the data exploration and model development stage, the most important feature of a visualization library is its ease of use. It should take as few steps as possible to go from having data as arrays of numbers (or CSVs or in a database) to having data displayed on a screen. The lifetime of graphs is also quite short: once the data scientist has learned all he can from the graph or visualization, it is normally discarded. By contrast, when developing visualization widgets for external stakeholders, one is willing to tolerate increased development time for greater flexibility. The visualizations can have significant lifetime, especially if the underlying data changes over time.

The tool of choice in Scala for the first type of visualization is breeze-viz. When developing visualizations for external stakeholders, web-based visualizations (such as D3) and Tableau tend to be favored.

In this chapter, we will explore breeze-viz. In *Chapter 14, Visualization with D3 and the Play Framework*, we will learn how to build Scala backends for JavaScript visualizations.

Breeze-viz is (no points for guessing) Breeze's visualization library. It wraps **JFreeChart**, a very popular Java charting library. Breeze-viz is still very experimental. In particular, it is much less feature-rich than matplotlib in Python, or R or MATLAB. Nevertheless, breeze-viz allows access to the underlying JFreeChart objects so one can always fall back to editing these objects directly. The syntax for breeze-viz is inspired by MATLAB and matplotlib.

Diving into Breeze

Let's get started. We will work in the Scala console, but a program similar to this example is available in `BreezeDemo.scala` in the examples corresponding to this chapter. Create a `build.sbt` file with the following lines:

```
scalaVersion := "2.11.7"

libraryDependencies += Seq(
  "org.scalanlp" %% "breeze" % "0.11.2",
  "org.scalanlp" %% "breeze-viz" % "0.11.2",
  "org.scalanlp" %% "breeze-natives" % "0.11.2"
)
```

Start an sbt console:

```
$ sbt console
```

```
scala> import breeze.linalg._
import breeze.linalg._
```

```
scala> import breeze.plot._
import breeze.plot._
```

```
scala> import breeze.numerics._
import breeze.numerics._
```

Let's start by plotting a sigmoid curve, $f(x) = 1/(1+e^{-x})$. We will first generate the data using Breeze. Recall that the `linspace` method creates a vector of doubles, uniformly distributed between two values:

```
scala> val x = linspace(-4.0, 4.0, 200)
x: DenseVector[Double] = DenseVector(-4.0, -3.959798...
```

```
scala> val fx = sigmoid(x)
fx: DenseVector[Double] = DenseVector(0.0179862099620915,...
```

We now have the data ready for plotting. The first step is to create a figure:

```
scala> val fig = Figure()
fig: breeze.plot.Figure = breeze.plot.Figure@37e36de9
```

This creates an empty Java Swing window (which may appear on your taskbar or equivalent). A figure can contain one or more plots. Let's add a plot to our figure:

```
scala> val plt = fig.subplot(0)
plt: breeze.plot.Plot = breeze.plot.Plot@171c2840
```

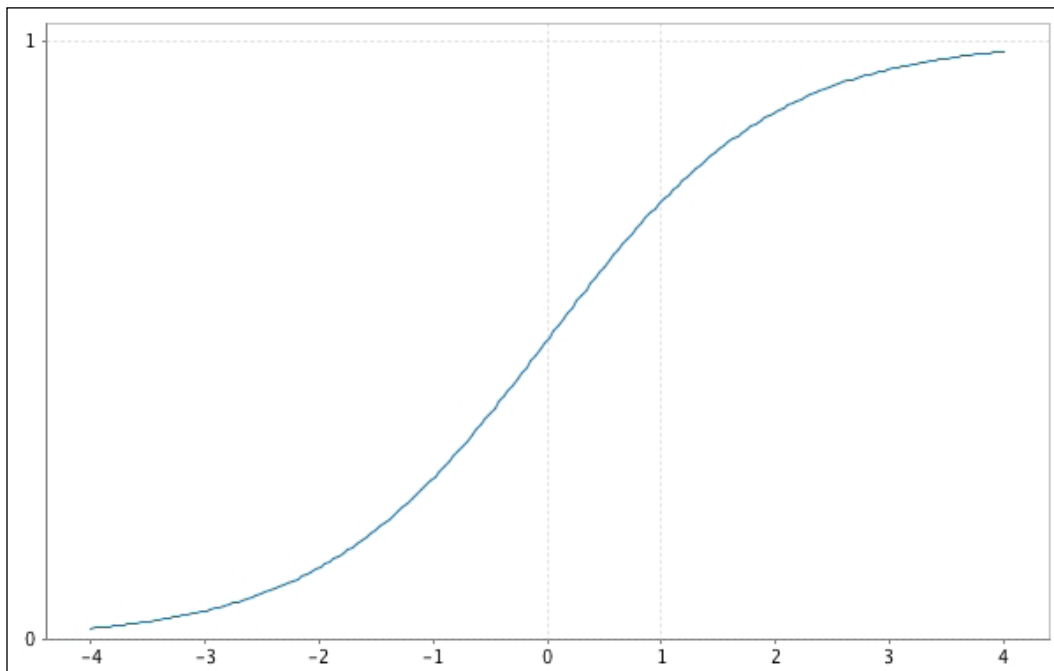
For now, let's ignore the 0 passed as argument to `.subplot`. We can add data points to our plot:

```
scala> plt += plot(x, fx)
breeze.plot.Plot = breeze.plot.Plot@63d6a0f8
```

The `plot` function takes two arguments, corresponding to the x and y values of the data series to be plotted. To view the changes, you need to refresh the figure:

```
scala> fig.refresh()
```

Look at the Swing window now. You should see a beautiful sigmoid, similar to the one below. Right-clicking on the window lets you interact with the plot and save the image as a PNG:



You can also save the image programmatically as follows:

```
scala> fig.saveas("sigmoid.png")
```

Breeze-viz currently only supports exporting to PNG.

Customizing plots

We now have a curve on our chart. Let's add a few more:

```
scala> val f2x = sigmoid(2.0*x)
f2x: breeze.linalg.DenseVector[Double] = DenseVector(3.353501304664E-4...
```

```
scala> val f10x = sigmoid(10.0*x)
f10x: breeze.linalg.DenseVector[Double] = DenseVector(4.2483542552
9E-18...
```

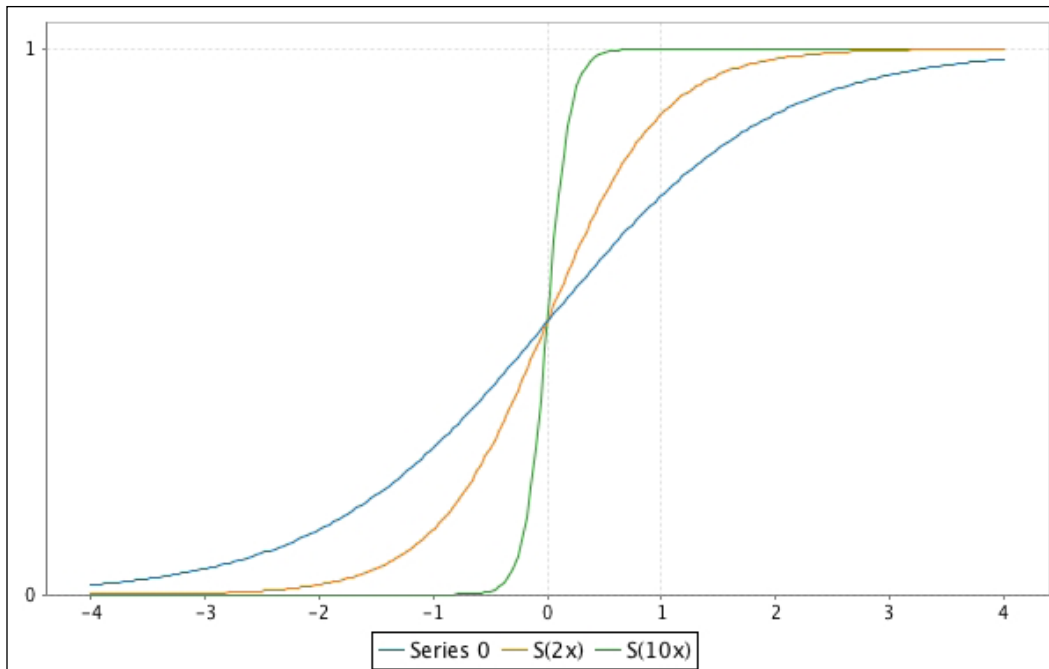
```
scala> plt += plot(x, f2x, name="S(2x)")
breeze.plot.Plot = breeze.plot.Plot@63d6a0f8
```

```
scala> plt += plot(x, f10x, name="S(10x)")
breeze.plot.Plot = breeze.plot.Plot@63d6a0f8
```

```
scala> fig.refresh()
```

Looking at the figure now, you should see all three curves in different colors. Notice that we named the data series as we added them to the plot, using the `name=""` keyword argument. To view the names, we must set the `legend` attribute:

```
scala> plt.legend = true
```



Our plot still leaves a lot to be desired. Let's start by restricting the range of the x axis to remove the bands of white space on either side of the plot:

```
scala> plt.xlim = (-4.0, 4.0)
plt.xlim: (Double, Double) = (-4.0,4.0)
```

Now, notice how, while the x ticks are sensibly spaced, there are only two y ticks: at 0 and 1 . It would be useful to have ticks every 0.1 increment. Breeze does not provide a way to set this directly. Instead, it exposes the underlying JFreeChart Axis object belonging to the current plot:

```
scala> plt.yaxis
org.jfree.chart.axis.NumberAxis = org.jfree.chart.axis.NumberAxis@0
```

The Axis object supports a `.setTickUnit` method that lets us set the tick spacing:

```
scala> import org.jfree.chart.axis.NumberTickUnit
import org.jfree.chart.axis.NumberTickUnit

scala> plt.yaxis.setTickUnit(new NumberTickUnit(0.1))
```

JFreeChart allows extensive customization of the `Axis` object. For a full list of methods available, consult the JFreeChart documentation (<http://www.jfree.org/jfreechart/api/javadoc/org/jfree/chart/axis/Axis.html>).

Let's also add a vertical line at $x=0$ and a horizontal line at $f(x)=1$. We will need to access the underlying JFreeChart plot to add these lines. This is available (somewhat confusingly) as the `.plot` attribute in our `Breeze Plot` object:

```
scala> plt.plot
org.jfree.chart.plot.XYPlot = org.jfree.chart.plot.XYPlot@17e4db6c
```

We can use the `.addDomainMarker` and `.addRangeMarker` methods to add vertical and horizontal lines to JFreeChart `XYPlot` objects:

```
scala> import org.jfree.chart.plot.ValueMarker
import org.jfree.chart.plot.ValueMarker

scala> plt.plot.addDomainMarker(new ValueMarker(0.0))

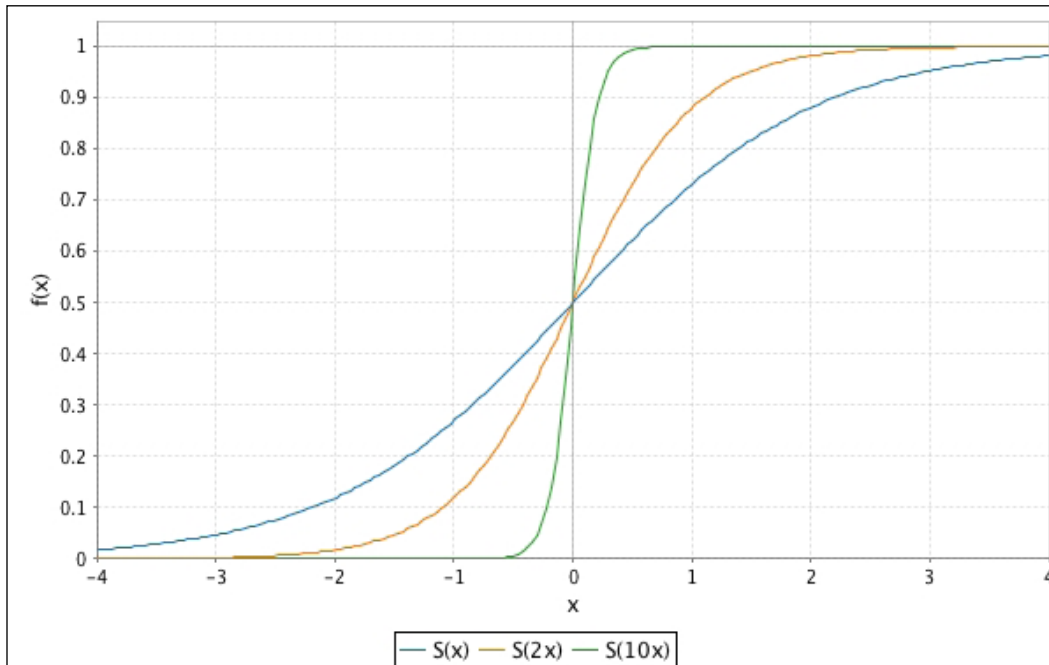
scala> plt.plot.addRangeMarker(new ValueMarker(1.0))
```

Let's also add labels to the axes:

```
scala> plt.xlabel = "x"
plt.xlabel: String = x

scala> plt.ylabel = "f(x)"
plt.ylabel: String = f(x)
```

If you have run all these commands, you should have a graph that looks like this:



We now know how to customize the basic building blocks of a graph. The next step is to learn how to change how curves are drawn.

Customizing the line type

So far, we have just plotted lines using the default settings. Breeze lets us customize how lines are drawn, at least to some extent.

For this example, we will use the height-weight data discussed in *Chapter 2, Manipulating Data with Breeze*. We will use the Scala shell here for demonstrative purposes, but you will find a program in `BreezeDemo.scala` that follows the example shell session.

The code examples for this chapter come with a module for loading the data, `HWDData.scala`, that loads the data from the CSVs:

```
scala> val data = HWDData.load
data: HWDData = HWDData [ 181 rows ]

scala> data.heights
```



```
breeze.linalg.DenseVector[Double] = DenseVector(182.0, ...
```

```
scala> data.weights
```

```
breeze.linalg.DenseVector[Double] = DenseVector(77.0, 58.0...
```

Let's create a scatter plot of the heights against the weights:

```
scala> val fig = Figure("height vs. weight")
```

```
fig: breeze.plot.Figure = breeze.plot.Figure@743f2558
```

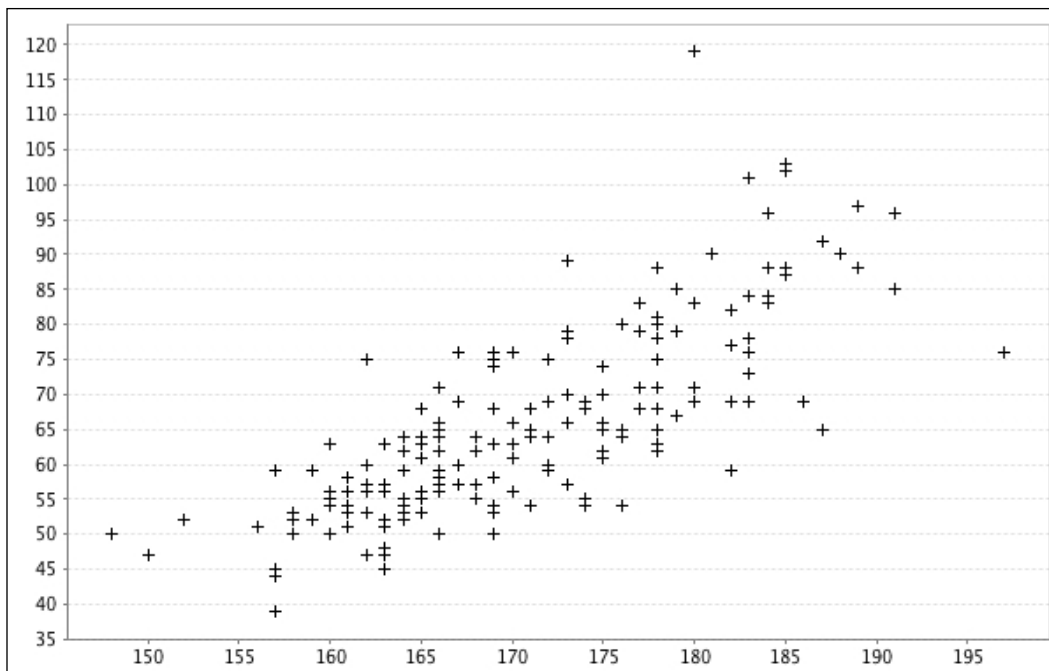
```
scala> val plt = fig.subplot(0)
```

```
plt: breeze.plot.Plot = breeze.plot.Plot@501ea274
```

```
scala> plt += plot(data.heights, data.weights, '+',  
  colorcode="black")
```

```
breeze.plot.Plot = breeze.plot.Plot@501ea274
```


This produces a scatter-plot of the height-weight data:



Note that we passed a third argument to the `plot` method, `'+'`. This controls the plotting style. As of this writing, there are three available styles: `'-'` (the default), `'+'`, and `'.'`. Experiment with these to see what they do. Finally, we pass a `colorcode="black"` argument to control the color of the line. This is either a color name or an RGB triple, written as a string. Thus, to plot red points, we could have passed `colorcode=" [255, 0, 0] "`.

Looking at the height-weight plot, there is clearly a trend between height and weight. Let's try and fit a straight line through the data points. We will fit the following function:

$$\text{weight}(\text{Kg}) = a + b \times \text{height}(\text{cm})$$

 Scientific literature suggests that it would be better to fit something more like $\text{mass} \propto \text{height}^2$. You should find it straightforward to fit a quadratic line to the data, should you wish to.

We will use Breeze's least squares function to find the values of a and b . The `leastSquares` method expects an input matrix of features and a target vector, just like the `LogisticRegression` class that we defined in the previous chapter. Recall that in *Chapter 2, Manipulating Data with Breeze*, when we prepared the training set for logistic regression classification, we introduced a dummy feature that was one for every participant to provide the degree of freedom for the y intercept. We will use the same approach here. Our feature matrix, therefore, contains two columns — one that is 1 everywhere and one for the height:

```
scala> val features = DenseMatrix.horzcat(
  DenseMatrix.ones[Double](data.npoints, 1),
  data.heights.toDenseMatrix.t
)
features: breeze.linalg.DenseMatrix[Double] =
1.0  182.0
1.0  161.0
1.0  161.0
1.0  177.0
1.0  157.0
...

scala> import breeze.stats.regression._
```

```
import breeze.stats.regression._

scala> val leastSquaresResult = leastSquares(features, data.weights)
leastSquaresResult: breeze.stats.regression.LeastSquaresRegressionResult
= <function1>
```

The `leastSquares` method returns an instance of `LeastSquareRegressionResult`, which contains a `coefficients` attribute containing the coefficients that best fit the data:

```
scala> leastSquaresResult.coefficients
breeze.linalg.DenseVector[Double] = DenseVector(-131.042322, 1.1521875)
```

The best-fit line is therefore:

$$weight(Kg) = -131.04 + 1.1522 \times height(cm)$$

Let's extract the coefficients. An elegant way of doing this is to use Scala's pattern matching capabilities:

```
scala> val Array(a, b) = leastSquaresResult.coefficients.toArray
a: Double = -131.04232269750622
b: Double = 1.1521875435418725
```

By writing `val Array(a, b) = ...`, we are telling Scala that the right-hand side of the expression is a two-element array and to bind the first element of that array to the value `a` and the second to the value `b`. See *Appendix, Pattern Matching and Extractors*, for a discussion of pattern matching.

We can now add the best-fit line to our graph. We start by generating evenly-spaced dummy height values:

```
scala> val dummyHeights = linspace(min(data.heights),
  max(data.heights), 200)
dummyHeights: breeze.linalg.DenseVector[Double] = DenseVector(148.0, ...
```

```
scala> val fittedWeights = a :+ (b :* dummyHeights)
fittedWeights: breeze.linalg.DenseVector[Double] = DenseVector(39.4814...
```

```
scala> plt += plot(dummyHeights, fittedWeights, colorcode="red")
breeze.plot.Plot = breeze.plot.Plot@501ea274
```

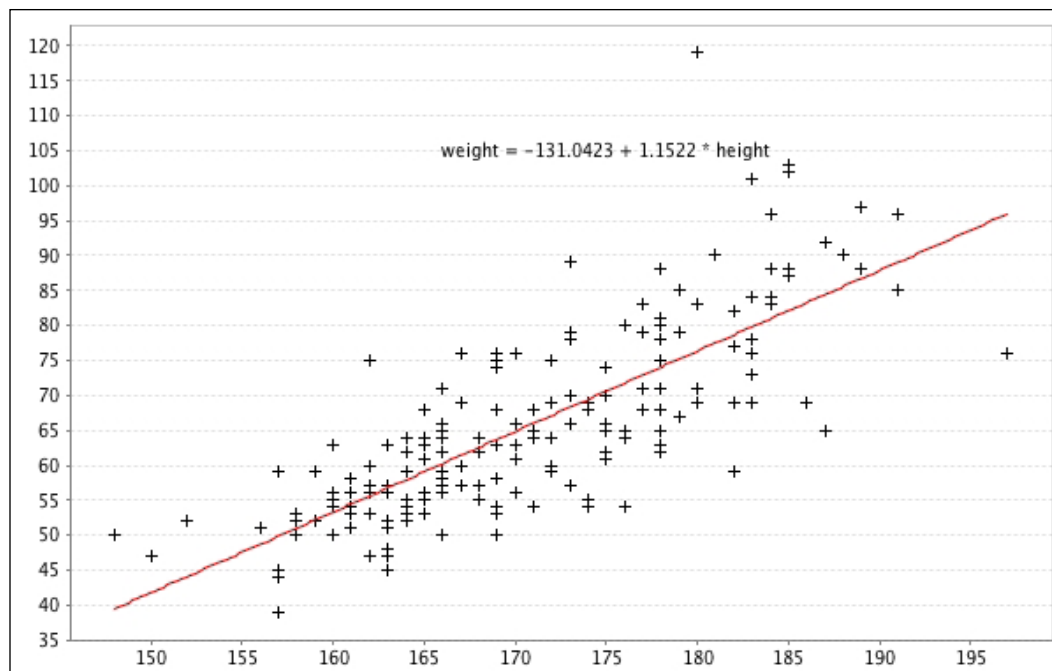
Let's also add the equation for the best-fit line to the graph as an annotation. We will first generate the label:

```
scala> val label = f"weight = $a%.4f + $b%.4f * height"  
label: String = weight = -131.0423 + 1.1522 * height
```

To add an annotation, we must access the underlying JFreeChart plot:

```
scala> import org.jfree.chart.annotations.XYTextAnnotation  
import org.jfree.chart.annotations.XYTextAnnotation  
  
scala> plt.plot.addAnnotation(new XYTextAnnotation(label, 175.0, 105.0))
```

The `XYTextAnnotation` constructor takes three parameters: the annotation string and a pair of (x, y) coordinates defining the centre of the annotation on the graph. The coordinates of the annotation are expressed in the coordinate system of the data. Thus, calling `new XYTextAnnotation(label, 175.0, 105.0)` generates an annotation whose centroid is at the point corresponding to a height of 175 cm and weight of 105 kg:



More advanced scatter plots

Breeze-viz offers a `scatter` function that adds a significant degree of customization to scatter plots. In particular, we can use the size and color of the marker points to add additional dimensions of information to the plot.

The `scatter` function takes, as its first two arguments, collections of x and y points. The third argument is a function mapping an integer i to a `Double` indicating the size of the i th point. The size of the point is measured in units of the x axis. If you have the sizes as a Scala collection or a Breeze vector, you can use that collection's `apply` method as the function. Let's see how this works in practice.

As with the previous examples, we will use the REPL, but you can find a sample program in `BreezeDemo.scala`:

```
scala> val fig = new Figure("Advanced scatter example")
fig: breeze.plot.Figure = breeze.plot.Figure@220821bc

scala> val plt = fig.subplot(0)
plt: breeze.plot.Plot = breeze.plot.Plot@668f8ae0

scala> val xs = linspace(0.0, 1.0, 100)
xs: breeze.linalg.DenseVector[Double] = DenseVector(0.0,
0.010101010101010102, 0.0202 ...

scala> val sizes = 0.025 * DenseVector.rand(100) // random sizes
sizes: breeze.linalg.DenseVector[Double] =
DenseVector(0.014879265631723166, 0.00219551...

scala> plt += scatter(xs, xs :^ 2.0, sizes.apply)
breeze.plot.Plot = breeze.plot.Plot@668f8ae0
```

Selecting custom colors works in a similar manner: we pass in a `colors` argument that maps an integer index to a `java.awt.Paint` object. Using these directly can be cumbersome, so Breeze provides some default palettes. For instance, the `GradientPaintScale` maps doubles in a given domain to a uniform color gradient. Let's map doubles in the range 0.0 to 1.0 to the colors between red and green:

```
scala> val palette = new GradientPaintScale(
  0.0, 1.0, PaintScale.RedToGreen)
palette: breeze.plot.GradientPaintScale[Double] = <function1>
```

```
scala> palette(0.5) // half-way between red and green
java.awt.Paint = java.awt.Color[r=127,g=127,b=0]
```

```
scala> palette(1.0) // green
java.awt.Paint = java.awt.Color[r=0,g=254,b=0]
```

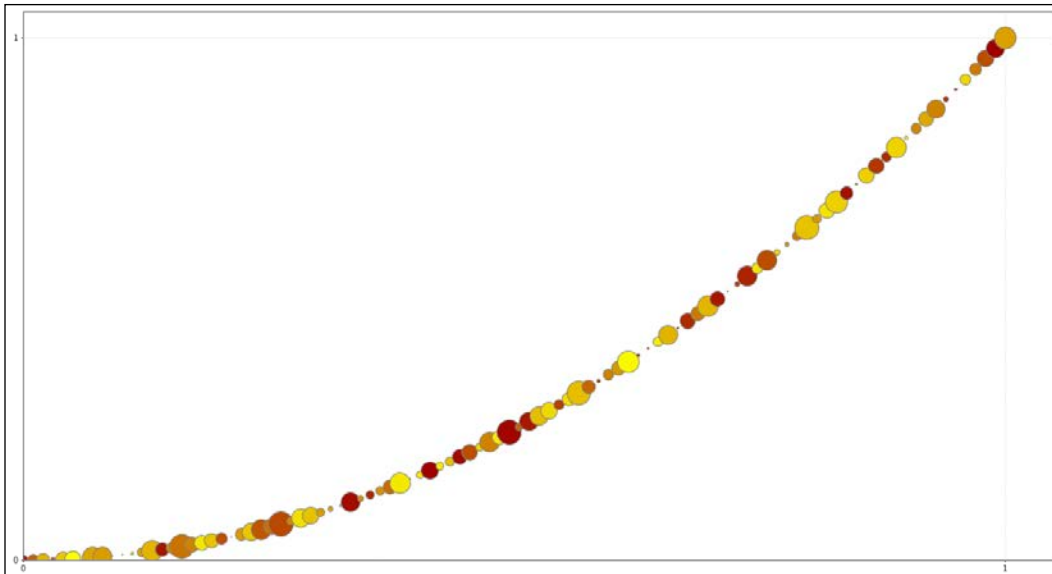
Besides the `GradientPaintScale`, `breeze-viz` provides a `CategoricalPaintScale` class for categorical palettes. For an overview of the different palettes, consult the source file `PaintScale.scala` at scala: <https://github.com/scalanlp/breeze/blob/master/viz/src/main/scala/breeze/plot/PaintScale.scala>.

Let's use our newfound knowledge to draw a multicolor scatter plot. We will assume the same initialization as the previous example. We will assign a random color to each point:

```
scala> val palette = new GradientPaintScale(0.0, 1.0,
  PaintScale.MaroonToGold)
palette: breeze.plot.GradientPaintScale[Double] = <function1>

scala> val colors = DenseVector.rand(100).mapValues(palette)
colors: breeze.linalg.DenseVector[java.awt.Paint] = DenseVector(java.awt.
Color[r=162,g=5,b=0], ...

scala> plt += scatter(xs, xs :^ 2.0, sizes.apply, colors.apply)
breeze.plot.Plot = breeze.plot.Plot@8ff7e27
```



Multi-plot example – scatterplot matrix plots

In this section, we will learn how to have several plots in the same figure.

The key new method that allows multiple plots in the same figure is `fig.subplot(nrows, ncols, plotIndex)`. This method, an overloaded version of the `fig.subplot` method we have been using up to now, both sets the number of rows and columns in the figure and returns a specific subplot. It takes three arguments:

- `nrows`: The number of rows of subplots in the figure
- `ncols`: The number of columns of subplots in the figure
- `plotIndex`: The index of the plot to return

Users familiar with MATLAB or matplotlib will note that the `.subplot` method is identical to the eponymous methods in these frameworks. This might seem a little complex, so let's look at an example (you will find the code for this in `BreezeDemo.scala`):

```
import breeze.plot._

def subplotExample {
  val data = HWData.load
```

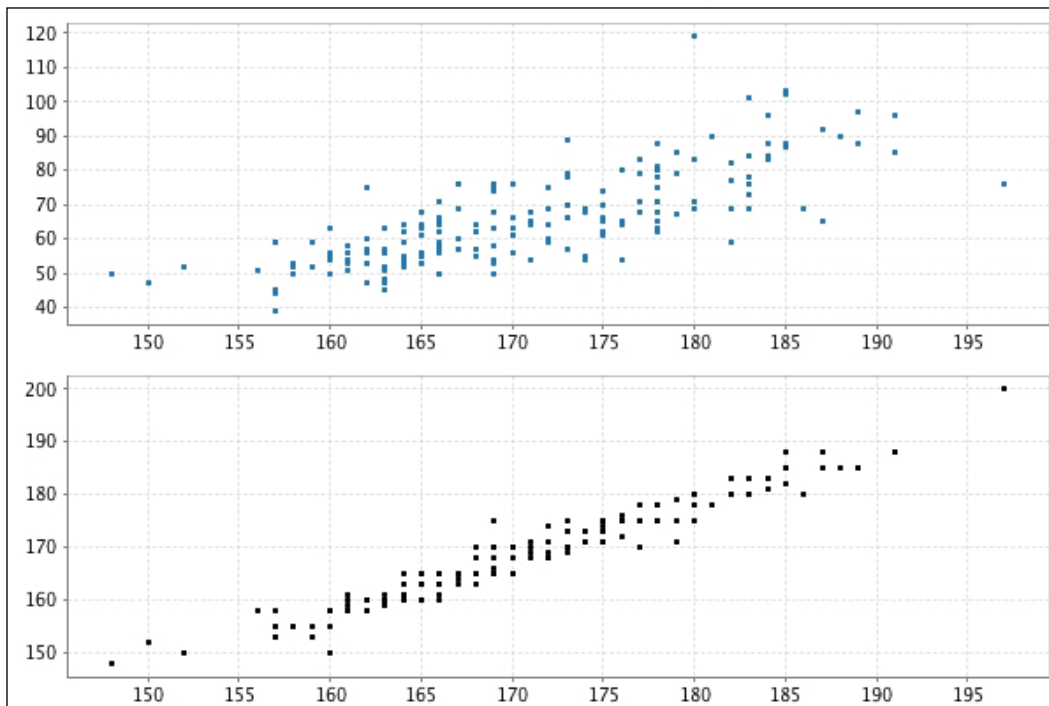
```
val fig = new Figure("Subplot example")

// upper subplot: plot index '0' refers to the first plot
var plt = fig.subplot(2, 1, 0)
plt += plot(data.heights, data.weights, '.')

// lower subplot: plot index '1' refers to the second plot
plt = fig.subplot(2, 1, 1)
plt += plot(data.heights, data.reportedHeights, '.',
            colorcode="black")

fig.refresh
}
```

Running this example produces the following plot:



Now that we have a basic grasp of how to add several subplots to the same figure, let's do something a little more interesting. We will write a class to draw scatterplot matrices. These are useful for exploring correlations between different features.

If you are not familiar with scatterplot matrices, have a look at the figure at the end of this section for an idea of what we are constructing. The idea is to build a square matrix of scatter plots for each pair of features. Element (i, j) in the matrix is a scatter plot of feature i against feature j . Since a scatter plot of a variable against itself is of limited use, one normally draws histograms of each feature along the diagonal. Finally, since a scatter plot of feature i against feature j contains the same information as a scatter plot of feature j against feature i , one normally only plots the upper triangle or the lower triangle of the matrix.

Let's start by writing functions for the individual plots. These will take a `Plot` object referencing the correct subplot and vectors of the data to plot:

```
import breeze.plot._
import breeze.linalg._

class ScatterplotMatrix(val fig:Figure) {

  /** Draw the histograms on the diagonal */
  private def plotHistogram(plt:Plot)(
    data:DenseVector[Double], label:String) {
    plt += hist(data)
    plt.xlabel = label
  }

  /** Draw the off-diagonal scatter plots */
  private def plotScatter(plt:Plot)(
    xdata:DenseVector[Double],
    ydata:DenseVector[Double],
    xlabel:String,
    ylabel:String) {
    plt += plot(xdata, ydata, '.')
    plt.xlabel = xlabel
    plt.ylabel = ylabel
  }

  ...
}
```

Notice the use of `hist(data)` to draw a histogram. The argument to `hist` must be a vector of data points. The `hist` method will bin these and represent them as a histogram.

Now that we have the machinery for drawing individual plots, we just need to wire everything together. The tricky part is to know how to select the correct subplot for a given row and column position in the matrix. We can select a single plot by calling `fig.subplot(nrows, ncolumns, plotIndex)`, but translating from a *(row, column)* index pair to a single `plotIndex` is not obvious. The plots are numbered in increasing order, first from left to right, then from top to bottom:

```
0 1 2 3
4 5 6 7
...
```

Let's write a short function to select a plot at a *(row, column)* index pair:

```
private def selectPlot(ncols:Int)(irow:Int, icol:Int):Plot = {
  fig.subplot(ncols, ncols, (irow)*ncols + icol)
}
```

We are now in a position to draw the matrix plot itself:

```
/** Draw a scatterplot matrix.
 *
 * This function draws a scatterplot matrix of the correlation
 * between each pair of columns in `featureMatrix`.
 *
 * @param featureMatrix A matrix of features, with each column
 *   representing a feature.
 * @param labels Names of the features.
 */
def plotFeatures(
  featureMatrix:DenseMatrix[Double],
  labels:List[String]
) {
  val ncols = featureMatrix.cols
  require(ncols == labels.size,
    "Number of columns in feature matrix "+
    "must match length of labels"
  )
  fig.clear
  fig.subplot(ncols, ncols, 0)

  (0 until ncols) foreach { irow =>
    val p = selectPlot(ncols)(irow, irow)
    plotHistogram(p)(featureMatrix(:, irow), labels(irow))

    (0 until irow) foreach { icol =>
```

```
        val p = selectPlot(ncols)(irow, icol)
        plotScatter(p)(
            featureMatrix(:, irow),
            featureMatrix(:, icol),
            labels(irow),
            labels(icol)
        )
    }
}
}
```

Let's write an example for our class. We will use the height-weight data again:

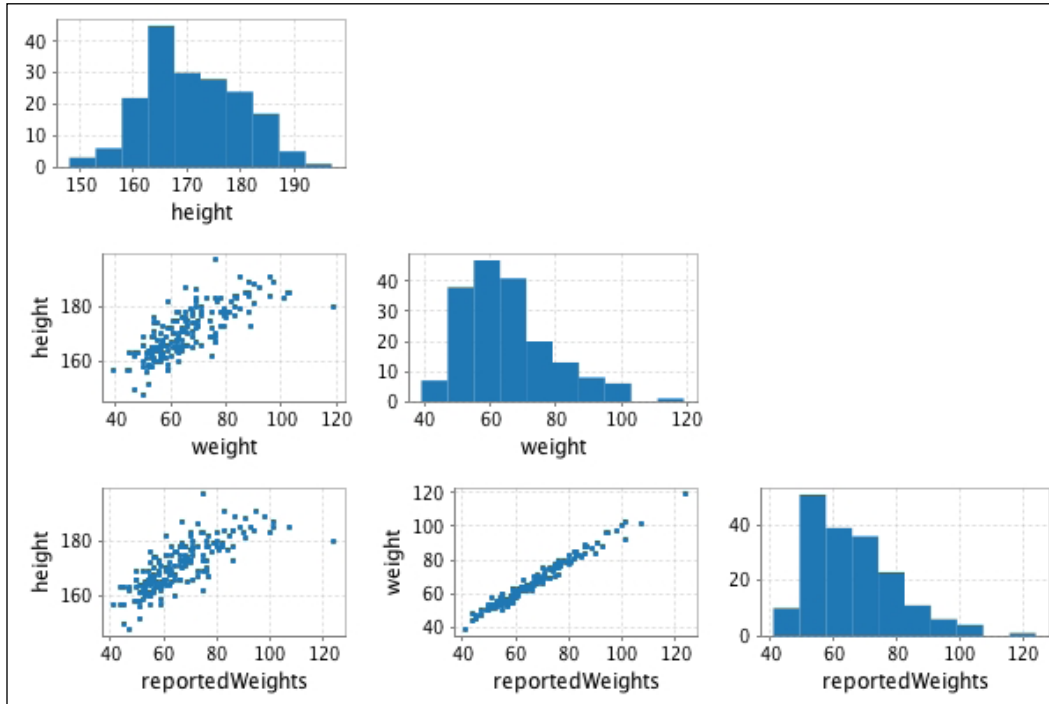
```
import breeze.linalg._
import breeze.numerics._
import breeze.plot._

object ScatterplotMatrixDemo extends App {

    val data = HWDData.load
    val m = new ScatterplotMatrix(Figure("Scatterplot matrix demo"))

    // Make a matrix with three columns: the height, weight and
    // reported weight data.
    val featureMatrix = DenseMatrix.horzcat(
        data.heights.toDenseMatrix.t,
        data.weights.toDenseMatrix.t,
        data.reportedWeights.toDenseMatrix.t
    )
    m.plotFeatures(featureMatrix,
        List("height", "weight", "reportedWeights"))
}
```

Running this through SBT produces the following plot:



Managing without documentation

Breeze-viz is unfortunately rather poorly documented. This can make the learning curve somewhat steep. Fortunately, it is still quite a small project: at the time of writing, there are just ten source files (<https://github.com/scalanlp/breeze/tree/master/viz/src/main/scala/breeze/plot>). A good way to understand exactly what breeze-viz does is to read the source code. For instance, to see what methods are available on a `Plot` object, read the source file `Plot.scala`. If you need functionality beyond that provided by Breeze, consult the documentation for JFreeChart to discover if you can implement what you need by accessing the underlying JFreeChart objects.

Breeze-viz reference

Writing a reference in a programming book is a dangerous exercise: you quickly become out of date. Nevertheless, given the paucity of documentation for breeze-viz, this section becomes more relevant – it is easier to compete against something that does not exist. Take this section with a pinch of salt, and if a command in this section does not work, head over to the source code:

Command	Description
<code>plt += plot(xs, ys)</code>	This plots a series of <code>(xs, ys)</code> values. The <code>xs</code> and <code>ys</code> values must be collection-like objects (Breeze vectors, Scala arrays, or lists, for instance).
<code>plt += scatter(xs, ys, size)</code> <code>plt += scatter(xs, ys, size, color)</code>	This plots a series of <code>(xs, ys)</code> values as a scatter plot. The <code>size</code> argument is an <code>(Int) => Double</code> function mapping the index of a point to its size (in the same units as the <code>x</code> axis). The <code>color</code> argument is an <code>(Int) => java.awt.Paint</code> function mapping from integers to colors. Read the <i>more advanced scatter plots</i> section for further details.
<code>plt += hist(xs)</code> <code>plt += hist(xs, bins=10)</code>	This bins <code>xs</code> and plots a histogram. The <code>bins</code> argument controls the number of bins.
<code>plt += image(mat)</code>	This plots an image or matrix. The <code>mat</code> argument should be <code>Matrix[Double]</code> . Read the <code>package.scala</code> source file in <code>breeze.plot</code> for details (https://github.com/scalanlp/breeze/blob/master/viz/src/main/scala/breeze/plot/package.scala).

It is also useful to summarize the options available on a `plot` object:

Attribute	Description
<code>plt.xlabel = "x-label"</code> <code>plt.ylabel = "y-label"</code>	This sets the axis label
<code>plt.xlim = (0.0, 1.0)</code> <code>plt.ylim = (0.0, 1.0)</code>	This sets the axis maximum and minimum value
<code>plt.logScaleX = true</code> <code>plt.logScaleY = true</code>	This switches the axis to a log scale
<code>plt.title = "title"</code>	This sets the plot title

Data visualization beyond breeze-viz

Other tools for data visualization in Scala are emerging: Spark notebooks (<https://github.com/andypetrella/spark-notebook#description>) based on the IPython notebook and Apache Zeppelin (<https://zeppelin.incubator.apache.org>). Both of these rely on Apache Spark, which we will explore later in this book.

Summary

In this chapter, we learned how to draw simple charts with breeze-viz. In the last chapter of this book, we will learn how to build interactive visualizations using JavaScript libraries.

Next, we will learn about basic Scala concurrency constructs – specifically, parallel collections.

4

Parallel Collections and Futures

Data science often involves processing medium or large amounts of data. Since the previously exponential growth in the speed of individual CPUs has slowed down and the amount of data continues to increase, leveraging computers effectively must entail parallel computation.

In this chapter, we will look at ways of parallelizing computation and data processing over a single computer. Virtually all new computers have more than one processing unit, and distributing a calculation over these cores can be an effective way of hastening medium-sized calculations.

Parallelizing calculations over a single chip is suitable for calculations involving gigabytes or a few terabytes of data. For larger data flows, we must resort to distributing the computation over several computers in parallel. We will discuss Apache Spark, a framework for parallel data processing in *Chapter 10, Distributed Batch Processing with Spark*.

In this book, we will look at three common ways of leveraging parallel architectures in a single machine: parallel collections, futures, and actors. We will consider the first two in this chapter, and leave the study of actors to *Chapter 9, Concurrency with Akka*.

Parallel collections

Parallel collections offer an extremely easy way to parallelize independent tasks. The reader, being familiar with Scala, will know that many tasks can be phrased as operations on collections, such as *map*, *reduce*, *filter*, or *groupBy*. Parallel collections are an implementation of Scala collections that parallelize these operations to run over several threads.

Let's start with an example. We want to calculate the frequency of occurrence of each letter in a sentence:

```
scala> val sentence = "The quick brown fox jumped over the lazy dog"
sentence: String = The quick brown fox jumped ...
```

Let's start by converting our sentence from a string to a vector of characters:

```
scala> val characters = sentence.toVector
Vector[Char] = Vector(T, h, e, , q, u, i, c, k, ...)
```

We can now convert `characters` to a *parallel* vector, a `ParVector`. To do this, we use the `par` method:

```
scala> val charactersPar = characters.par
ParVector[Char] = ParVector(T, h, e, , q, u, i, c, k, , ...)
```

`ParVector` collections support the same operations as regular vectors, but their methods are executed in parallel over several threads.

Let's start by filtering out the spaces in `charactersPar`:

```
scala> val lettersPar = charactersPar.filter { _ != ' ' }
ParVector[Char] = ParVector(T, h, e, q, u, i, c, k, ...)
```

Notice how Scala hides the execution details. The `filter` operation was performed using multiple threads, and you barely even noticed! The interface and behavior of a parallel vector is identical to its serial counterpart, save for a few details that we will explore in the next section.

Let's now use the `toLowerCase` function to make the letters lowercase:

```
scala> val lowerLettersPar = lettersPar.map { _.toLowerCase }
ParVector[Char] = ParVector(t, h, e, q, u, i, c, k, ...)
```

As before, the `map` method was applied in parallel. To find the frequency of occurrence of each letter, we use the `groupBy` method to group characters into vectors containing all the occurrences of that character:

```
scala> val intermediateMap = lowerLettersPar.groupBy(identity)
ParMap[Char,ParVector[Char]] = ParMap(e -> ParVector(e, e, e, e), ...)
```

Note how the `groupBy` method has created a `ParMap` instance, the parallel equivalent of an immutable map. To get the number of occurrences of each letter, we do a `mapValues` call on `intermediateMap`, replacing each vector by its length:

```
scala> val occurrenceNumber = intermediateMap.mapValues { _.length }
ParMap[Char,Int] = ParMap(e -> 4, x -> 1, n -> 1, j -> 1, ...)
```

Congratulations! We've written a multi-threaded algorithm for finding the frequency of occurrence of each letter in a few lines of code. You should find it straightforward to adapt this to find the frequency of occurrence of each word in a document, a common preprocessing problem for analyzing text data.

Parallel collections make it very easy to parallelize some operation pipelines: all we had to do was call `.par` on the `characters` vector. All subsequent operations were parallelized. This makes switching from a serial to a parallel implementation very easy.

Limitations of parallel collections

Part of the power and the appeal of parallel collections is that they present the same interface as their serial counterparts: they have a `map` method, a `foreach` method, a `filter` method, and so on. By and large, these methods work in the same way on parallel collections as they do in serial. There are, however, some notable caveats. The most important one has to do with side effects. If an operation on a parallel collection has a side effect, this may result in a race condition: a situation in which the final result depends on the order in which the threads perform their operations.

Side effects in collections arise most commonly when we update a variable defined outside of the collection. To give a trivial example of unexpected behavior, let's define a `count` variable and increment it a thousand times using a parallel range:

```
scala> var count = 0
count: Int = 0

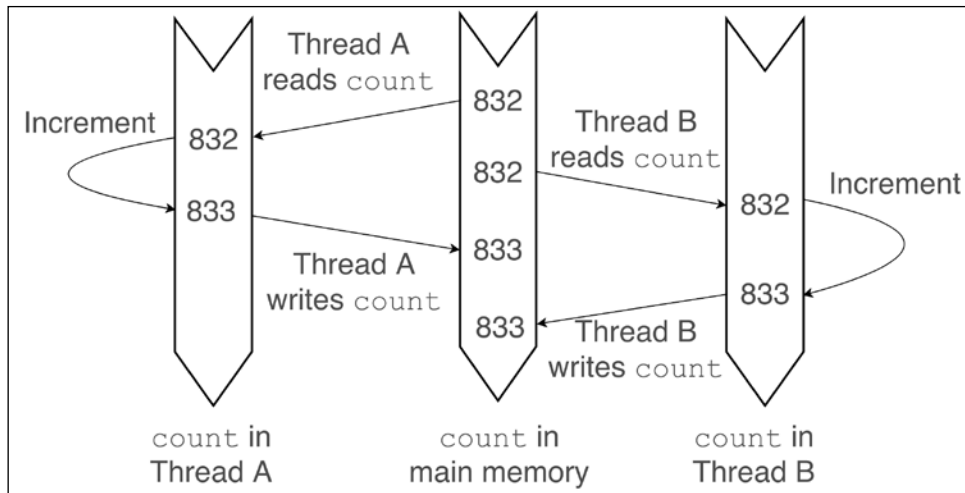
scala> (0 until 1000).par.foreach { i => count += 1 }

scala> count
count: Int = 874 // not 1000!
```

What happened here? The function passed to `foreach` has a side effect: it increments `count`, a variable outside of the scope of the function. This is a problem because the `+=` operator is a sequence of two operations:

- Retrieve the value of `count` and add one to it
- Assign the result back to `count`

To understand why this causes unexpected behavior, let's imagine that the `foreach` loop has been parallelized over two threads. **Thread A** might read the `count` variable when it is **832** and add one to it to give **833**. Before it has time to reassign **833** to `count`, **Thread B** reads `count`, still at **832**, and adds one to give **833**. **Thread A** then assigns **833** to `count`. **Thread B** then assigns **833** to `count`. We've run through two updates but only incremented the count by one. The problem arises because `+=` can be separated into two instructions: it is not *atomic*. This leaves room for threads to interleave their operations:



The anatomy of a race condition: both thread A and thread B are trying to update `count` concurrently, resulting in one of the updates being overwritten. The final value of `count` is 833 instead of 834.

To give a somewhat more realistic example of problems caused by non-atomicity, let's look at a different method for counting the frequency of occurrence of each letter in our sentence. We define a mutable `Char -> Int` hash map outside of the loop. Each time we encounter a letter, we increment the corresponding integer in the map:

```
scala> import scala.collection.mutable
import scala.collection.mutable

scala> val occurrenceNumber = mutable.Map.empty[Char, Int]
```

```
occurrenceNumber: mutable.Map[Char,Int] = Map()

scala> lowerLettersPar.foreach { c =>
  occurrenceNumber(c) = occurrenceNumber.getOrElse(c, 0) + 1
}

scala> occurrenceNumber('e') // Should be 4
Int = 2
```

The discrepancy occurs because of the non-atomicity of the operations in the `foreach` loop.

In general, it is good practice to avoid side effects in higher-order functions on collections. They make the code harder to understand and preclude switching from serial to parallel collections. It is also good practice to avoid exposing mutable state: immutable objects can be shared freely between threads and cannot be affected by side effects.

Another limitation of parallel collections occurs in reduction (or folding) operations. The function used to combine items together must be *associative*. For instance:

```
scala> (0 until 1000).par.reduce { _ - _ } // should be -499500
Int = 63620
```

The *minus* operator, `-`, is not associative. The order in which consecutive operations are applied matters: $(a - b) - c$ is not the same as $a - (b - c)$. The function used to reduce a parallel collection must be associative because the order in which the reduction occurs is not tied to the order of the collection.

Error handling

In single-threaded programs, exception handling is relatively straightforward: if an exception occurs, the function can either handle it or escalate it. This is not nearly as obvious when parallelism is introduced: a single thread might fail, but the others might return successfully.

Parallel collection methods will throw an exception if they fail on any element, just like their serial counterparts:

```
scala> Vector(2, 0, 5).par.map { 10 / _ }
java.lang.ArithmeticException: / by zero
...
```

There are cases when this isn't the behavior that we want. For instance, we might be using a parallel collection to retrieve a large number of web pages in parallel. We might not mind if a few of the pages cannot be fetched.

Scala's `Try` type was designed for sandboxing code that might throw exceptions. It is similar to `Option` in that it is a one-element container:

```
scala> import scala.util._
import scala.util._
```

```
scala> Try { 2 + 2 }
Try[Int] = Success(4)
```

Unlike the `Option` type, which indicates whether an expression has a useful value, the `Try` type indicates whether an expression can be executed without throwing an exception. It takes on the following two values:

- `Try { 2 + 2 } == Success(4)` if the expression in the `Try` statement is evaluated successfully
- `Try { 2 / 0 } == Failure(java.lang.ArithmeticException: / by zero)` if the expression in the `Try` block results in an exception

This will make more sense with an example. To see the `Try` type in action, we will try to fetch web pages in a fault tolerant manner. We will use the built-in `Source.fromURL` method which fetches a web page and opens an iterator of the page's content. If it fails to fetch the web page, it throws an error:

```
scala> import scala.io.Source
import scala.io.Source

scala> val html = Source.fromURL("http://www.google.com")
scala.io.BufferedSource = non-empty iterator

scala> val html = Source.fromURL("garbage")
java.net.MalformedURLException: no protocol: garbage
...
```

Instead of letting the expression propagate out and crash the rest of our code, we can wrap the call to `Source.fromURL` in `Try`:

```
scala> Try { Source.fromURL("http://www.google.com") }
```

```
Try[BufferedSource] = Success(non-empty iterator)
```

```
scala> Try { Source.fromURL("garbage") }  
Try[BufferedSource] = Failure(java.net.MalformedURLException: no  
protocol: garbage)
```

To see the power of our Try statement, let's now retrieve a list of URLs in parallel in a fault tolerant manner:

```
scala> val URLs = Vector("http://www.google.com",  
    "http://www.bbc.co.uk",  
    "not-a-url"  
)  
URLs: Vector[String] = Vector(http://www.google.com, http://www.bbc.  
co.uk, not-a-url)  
  
scala> val pages = URLs.par.map { url =>  
    url -> Try { Source.fromURL(url) }  
}  
pages: ParVector[(String, Try[BufferedSource])] = ParVector((http://  
www.google.com,Success(non-empty iterator)), (http://www.bbc.  
co.uk,Success(non-empty iterator)), (not-a-url,Failure(java.net.  
MalformedURLException: no protocol: not-a-url)))
```

We can then use a collect statement to act on the pages we could fetch successfully. For instance, to get the number of characters on each page:

```
scala> pages.collect { case(url, Success(it)) => url -> it.size }  
ParVector[(String, Int)] = ParVector((http://www.google.com,18976),  
(http://www.bbc.co.uk,132893))
```

By making good use of Scala's built-in Try classes and parallel collections, we have built a fault tolerant, multithreaded URL retriever in a few lines of code. (Compare this to the myriad of Java/C++ books that prefix code examples with 'error handling is left out for clarity'.)

The Try type versus try/catch statements

Programmers with imperative or object-oriented backgrounds will be more familiar with try/catch blocks for handling exceptions. We could have accomplished similar functionality here by wrapping the code for fetching URLs in a try block, returning null if the call raises an exception.



However, besides being more verbose, returning null is less satisfactory: we lose all information about the exception and null is less expressive than `Failure(exception)`. Furthermore, returning a `Try[T]` type forces the caller to consider the possibility that the function might fail, by encoding this possibility in the type of the return value. In contrast, just returning `T` and coding failure with a null value allows the caller to ignore failure, raising the possibility of a confusing `NullPointerException` being thrown at a completely different point in the program.

In short, `Try[T]` is just another higher-order type, like `Option[T]` or `List[T]`. Treating the possibility of failure in the same way as the rest of the code adds coherence to the program and encourages programmers to tackle the possibility of exceptions explicitly.

Setting the parallelism level

So far, we have considered parallel collections as black boxes: add `par` to a normal collection and all the operations are performed in parallel. Often, we will want more control over how the tasks are executed.

Internally, parallel collections work by distributing an operation over multiple threads. Since the threads share memory, parallel collections do not need to copy any data. Changing the number of threads available to the parallel collection will change the number of CPUs that are used to perform the tasks.

Parallel collections have a `taskSupport` attribute that controls task execution:

```
scala> val parRange = (0 to 100).par
parRange: ParRange = ParRange(0, 1, 2, 3, 4, 5, ...

scala> parRange.taskSupport
TaskSupport = scala.collection.parallel.ExecutionContextTaskSupport@311a0b3e

scala> parRange.taskSupport.parallelismLevel
Int = 8 // Number of threads to be used
```

The task support object of a collection is an *execution context*, an abstraction capable of executing Scala expressions in a separate thread. By default, the execution context in Scala 2.11 is a *work-stealing thread pool*. When a parallel collection submits tasks, the context allocates these tasks to its threads. If a thread finds that it has finished its queued tasks, it will try and steal outstanding tasks from the other threads. The default execution context maintains a thread pool with number of threads equal to the number of CPUs.

The number of threads over which the parallel collection distributes the work can be changed by changing the task support. For instance, to parallelize the operations performed by a range over four threads:

```
scala> import scala.collection.parallel._
import scala.collection.parallel._

scala> parRange.taskSupport = new ForkJoinTaskSupport(
  new scala.concurrent.forkjoin.ForkJoinPool(4)
)
parRange.taskSupport: scala.collection.parallel.TaskSupport = scala.
collection.parallel.ForkJoinTaskSupport@6e1134e1

scala> parRange.taskSupport.parallelismLevel
Int: 4
```

An example – cross-validation with parallel collections

Let's apply what you have learned so far to solve data science problems. There are many parts of a machine learning pipeline that can be parallelized trivially. One such part is cross-validation.

We will give a brief description of cross-validation here, but you can refer to *The Elements of Statistical Learning*, by Hastie, Tibshirani, and Friedman for a more in-depth discussion.

Typically, a supervised machine learning problem involves training an algorithm over a training set. For instance, when we built a model to calculate the probability of a person being male based on their height and weight, the training set was the (height, weight) data for each participant, together with the male/female label for each row. Once the algorithm is trained on the training set, we can use it to classify new data. This process only really makes sense if the training set is representative of the new data that we are likely to encounter.

The training set has a finite number of entries. It will thus, inevitably, have idiosyncrasies that are not representative of the population at large, merely due to its finite nature. These idiosyncrasies will result in prediction errors when predicting whether a new person is male or female, over and above the prediction error of the algorithm on the training set itself. Cross-validation is a tool for estimating the error caused by the idiosyncrasies of the training set that do not reflect the population at large.

Cross-validation works by dividing the training set in two parts: a smaller, new training set and a cross-validation set. The algorithm is trained on the reduced training set. We then see how well the algorithm models the cross-validation set. Since we know the right answer for the cross-validation set, we can measure how well our algorithm is performing when shown new information. We repeat this procedure many times with different cross-validation sets.

There are several different types of cross-validation, which differ in how we choose the cross-validation set. In this chapter, we will look at repeated random subsampling: we select k rows at random from the training data to form the cross-validation set. We do this many times, calculating the cross-validation error for each subsample. Since each iteration is independent of the previous ones, we can parallelize this process trivially. It is therefore a good candidate for parallel collections. We will look at an alternative form of cross-validation, *k-fold cross-validation*, in *Chapter 12, Distributed Machine Learning with MLlib*.

We will build a class that performs cross-validation in parallel. I encourage you to write the code as you go, but you will find the source code corresponding to these examples on GitHub (<https://github.com/pbugnion/s4ds>). We will use parallel collections to handle the parallelism and Breeze data types in the inner loop. The `build.sbt` file is identical to the one we used in *Chapter 2, Manipulating Data with Breeze*:

```
scalaVersion := "2.11.7"

libraryDependencies += Seq(
  "org.scalanlp" %% "breeze" % "0.11.2",
  "org.scalanlp" %% "breeze-natives" % "0.11.2"
)
```

We will build a `RandomSubsample` class. The class exposes a type alias, `CVFunction`, for a function that takes two lists of indices—the first corresponding to the reduced training set and the second to the validation set—and returns a `Double` corresponding to the cross-validation error:

```
type CVFunction = (Seq[Int], Seq[Int]) => Double
```

The `RandomSubsample` class will expose a single method, `mapSamples`, which takes a `CVFunction`, repeatedly passes it different partitions of indices, and returns a vector of the errors. This is what the class looks like:

```
// RandomSubsample.scala

import breeze.linalg._
import breeze.numerics._

/** Random subsample cross-validation
 *
 * @param nElems Total number of elements in the training set.
 * @param nCrossValidation Number of elements to leave out of
 * training set.
 */
class RandomSubsample(val nElems: Int, val nCrossValidation: Int) {

  type CVFunction = (Seq[Int], Seq[Int]) => Double

  require(nElems > nCrossValidation,
    "nCrossValidation, the number of elements " +
    "withheld, must be < nElems")

  private val indexList = DenseVector.range(0, nElems)

  /** Perform multiple random sub-sample CV runs on f
   *
   * @param nShuffles Number of random sub-sample runs.
   * @param f user-defined function mapping from a list of
   * indices in the training set and a list of indices in the
   * test-set to a double indicating the out-of sample score
   * for this split.
   * @returns DenseVector of the CV error for each random split.
   */
  def mapSamples(nShuffles: Int)(f: CVFunction)
  : DenseVector[Double] = {
    val cvResults = (0 to nShuffles).par.map { i =>

      // Randomly split indices between test and training
      val shuffledIndices = breeze.linalg.shuffle(indexList)
      val Seq(testIndices, trainingIndices) =
        split(shuffledIndices, Seq(nCrossValidation))

      // Apply f for this split

```

```
        f(trainingIndices.toScalaVector,  
          testIndices.toScalaVector)  
      }  
      DenseVector(cvResults.toArray)  
    }  
  }
```

Let's look at what happens in more detail, starting with the arguments passed to the constructor:

```
class RandomSubsample(val nElems:Int, val nCrossValidation:Int)
```

We pass the total number of elements in the training set and the number of elements to leave out for cross-validation in the class constructor. Thus, passing 100 to `nElems` and 20 to `nCrossValidation` implies that our training set will have 80 random elements of the total data and that the test set will have 20 elements.

We then construct a list of all integers between 0 and `nElems`:

```
private val indexList = DenseVector.range(0, nElems)
```

For each iteration of the cross-validation, we will shuffle this list and take the first `nCrossValidation` elements to be the indices of rows in our test set and the remaining to be the indices of rows in our training set.

Our class exposes a single method, `mapSamples`, that takes two curried arguments: `nShuffles`, the number of times to perform random subsampling, and `f`, a `CVFunction`:

```
def mapSamples(nShuffles:Int)(f:CVFunction):DenseVector[Double]
```

With all this set up, the code for doing cross-validation is deceptively simple. We generate a parallel range from 0 to `nShuffles` and, for each item in the range, generate a new train-test split and calculate the cross-validation error:

```
val cvResults = (0 to nShuffles).par.map { i =>  
  val shuffledIndices = breeze.linalg.shuffle(indexList)  
  val Seq(testIndices, trainingIndices) =  
    split(shuffledIndices, Seq(nCrossValidation))  
  f(trainingIndices.toScalaVector, testIndices.toScalaVector)  
}
```

The only tricky part of this function is splitting the shuffled index list into a list of indices for the training set and a list of indices for the test set. We use Breeze's `split` method. This takes a vector as its first argument and a list of split-points as its second, and returns a list of fragments of the original vector. We then use pattern matching to extract the individual parts.

Finally, `mapSamples` converts `cvResults` to a Breeze vector:

```
DenseVector(cvResults.toArray)
```

Let's see this in action. We can test our class by running cross-validation on the logistic regression example developed in *Chapter 2, Manipulating Data with Breeze*. In that chapter, we developed a `LogisticRegression` class that takes a training set (in the form of a `DenseMatrix`) and target (in the form of a `DenseVector`) at construction time. The class then calculates the parameters that best represent the training set. We will first add two methods to the `LogisticRegression` class to use the trained model to classify previously unseen examples:

- The `predictProbabilitiesMany` method uses the trained model to calculate the probability of having the target variable set to one. In the context of our example, this is the probability of being male, given a height and weight.
- The `classifyMany` method assigns classification labels (one or zero) to members of a test set. We will assign a one if `predictProbabilitiesMany` returns a value greater than 0.5.

With these two functions, our `LogisticRegression` class becomes:

```
// Logistic Regression.scala

class LogisticRegression(
  val training:DenseMatrix[Double],
  val target:DenseVector[Double]
) {
  ...
  /** Probability of classification for each row
   * in test set.
   */
  def predictProbabilitiesMany(test:DenseMatrix[Double])
  :DenseVector[Double] = {
    val xBeta = test * optimalCoefficients
    sigmoid(xBeta)
  }

  /** Predict the value of the target variable
   * for each row in test set.
   */
  def classifyMany(test:DenseMatrix[Double])
  :DenseVector[Double] = {
    val probabilities = predictProbabilitiesMany(test)
    I((probabilities > 0.5).toDenseVector)
  }
  ...
}
```

We can now put together an example program for our `RandomSubsample` class. We will use the same height-weight data as in *Chapter 2, Manipulating Data with Breeze*. The data preprocessing will be similar. The code examples for this chapter provide a helper module, `HWDData`, to load the height-weight data into Breeze vectors. The data itself is in the `data/` directory of the code examples for this chapter (available on GitHub at <https://github.com/pbugnion/s4ds/tree/master/chap04>).

For each new subsample, we create a new `LogisticRegression` instance, train it on the subset of the training set to get the best coefficients for this train-test split, and use `classifyMany` to generate predictions on the cross-validation set in this split. We then calculate the classification error and report the average classification error over every train-test split:

```
// RandomSubsampleDemo.scala

import breeze.linalg._
import breeze.linalg.functions.manhattanDistance
import breeze.numerics._
import breeze.stats._

object RandomSubsampleDemo extends App {

  /* Load and pre-process data */
  val data = HWDData.load

  val rescaledHeights:DenseVector[Double] =
    (data.heights - mean(data.heights)) / stddev(data.heights)

  val rescaledWeights:DenseVector[Double] =
    (data.weights - mean(data.weights)) / stddev(data.weights)

  val featureMatrix:DenseMatrix[Double] =
    DenseMatrix.horzcat(
      DenseMatrix.ones[Double](data.npoints, 1),
      rescaledHeights.toDenseMatrix.t,
      rescaledWeights.toDenseMatrix.t
    )

  val target:DenseVector[Double] = data.genders.values.map {
    gender => if(gender == 'M') 1.0 else 0.0
  }

  /* Cross-validation */
  val testSize = 20
```

```

val cvCalculator = new RandomSubsample(data.npoints, testSize)

// Start parallel CV loop
val cvErrors = cvCalculator.mapSamples(1000) {
  (trainingIndices, testIndices) =>

  val regressor = new LogisticRegression(
    data.featureMatrix(trainingIndices, :).toDenseMatrix,
    data.target(trainingIndices).toDenseVector
  )
  // Predictions on test-set
  val genderPredictions = regressor.classifyMany(
    data.featureMatrix(testIndices, :).toDenseMatrix
  )
  // Calculate number of mis-classified examples
  val dist = manhattanDistance(
    genderPredictions, data.target(testIndices)
  )
  // Calculate mis-classification rate
  dist / testSize.toDouble
}

println(s"Mean classification error: ${mean(cvErrors)}")
}

```

Running this program on the height-weight data gives a classification error of 10%.

We now have a fully working, parallelized cross-validation class. Scala's parallel range made it simple to repeatedly compute the same function in different threads.

Futures

Parallel collections offer a simple, yet powerful, framework for parallel operations. However, they are limited in one respect: the total amount of work must be known in advance, and each thread must perform the same function (possibly on different inputs).

Imagine that we want to write a program that fetches a web page (or queries a web API) every few seconds and extracts data for further processing from this web page. A typical example might involve querying a web API to maintain an up-to-date value of a particular stock price. Fetching data from an external web page takes a few hundred milliseconds, typically. If we perform this operation on the main thread, it will needlessly waste CPU cycles waiting for the web server to reply.

The solution is to wrap the code for fetching the web page in a *future*. A future is a one-element container containing the future result of a computation. When you create a future, the computation in it gets off-loaded to a different thread in order to avoid blocking the main thread. When the computation finishes, the result is written to the future and thus made accessible to the main thread.

As an example, we will write a program that queries the "Markit on demand" API to fetch the price of a given stock. For instance, the URL for the current price of a Google share is `http://dev.markitondemand.com/MODApis/Api/v2/Quote?symbol=GOOG`. Go ahead and paste this in the address box of your web browser. You will see an XML string appear with, among other things, the current stock price. Let's fetch this programmatically without resorting to a future first:

```
scala> import scala.io._
import scala.io_

scala> val url = "http://dev.markitondemand.com/MODApis/Api/v2/
Quote?symbol=GOOG"
url: String = http://dev.markitondemand.com/MODApis/Api/v2/
Quote?symbol=GOOG

scala> val response = Source.fromURL(url).mkString
response: String = <StockQuote><Status>SUCCESS</Status>
...
```

Notice how it takes a little bit of time to query the API. Let's now do the same, but using a future (don't worry about the imports for now, we will discuss what they mean in more detail further on):

```
scala> import scala.concurrent._
import scala.concurrent._

scala> import scala.util._
import scala.util._

scala> import scala.concurrent.ExecutionContext.Implicits.global
import scala.concurrent.ExecutionContext.Implicits.global

scala> val response = Future { Source.fromURL(url).mkString }
response: Future[String] = Promise$DefaultPromise@33301801b
```

If you run this, you will notice that control returns to the shell instantly before the API has had a chance to respond. To make this evident, let's simulate a slow connection by adding a call to `Thread.sleep`:

```
scala> val response = Future {
  Thread.sleep(10000) // sleep for 10s
  Source.fromURL(url).mkString
}
response: Future[String] = Promise$DefaultPromise@231f98ef
```

When you run this, you do not have to wait for ten seconds for the next prompt to appear: you regain control of the shell straightaway. The bit of code in the future is executed asynchronously: its execution is independent of the main program flow.

How do we retrieve the result of the computation? We note that `response` has type `Future[String]`. We can check whether the computation wrapped in the future has finished by querying the future's `isCompleted` attribute:

```
scala> response.isCompleted
Boolean = true
```

The future exposes a `value` attribute that contains the computation result:

```
scala> response.value
Option[Try[String]] = Some(Success(<StockQuote><Status>SUCCESS</Status>
...)
```

The `value` attribute of a future has type `Option[Try[T]]`. We have already seen how to use the `Try` type to handle exceptions gracefully in the context of parallel collections. It is used in the same way here. A future's `value` attribute is `None` until the future is complete, then it is set to `Some(Success(value))` if the future ran successfully, or `Some(Failure(error))` if an exception was thrown.

Repeatedly calling `f.value` until the future completes works well in the shell, but it does not generalize to more complex programs. Instead, we want to tell the computer to do something once the future is complete: we want to bind a *callback* function to the future. We can do this by setting the future's `onComplete` attribute. Let's tell the future to print the API response when it completes:

```
scala> response.onComplete {
  case Success(s) => println(s)
```



```
    case Failure(e) => println(s"Error fetching page: $e")
  }

scala>
// Wait for response to complete, then prints:
<StockQuote><Status>SUCCESS</Status><Name>Alphabet Inc</
Name><Symbol>GOOGL</Symbol><LastPrice>695.22</LastPrice><Chan...
```

The function passed to `onComplete` runs when the future is finished. It takes a single argument of type `Try[T]` containing the result of the future.



Failure is normal: how to build resilient applications

By wrapping the output of the code that it runs in a `Try` type, futures force the client code to consider the possibility that the code might fail. The client can isolate the effect of failure to avoid crashing the whole application. They might, for instance, log the exception. In the case of a web API query, they might add the offending URL to be queried again at a later date. In the case of a database failure, they might roll back the transaction.

By treating failure as a first-class citizen rather than through exceptional control flow bolted on at the end, we can build applications that are much more resilient.

Future composition – using a future's result

In the previous section, you learned about the `onComplete` method to bind a callback to a future. This is useful to cause a side effect to happen when the future is complete. It does not, however, let us transform the future's return value easily.

To carry on with our stocks example, let's imagine that we want to convert the query response from a string to an XML object. Let's start by including the `scala-xml` library as a dependency in `build.sbt`:

```
libraryDependencies += "org.scala-lang" % "scala-xml" % "2.11.0-M4"
```

Let's restart the console and reimport the dependencies on `scala.concurrent._`, `scala.concurrent.ExecutionContext.Implicits.global`, and `scala.io._`. We also want to import the XML library:

```
scala> import scala.xml.XML
import scala.xml.XML
```

We will use the same URL as in the previous section:

```
http://dev.markitondemand.com/MODAPIS/Api/v2/Quote?symbol=GOOG
```

It is sometimes useful to think of a future as a collection that either contains one element if a calculation has been successful, or zero elements if it has failed. For instance, if the web API has been queried successfully, our future contains a string representation of the response. Like other container types in Scala, futures support a `map` method that applies a function to the element contained in the future, returning a new future, and does nothing if the calculation in the future failed. But what does this mean in the context of a computation that might not be finished yet? The `map` method gets applied as soon as the future is complete, like the `onComplete` method.

We can use the future's `map` method to apply a transformation to the result of the future asynchronously. Let's poll the "Markit on demand" API again. This time, instead of printing the result, we will parse it as XML.

```
scala> val strResponse = Future {
  Thread.sleep(20000) // Sleep for 20s
  val res = Source.fromURL(url).mkString
  println("finished fetching url")
  res
}
strResponse: Future[String] = Promise$DefaultPromise@1dda9bc8

scala> val xmlResponse = strResponse.map { s =>
  println("applying string to xml transformation")
  XML.loadString(s)
}
xmlResponse: Future[xml.Elem] = Promise$DefaultPromise@25d1262a

// wait while the remainder of the 20s elapses
finished fetching url
applying string to xml transformation

scala> xmlResponse.value
Option[Try[xml.Elem]] = Some(Success(<StockQuote><Status>SUCCESS</
Status>...
```

By registering subsequent maps on futures, we are providing a road map to the executor running the future for what to do.

If any of the steps fail, the failed `Try` instance containing the exception gets propagated instead:

```
scala> val strResponse = Future {
  Source.fromURL("empty").mkString
}

scala> val xmlResponse = strResponse.map {
  s => XML.loadString(s)
}

scala> xmlResponse.value
Option[Try[xml.Elem]] = Some(Failure(MalformedURLException: no protocol:
empty))
```

This behavior makes sense if you think of a failed future as an empty container. When applying a map to an empty list, it returns the same empty list. Similarly, when applying a map to an empty (failed) future, the empty future is returned.

Blocking until completion

The code for fetching stock prices works fine in the shell. However, if you paste it in a standalone program, you will notice that nothing gets printed and the program finishes straightaway. Let's look at a trivial example of this:

```
// BlockDemo.scala
import scala.concurrent._
import scala.concurrent.ExecutionContext.Implicits.global
import scala.concurrent.duration._

object BlockDemo extends App {
  val f = Future { Thread.sleep(10000) }
  f.onComplete { _ => println("future completed") }
  // "future completed" is not printed
}
```

The program stops running as soon as the main thread has completed its tasks, which, in this example, just involves creating the futures. In particular, the line "future completed" is never printed. If we want the main thread to wait for a future to execute, we must explicitly tell it to block execution until the future has finished running. This is done using the `Await.ready` or `Await.result` methods. Both these methods block the execution of the main thread until the future completes. We could make the above program work as intended by adding this line:

```
Await.ready(f, 1 minute)
```

The `Await` methods take the future as their first argument and a `Duration` object as the second. If the future takes longer to complete than the specified duration, a `TimeoutException` is thrown. Pass `Duration.Inf` to set an infinite timeout.

The difference between `Await.ready` and `Await.result` is that the latter returns the value inside the future. In particular, if the future resulted in an exception, that exception will get thrown. In contrast, `Await.ready` returns the future itself.

In general, one should try to avoid blocking as much as possible: the whole point of futures is to run code in background threads in order to keep the main thread of execution responsive. However, a common, legitimate use case for blocking is at the end of a program. If we are running a large-scale integration process, we might dispatch several futures to query web APIs, read from text files, or insert data into a database. Embedding the code in futures is more scalable than performing these operations sequentially. However, as the majority of the intensive work is running in background threads, we are left with many outstanding futures when the main thread completes. It makes sense, at this stage, to block until all the futures have completed.

Controlling parallel execution with execution contexts

Now that we know how to define futures, let's look at controlling how they run. In particular, you might want to control the number of threads to use when running a large number of futures.

When a future is defined, it is passed an *execution context*, either directly or implicitly. An execution context is an object that exposes an `execute` method that takes a block of code and runs it, possibly asynchronously. By changing the execution context, we can change the "backend" that runs the futures. We have already seen how to use execution contexts to control the execution of parallel collections.

So far, we have just been using the default execution context by importing `scala.concurrent.ExecutionContext.Implicits.global`. This is a fork / join thread pool with as many threads as there are underlying CPUs.

Let's now define a new execution context that uses sixteen threads:

```
scala> import java.util.concurrent.Executors
import java.util.concurrent.Executors

scala> val ec = ExecutionContext.fromExecutorService(
  Executors.newFixedThreadPool(16)
)
ec: ExecutionContextExecutorService = ExecutionContextImpl$$anon$1@1351ce60
```

Having defined the execution context, we can pass it explicitly to futures as they are defined:

```
scala> val f = Future { Thread.sleep(1000) } (ec)
f: Future[Unit] = Promise$DefaultPromise@458b456
```

Alternatively, we can define the execution context implicitly:

```
scala> implicit val context = ec
context: ExecutionContextExecutorService = ExecutionContextImpl$$anon$1@1351ce60
```

It is then passed as an implicit parameter to all new futures as they are constructed:

```
scala> val f = Future { Thread.sleep(1000) }
f: Future[Unit] = Promise$DefaultPromise@3c4b7755
```

You can shut the execution context down to destroy the thread pool:

```
scala> ec.shutdown()
```

When an execution context receives a shutdown command, it will finish executing its current tasks but will refuse any new tasks.

Futures example – stock price fetcher

Let's bring some of the concepts that we covered in this section together to build a command-line application that prompts the user for the name of a stock and fetches the value of that stock. The catch is that, to keep the UI responsive, we will fetch the stock using a future:

```
// StockPriceDemo.scala

import scala.concurrent._
```

```
import scala.concurrent.ExecutionContext.Implicits.global
import scala.io._
import scala.xml.XML
import scala.util._

object StockPriceDemo extends App {

  /* Construct URL for a stock symbol */
  def urlFor(stockSymbol:String) =
    ("http://dev.markitondemand.com/MODApis/Api/v2/Quote?" +
     s"symbol=${stockSymbol}")

  /* Build a future that fetches the stock price */
  def fetchStockPrice(stockSymbol:String):Future[BigDecimal] = {
    val url = urlFor(stockSymbol)
    val strResponse = Future { Source.fromURL(url).mkString }
    val xmlResponse = strResponse.map { s => XML.loadString(s) }
    val price = xmlResponse.map {
      r => BigDecimal((r \ "LastPrice").text)
    }
    price
  }

  /* Command line interface */
  println("Enter symbol at prompt.")
  while (true) {
    val symbol = readLine("> ") // Wait for user input
    // When user puts in symbol, fetch data in background
    // thread and print to screen when complete
    fetchStockPrice(symbol).onComplete { res =>
      println()
      res match {
        case Success(price) => println(s"$symbol: USD $price")
        case Failure(e) => println(s"Error fetching $symbol: $e")
      }
    }
    print("> ") // Simulate the appearance of a new prompt
  }
}
```

Try running the program and entering the code for some stocks:

```
[info] Running StockPriceDemo
Enter symbol at prompt:
> GOOG
> MSFT
>
GOOG: USD 695.22
>
MSFT: USD 47.48
> AAPL
>
AAPL: USD 111.01
```

Let's summarize how the code works. when you enter a stock, the main thread constructs a future that fetches the stock information from the API, converts it to XML, and extracts the price. We use `(r \ "LastPrice").text` to extract the text inside the `LastPrice` tag from the XML node `r`. We then convert the value to a big decimal. When the transformations are complete, the result is printed to screen by binding a callback through `onComplete`. Exception handling is handled naturally through our use of `.map` methods to handle transformations.

By wrapping the code for fetching a stock price in a future, we free up the main thread to just respond to the user. This means that the user interface does not get blocked if we have, for instance, a slow internet connection.

This example is somewhat artificial, but you could easily wrap much more complicated logic: stock prices could be written to a database and we could add additional commands to plot the stock price over time, for instance.

We have only scratched the surface of what futures can offer in this section. We will revisit futures in more detail when we look at polling web APIs in *Chapter 7, Web APIs* and *Chapter 9, Concurrency with Akka*.

Futures are a key part of the data scientist's toolkit for building scalable systems. Moving expensive computation (either in terms of CPU time or wall time) to background threads improves scalability greatly. For this reason, futures are an important part of many Scala libraries such as **Akka** and the **Play** framework.

Summary

By providing high-level concurrency abstractions, Scala makes writing parallel code intuitive and straightforward. Parallel collections and futures form an invaluable part of a data scientist's toolbox, allowing them to parallelize their code with minimal effort. However, while these high-level abstractions obviate the need to deal directly with threads, an understanding of the internals of Scala's concurrency model is necessary to avoid race conditions.

In the next chapter, we will put concurrency on hold and study how to interact with SQL databases. However, this is only temporary: futures will play an important role in many of the remaining chapters in this book.

References

Aleksandar Prokopec, Learning Concurrent Programming in Scala. This is a detailed introduction to the basics of concurrent programming in Scala. In particular, it explores parallel collections and futures in much greater detail than this chapter.

Daniel Westheide's blog gives an excellent introduction to many Scala concepts, in particular:

- **Futures:** <http://danielwestheide.com/blog/2013/01/09/the-neophytes-guide-to-scala-part-8-welcome-to-the-future.html>
- **The Try type:** <http://danielwestheide.com/blog/2012/12/26/the-neophytes-guide-to-scala-part-6-error-handling-with-try.html>

For a discussion of cross-validation, see *The Elements of Statistical Learning* by Hastie, Tibshirani, and Friedman.

5

Scala and SQL through JDBC

One of data science's *raison d'être* is the difficulty of manipulating large datasets. Much of the data of interest to a company or research group cannot fit conveniently in a single computer's RAM. Storing the data in a way that is easy to query is therefore a complex problem.

Relational databases have been successful at solving the data storage problem. Originally proposed in 1970 (<http://www.seas.upenn.edu/~zives/03f/cis550/codd.pdf>), the overwhelming majority of databases in active use today are still relational. In that time, the price of RAM per megabyte has decreased by a factor of a hundred million. Similarly, hard drive capacity has increased from tens or hundreds of megabytes to terabytes. It is remarkable that, despite this exponential growth in data storage capacity, the relational model has remained dominant.

Virtually all relational databases are described and queried with variants of **SQL (Structured Query Language)**. With the advent of distributed computing, the position of SQL databases as the *de facto* data storage standard is being challenged by other types of databases, commonly grouped under the umbrella term NoSQL. Many NoSQL databases are more partition-tolerant than SQL databases: they can be split into several parts residing on different computers. While this author expects that NoSQL databases will become increasingly popular, SQL databases are likely to remain prevalent as a data persistence mechanism; hence, a significant portion of this book is devoted to interacting with SQL from Scala.

While SQL is standardized, most implementations do not follow the full standard. Additionally, most implementations provide extensions to the standard. This means that, while many of the concepts in this book will apply to all SQL backends, the exact syntax will need to be adjusted. We will consider only the MySQL implementation here.

In this chapter, you will learn how to interact with SQL databases from Scala using JDBC, a bare bones Java API. In the next chapter, we will consider Slick, an **Object Relational Mapper (ORM)** that gives a more Scala-esque feel to interacting with SQL.

This chapter is roughly composed of two sections: we will first discuss the basic functionality for connecting and interacting with SQL databases, and then discuss useful functional patterns that can be used to create an elegant, loosely coupled, and coherent data access layer.

This chapter assumes that you have a basic working knowledge of SQL. If you do not, you would be better off first reading one of the reference books mentioned at the end of the chapter.

Interacting with JDBC

JDBC is an API for connecting to SQL databases in Java. It remains the simplest way of connecting to SQL databases from Scala. Furthermore, the majority of higher-level abstractions for interacting with databases still use JDBC as a backend.

JDBC is not a library in itself. Rather, it exposes a set of interfaces to interact with databases. Relational database vendors then provide specific implementations of these interfaces.

Let's start by creating a `build.sbt` file. We will declare a dependency on the MySQL JDBC connector:

```
scalaVersion := "2.11.7"

libraryDependencies += "mysql" % "mysql-connector-java" % "5.1.36"
```

First steps with JDBC

Let's start by connecting to JDBC from the command line. To follow with the examples, you will need access to a running MySQL server. If you added the MySQL connector to the list of dependencies, open a Scala console by typing the following command:

```
$ sbt console
```

Let's import JDBC:

```
scala> import java.sql._
import java.sql._
```

We then need to tell JDBC to use a specific connector. This is normally done using reflection, loading the driver at runtime:

```
scala> Class.forName("com.mysql.jdbc.Driver")
Class[_] = class com.mysql.jdbc.Driver
```

This loads the appropriate driver into the namespace at runtime. If this seems somewhat magical to you, it's probably not worth worrying about exactly how this works. This is the only example of reflection that we will consider in this book, and it is not particularly idiomatic Scala.

Connecting to a database server

Having specified the SQL connector, we can now connect to a database. Let's assume that we have a database called `test` on host `127.0.0.1`, listening on port `3306`. We create a connection as follows:

```
scala> val connection = DriverManager.getConnection(
  "jdbc:mysql://127.0.0.1:3306/test",
  "root", // username when connecting
  "" // password
)
java.sql.Connection = com.mysql.jdbc.JDBC4Connection@12e78a69
```

The first argument to `getConnection` is a URL-like string with `jdbc:mysql://host[:port]/database`. The second and third arguments are the username and password. Pass in an empty string if you can connect without a password.

Creating tables

Now that we have a database connection, let's interact with the server. For these examples, you will find it useful to have a MySQL shell open (or a MySQL GUI such as **MySQLWorkbench**) as well as the Scala console. You can open a MySQL shell by typing the following command in a terminal:

```
$ mysql
```

As an example, we will create a small table to keep track of famous physicists. In a `mysql` shell, we would run the following command:

```
mysql> USE test;
mysql> CREATE TABLE physicists (
  id INT(11) AUTO_INCREMENT PRIMARY KEY,
  name VARCHAR(32) NOT NULL
);
```

To achieve the same with Scala, we send a JDBC statement to the connection:

```
scala> val statementString = """
CREATE TABLE physicists (
  id INT(11) AUTO_INCREMENT PRIMARY KEY,
  name VARCHAR(32) NOT NULL
)
"""

scala> val statement = connection.prepareStatement(statementString)
PreparedStatement = JDBC4PreparedStatement@c983201: CREATE TABLE ...

scala> statement.executeUpdate()
results: Int = 0
```

Let's ignore the return value of `executeUpdate` for now.

Inserting data

Now that we have created a table, let's insert some data into it. We can do this with a SQL `INSERT` statement:

```
scala> val statement = connection.prepareStatement("""
  INSERT INTO physicists (name) VALUES ('Isaac Newton')
""")

scala> statement.executeUpdate()
Int = 1
```

In this case, `executeUpdate` returns 1. When inserting rows, it returns the number of rows that were inserted. Similarly, if we had used a SQL `UPDATE` statement, this would return the number of rows that were updated. For statements that do not manipulate rows directly (such as the `CREATE TABLE` statement in the previous section), `executeUpdate` just returns 0.

Let's just jump into a `mysql` shell to verify the insertion performed correctly:

```
mysql> select * from physicists ;
+----+-----+
| id | name      |
+----+-----+
|  1 | Isaac Newton |
+----+-----+
1 row in set (0.00 sec)
```

Let's quickly summarize what we have seen so far: to execute SQL statements that do not return results, use the following:

```
val statement = connection.prepareStatement("SQL statement string")
statement.executeUpdate()
```

In the context of data science, we frequently need to insert or update many rows at a time. For instance, we might have a list of physicists:

```
scala> val physicistNames = List("Marie Curie", "Albert Einstein", "Paul Dirac")
```

We want to insert all of these into the database. While we could create a statement for each physicist and send it to the database, this is quite inefficient. A better solution is to create a *batch* of statements and send them to the database together. We start by creating a statement template:

```
scala> val statement = connection.prepareStatement("""
    INSERT INTO physicists (name) VALUES (?)
""")
PreparedStatement = JDBC4PreparedStatement@621a8225: INSERT INTO
physicists (name) VALUES (** NOT SPECIFIED **)
```

This is identical to the previous `prepareStatement` calls, except that we replaced the physicist's name with a `?` placeholder. We can set the placeholder value with the `statement.setString` method:

```
scala> statement.setString(1, "Richard Feynman")
```

This replaces the first placeholder in the statement with the string `Richard Feynman`:

```
scala> statement
com.mysql.jdbc.JDBC4PreparedStatement@5fdd16c3:
INSERT INTO physicists (name) VALUES ('Richard Feynman')
```

Note that JDBC, somewhat counter-intuitively, counts the placeholder positions from 1 rather than 0.

We have now created the first statement in the batch of updates. Run the following command:

```
scala> statement.addBatch()
```

By running the preceding command, we initiate a batch insert: the statement is added to a temporary buffer that will be executed when we run the `executeBatch` method. Let's add all the physicists in our list:

```
scala> physicistNames.foreach { name =>
  statement.setString(1, name)
  statement.addBatch()
}
```

We can now execute all the statements in the batch:

```
scala> statement.executeBatch
Array[Int] = Array(1, 1, 1, 1)
```

The return value of `executeBatch` is an array of the number of rows altered or inserted by each item in the batch.

Note that we used `statement.setString` to fill in the template with a particular name. The `PreparedStatement` object has `setXXX` methods for all basic types. To get a complete list, read the `PreparedStatement` API documentation (<http://docs.oracle.com/javase/7/docs/api/java/sql/PreparedStatement.html>).

Reading data

Now that we know how to insert data into a database, let's look at the converse: reading data. We use SQL `SELECT` statements to query the database. Let's do this in the MySQL shell first:

```
mysql> SELECT * FROM physicists;
+----+-----+
| id | name          |
```

```
+-----+-----+
| 1 | Isaac Newton |
| 2 | Richard Feynman |
| 3 | Marie Curie |
| 4 | Albert Einstein |
| 5 | Paul Dirac |
+-----+-----+
5 rows in set (0.01 sec)
```

To extract this information in Scala, we define a `PreparedStatement`:

```
scala> val statement = connection.prepareStatement("""
    SELECT name FROM physicists
""")
PreparedStatement = JDBC4PreparedStatement@3c577c9d:
SELECT name FROM physicists
```

We execute this statement by running the following command:

```
scala> val results = statement.executeQuery()
results: java.sql.ResultSet = com.mysql.jdbc.JDBC4ResultSet@74a2e158
```

This returns a `JDBC ResultSet` instance. The `ResultSet` is an abstraction representing a set of rows from the database. Note that we used `statement.executeQuery` rather than `statement.executeUpdate`. In general, one should execute statements that return data (in the form of `ResultSet`) with `executeQuery`. Statements that modify the database without returning data (insert, create, alter, or update statements, among others) are executed with `executeUpdate`.

The `ResultSet` object behaves somewhat like an iterator. It exposes a `next` method that advances itself to the next record, returning `true` if there are records left in `ResultSet`:

```
scala> results.next // Advance to the first record
Boolean = true
```

When the `ResultSet` instance points to a record, we can extract fields in this record by passing in the field name:

```
scala> results.getString("name")
String = Isaac Newton
```

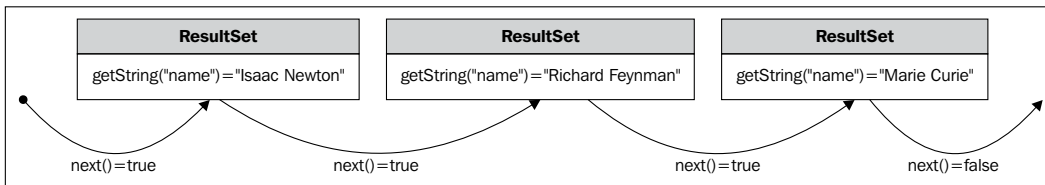

We can also extract fields using positional arguments. The fields are indexed from one:

```
scala> results.getString(1) // first positional argument
String = Isaac Newton
```

When we are done with a particular record, we call the `next` method to advance the `ResultSet` to the next record:

```
scala> results.next // advances the ResultSet by one record
Boolean = true
```

```
scala> results.getString("name")
String = Richard Feynman
```



A `ResultSet` object supports the `getXXX(fieldName)` methods to access the fields of a record and a `next` method to advance to the next record in the result set.

One can iterate over a result set using a `while` loop:

```
scala> while(results.next) { println(results.getString("name")) }
Marie Curie
Albert Einstein
Paul Dirac
```



A word of warning applies to reading fields that are nullable. While one might expect JDBC to return null when faced with a null SQL field, the return type depends on the `getXXX` command used. For instance, `getInt` and `getLong` will return 0 for any field that is null. Similarly, `getDouble` and `getFloat` return 0.0. This can lead to some subtle bugs in code. In general, one should be careful with getters that return Java value types (`int`, `long`) rather than objects. To find out if a value is null in the database, query it first with `getInt` (or `getLong` or `getDouble`, as appropriate), then use the `wasNull` method that returns a `Boolean` if the last read value was null:

```
scala> rs.getInt("field")
0
scala> rs.wasNull // was the last item read null?
true
```

This (surprising) behavior makes reading from `ResultSet` instances error-prone. One of the goals of the second part of this chapter is to give you the tools to build an abstraction layer on top of the `ResultSet` interface to avoid having to call methods such as `getInt` directly.

Reading values directly from `ResultSet` objects feels quite unnatural in Scala. We will look, further on in this chapter, at constructing a layer through which you can access the result set using type classes.

We now know how to read and write to a database. Having finished with the database for now, we close the result sets, prepared statements, and connections:

```
scala> results.close
```

```
scala> statement.close
```

```
scala> connection.close
```

While closing statements and connections is not important in the Scala shell (they will get closed when you exit), it is important when you run programs; otherwise, the objects will persist, leading to "out of memory exceptions". In the next sections, we will look at establishing connections and statements with the **loan pattern**, a design pattern that closes a resource automatically when we finish using it.

JDBC summary

We now have an overview of JDBC. The rest of this chapter will concentrate on writing abstractions that sit above JDBC, making database accesses feel more natural. Before we do this, let's summarize what we have seen so far.

We have used three JDBC classes:

- The `Connection` class represents a connection to a specific SQL database. Instantiate a connection as follows:

```
import java.sql._
Class.forName("com.mysql.jdbc.Driver")
val connection = DriverManager.getConnection(
  "jdbc:mysql://127.0.0.1:3306/test",
  "root", // username when connecting
  "" // password
)
```

Our main use of `Connection` instances has been to generate `PreparedStatement` objects:

```
connection.prepareStatement("SELECT * FROM physicists")
```

- A `PreparedStatement` instance represents a SQL statement about to be sent to the database. It also represents the template for a SQL statement with placeholders for values yet to be filled in. The class exposes the following methods:

<code>statement.executeUpdate</code>	This sends the statement to the database. Use this for SQL statements that modify the database and do not return any data, such as <code>INSERT</code> , <code>UPDATE</code> , <code>DELETE</code> , and <code>CREATE</code> statements.
<code>val results = statement.executeQuery</code>	This sends the statement to the database. Use this for SQL statements that return data (predominantly, the <code>SELECT</code> statements). This returns a <code>ResultSet</code> instance.
<code>statement.addBatch</code> <code>statement.executeBatch</code>	The <code>addBatch</code> method adds the current statement to a batch of statements, and <code>executeBatch</code> sends the batch of statements to the database.

<pre>statement.setString(1, "Scala") statement.setInt(1, 42) statement.setBoolean(1, true)</pre>	<p>Fill in the placeholder values in the <code>PreparedStatement</code>. The first argument is the position in the statement (counting from 1). The second argument is the value.</p> <p>One common use case for these is in a batch update or insert: we might have a Scala list of objects that we want to insert into the database. We fill in the placeholders for each object in the list using the <code>.setXXX</code> methods, then add this statement to the batch using <code>.addBatch</code>. We can then send the entire batch to the database using <code>.executeBatch</code>.</p>
<pre>statement.setNull(1, java.sql.Types.BOOLEAN)</pre>	<p>This sets a particular item in the statement to <code>NULL</code>. The second argument specifies the <code>NULL</code> type. If we are setting a cell in a Boolean column, for instance, this should be <code>Types.BOOLEAN</code>. A full list of types is given in the API documentation for the <code>java.sql.Types</code> package (http://docs.oracle.com/javase/7/docs/api/java/sql/Types.html).</p>

- A `ResultSet` instance represents a set of rows returned by a `SELECT` or `SHOW` statement. `ResultSet` exposes methods to access fields in the current row:

<pre>rs.getString(i) rs.getInt(i)</pre>	<p>These methods get the value of the <code>i</code>th field in the current row; <code>i</code> is measured from 1.</p>
<pre>rs.getString("name") rs.getInt("age")</pre>	<p>These methods get the value of a specific field, which is indexed by the column name.</p>
<pre>rs.wasNull</pre>	<p>This returns whether the last column read was <code>NULL</code>. This is particularly important when reading Java value types, such as <code>getInt</code>, <code>getBoolean</code>, or <code>getDouble</code>, as these return a default value when reading a <code>NULL</code> value.</p>

The `ResultSet` instance exposes the `.next` method to move to the next row; `.next` returns `true` until the `ResultSet` has advanced to just beyond the last row.

Functional wrappers for JDBC

We now have a basic overview of the tools afforded by JDBC. All the objects that we have interacted with so far feel somewhat clunky and out of place in Scala. They do not encourage a functional style of programming.

Of course, elegance is not necessarily a goal in itself (or, at least, you will probably struggle to convince your CEO that he should delay the launch of a product because the code lacks elegance). However, it is usually a symptom: either the code is not extensible or too tightly coupled, or it is easy to introduce bugs. The latter is particularly the case for JDBC. Forgot to check `wasNull`? That will come back to bite you. Forgot to close your connections? You'll get an "out of memory exception" (hopefully not in production).

In the next sections, we will look at patterns that we can use to wrap JDBC types in order to mitigate many of these risks. The patterns that we introduce here are used very commonly in Scala libraries and applications. Thus, besides writing robust classes to interact with JDBC, learning about these patterns will, I hope, give you greater understanding of Scala programming.

Safer JDBC connections with the loan pattern

We have already seen how to connect to a JDBC database and send statements to the database for execution. This technique, however, is somewhat error prone: you have to remember to close statements; otherwise, you will quickly run out of memory. In more traditional imperative style, we write the following try-finally block around every connection:

```
// WARNING: poor Scala code
val connection = DriverManager.getConnection(url, user, password)
try {
  // do something with connection
}
finally {
  connection.close()
}
```

Scala, with first-class functions, provides us with an alternative: the *loan pattern*. We write a function that is responsible for opening the connection, loaning it to the client code to do something interesting with it, and then closing it when the client code is done. Thus, the client code is not responsible for closing the connection any more.

Let's create a new `SqlUtils` object with a `usingConnection` method that leverages the loan pattern:

```
// SqlUtils.scala

import java.sql._

object SqlUtils {

  /** Create an auto-closing connection using
   * the loan pattern */
  def usingConnection[T] (
    db:String,
    host:String="127.0.0.1",
    user:String="root",
    password:String="",
    port:Int=3306
  ) (f:Connection => T):T = {

    // Create the connection
    val Url = s"jdbc:mysql://$host:$port/$db"
    Class.forName("com.mysql.jdbc.Driver")
    val connection = DriverManager.getConnection(
      Url, user, password)

    // give the connection to the client, through the callable
    // `f` passed in as argument
    try {
      f(connection)
    }
    finally {
      // When client is done, close the connection
      connection.close()
    }
  }
}
```

Let's see this function in action:

```
scala> SqlUtils.usingConnection("test") {
  connection => println(connection)
}
com.mysql.jdbc.JDBC4Connection@46fd3d66
```

Thus, the client doesn't have to remember to close the connection, and the resultant code (for the client) feels much more like Scala.

How does our `usingConnection` function work? The function definition is `def usingConnection(...)(f : Connection => T):T`. It takes, as its second set of arguments, a function that acts on a `Connection` object. The body of `usingConnection` creates the connection, then passes it to `f`, and finally closes the connection. This syntax is somewhat similar to code blocks in Ruby or the `with` statement in Python.



Be careful when mixing the loan pattern with lazy operations. This applies particularly to returning iterators, streams, and futures from `f`. As soon as the thread of execution leaves `f`, the connection will be closed. Any data structure that is not materialized at this point will not be able to carry on accessing the connection.

The loan pattern is, of course, not exclusive to database connections. It is useful whenever you have the following pattern, in pseudocode:

```
open resource (eg. database connection, file ...)
use resource somehow // loan resource to client for this part.
close resource
```

Enriching JDBC statements with the "pimp my library" pattern

In the previous section, we saw how to create self-closing connections with the loan pattern. This allows us to open connections to the database without having to remember to close them. However, we still have to remember to close any `ResultSet` and `PreparedStatement` that we open:

```
// WARNING: Poor Scala code
SqlUtils.usingConnection("test") { connection =>
  val statement = connection.prepareStatement(
    "SELECT * FROM physicists")
  val results = statement.executeQuery
  // do something useful with the results
  results.close
  statement.close
}
```

Having to open and close the statement is somewhat ugly and error prone. This is another natural use case for the loan pattern. Ideally, we would like to write the following:

```
usingConnection("test") { connection =>
  connection.withQuery("SELECT * FROM physicists") {
    resultSet => // process results
  }
}
```

How can we define a `.withQuery` method on the `Connection` class? We do not control the `Connection` class definition as it is part of the JDBC API. We would like to be able to somehow reopen the `Connection` class definition to add the `withQuery` method.

Scala does not let us reopen classes to add new methods (a practice known as monkey-patching). We can still, however, enrich existing libraries with implicit conversions using the **pimp my library** pattern (<http://www.artima.com/weblogs/viewpost.jsp?thread=179766>). We first define a `RichConnection` class that contains the `withQuery` method. This `RichConnection` class is created from an existing `Connection` instance.

```
// RichConnection.scala

import java.sql.{Connection, ResultSet}

class RichConnection(val underlying:Connection) {

  /** Execute a SQL query and process the ResultSet */
  def withQuery[T](query:String)(f:ResultSet => T):T = {
    val statement = underlying.prepareStatement(query)
    val results = statement.executeQuery
    try {
      f(results) // loan the ResultSet to the client
    }
    finally {
      // Ensure all the resources get freed.
      results.close
      statement.close
    }
  }
}
```


We could use this class by just wrapping every `Connection` instance in a `RichConnection` instance:

```
// Warning: poor Scala code
SqlUtils.usingConnection("test") { connection =>
  val richConnection = new RichConnection(connection)
  richConnection.withQuery("SELECT * FROM physicists") {
    resultSet => // process resultSet
  }
}
```

This adds unnecessary boilerplate: we have to remember to convert every connection instance to `RichConnection` to use `withQuery`. Fortunately, Scala provides an easier way with implicit conversions: we tell Scala how to convert from `Connection` to `RichConnection` and vice versa, and tell it to perform this conversion automatically (implicitly), if necessary:

```
// Implicits.scala
import java.sql.Connection

// Implicit conversion methods are often put in
// an object called Implicits.
object Implicits {
  implicit def pimpConnection(conn:Connection) =
    new RichConnection(conn)
  implicit def depimpConnection(conn:RichConnection) =
    conn.underlying
}
```

Now, whenever `pimpConnection` and `depimpConnection` are in the current scope, Scala will automatically use them to convert from `Connection` instances to `RichConnection` and back as needed.

We can now write the following (I have added type information for emphasis):

```
// Bring the conversion functions into the current scope
import Implicits._

SqlUtils.usingConnection("test") { (connection:Connection) =>
  connection.withQuery("SELECT * FROM physicists") {
    // Wow! It's like we have just added
    // .withQuery to the JDBC Connection class!
    resultSet => // process results
  }
}
```

This might look like magic, so let's step back and look at what happens when we call `withQuery` on a `Connection` instance. The Scala compiler will first look to see if the class definition of `Connection` defines a `withQuery` method. When it finds that it does not, it will look for implicit methods that convert a `Connection` instance to a class that defines `withQuery`. It will find that the `pimpConnection` method allows conversion from `Connection` to `RichConnection`, which defines `withQuery`. The Scala compiler automatically uses `pimpConnection` to transform the `Connection` instance to `RichConnection`.

Note that we used the names `pimpConnection` and `depimpConnection` for the conversion functions, but they could have been anything. We never call these methods explicitly.

Let's summarize how to use the *pimp my library* pattern to add methods to an existing class:

1. Write a class that wraps the class you want to enrich: `class RichConnection(val underlying: Connection)`. Add all the methods that you wish the original class had.
2. Write a method to convert from your original class to your enriched class as part of an object called (conventionally) `Implicits`. Make sure that you tell Scala to use this conversion automatically with the `implicit` keyword: `implicit def pimpConnection(conn: Connection): RichConnection`. You can also tell Scala to automatically convert back from the enriched class to the original class by adding the reverse conversion method.
3. Allow implicit conversions by importing the implicit conversion methods: `import Implicits._`.

Wrapping result sets in a stream

The JDBC `ResultSet` object plays very badly with Scala collections. The only real way of doing anything useful with it is to loop through it directly with a `while` loop. For instance, to get a list of the names of physicists in our database, we could write the following code:

```
// WARNING: poor Scala code
import Implicits._ // import implicit conversions

SqlUtils.usingConnection("test") { connection =>
  connection.withQuery("SELECT * FROM physicists") { resultSet =>
    var names = List.empty[String]
    while(resultSet.next) {
```

```
        val name = resultSet.getString("name")
        names = name :: names
    }
    names
}
}
//=> List[String] = List(Paul Dirac, Albert Einstein, Marie Curie,
Richard Feynman, Isaac Newton)
```

The `ResultSet` interface feels unnatural because it behaves very differently from Scala collections. In particular, it does not support the higher-order functions that we take for granted in Scala: no `map`, `filter`, `fold`, or `for` comprehensions. Thankfully, writing a *stream* that wraps `ResultSet` is quite straightforward. A Scala stream is a lazily evaluated list: it evaluates the next element in the collection when it is needed and forgets previous elements when they are no longer used.

We can define a `stream` method that wraps `ResultSet` as follows:

```
// SqlUtils.scala
object SqlUtils {
    ...
    def stream(results:ResultSet):Stream[ResultSet] =
        if (results.next) { results #:: stream(results) }
        else { Stream.empty[ResultSet] }
}
```

This might look quite confusing, so let's take it slowly. We define a `stream` method that wraps `ResultSet`, returning a `Stream[ResultSet]`. When the client calls `stream` on an empty result set, this just returns an empty stream. When the client calls `stream` on a non-empty `ResultSet`, the `ResultSet` instance is advanced by one row, and the client gets back `results #:: stream(results)`. The `#::` operator on a stream is similar to the `cons` operator, `::`, on a list: it prepends `results` to an existing stream. The critical difference is that, unlike a list, `stream(results)` does not get evaluated until necessary. This, therefore, avoids duplicating the entire `ResultSet` in memory.

Let's use our brand new `stream` function to get the name of all the physicists in our database:

```
import Implicits._

SqlUtils.usingConnection("test") { connection =>
    connection.withQuery("SELECT * FROM physicists") { results =>
        val resultsStream = SqlUtils.stream(results)
    }
}
```

```

        resultsStream.map { _.getString("name") }.toVector
    }
}
//=> Vector(Richard Feynman, Albert Einstein, Marie Curie, Paul Dirac)

```

Streaming the results, rather than using the result set directly, lets us interact with the data much more naturally as we are now dealing with just a Scala collection.

When you use `stream` in a `withQuery` block (or, generally, in a block that automatically closes the result set), you must always materialize the stream within the function, hence the call to `toVector`. Otherwise, the stream will wait until its elements are needed to materialize them, and by then, the `ResultSet` instance will be closed.

Looser coupling with type classes

So far, we have been reading and writing simple types to the database. Let's imagine that we want to add a `gender` column to our database. We will store the gender as an enumeration in our physicists database. Our table is now as follows:

```

mysql> CREATE TABLE physicists (
    id INT(11) AUTO_INCREMENT PRIMARY KEY,
    name VARCHAR(32) NOT NULL,
    gender ENUM("Female", "Male") NOT NULL
);

```

How can we represent genders in Scala? A good way of doing this is with an enumeration:

```

// Gender.scala

object Gender extends Enumeration {
    val Male = Value
    val Female = Value
}

```

However, we now have a problem when deserializing objects from the database: JDBC has no built-in mechanism to convert from a SQL `ENUM` type to a Scala `Gender` type. We could achieve this by just converting manually every time we need to read gender information:

```

resultsStream.map {
    rs => Gender.withName(rs.getString("gender"))
}.toVector

```

However, we would need to write this everywhere that we want to read the `gender` field. This goes against the DRY (don't repeat yourself) principle, leading to code that is difficult to maintain. If we decide to change the way gender is stored in the database, we would need to find every instance in the code where we read the gender field and change it.

A somewhat better solution would be to add a `getGender` method to the `ResultSet` class using the pimp my library idiom that we used extensively in this chapter. This solution is still not optimal. We are adding unnecessary specificity to `ResultSet`: it is now coupled to the structure of our databases.

We could create a subclass of `ResultSet` using inheritance, such as `PhysicistResultSet`, that can read the fields in a specific table. However, this approach is not composable: if we had another table that kept track of pets, with name, species, and gender fields, we would have to either reimplement the code for reading gender in a new `PetResultSet` or factor out a `GenderedResultSet` superclass. As the number of tables grows, the inheritance hierarchy would become unmanageable. A better approach would let us compose the functionality that we need. In particular, we want to decouple the process of extracting Scala objects from a result set from the code for iterating over a result set.

Type classes

Scala provides an elegant solution using *type classes*. Type classes are a very powerful arrow in the Scala architect's quiver. However, they can present a bit of a learning curve, especially as there is no direct equivalent in object-oriented programming.

Instead of presenting an abstract explanation, I will dive into an example: I will describe how we can leverage type classes to convert fields in a `ResultSet` to Scala types. The aim is to define a `read[T] (field)` method on `ResultSet` that knows exactly how to deserialize to objects of type `T`. This method will replace and extend the `getXXX` methods in `ResultSet`:

```
// results is a ResultSet instance
val name = results.read[String] ("name")
val gender = results.read[Gender.Value] ("gender")
```

We start by defining an abstract `SqlReader[T]` trait that exposes a `read` method to read a specific field from a `ResultSet` and return an instance of type `T`:

```
// SqlReader.scala

import java.sql._

trait SqlReader[T] {
  def read(results:ResultSet, field:String):T
}
```

We now need to provide a concrete implementation of `SqlReader[T]` for every `T` type that we want to read. Let's provide concrete implementations for the `Gender` and `String` fields. We will place the implementation in a `SqlReader` companion object:

```
// SqlReader.scala

object SqlReader {
  implicit object StringReader extends SqlReader[String] {
    def read(results:ResultSet, field:String):String =
      results.getString(field)
  }

  implicit object GenderReader extends SqlReader[Gender.Value] {
    def read(results:ResultSet, field:String):Gender.Value =
      Gender.withName(StringReader.read(results, field))
  }
}
```

We could now use our `ReadableXXX` objects to read from a result set:

```
import SqlReader._
val name = StringReader.read(results, "name")
val gender = GenderReader.read(results, "gender")
```

This is already somewhat better than using the following:

```
Gender.withName(results.getString("gender"))
```

This is because the code to map from a `ResultSet` field to `Gender.Value` is centralized in a single place: `ReadableGender`. However, it would be great if we could tell Scala to use `ReadableGender` whenever it needs to read `Gender.Value`, and use `ReadableString` whenever it needs to read a `String` value. This is exactly what type classes do.

Coding against type classes

We defined a `Readable[T]` interface that abstracts how to read an object of type `T` from a field in a `ResultSet`. How do we tell Scala that it needs to use this `Readable` object to convert from the `ResultSet` fields to the appropriate Scala type?

The key is the `implicitly` keyword that we used to prefix the `GenderReader` and `StringReader` object definitions. It lets us write:

```
implicitly[SqlReader[Gender.Value]].read(results, "gender")
implicitly[SqlReader[String]].read(results, "name")
```

By writing `implicitly[SqlReader[T]]`, we are telling the Scala compiler to find a class (or an object) that extends `SqlReader[T]` that is marked for implicit use. Try this out by pasting the following in the command line, for instance:

```
scala> :paste
```

```
import Implicits._ // Connection to RichConnection conversion
SqlUtils.usingConnection("test") {
  _.withQuery("select * from physicists") {
    rs => {
      rs.next() // advance to first record
      implicitly[SqlReader[Gender.Value]].read(rs, "gender")
    }
  }
}
```

Of course, using `implicitly[SqlReader[T]]` everywhere is not particularly elegant. Let's use the `pimp my library` idiom to add a `read[T]` method to `ResultSet`. We first define a `RichResultSet` class that we can use to "pimp" the `ResultSet` class:

```
// RichResultSet.scala

import java.sql.ResultSet

class RichResultSet(val underlying:ResultSet) {
  def read[T : SqlReader](field:String):T = {
    implicitly[SqlReader[T]].read(underlying, field)
  }
}
```

The only unfamiliar part of this should be the `read[T : SqlReader]` generic definition. We are stating here that `read` will accept any `T` type, provided an instance of `SqlReader[T]` exists. This is called a *context bound*.

We must also add implicit methods to the `Implicits` object to convert from `ResultSet` to `RichResultSet`. You should be familiar with this now, so I will not bore you with the details. You can now call `results.read[T](fieldName)` for any `T` for which you have a `SqlReader[T]` implicit object defined:

```
import Implicits._

SqlUtils.usingConnection("test") { connection =>
  connection.withQuery("SELECT * FROM physicists") {
    results =>
      val resultStream = SqlUtils.stream(results)
      resultStream.map { row =>
        val name = row.read[String]("name")
        val gender = row.read[Gender.Value]("gender")
        (name, gender)
      }.toVector
    }
  }
//=> Vector[(String, Gender.Value)] = Vector((Albert Einstein, Male),
(Marie Curie, Female))
```

Let's summarize the steps needed for type classes to work. We will do this in the context of deserializing from SQL, but you will be able to adapt these steps to solve other problems:

- Define an abstract generic trait that provides the interface for the type class, for example, `SqlReader[T]`. Any functionality that is independent of `T` can be added to this base trait.
- Create the companion object for the base trait and add implicit objects extending the trait for each `T`, for example,


```
implicit object StringReader extends SqlReader[T].
```
- Type classes are always used in generic methods. A method that relies on the existence of a type class for an argument must contain a context bound in the generic definition, for example, `def read[T : SqlReader](field:String):T`. To access the type class in this method, use the `implicitly` keyword: `implicitly[SqlReader[T]]`.

When to use type classes

Type classes are useful when you need a particular behavior for many different types, but exactly how this behavior is implemented varies between these types. For instance, we need to be able to read several different types from `ResultSet`, but exactly how each type is read differs between types: for strings, we must read from `ResultSet` using `getString`, whereas for integers, we must use `getInt` followed by `wasNull`.

A good rule of thumb is when you start thinking "Oh, I could just write a generic method to do this. Ah, but wait, I will have to write the `Int` implementation as a specific edge case as it behaves differently. Oh, and the `Gender` implementation. I wonder if there's a better way?", then type classes might be useful.

Benefits of type classes

Data scientists frequently have to deal with new input streams, changing requirements, and new data types. Having an object-relational mapping layer that is easy to extend or alter is therefore critical to responding to changes efficiently. Minimizing coupling between code entities and separation of concerns are the only ways to ensure that the code can be changed in response to new data.

With type classes, we maintain orthogonality between accessing records in the database (through the `ResultSet` class) and how individual fields are transformed to Scala objects: both can vary independently. The only coupling between these two concerns is through the `SqlReader[T]` interface.

This means that both concerns can evolve independently: to read a new data type, we just need to implement a `SqlReader[T]` object. Conversely, we can add functionality to `ResultSet` without needing to reimplement how fields are converted. For instance, we could add a `getColumn` method that returns a `Vector[T]` of all the values of a field in a `ResultSet` instance:

```
def getColumn[T : SqlReader](field:String):Vector[T] = {
  val resultStream = SqlUtils.stream(results)
  resultStream.map { _.read[T](field) }.toVector
}
```

Note how we could do this without increasing the coupling to the way in which individual fields are read.

Creating a data access layer

Let's bring together everything that we have seen and build a *data-mapper* class for fetching `Physicist` objects from the database. These classes (also called *data access objects*) are useful to decouple the internal representation of an object from its representation in the database.

We start by defining the `Physicist` class:

```
// Physicist.scala
case class Physicist(
  val name:String,
  val gender:Gender.Value
)
```

The data access object will expose a single method, `readAll`, that returns a `Vector[Physicist]` of all the physicists in our database:

```
// PhysicistDao.scala

import java.sql.{ ResultSet, Connection }
import Implicits._ // implicit conversions

object PhysicistDao {

  /* Helper method for reading a single row */
  private def readFromResultSet(results:ResultSet):Physicist = {
    Physicist(
      results.read[String]("name"),
      results.read[Gender.Value]("gender")
    )
  }

  /* Read the entire 'physicists' table. */
  def readAll(connection:Connection):Vector[Physicist] = {
    connection.withQuery("SELECT * FROM physicists") {
      results =>
        val resultStream = SqlUtils.stream(results)
        resultStream.map(readFromResultSet).toVector
    }
  }
}
```

The data access layer can be used by client code as in the following example:

```
object PhysicistDaoDemo extends App {  
  
    val physicists = SqlUtils.usingConnection("test") {  
        connection => PhysicistDao.readAll(connection)  
    }  
  
    // physicists is a Vector[Physicist] instance.  
    physicists.foreach { println }  
    //=> Physicist(Albert Einstein, Male)  
    //=> Physicist(Marie Curie, Female)  
}
```

Summary

In this chapter, we learned how to interact with SQL databases using JDBC. We wrote a library to wrap native JDBC objects, aiming to give them a more functional interface.

In the next chapter, you will learn about Slick, a Scala library that provides functional wrappers to interact with relational databases.

References

The API documentation for JDBC is very complete: <http://docs.oracle.com/javase/7/docs/api/java/sql/package-summary.html>

The API documentation for the `ResultSet` interface (<http://docs.oracle.com/javase/7/docs/api/java/sql/ResultSet.html>), for the `PreparedStatement` class (<http://docs.oracle.com/javase/7/docs/api/java/sql/PreparedStatement.html>) and the `Connection` class (<http://docs.oracle.com/javase/7/docs/api/java/sql/Connection.html>) is particularly relevant.

The data mapper pattern is described extensively in Martin Fowler's *Patterns of Enterprise Application Architecture*. A brief description is also available on his website (<http://martinfowler.com/eaCatalog/dataMapper.html>).

For an introduction to SQL, I suggest *Learning SQL* by Alan Beaulieu (O'Reilly).

For another discussion of type classes, read <http://danielwestheide.com/blog/2013/02/06/the-neophytes-guide-to-scala-part-12-type-classes.html>.

This post describes how some common object-oriented design patterns can be reimplemented more elegantly in Scala using type classes:

<https://staticallytyped.wordpress.com/2013/03/24/gang-of-four-patterns-with-type-classes-and-implicits-in-scala-part-2/>

This post by *Martin Odersky* details the *Pimp my Library* pattern:

<http://www.artima.com/weblogs/viewpost.jsp?thread=179766>

6

Slick – A Functional Interface for SQL

In *Chapter 5, Scala and SQL through JDBC*, we investigated how to access SQL databases with JDBC. As interacting with JDBC feels somewhat unnatural, we extended JDBC using custom wrappers. The wrappers were developed to provide a functional interface to hide the imperative nature of JDBC.

With the difficulty of interacting directly with JDBC from Scala and the ubiquity of SQL databases, you would expect there to be existing Scala libraries that wrap JDBC. *Slick* is such a library.

Slick styles itself as a *functional-relational mapping* library, a play on the more traditional *object-relational mapping* name used to denote libraries that build objects from relational databases. It presents a functional interface to SQL databases, allowing the client to interact with them in a manner similar to native Scala collections.

FEC data

In this chapter, we will use a somewhat more involved example dataset. The **Federal Electoral Commission of the United States (FEC)** records all donations to presidential candidates greater than \$200. These records are publicly available. We will look at the donations for the campaign leading up to the 2012 general elections that resulted in Barack Obama's re-election. The data includes donations to the two presidential candidates, Obama and Romney, and also to the other contenders in the Republican primaries (there were no Democrat primaries).

In this chapter, we will take the transaction data provided by the FEC, store it in a table, and learn how to query and analyze it.

The first step is to acquire the data. If you have downloaded the code samples from the Packt website, you should already have two CSVs in the data directory of the code samples for this chapter. If not, you can download the files using the following links:

- data.scala4datascience.com/fec/ohio.csv.gz (or [ohio.csv.zip](http://data.scala4datascience.com/fec/ohio.csv.zip))
- data.scala4datascience.com/fec/us.csv.gz (or [us.csv.zip](http://data.scala4datascience.com/fec/us.csv.zip))

Decompress the two files and place them in a directory called `data/` in the same location as the source code examples for this chapter. The data files correspond to the following:

- The `ohio.csv` file is a CSV of all the donations made by donors in Ohio.
- The `us.csv` file is a CSV of all the donations made by donors across the country. This is quite a large file, with six million rows.

The two CSV files contain identical columns. Use the Ohio dataset for more responsive behavior, or the nationwide data file if you want to wrestle with a larger dataset. The dataset is adapted from a list of contributions downloaded from <http://www.fec.gov/disclosurerep/PDownload.do>.

Let's start by creating a Scala case class to represent a transaction. In the context of this chapter, a transaction is a single donation from an individual to a candidate:

```
// Transaction.scala
import java.sql.Date

case class Transaction(
  id:Option[Int], // unique identifier
  candidate:String, // candidate receiving the donation
  contributor:String, // name of the contributor
  contributorState:String, // contributor state
  contributorOccupation:Option[String], // contributor job
  amount:Long, // amount in cents
  date:Date // date of the donation
)
```

The code repository for this chapter includes helper functions in an `FECData` singleton object to load the data from CSVs:

```
scala> val ohioData = FECData.loadOhio
s4ds.FECData = s4ds.FECData@718454de
```

Calling `FECData.loadOhio` or `FECData.loadAll` will create an `FECData` object with a single attribute, `transactions`, which is an iterator over all the donations coming from Ohio or the entire United States:

```
scala> val ohioTransactions = ohioData.transactions
Iterator[Transaction] = non-empty iterator

scala> ohioTransactions.take(5).foreach(println)
Transaction(None,Paul, Ron,BROWN, TODD W MR.,OH,Some(ENGINE
ER),5000,2011-01-03)
Transaction(None,Paul, Ron,DIEHL, MARGO SONJA,OH,Some(RETIR
ED),2500,2011-01-03)
Transaction(None,Paul, Ron,KIRCHMEYER, BENJAMIN,OH,Some(COMPUTER
PROGRAMMER),20120,2011-01-03)
Transaction(None,Obama, Barack,KEYES, STEPHEN,OH,Some(HR EXECUTIVE /
ATTORNEY),10000,2011-01-03)
Transaction(None,Obama, Barack,MURPHY, MIKE W,OH,Some(MANAG
ER),5000,2011-01-03)
```

Now that we have some data to play with, let's try and put it in the database so that we can run some useful queries on it.

Importing Slick

To add Slick to the list of dependencies, you will need to add `"com.typesafe.slick" %% "slick" % "2.1.0"` to the list of dependencies in your `build.sbt` file. You will also need to make sure that Slick has access to a JDBC driver. In this chapter, we will connect to a MySQL database, and must, therefore, add the MySQL connector `"mysql" % "mysql-connector-java" % "5.1.37"` to the list of dependencies.

Slick is imported by importing a specific database driver. As we are using MySQL, we must import the following:

```
scala> import slick.driver.MySQLDriver.simple._
import slick.driver.MySQLDriver.simple._
```

To connect to a different flavor of SQL database, import the relevant driver. The easiest way of seeing what drivers are available is to consult the API documentation for the `slick.driver` package, which is available at <http://slick.typesafe.com/doc/2.1.0/api/#scala.slick.driver.package>. All the common SQL flavors are supported (including **H2**, **PostgreSQL**, **MS SQL Server**, and **SQLite**).

Defining the schema

Let's create a table to represent our transactions. We will use the following schema:

```
CREATE TABLE transactions (  
  id INT(11) AUTO_INCREMENT PRIMARY KEY,  
  candidate VARCHAR(254) NOT NULL,  
  contributor VARCHAR(254) NOT NULL,  
  contributor_state VARCHAR(2) NOT NULL,  
  contributor_occupation VARCHAR(254),  
  amount BIGINT(20) NOT NULL,  
  date DATE  
);
```

Note that the donation amount is in *cents*. This allows us to use an integer field (rather than a fixed point decimal, or worse, a float).



You should never use a floating point format to represent money or, in fact, any discrete quantity because floats cannot represent most fractions exactly:

```
scala> 0.1 + 0.2  
Double = 0.30000000000000004
```

This seemingly nonsensical result occurs because there is no way to store 0.3 exactly in doubles.

This post gives an extensive discussion of the limitations of the floating point format:

http://docs.oracle.com/cd/E19957-01/806-3568/ncg_goldberg.html

To use Slick with tables in our database, we first need to tell Slick about the database schema. We do this by creating a class that extends the `Table` abstract class. The way in which a schema is defined is quite straightforward, so let's dive straight into the code. We will store our schema in a `Tables` singleton. We define a `Transactions` class that provides the mapping to go from collections of `Transaction` instances to SQL tables structured like the `transactions` table:

```
// Tables.scala  
  
import java.sql.Date  
import slick.driver.MySQLDriver.simple._  
  
/** Singleton object for table definitions */
```

```

object Tables {

  // Transactions table definition
  class Transactions(tag:Tag)
  extends Table[Transaction](tag, "transactions") {
    def id = column[Int]("id", O.PrimaryKey, O.AutoInc)
    def candidate = column[String]("candidate")
    def contributor = column[String]("contributor")
    def contributorState = column[String](
      "contributor_state", O.DBType("VARCHAR(2)"))
    def contributorOccupation = column[Option[String]](
      "contributor_occupation")
    def amount = column[Long]("amount")
    def date = column[Date]("date")

    def * = (id.?, candidate, contributor,
      contributorState, contributorOccupation, amount, date) <> (
      Transaction.tupled, Transaction.unapply)
  }

  val transactions = TableQuery[Transactions]
}

```

Let's go through this line by line. We first define a `Transactions` class, which must take a Slick `Tag` object as its first argument. The `Tag` object is used by Slick internally to construct SQL statements. The `Transactions` class extends a `Table` object, passing it the tag and name of the table in the database. We could, optionally, have added a database name by extending `Table[Transaction](tag, Some("fec"), "transactions")` rather than just `Table[Transaction](tag, "transactions")`. The `Table` type is parametrized by `Transaction`. This means that running `SELECT` statements on the database returns `Transaction` objects. Similarly, we will insert data into the database by passing a transaction or list of transactions to the relevant Slick methods.

Let's look at the `Transactions` class definition in more detail. The body of the class starts by listing the database columns. For instance, the `id` column is defined as follows:

```
def id = column[Int]("id", O.PrimaryKey, O.AutoInc)
```

We tell Slick that it should read the column called `id` and transform it to a Scala integer. Additionally, we tell Slick that this column is the primary key and that it is auto-incrementing. The Slick documentation contains a list of available options for `column`.

The `candidate` and `contributor` columns are straightforward: we tell Slick to read these as `String` from the database. The `contributor_state` column is a little more interesting. Besides specifying that it should be read from the database as a `String`, we also tell Slick that it should be stored in the database with type `VARCHAR(2)`.

The `contributor_occupation` column in our table can contain `NULL` values. When defining the schema, we pass the `Option[String]` type to the column method:

```
def contributorOccupation =  
  column[Option[String]]("contributor_occupation")
```

When reading from the database, a `NULL` field will get converted to `None` for columns specified as `Option[T]`. Conversely, if the field has a value, it will be returned as `Some(value)`.

The last line of the class body is the most interesting part: it specifies how to transform the raw data read from the database into a `Transaction` object and how to convert a `Transaction` object to raw fields ready for insertion:

```
def * = (id.?, candidate, contributor,  
  contributorState, contributorOccupation, amount, date) <> (  
  Transaction.tupled, Transaction.unapply)
```

The first part is just a tuple of fields to be read from the database: `(id.?, candidate, contributor, contributorState, contributorOccupation, amount, date)`, with a small amount of metadata. The second part is a pair of functions that describe how to transform this tuple into a `Transaction` object and back. In this case, as `Transaction` is a case class, we can take advantage of the `Transaction.tupled` and `Transaction.unapply` methods automatically provided for case classes.

Notice how we followed the `id` entry with `.?`. In our `Transaction` class, the donation `id` has the `Option[Int]` type, but the column in the database has the `INT` type with the additional `O.AutoInc` option. The `.?` suffix tells Slick to use the default value provided by the database (in this case, the database's auto-increment) if `id` is `None`.

Finally, we define the value:

```
val transactions = TableQuery[Transactions]
```

This is the handle that we use to actually interact with the database. For instance, as we will see later, to get a list of donations to Barack Obama, we run the following query (don't worry about the details of the query for now):

```
Tables.transactions.filter {_.candidate === "Obama, Barack"}.list
```

Let's summarize the parts of our `Transactions` mapper class:

- The `Transactions` class must extend the `Table` abstract class parametrized by the type that we want to return: `Table[Transaction]`.
- We define the columns to read from the database explicitly using `column`, for example, `def contributorState = column[String]("contributor_state", O.DBType("VARCHAR(2)"))`. The `[String]` type parameter defines the Scala type that this column gets read as. The first argument is the SQL column name. Consult the Slick documentation for a full list of additional arguments (<http://slick.typesafe.com/doc/2.1.0/schemas.html>).
- We describe how to convert from a tuple of the column values to a Scala object and vice versa using `def * = (id.?, candidate, ...) <> (Transaction.tupled, Transaction.unapply)`.

Connecting to the database

So far, you have learned how to define `Table` classes that encode the transformation from rows in a SQL table to Scala case classes. To move beyond table definitions and start interacting with a database server, we must connect to a database. As in the previous chapter, we will assume that there is a MySQL server running on localhost on port 3306.

We will use the console to demonstrate the functionality in this chapter, but you can find an equivalent sample program in `SlickDemo.scala`. Let's open a Scala console and connect to the database running on port 3306:

```
scala> import slick.driver.MySQLDriver.simple._
import slick.driver.MySQLDriver.simple._

scala> val db = Database.forURL(
  "jdbc:mysql://127.0.0.1:3306/test",
  driver="com.mysql.jdbc.Driver"
)

db: slick.driver.MySQLDriver.backend.DatabaseDef = slick.jdbc.JdbcBackend
$DatabaseDef@3632d1dd
```

If you have read the previous chapter, you will recognize the first argument as a JDBC-style URL. The URL starts by defining a protocol, in this case, `jdbc:mysql`, followed by the IP address and port of the database server, followed by the database name (`test`, here).

The second argument to `forURL` is the class name of the JDBC driver. This driver is imported at runtime using reflection. Note that the driver specified here must match the Slick driver imported statically.

Having defined the database, we can now use it to create a connection:

```
scala> db.withSession { implicit session =>
  // do something useful with the database
  println(session)
}
scala.slick.jdbc.JdbcBackend$BaseSession@af5a276
```

Slick functions that require access to the database take a `Session` argument implicitly: if a `Session` instance marked as `implicit` is available in scope, they will use it. Thus, preceding `session` with the `implicit` keyword saves us having to pass `session` explicitly every time we run an operation on the database.

If you have read the previous chapter, you will recognize that Slick deals with the need to close connections with the *loan pattern*: a database connection is created in the form of a `session` object and passed temporarily to the client. When the client code returns, the session is closed, ensuring that all opened connections are closed. The client code is therefore spared the responsibility of closing the connection.

The loan pattern is very useful in production code, but it can be somewhat cumbersome in the shell. Slick lets us create a session explicitly as follows:

```
scala> implicit val session = db.createSession
session: slick.driver.MySQLDriver.backend.Session = scala.slick.jdbc.JdbcBackend$BaseSession@2b775b49

scala> session.close
```

Creating tables

Let's use our new connection to create the transaction table in the database. We can access methods to create and drop tables using the `ddl` attribute on our `TableQuery[Transactions]` instance:

```
scala> db.withSession { implicit session =>
  Tables.transactions.ddl.create
}
```

If you jump into a `mysql` shell, you will see that a `transactions` table has been created:

```
mysql> describe transactions ;
+-----+-----+-----+-----+
| Field          | Type          | Null | Key |
+-----+-----+-----+-----+
| id             | int(11)       | NO   | PRI |
| candidate      | varchar(254)  | NO   |     |
| contributor    | varchar(254)  | NO   |     |
| contributor_state | varchar(2)    | NO   |     |
| contributor_occupation | varchar(254) | YES  |     |
| amount        | bigint(20)    | NO   |     |
| date          | date          | NO   |     |
+-----+-----+-----+-----+
7 rows in set (0.01 sec)
```

The `ddl` attribute also includes a `drop` method to drop the table. Incidentally, `ddl` stands for "data-definition language" and is commonly used to refer to the parts of SQL relevant to schema and constraint definitions.

Inserting data

Slick `TableQuery` instances let us interact with SQL tables with an interface similar to Scala collections.

Let's create a transaction first. We will pretend that a donation occurred on the 22nd of June, 2010. Unfortunately, the code to create dates in Scala and pass these to JDBC is particularly clunky. We first create a `java.util.Date` instance, which we must then convert to a `java.sql.Date` to use in our newly created transaction:

```
scala> import java.text.SimpleDateFormat
import java.text.SimpleDateFormat

scala> val date = new SimpleDateFormat("dd-MM-yyyy").parse("22-06-2010")
date: java.util.Date = Tue Jun 22 00:00:00 BST 2010

scala> val sqlDate = new java.sql.Date(date.getTime())
sqlDate: java.sql.Date = 2010-06-22

scala> val transaction = Transaction(
```

```
    None, "Obama, Barack", "Doe, John", "TX", None, 200, sqlDate
  )
transaction: Transaction = Transaction(None,Obama, Barack,Doe,
John,TX,None,200,2010-06-22)
```

Much of the interface provided by the `TableQuery` instance mirrors that of a mutable list. To insert a single row in the transaction table, we can use the `+=` operator:

```
scala> db.withSession {
  implicit session => Tables.transactions += transaction
}
Int = 1
```

Under the hood, this will create a JDBC prepared statement and run this statement's `executeUpdate` method.

If you are committing many rows at a time, you should use Slick's bulk insert operator: `++=`. This takes a `List[Transaction]` as input and inserts all the transactions in a single batch by taking advantage of JDBC's `addBatch` and `executeBatch` functionality.

Let's insert all the FEC transactions so that we have some data to play with when running queries in the next section. We can load an iterator of transactions for Ohio by calling the following:

```
scala> val transactions = FECDData.loadOhio.transactions
transactions: Iterator[Transaction] = non-empty iterator
```

We can also load the transactions for the whole of United States:

```
scala> val transactions = FECDData.loadAll.transactions
transactions: Iterator[Transaction] = non-empty iterator
```

To avoid materializing all the transactions in a single fell swoop – thus potentially exceeding our computer's available memory – we will take batches of transactions from the iterator and insert them:

```
scala> val batchSize = 100000
batchSize: Int = 100000

scala> val transactionBatches = transactions.grouped(batchSize)
transactionBatches: transactions.GroupedIterator[Transaction] = non-empty iterator
```

An iterator's `grouped` method splits the iterator into batches. It is useful to split a long collection or iterator into manageable batches that can be processed one after the other. This is important when integrating or processing large datasets.

All that we have to do now is iterate over our batches, inserting them into the database as we go:

```
scala> db.withSession { implicit session =>
  transactionBatches.foreach {
    batch => Tables.transactions += batch.toList
  }
}
```

While this works, it is sometimes useful to see progress reports when doing long-running integration processes. As we have split the integration into batches, we know (to the nearest batch) how far into the integration we are. Let's print the progress information at the beginning of every batch:

```
scala> db.withSession { implicit session =>
  transactionBatches.zipWithIndex.foreach {
    case (batch, batchNumber) =>
      println(s"Processing row ${batchNumber*batchSize}")
      Tables.transactions += batch.toList
  }
}
Processing row 0
Processing row 100000
...
```

We use the `.zipWithIndex` method to transform our iterator over batches into an iterator of *(batch, current index)* pairs. In a full-scale application, the progress information would probably be written to a log file rather than to the screen.

Slick's well-designed interface makes inserting data very intuitive, integrating well with native Scala types.

Querying data

In the previous section, we used Slick to insert donation data into our database. Let's explore this data now.

When defining the `Transactions` class, we defined a `TableQuery` object, `transactions`, that acts as the handle for accessing the transaction table. It exposes an interface similar to Scala iterators. For instance, to see the first five elements in our database, we can call `take(5)`:

```
scala> db.withSession { implicit session =>
  Tables.transactions.take(5).list
}
List[Tables.Transactions#TableElementType] =
List(Transaction(Some(1),Obama, Barack,Doe, ...
```

Internally, Slick implements the `.take` method using a SQL `LIMIT`. We can, in fact, get the SQL statement using the `.selectStatement` method on the query:

```
scala> db.withSession { implicit session =>
  println(Tables.transactions.take(5).selectStatement)
}
select x2.`id`, x2.`candidate`, x2.`contributor`, x2.`contributor_
state`, x2.`contributor_occupation`, x2.`amount`, x2.`date` from
(select x3.`date` as `date`, x3.`contributor` as `contributor`,
x3.`amount` as `amount`, x3.`id` as `id`, x3.`candidate` as `candidate`,
x3.`contributor_state` as `contributor_state`, x3.`contributor_
occupation` as `contributor_occupation` from `transactions` x3 limit 5)
x2
```

Our Slick query is made up of the following two parts:

- `.take(n)`: This part is called the *invoker*. Invokers build up the SQL statement but do not actually fire it to the database. You can chain many invokers together to build complex SQL statements.
- `.list`: This part sends the statement prepared by the invoker to the database and converts the result to Scala object. This takes a `session` argument, possibly implicitly.

Invokers

Invokers are the components of a Slick query that build up the SQL select statement. Slick exposes a variety of invokers that allow the construction of complex queries. Let's look at some of these invokers here:

- The `map` invoker is useful to select individual columns or apply operations to columns:

```
scala> db.withSession { implicit session =>
  Tables.transactions.map {
    _.candidate
  }.take(5).list
}
List[String] = List(Obama, Barack, Paul, Ron, Paul, Ron, Paul,
Ron, Obama, Barack)
```

- The `filter` invoker is the equivalent of the `WHERE` statements in SQL. Note that Slick fields must be compared using `===`:

```
scala> db.withSession { implicit session =>
  Tables.transactions.filter {
    _.candidate === "Obama, Barack"
  }.take(5).list
}
List[Tables.Transactions#TableElementType] =
List(Transaction(Some(1),Obama, Barack,Doe,
John,TX,None,200,2010-06-22), ...)
```

Similarly, to filter out donations to Barack Obama, use the `!=` operator:

```
scala> db.withSession { implicit session =>
  Tables.transactions.filter {
    _.candidate != "Obama, Barack"
  }.take(5).list
}
List[Tables.Transactions#TableElementType] =
List(Transaction(Some(2),Paul, Ron,BROWN, TODD W MR.,OH,...)
```

- The `sortBy` invoker is the equivalent of the `ORDER BY` statement in SQL:

```
scala> db.withSession { implicit session =>
  Tables.transactions.sortBy {
    _.date.desc
  }
```

```
    }.take(5).list
  }
List[Tables.Transactions#TableElementType] = List(Transaction(Some(65536),Obama,Barack,COPELAND,THOMAS,OH,Some(COLLEGE TEACHING),10000,2012-01-02))
```

- The `leftJoin`, `rightJoin`, `innerJoin`, and `outerJoin` invokers are used for joining tables. As we do not cover interactions between multiple tables in this tutorial, we cannot demonstrate joins. See the Slick documentation (<http://slick.typesafe.com/doc/2.1.0/queries.html#joining-and-zipping>) for examples of these.
- Aggregation invokers such as `length`, `min`, `max`, `sum`, and `avg` can be used for computing summary statistics. These must be executed using `.run`, rather than `.list`, as they return single numbers. For instance, to get the total donations to Barack Obama:

```
scala> db.withSession { implicit session =>
  Tables.transactions.filter {
    _.candidate === "Obama, Barack"
  }.map { _.amount }.sum.run
}
Option[Int] = Some(849636799) // (in cents)
```

Operations on columns

In the previous section, you learned about the different invokers and how they mapped to SQL statements. We brushed over the methods supported by columns themselves, however: we can compare for equality using `===`, but what other operations are supported by Slick columns?

Most of the SQL functions are supported. For instance, to get the total donations to candidates whose name starts with "O", we could run the following:

```
scala> db.withSession { implicit session =>
  Tables.transactions.filter {
    _.candidate.startsWith("O")
  }.take(5).list
}
List[Tables.Transactions#TableElementType] = List(Transaction(Some(1594098)...
```

Similarly, to count donations that happened between January 1, 2011 and February 1, 2011, we can use the `.between` method on the `date` column:

```
scala> val dateParser = new SimpleDateFormat("dd-MM-yyyy")
dateParser: java.text.SimpleDateFormat = SimpleDateFormat

scala> val startDate = new java.sql.Date(dateParser.parse("01-01-2011").
getTime())
startDate: java.sql.Date = 2011-01-01

scala> val endDate = new java.sql.Date(dateParser.parse("01-02-2011").
getTime())
endDate: java.sql.Date = 2011-02-01

scala> db.withSession { implicit session =>
  Tables.transactions.filter {
    _.date.between(startDate, endDate)
  }.length.run
}
Int = 9772
```

The equivalent of the SQL `IN (...)` operator that selects values in a specific set is `inSet`. For instance, to select all transactions to Barack Obama and Mitt Romney, we can use the following:

```
scala> val candidateList = List("Obama, Barack", "Romney, Mitt")
candidateList: List[String] = List(Obama, Barack, Romney, Mitt)

scala> val donationCents = db.withSession { implicit session =>
  Tables.transactions.filter {
    _.candidate.inSet(candidateList)
  }.map { _.amount }.sum.run
}
donationCents: Option[Long] = Some(2874484657)

scala> val donationDollars = donationCents.map { _ / 100 }
donationDollars: Option[Long] = Some(28744846)
```

So, between them, Mitt Romney and Barack Obama received over 28 million dollars in registered donations.

We can also negate a Boolean column with the `!` operator. For instance, to calculate the total amount of donations received by all candidates apart from Barack Obama and Mitt Romney:

```
scala> db.withSession { implicit session =>
  Tables.transactions.filter {
    ! _.candidate.inSet(candidateList)
  }.map { _.amount }.sum.run
}.map { _ / 100 }
Option[Long] = Some(1930747)
```

Column operations are added by implicit conversion on the base `Column` instances. For a full list of methods available on String columns, consult the API documentation for the `StringColumnExtensionMethods` class (<http://slick.typesafe.com/doc/2.1.0/api/#scala.slick.lifted.StringColumnExtensionMethods>). For the methods available on Boolean columns, consult the API documentation for the `BooleanColumnExtensionMethods` class (<http://slick.typesafe.com/doc/2.1.0/api/#scala.slick.lifted.BooleanColumnExtensionMethods>). For the methods available on numeric columns, consult the API documentation for `NumericColumnExtensionMethods` (<http://slick.typesafe.com/doc/2.1.0/api/#scala.slick.lifted.NumericColumnExtensionMethods>).

Aggregations with "Group by"

Slick also provides a `groupBy` method that behaves like the `groupBy` method of native Scala collections. Let's get a list of candidates with all the donations for each candidate:

```
scala> val grouped = Tables.transactions.groupBy { _.candidate }
grouped: scala.slick.lifted.Query[(scala.slick.lifted.Column[...

scala> val aggregated = grouped.map {
  case (candidate, group) =>
    (candidate -> group.map { _.amount }.sum)
}
aggregated: scala.slick.lifted.Query[(scala.slick.lifted.Column[...

scala> val groupedDonations = db.withSession {
  implicit session => aggregated.list
}
```

```
groupedDonations: List[(String, Option[Long])] = List((Bachmann,
Michele,Some(7439272)),...
```

Let's break this down. The first statement, `transactions.groupBy { _.candidate }`, specifies the key by which to group. You can think of this as building an intermediate list of `(String, List[Transaction])` tuples mapping the group key to a list of all the table rows that satisfy this key. This behavior is identical to calling `groupBy` on a Scala collection.

The call to `groupBy` must be followed by a `map` that aggregates the groups. The function passed to `map` must take the tuple `(String, List[Transaction])` pair created by the `groupBy` call as its sole argument. The `map` call is responsible for aggregating the `List[Transaction]` object. We choose to first pick out the amount field of each transaction, and then to run a sum over these. Finally, we call `.list` on the whole pipeline to actually run the query. This just returns a Scala list. Let's convert the total donations from cents to dollars:

```
scala> val groupedDonationDollars = groupedDonations.map {
  case (candidate, donationCentsOption) =>
    candidate -> (donationCentsOption.getOrElse(0L) / 100)
}
groupedDonationDollars: List[(String, Long)] = List((Bachmann,
Michele,74392),...
```

```
scala> groupedDonationDollars.sortBy {
  _._2
}.reverse.foreach { println }
(Romney, Mitt,20248496)
(Obama, Barack,8496347)
(Paul, Ron,565060)
(Santorum, Rick,334926)
(Perry, Rick,301780)
(Gingrich, Newt,277079)
(Cain, Herman,210768)
(Johnson, Gary Earl,83610)
(Bachmann, Michele,74392)
(Pawlenty, Timothy,42500)
(Huntsman, Jon,23571)
(Roemer, Charles E. 'Buddy' III,8579)
(Stein, Jill,5270)
(McCotter, Thaddeus G,3210)
```

Accessing database metadata

Commonly, especially during development, you might start the script by dropping the table if it exists, then recreating it. We can find if a table is defined by accessing the database metadata through the `MTable` object. To get a list of tables with name matching a certain pattern, we can run `MTable.getTables(pattern)`:

```
scala> import slick.jdbc.meta.MTable
import slick.jdbc.meta.MTable

scala> db.withSession { implicit session =>
  MTable.getTables("transactions").list
}
List[scala.slick.jdbc.meta.MTable] = List(MTable(MQName(fec.transactions),TABLE,,None,None,None) ...)
```

Thus, to drop the transactions table if it exists, we can run the following:

```
scala> db.withSession { implicit session =>
  if(MTable.getTables("transactions").list.nonEmpty) {
    Tables.transactions.ddl.drop
  }
}
```

The `MTable` instance contains a lot of metadata about the table. Go ahead and recreate the `transactions` table if you dropped it in the previous example. Then, to find information about the table's primary keys:

```
scala> db.withSession { implicit session =>
  val tableMeta = MTable.getTables("transactions").first
  tableMeta.getPrimaryKeys.list
}
List[MPrimaryKey] = List(MPrimaryKey(MQName(test.transactions),id,1,Some(PRIMARY)))
```

For a full list of methods available on `MTable` instances, consult the Slick documentation (<http://slick.typesafe.com/doc/2.1.0/api/index.html#scala.slick.jdbc.meta.MTable>).

Slick versus JDBC

This chapter and the previous one introduced two different ways of interacting with SQL. In the previous chapter, we described how to use JDBC and build extensions on top of JDBC to make it more usable. In this chapter, we introduced Slick, a library that provides a functional interface on top of JDBC.

Which method should you choose? If you are starting a new project, you should consider using Slick. Even if you spend a considerable amount of time writing wrappers that sit on top of JDBC, it is unlikely that you will achieve the fluidity that Slick offers.

If you are working on an existing project that makes extensive use of JDBC, I hope that the previous chapter demonstrates that, with a little time and effort, you can write JDBC wrappers that reduce the impedance between the imperative style of JDBC and Scala's functional approach.

Summary

In the previous two chapters, we looked extensively at how to query relational databases from Scala. In this chapter, you learned how to use Slick, a "functional-relational" mapper that allows interacting with SQL databases as one would with Scala collections.

In the next chapter, you will learn how to ingest data by querying web APIs.

References

To learn more about Slick, you can refer to the Slick documentation (<http://slick.typesafe.com/doc/2.1.0/>) and its API documentation (<http://slick.typesafe.com/doc/2.1.0/api/#package>).

7

Web APIs

Data scientists and data engineers get data from a variety of different sources. Often, data might come as CSV files or database dumps. Sometimes, we have to obtain the data through a web API.

An individual or organization sets up a web API to distribute data to programs over the Internet (or an internal network). Unlike websites, where the data is intended to be consumed by a web browser and shown to the user, the data provided by a web API is agnostic to the type of program querying it. Web servers serving HTML and web servers backing an API are queried in essentially the same way: through HTTP requests.

We have already seen an example of a web API in *Chapter 4, Parallel Collections and Futures*, where we queried the "Markit on demand" API for current stock prices. In this chapter, we will explore how to interact with web APIs in more detail; specifically, how to convert the data returned by the API to Scala objects and how to [add additional information to the request](#) through HTTP headers (for authentication, for instance).

The "Markit on demand" API returned the data formatted as an XML object, but increasingly, new web APIs return data formatted as JSON. We will therefore focus on JSON in this chapter, but the concepts will port easily to XML.

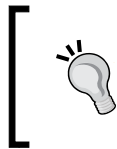
JSON is a language for formatting structured data. Many readers will have come across JSON in the past, but if not, there is a brief introduction to the syntax and concepts later on in this chapter. You will find it quite straightforward.

In this chapter, we will poll the GitHub API. GitHub has, over the last few years, become the de facto tool for collaborating on open source software. It provides a powerful, feature-rich API that gives programmatic access to nearly all the data available through the website.

Let's get a taste of what we can do. Type `api.github.com/users/odersky` in your web browser address bar. This will return the data offered by the API on a particular user (Martin Odersky, in this case):

```
{
  "login": "odersky",
  "id": 795990,
  ...
  "public_repos": 8,
  "public_gists": 3,
  "followers": 707,
  "following": 0,
  "created_at": "2011-05-18T14:51:21Z",
  "updated_at": "2015-09-15T15:14:33Z"
}
```

The data is returned as a JSON object. This chapter is devoted to learning how to access and parse this data programmatically. In *Chapter 13, Web APIs with Play*, you will learn how to build your own web API.



The GitHub API is extensive and very well-documented. We will explore some of the features of the API in this chapter. To see the full extent of the API, visit the documentation (<https://developer.github.com/v3/>).

A whirlwind tour of JSON

JSON is a format for transferring structured data. It is flexible, easy for computers to generate and parse, and relatively readable for humans. It has become very common as a means of persisting program data structures and transferring data between programs.

JSON has four basic types: **Numbers**, **Strings**, **Booleans**, and **null**, and two compound types: **Arrays** and **Objects**. Objects are unordered collections of key-value pairs, where the key is always a string and the value can be any simple or compound type. We have already seen a JSON object: the data returned by the API call `api.github.com/users/odersky`.

Arrays are ordered lists of simple or compound types. For instance, type `api.github.com/users/odersky/repos` in your browser to get an array of objects, each representing a GitHub repository:

```
[
  {
    "id": 17335228,
    "name": "dotty",
    "full_name": "odersky/dotty",
    ...
  },
  {
    "id": 15053153,
    "name": "frontend",
    "full_name": "odersky/frontend",
    ...
  },
  ...
]
```

We can construct complex structures by nesting objects within other objects or arrays. Nevertheless, most web APIs return JSON structures with no more than one or two levels of nesting. If you are not familiar with JSON, I encourage you to explore the GitHub API through your web browser.

Querying web APIs

The easiest way of querying a web API from Scala is to use `Source.fromURL`. We have already used this in *Chapter 4, Parallel Collections and Futures*, when we queried the "Markit on demand" API. `Source.fromURL` presents an interface similar to `Source.fromFile`:

```
scala> import scala.io._
import scala.io._

scala> val response = Source.fromURL(
  "https://api.github.com/users/odersky"
).mkString
response: String = {"login":"odersky","id":795990, ...
```

`Source.fromURL` returns an iterator over the characters of the response. We materialize the iterator into a string using its `.mkString` method. We now have the response as a Scala string. The next step is to parse the string with a JSON parser.

JSON in Scala – an exercise in pattern matching

There are several libraries for manipulating JSON in Scala. We prefer `json4s`, but if you are a die-hard fan of another JSON library, you should be able to readily adapt the examples in this chapter. Let's create a `build.sbt` file with a dependency on `json4s`:

```
// build.sbt
scalaVersion := "2.11.7"

libraryDependencies += "org.json4s" %% "json4s-native" % "3.2.11"
```

We can then import `json4s` into an SBT console session with:

```
scala> import org.json4s._
import org.json4s._

scala> import org.json4s.native.JsonMethods._
import org.json4s.native.JsonMethods._
```

Let's use `json4s` to parse the response to our GitHub API query:

```
scala> val jsonResponse = parse(response)
jsonResponse: org.json4s.JValue = JObject(List((login,JString(odersky)),(
id,JInt(795990)),...
```

The `parse` method takes a string (that contains well-formatted JSON) and converts it to a `JValue`, a supertype for all `json4s` objects. The runtime type of the response to this particular query is `JObject`, which is a `json4s` type representing a JSON object.

`JObject` is a wrapper around a `List[JField]`, and `JField` represents an individual key-value pair in the object. We can use *extractors* to access this list:

```
scala> val JObject(fields) = jsonResponse
fields: List[JField] = List((login,Jstring(odersky)),...
```

What's happened here? By writing `val JObject(fields) = ...`, we are telling Scala:

- The right-hand side has runtime type of `JObject`
- Go into the `JObject` instance and bind the list of fields to the constant `fields`

Readers familiar with Python might recognize the similarity with tuple unpacking, though Scala extractors are much more powerful and versatile. Extractors are used extensively to extract Scala types from `json4s` types.

Pattern matching using case classes

How exactly does the Scala compiler know what to do with an extractor such as:

```
val JObject(fields) = ...
```



`JObject` is a case class with the following constructor:

```
case class JObject(obj:List[JField])
```

Case classes all come with an extractor that reverses the constructor exactly. Thus, writing `val JObject(fields)` will bind `fields` to the `obj` attribute of the `JObject`. For further details on how extractors work, read *Appendix, Pattern Matching and Extractors*.

We have now extracted `fields`, a (plain old Scala) list of fields from the `JObject`. A `JField` is a key-value pair, with the key being a string and value being a subtype of `JValue`. Again, we can use extractors to extract the values in the field:

```
scala> val firstField = fields.head
firstField: JField = (login,JString(odersky))
```

```
scala> val JField(key, JString(value)) = firstField
key: String = login
value: String = odersky
```

We matched the right-hand side against the pattern `JField(_, JString(_))`, binding the first element to `key` and the second to `value`. What happens if the right-hand side does not match the pattern?

```
scala> val JField(key, JInt(value)) = firstField
scala.MatchError: (login,JString(odersky)) (of class scala.Tuple2)
...
```

The code throws a `MatchError` at runtime. These examples demonstrate the power of nested pattern matching: in a single line, we managed to verify the type of `firstField`, that its value has type `JString`, and we have bound the key and value to the `key` and `value` variables, respectively. As another example, if we *know* that the first field is the login field, we can both verify this and extract the value:

```
scala> val JField("login", JString(loginName)) = firstField
loginName: String = odersky
```

Notice how this style of programming is *declarative* rather than *imperative*: we declare that we want a `JField("login", JString(_))` variable on the right-hand side. We then let the language figure out how to check the variable types. Pattern matching is a recurring theme in functional languages.

We can also use pattern matching in a for loop when looping over fields. When used in a for loop, a pattern match defines a *partial function*: only elements that match the pattern pass through the loop. This lets us filter the collection for elements that match a pattern and also apply a transformation to these elements. For instance, we can extract every string field in our `fields` list:

```
scala> for {
  JField(key, JString(value)) <- fields
} yield (key -> value)
List[(String, String)] = List((login,odersky), (avatar_url,https://avatars.githubusercontent.com/...
```

We can use this to search for specific fields. For instance, to extract the "followers" field:

```
scala> val followersList = for {
  JField("followers", JInt(followers)) <- fields
} yield followers
followersList: List[Int] = List(707)

scala> val followers = followersList.headOption
blogURL: Option[Int] = Some(707)
```

We first extracted all fields that matched the pattern `JField("follower", JInt(_))`, returning the integer inside the `JInt`. As the source collection, `fields`, is a list, this returns a list of integers. We then extract the first value from this list using `headOption`, which returns the head of the list if the list has at least one element, or `None` if the list is empty.

We are not limited to extracting a single field at a time. For instance, to extract the "id" and "login" fields together:

```
scala> {
  for {
    JField("login", JString(loginName)) <- fields
    JField("id", JInt(id)) <- fields
  } yield (id -> loginName)
}.headOption
Option[(BigInt, String)] = Some((795990,odersky))
```

Scala's pattern matching and extractors provide you with an extremely powerful way of traversing the `json4s` tree, extracting the fields that we need.

JSON4S types

We have already discovered parts of `json4s`'s type hierarchy: strings are wrapped in `JString` objects, integers (or big integers) are wrapped in `JInt`, and so on. In this section, we will take a step back and formalize the type structure and what Scala types they extract to. These are the `json4s` runtime types:

- `val JString(s) // => extracts to a String`
- `val JDouble(d) // => extracts to a Double`
- `val JDecimal(d) // => extracts to a BigDecimal`
- `val JInt(i) // => extracts to a BigInt`
- `val JBool(b) // => extracts to a Boolean`
- `val JObject(l) // => extracts to a List[JField]`
- `val JArray(l) // => extracts to a List[JValue]`
- `JNull // => represents a JSON null`

All these types are subclasses of `JValue`. The compile-time result of `parse` is `JValue`, which you normally need to cast to a concrete type using an extractor.

The last type in the hierarchy is `JField`, which represents a key-value pair. `JField` is just a type alias for the `(String, JValue)` tuple. It is thus not a subtype of `JValue`. We can extract the key and value using the following extractor:

```
val JField(key, JInt(value)) = ...
```


Extracting fields using XPath

In the previous sections, you learned how to traverse JSON objects using extractors. In this section, we will look at a different way of traversing JSON objects and extracting specific fields: the *XPath DSL* (domain-specific language). XPath is a query language for traversing tree-like structures. It was originally designed for addressing specific nodes in an XML document, but it works just as well with JSON. We have already seen an example of XPath syntax when we extracted the stock price from the XML document returned by the "Markit on demand" API in *Chapter 4, Parallel Collections and Futures*. We extracted the node with tag "LastPrice" using `r \ "LastPrice"`. The `\` operator was defined by the `scala.xml` package.

The `json4s` package exposes a similar DSL to extract fields from `JObject` instances. For instance, we can extract the "login" field from the JSON object `jsonResponse`:

```
scala> jsonResponse \ "login"
org.json4s.JValue = JString(odersky)
```

This returns a `JValue` that we can transform into a Scala string using an extractor:

```
scala> val JString(loginName) = jsonResponse \ "login"
loginName: String = odersky
```

Notice the similarity between the XPath DSL and traversing a filesystem: we can think of `JObject` instances as directories. Field names correspond to file names and the field value to the content of the file. This is more evident for nested structures. The `users` endpoint of the GitHub API does not have nested documents, so let's try another endpoint. We will query the API for the repository corresponding to this book: "`https://api.github.com/repos/pbugnion/s4ds`". The response has the following structure:

```
{
  "id": 42269470,
  "name": "s4ds",
  ...
  "owner": { "login": "pbugnion", "id": 1392879 ... }
  ...
}
```

Let's fetch this document and use the XPath syntax to extract the repository owner's login name:

```
scala> val jsonResponse = parse(Source.fromURL(
  "https://api.github.com/repos/pbugnion/s4ds"
).mkString)
jsonResponse: JValue = JObject(List((id,JInt(42269470)),
(name,JString(s4ds))...)

scala> val JString(ownerLogin) = jsonResponse \ "owner" \ "login"
ownerLogin: String = pbugnion
```

Again, this is much like traversing a filesystem: `jsonResponse \ "owner"` returns a `JObject` corresponding to the "owner" object. This `JObject` can, in turn, be queried for the "login" field, returning the value `JString(pbugnion)` associated with this key.

What if the API response is an array? The filesystem analogy breaks down somewhat. Let's query the API endpoint listing Martin Odersky's repositories: `https://api.github.com/users/odersky/repos`. The response is an array of JSON objects, each of which represents a repository:

```
[
  {
    "id": 17335228,
    "name": "dotty",
    "size": 14699,
    ...
  },
  {
    "id": 15053153,
    "name": "frontend",
    "size": 392
    ...
  },
  {
    "id": 2890092,
    "name": "scala",
    "size": 76133,
    ...
  },
  ...
]
```

Let's fetch this and parse it as JSON:

```
scala> val jsonResponse = parse(Source.fromURL(
  "https://api.github.com/users/odersky/repos"
).mkString)
jsonResponse: JValue = JArray(List(JObject(List((id,JInt(17335228)),
(name,Jstring(dotty)), ...
```

This returns a `JArray`. The XPath DSL works in the same way on a `JArray` as on a `JObject`, but now, instead of returning a single `JValue`, it returns an array of fields matching the path in every object in the array. Let's get the size of all Martin Odersky's repositories:

```
scala> jsonResponse \ "size"
JValue = JArray(List(JInt(14699), JInt(392), ...
```

We now have a `JArray` of the values corresponding to the "size" field in every repository. We can iterate over this array with a `for` comprehension and use extractors to convert elements to Scala objects:

```
scala> for {
  JInt(size) <- (jsonResponse \ "size")
} yield size
List[BigInt] = List(14699, 392, 76133, 32010, 98166, 1358, 144, 273)
```

Thus, combining extractors with the XPath DSL gives us powerful, complementary tools to extract information from JSON objects.

There is much more to the XPath syntax than we have space to cover here, including the ability to extract fields nested at any level of depth below the current root or fields that match a predicate or a certain type. We find that well-designed APIs obviate the need for many of these more powerful functions, but do consult the documentation (json4s.org) to get an overview of what you can do.

In the next section, we will look at extracting JSON directly into case classes.

Extraction using case classes

In the previous sections, we extracted specific fields from the JSON response using Scala extractors. We can do one better and extract full case classes.

When moving beyond the REPL, programming best practice dictates that we move from `json4s` types to Scala objects as soon as possible rather than passing `json4s` types around the program. Converting from `json4s` types to Scala types (or case classes representing domain objects) is good practice because:

- It decouples the program from the structure of the data that we receive from the API, something we have little control over.
- It improves type safety: a `JObject` is, as far as the compiler is concerned, always a `JObject`, whatever fields it contains. By contrast, the compiler will never mistake a `User` for a `Repository`.

`Json4s` lets us extract case classes directly from `JObject` instances, making writing the layer converting `JObject` instances to custom types easy.

Let's define a case class representing a GitHub user:

```
scala> case class User(id:Long, login:String)
defined class User
```

To extract a case class from a `JObject`, we must first define an implicit `Formats` value that defines how simple types should be serialized and deserialized. We will use the default `DefaultFormats` provided with `json4s`:

```
scala> implicit val formats = DefaultFormats
formats: DefaultFormats.type = DefaultFormats$@750e685a
```

We can now extract instances of `User`. Let's do this for Martin Odersky:

```
scala> val url = "https://api.github.com/users/odersky"
url: String = https://api.github.com/users/odersky

scala> val jsonResponse = parse(Source.fromURL(url).mkString)
jsonResponse: JValue = JObject(List((login,JString(odersky)), ...

scala> jsonResponse.extract[User]
User = User(795990,odersky)
```

This works as long as the object is well-formatted. The `extract` method looks for fields in the `JObject` that match the attributes of `User`. In this case, `extract` will note that the `JObject` contains the `"login": "odersky"` field and that `JString("odersky")` can be converted to a Scala string, so it binds `"odersky"` to the `login` attribute in `User`.

What if the attribute names differ from the field names in the JSON object? We must first transform the object to have the correct fields. For instance, let's rename the login attribute to userName in our User class:

```
scala> case class User(id:Long, userName:String)
defined class User
```

If we try to use `extract [User]` on `jsonResponse`, we will get a mapping error because the deserializer is missing a login field in the response. We can fix this using the `transformField` method on `jsonResponse` to rename the login field:

```
scala> jsonResponse.transformField {
  case("login", n) => "userName" -> n
}.extract [User]
User = User(795990,odersky)
```

What about optional fields? Let's assume that the JSON object returned by the GitHub API does not always contain the login field. We could symbolize this in our object model by giving the login parameter the type `Option[String]` rather than `String`:

```
scala> case class User(id:Long, login:Option[String])
defined class User
```

This works just as you would expect. When the response contains a non-null login field, calling `extract [User]` will deserialize it to `Some(value)`, and when it's missing or `JNull`, it will produce `None`:

```
scala> jsonResponse.extract [User]
User = User(795990,Some(odersky))
```

```
scala> jsonResponse.removeField {
  case(k, _) => k == "login" // remove the "login" field
}.extract [User]
User = User(795990,None)
```

Let's wrap this up in a small program. The program will take a single command-line argument, the user's login name, extract a `User` instance, and print it to screen:

```
// GitHubUser.scala

import scala.io._
import org.json4s._
```

```
import org.json4s.native.JsonMethods._

object GitHubUser {

  implicit val formats = DefaultFormats

  case class User(id:Long, userName:String)

  /** Query the GitHub API corresponding to `url`
    * and convert the response to a User.
    */
  def fetchUserFromUrl(url:String):User = {
    val response = Source.fromURL(url).mkString
    val jsonResponse = parse(response)
    extractUser(jsonResponse)
  }

  /** Helper method for transforming the response to a User */
  def extractUser(obj:JValue):User = {
    val transformedObject = obj.transformField {
      case ("login", name) => ("userName", name)
    }
    transformedObject.extract[User]
  }

  def main(args:Array[String]) {
    // Extract username from argument list
    val name = args.headOption.getOrElse {
      throw new IllegalArgumentException(
        "Missing command line argument for user.")
    }

    val user = fetchUserFromUrl(
      s"https://api.github.com/users/$name")

    println(s"*** Extracted for $name:")
    println()
    println(user)
  }
}
```

We can run this from an SBT console as follows:

```
$ sbt
> runMain GitHubUser pbugnion
** Extracted for pbugnion:
User(1392879,pbugnion)
```

Concurrency and exception handling with futures

While the program that we wrote in the previous section works, it is very brittle. It will crash if we enter a non-existent user name or the GitHub API changes or returns a badly-formatted response. We need to make it fault-tolerant.

What if we also wanted to fetch multiple users? The program, as written, is entirely single-threaded. The `fetchUserFromUrl` method fires a call to the API and blocks until the API sends data back. A better solution would be to fetch multiple users in parallel.

As you learned in *Chapter 4, Parallel Collections and Futures*, there are two straightforward ways to implement both fault tolerance and parallel execution: we can either put all the user names in a parallel collection and wrap the code for fetching and extracting the user in a `Try` block or we can wrap each query in a future.

When querying web APIs, it is sometimes the case that a request can take abnormally long. To prevent this from blocking the other threads, it is preferable to rely on futures rather than parallel collections for concurrency, as we saw in the *Parallel collection or Future?* section at the end of *Chapter 4, Parallel Collections and Futures*.

Let's rewrite the code from the previous section to handle fetching multiple users concurrently in a fault-tolerant manner. We will change the `fetchUserFromUrl` method to query the API asynchronously. This is not terribly different from *Chapter 4, Parallel Collections and Futures*, in which we queried the "Markit on demand" API:

```
// GitHubUserConcurrent.scala

import scala.io._
import scala.concurrent._
import scala.concurrent.duration._
import ExecutionContext.Implicits.global
import scala.util._

import org.json4s._
```

```
import org.json4s.native.JsonMethods._

object GitHubUserConcurrent {

  implicit val formats = DefaultFormats

  case class User(id:Long, userName:String)

  // Fetch and extract the `User` corresponding to `url`
  def fetchUserFromUrl(url:String):Future[User] = {
    val response = Future { Source.fromURL(url).mkString }
    val parsedResponse = response.map { r => parse(r) }
    parsedResponse.map { extractUser }
  }

  // Helper method for extracting a user from a JObject
  def extractUser(jsonResponse:JValue):User = {
    val o = jsonResponse.transformField {
      case ("login", name) => ("userName", name)
    }
    o.extract[User]
  }

  def main(args:Array[String]) {
    val names = args.toList

    // Loop over each username and send a request to the API
    // for that user
    val name2User = for {
      name <- names
      url = s"https://api.github.com/users/$name"
      user = fetchUserFromUrl(url)
    } yield name -> user

    // callback function
    name2User.foreach { case(name, user) =>
      user.onComplete {
        case Success(u) => println(s" ** Extracted for $name: $u")
        case Failure(e) => println(s" ** Error fetching $name:
          $e")
      }
    }

    // Block until all the calls have finished.
  }
}
```



```
        Await.ready(Future.sequence(name2User.map { _._2 }), 1 minute)
    }
}
```

Let's run the code through sbt:

```
$ sbt
> runMain GitHubUserConcurrent odersky derekwyatt not-a-user-675
** Error fetching user not-a-user-675: java.io.FileNotFoundException:
https://api.github.com/users/not-a-user-675
** Extracted for odersky: User(795990,odersky)
** Extracted for derekwyatt: User(62324,derekwyatt)
```

The code itself should be straightforward. All the concepts used here have been explored in this chapter or in *Chapter 4, Parallel Collections and Futures*, apart from the last line:

```
Await.ready(Future.sequence(name2User.map { _._2 }), 1 minute)
```

This statement tells the program to wait until all futures in our list have been completed. `Await.ready(..., 1 minute)` takes a future as its first argument and blocks execution until this future returns. The second argument is a time-out on this future. The only catch is that we need to pass a single future to `Await` rather than a list of futures. We can use `Future.sequence` to merge a collection of futures into a single future. This future will be completed when all the futures in the sequence have completed.

Authentication – adding HTTP headers

So far, we have been using the GitHub API without authentication. This limits us to sixty requests per hour. Now that we can query the API in parallel, we could exceed this limit in seconds.

Fortunately, GitHub is much more generous if you authenticate when you query the API. The limit increases to 5,000 requests per hour. You must have a GitHub user account to authenticate, so go ahead and create one now if you need to. After creating an account, navigate to <https://github.com/settings/tokens> and click on the **Generate new token** button. Accept the default settings and enter a token description and a long hexadecimal number should appear on the screen. Copy the token for now.

HTTP – a whirlwind overview

Before using our newly generated token, let's take a few minutes to review how HTTP works.

HTTP is a protocol for transferring information between different computers. It is the protocol that we have been using throughout the chapter, though Scala hid the details from us in the call to `Source.fromURL`. It is also the protocol that you use when you point your web browser to a website, for instance.

In HTTP, a computer will typically make a *request* to a remote server, and the server will send back a *response*. Requests contain a *verb*, which defines the type of request, and a URL identifying a *resource*. For instance, when we typed `api.github.com/users/pbugnion` in our browsers, this was translated into a GET (the verb) request for the `users/pbugnion` resource. All the calls that we have made so far have been GET requests. You might use a different type of request, for instance, a POST request, to modify (rather than just view) some content on GitHub.

Besides the verb and resource, there are two more parts to an HTTP request:

- The *headers* include metadata about the request, such as the expected format and character set of the response or the authentication credentials. Headers are just a list of key-value pairs. We will pass the OAuth token that we have just generated to the API using the `Authorization` header. This Wikipedia article lists commonly used header fields: en.wikipedia.org/wiki/List_of_HTTP_header_fields.
- The request body is not used in GET requests but becomes important for requests that modify the resource they query. For instance, if I wanted to create a new repository on GitHub programmatically, I would send a POST request to `/pbugnion/repos`. The POST body would then be a JSON object describing the new repository. We will not use the request body in this chapter.

Adding headers to HTTP requests in Scala

We will pass the OAuth token as a header with our HTTP request. Unfortunately, the `Source.fromURL` method is not particularly suited to adding headers when creating a GET request. We will, instead, use a library, `scalaj-http`.

Let's add `scalaj-http` to the dependencies in our `build.sbt`:

```
libraryDependencies += "org.scalaj" %% "scalaj-http" % "1.1.6"
```

We can now import `scalaj-http`:


```
scala> import scalaj.http._
import scalaj.http._
```

We start by creating an `HttpRequest` object:

```
scala> val request = Http("https://api.github.com/users/pbugnion")
request:scalaj.http.HttpRequest = HttpRequest(api.github.com/users/
pbugnion,GET,...)
```

We can now add the authorization header to the request (add your own token string here):

```
scala> val authorizedRequest = request.header("Authorization", "token
e836389ce ...")
authorizedRequest:scalaj.http.HttpRequest = HttpRequest(api.github.com/
users/pbugnion,GET,...)
```

 The `.header` method returns a new `HttpRequest` instance. It does not modify the request in place. Thus, just calling `request.header(...)` does not actually add the header to request itself, which can be a source of confusion.

Let's fire the request. We do this through the request's `asString` method, which queries the API, fetches the response, and parses it as a Scala `String`:

```
scala> val response = authorizedRequest.asString
response:scalaj.http.HttpResponse[String] = HttpResponse>{"login":"pbugni
on",...}
```

The response is made up of three components:

- The status code, which should be `200` for a successful request:

```
scala> response.code
Int = 200
```
- The response body, which is the part that we are interested in:

```
scala> response.body
String = {"login":"pbugnion","id":1392879,...}
```
- The response headers (metadata about the response):

```
scala> response.headers
Map[String,String] = Map(Access-Control-Allow-Credentials -> true,
...)
```

To verify that the authorization was successful, query the `X-RateLimit-Limit` header:

```
scala> response.headers("X-RateLimit-Limit")
String = 5000
```

This value is the maximum number of requests per hour that you can make to the GitHub API from a single IP address.

Now that we have some understanding of how to add authentication to GET requests, let's modify our script for fetching users to use the OAuth token for authentication. We first need to import `scalaj-http`:

```
import scalaj.http._
```

Injecting the value of the token into the code can be somewhat tricky. You might be tempted to hardcode it, but this prohibits you from sharing the code. A better solution is to use an *environment variable*. Environment variables are a set of variables present in your terminal session that are accessible to all processes running in that session. To get a list of the current environment variables, type the following on Linux or Mac OS:

```
$ env
HOME=/Users/pascal
SHELL=/bin/zsh
...
```

On Windows, the equivalent command is `SET`. Let's add the GitHub token to the environment. Use the following command on Mac OS or Linux:

```
$ export GHTOKEN="e83638..." # enter your token here
```

On Windows, use the following command:

```
$ SET GHTOKEN="e83638..."
```

If you were to reuse this environment variable across many projects, entering `export GHTOKEN=...` in the shell for every session gets old quite quickly. A more permanent solution is to add `export GHTOKEN="e83638..."` to your shell configuration file (your `.bashrc` file if you are using Bash). This is safe provided your `.bashrc` is readable by the user only. Any new shell session will have access to the `GHTOKEN` environment variable.

We can access environment variables from a Scala program using `sys.env`, which returns a `Map[String, String]` of the variables. Let's add a lazy `val token` to our class, containing the token value:

```
lazy val token:Option[String] = sys.env.get("GHTOKEN") orElse {
  println("No token found: continuing without authentication")
  None
}
```

Now that we have the token, the only part of the code that must change, to add authentication, is the `fetchUserFromUrl` method:

```
def fetchUserFromUrl(url:String):Future[User] = {
  val baseRequest = Http(url)
  val request = token match {
    case Some(t) => baseRequest.header(
      "Authorization", s"token $t")
    case None => baseRequest
  }
  val response = Future {
    request.asString.body
  }
  val parsedResponse = response.map { r => parse(r) }
  parsedResponse.map(extractUser)
}
```

Additionally, we can, to gain clearer error messages, check that the response's status code is 200. As this is straightforward, it is left as an exercise.

Summary

In this chapter, you learned how to query the GitHub API, converting the response to Scala objects. Of course, merely printing results to screen is not terribly interesting. In the next chapter, we will look at the next step of the data ingestion process: storing data in a database. We will query the GitHub API and store the results in a MongoDB database.

In *Chapter 13, Web APIs with Play*, we will look at building our own simple web API.

References

The GitHub API, with its extensive documentation, is a good place to explore how a rich API is constructed. It has a **Getting Started** section that is worth reading:

<https://developer.github.com/guides/getting-started/>

Of course, this is not specific to Scala: it uses cURL to query the API.

Read the documentation (<http://json4s.org>) and source code (<https://github.com/json4s/json4s>) for `json4s` for a complete reference. There are many parts of this package that we have not explored, in particular, how to build JSON from Scala.

8

Scala and MongoDB

In *Chapter 5, Scala and SQL through JDBC*, and *Chapter 6, Slick – A Functional Interface for SQL*, you learned how to insert, transform, and read data in SQL databases. These databases remain (and are likely to remain) very popular in data science, but NoSQL databases are emerging as strong contenders.

The needs for data storage are growing rapidly. Companies are producing and storing more data points in the hope of acquiring better business intelligence. They are also building increasingly large teams of data scientists, who all need to access the data store. Maintaining constant access time as the data load increases requires taking advantage of parallel architectures: we need to distribute the database across several computers so that, as the load on the server increases, we can just add more machines to improve throughput.

In MySQL databases, the data is naturally split across different tables. Complex queries necessitate joining across several tables. This makes partitioning the database across different computers difficult. NoSQL databases emerged to fill this gap.

In this chapter, you will learn to interact with MongoDB, an open source database that offers high performance and can be distributed easily. MongoDB is one of the more popular NoSQL databases with a strong community. It offers a reasonable balance of speed and flexibility, making it a natural alternative to SQL for storing large datasets with uncertain query requirements, as might happen in data science. Many of the concepts and recipes in this chapter will apply to other NoSQL databases.

MongoDB

MongoDB is a *document-oriented* database. It contains collections of documents. Each document is a JSON-like object:

```
{
  _id: ObjectId("558e846730044ede70743be9"),
  name: "Gandalf",
  age: 2000,
  pseudonyms: [ "Mithrandir", "Olorin", "Greyhame" ],
  possessions: [
    { name: "Glamdring", type: "sword" },
    { name: "Narya", type: "ring" }
  ]
}
```

Just as in JSON, a document is a set of key-value pairs, where the values can be strings, numbers, Booleans, dates, arrays, or subdocuments. Documents are grouped in collections, and collections are grouped in databases.

You might be thinking that this is not very different from SQL: a document is similar to a row and a collection corresponds to a table. There are two important differences:

- The values in documents can be simple values, arrays, subdocuments, or arrays of subdocuments. This lets us encode one-to-many and many-to-many relationships in a single collection. For instance, consider the wizard collection. In SQL, if we wanted to store pseudonyms for each wizard, we would have to use a separate `wizard2pseudonym` table with a row for each wizard-pseudonym pair. In MongoDB, we can just use an array. In practice, this means that we can normally use a single document to represent an entity (a customer, transaction, or wizard, for instance). In SQL, we would normally have to join across several tables to retrieve all the information on a specific entity.
- MongoDB is *schemaless*. Documents in a collection can have varying sets of fields with different types for the same field across different documents. In practice, MongoDB collections have a loose schema enforced either client side or by convention: most documents will have a subset of the same fields, and fields will, in general, contain the same data type. Having a flexible schema makes adjusting the data structure easy as there is no need for time-consuming `ALTER TABLE` statements. The downside is that there is no easy way of enforcing our flexible schema on the database side.

Note the `_id` field: this is a unique key. MongoDB will generate one automatically if we insert a document without an `_id` field.

This chapter gives recipes for interacting with a MongoDB database from Scala, including maintaining type safety and best practices. We will not cover advanced MongoDB functionality (such as aggregation or distributing the database). We will assume that you have MongoDB installed on your computer (<http://docs.mongodb.org/manual/installation/>). It will also help to have a very basic knowledge of MongoDB (we discuss some references at the end of this chapter, but any basic tutorial available online will be sufficient for the needs of this chapter).

Connecting to MongoDB with Casbah

The official MongoDB driver for Scala is called **Casbah**. Rather than a fully-fledged driver, Casbah wraps the Java Mongo driver, providing a more functional interface. There are other MongoDB drivers for Scala, which we will discuss briefly at the end of this chapter. For now, we will stick to Casbah.

Let's start by adding Casbah to our `build.sbt` file:

```
scalaVersion := "2.11.7"

libraryDependencies += "org.mongodb" %% "casbah" % "3.0.0"
```

Casbah also expects `slf4j` bindings (a Scala logging framework) to be available, so let's also add `slf4j-nop`:

```
libraryDependencies += "org.slf4j" % "slf4j-nop" % "1.7.12"
```

We can now start an SBT console and import Casbah in the Scala shell:

```
$ sbt console
scala> import com.mongodb.casbah.Imports._
import com.mongodb.casbah.Imports._

scala> val client = MongoClient()
client: com.mongodb.casbah.MongoClient = com.mongodb.casbah.
MongoClient@4ac17318
```

This connects to a MongoDB server on the default host (`localhost`) and default port (`27017`). To connect to a different server, pass the host and port as arguments to `MongoClient`:

```
scala> val client = MongoClient("192.168.1.1", 27017)
client: com.mongodb.casbah.MongoClient = com.mongodb.casbah.
MongoClient@584c6b02
```

Note that creating a client is a lazy operation: it does not attempt to connect to the server until it needs to. This means that if you enter the wrong URL or password, you will not know about it until you try and access documents on the server.

Once we have a connection to the server, accessing a database is as simple as using the client's `apply` method. For instance, to access the `github` database:

```
scala> val db = client("github")
db: com.mongodb.casbah.MongoDB = DB{name='github'}
```

We can then access the "users" collection:

```
scala> val coll = db("users")
coll: com.mongodb.casbah.MongoCollection = users
```

Connecting with authentication

MongoDB supports several different authentication mechanisms. In this section, we will assume that your server is using the **SCRAM-SHA-1** mechanism, but you should find adapting the code to a different type of authentication straightforward.

The easiest way of authenticating is to pass `username` and `password` in the URI when connecting:

```
scala> val username = "USER"
username: String = USER

scala> val password = "PASSWORD"
password: String = PASSWORD

scala> val uri = MongoClientURI(
  s"mongodb://$username:$password@localhost/?authMechanism=SCRAM-SHA-1"
)
uri: MongoClientURI = mongodb://USER:PASSWORD@localhost/?authMechanism=SCRAM-SHA-1

scala> val mongoClient = MongoClient(uri)
client: com.mongodb.casbah.MongoClient = com.mongodb.casbah.MongoClient@4ac17318
```

In general, you will not want to put your password in plain text in the code. You can either prompt for a password on the command line or pass it through environment variables, as we did with the GitHub OAuth token in *Chapter 7, Web APIs*. The following code snippet demonstrates how to pass credentials through the environment:

```
// Credentials.scala

import com.mongodb.casbah.Imports._

object Credentials extends App {

  val username = sys.env.getOrElse("MONGOUSER",
    throw new IllegalStateException(
      "Need a MONGOUSER variable in the environment")
  )
  val password = sys.env.getOrElse("MONGOPASSWORD",
    throw new IllegalStateException(
      "Need a MONGOPASSWORD variable in the environment")
  )

  val host = "127.0.0.1"
  val port = 27017

  val uri = s"mongodb:
    //${username}:${password}@${host}:${port}/?authMechanism=SCRAM-SHA-1"

  val client = MongoClient(MongoClientURI(uri))
}
```

You can run it through SBT as follows:

```
$ MONGOUSER="pascal" MONGOPASSWORD="scalarulez" sbt
> runMain Credentials
```

Inserting documents

Let's insert some documents into our newly created database. We want to store information about GitHub users, using the following document structure:

```
{
  id: <mongodb object id>,
  login: "pbugnion",
  github_id: 1392879,
  repos: [
    {
      name: "scikit-monaco",
      id: 14821551,
      language: "Python"
    },
    {
      name: "contactpp",
      id: 20448325,
      language: "Python"
    }
  ]
}
```

Casbah provides a `DBObject` class to represent MongoDB documents (and subdocuments) in Scala. Let's start by creating a `DBObject` instance for each repository subdocument:

```
scala> val repo1 = DBObject("name" -> "scikit-monaco", "id" -> 14821551,
"language" -> "Python")
repo1: DBObject = { "name" : "scikit-monaco" , "id" : 14821551,
"language" : "Python" }
```

As you can see, a `DBObject` is just a list of key-value pairs, where the keys are strings. The values have compile-time type `AnyRef`, but Casbah will fail (at runtime) if you try to add a value that cannot be serialized.

We can also create `DBObject` instances from lists of key-value pairs directly. This is particularly useful when converting from a Scala map to a `DBObject`:

```
scala> val fields:Map[String, Any] = Map(
  "name" -> "contactpp",
  "id" -> 20448325,
  "language" -> "Python"
)
```

```
Map[String, Any] = Map(name -> contactpp, id -> 20448325, language ->
Python)
```

```
scala> val repo2 = DBObject(fields.toList)
repo2: dDBObject = { "name" : "contactpp" , "id" : 20448325, "language" :
"Python" }
```

The `DBObject` class provides many of the same methods as a map. For instance, we can address individual fields:

```
scala> repo1("name")
AnyRef = scikit-monaco
```

We can construct a new object by adding a field to an existing object:

```
scala> repo1 + ("fork" -> true)
mutable.Map[String,Any] = { "name" : "scikit-monaco" , "id" : 14821551,
"language" : "python", "fork" : true }
```

Note the return type: `mutable.Map[String,Any]`. Rather than implementing methods such as `+` directly, Casbah adds them to `DBObject` by providing an implicit conversion to and from `mutable.Map`.

New `DBObject` instances can also be created by concatenating two existing instances:

```
scala> repo1 ++ DBObject(
  "locs" -> 6342,
  "description" -> "Python library for Monte Carlo integration"
)
DBObject = { "name" : "scikit-monaco" , "id" : 14821551, "language" :
"Python", "locs" : 6342 , "description" : "Python library for Monte Carlo
integration" }
```

`DBObject` instances can then be inserted into a collection using the `+=` operator. Let's insert our first document into the `user` collection:

```
scala> val userDocument = DBObject(
  "login" -> "pbugnion",
  "github_id" -> 1392879,
  "repos" -> List(repo1, repo2)
)
```

```
userDocument: DBObject = { "login" : "pbugnion" , ... }

scala> val coll = MongoClient("github")("users")
coll: com.mongodb.casbah.MongoCollection = users

scala> coll += userDocument
com.mongodb.casbah.TypeImports.WriteResult = WriteResult{, n=0,
updateOfExisting=false, upsertedId=null}
```

A database containing a single document is a bit boring, so let's add a few more documents queried directly from the GitHub API. You learned how to query the GitHub API in the previous chapter, so we won't dwell on how to do this here.

In the code examples for this chapter, we have provided a class called `GitHubUserIterator` that queries the GitHub API (specifically the `/users` endpoint) for user documents, converts them to a case class, and offers them as an iterator. You will find the class in the code examples for this chapter (available on GitHub at <https://github.com/pbugnion/s4ds/tree/master/chap08>) in the `GitHubUserIterator.scala` file. The easiest way to have access to the class is to open an SBT console in the directory of the code examples for this chapter. The API then fetches users in increasing order of their login ID:

```
scala> val it = new GitHubUserIterator
it: GitHubUserIterator = non-empty iterator

scala> it.next // Fetch the first user
User = User(mojombo,1,List(Repo(...
```

`GitHubUserIterator` returns instances of the `User` case class, defined as follows:

```
// User.scala
case class User(login:String, id:Long, repos>List[Repo])

// Repo.scala
case class Repo(name:String, id:Long, language:String)
```

Let's write a short program to fetch 500 users and insert them into the MongoDB database. We will need to authenticate with the GitHub API to retrieve these users. The constructor for `GitHubUserIterator` takes the GitHub OAuth token as an optional argument. We will inject the token through the environment, as we did in the previous chapter.

We first give the entire code listing before breaking it down – if you are typing this out, you will need to copy `GitHubUserIterator.scala` from the code examples for this chapter to the directory in which you are running this to access the `GitHubUserIterator` class. The class relies on `scalaj-http` and `json4s`, so either copy the `build.sbt` file from the code examples or specify those packages as dependencies in your `build.sbt` file.

```
// InsertUsers.scala

import com.mongodb.casbah.Imports._

object InsertUsers {

  /** Function for reading GitHub token from environment. */
  lazy val token:Option[String] = sys.env.get("GHTOKEN") orElse {
    println("No token found: continuing without authentication")
    None
  }

  /** Transform a Repo instance to a DBObject */
  def repoToDBObject(repo:Repo):DBObject = DBObject(
    "github_id" -> repo.id,
    "name" -> repo.name,
    "language" -> repo.language
  )

  /** Transform a User instance to a DBObject */
  def userToDBObject(user:User):DBObject = DBObject(
    "github_id" -> user.id,
    "login" -> user.login,
    "repos" -> user.repos.map(repoToDBObject)
  )

  /** Insert a list of users into a collection. */
  def insertUsers(coll:MongoCollection)(users:Iterable[User]) {
    users.foreach { user => coll += userToDBObject(user) }
  }

  /** Fetch users from GitHub and passes them to `inserter` */
  def ingestUsers(nusers:Int)(inserter:Iterable[User] => Unit) {
    val it = new GitHubUserIterator(token)
    val users = it.take(nusers).toList
    inserter(users)
  }
}
```



```
    }

    def main(args:Array[String]) {
      val coll = MongoClient("github")("users")
      val nusers = 500
      coll.dropCollection()
      val inserter = insertUsers(coll)_
      ingestUsers(inserter)(nusers)
    }
  }
}
```

Before diving into the details of how this program works, let's run it through SBT. You will want to query the API with authentication to avoid hitting the rate limit. Recall that we need to set the `GHTOKEN` environment variable:

```
$ GHTOKEN="e83638..." sbt
$ runMain InsertUsers
```

The program will take about five minutes to run (depending on your Internet connection). To verify that the program works, we can query the number of documents in the `users` collection of the `github` database:

```
$ mongo github --quiet --eval "db.users.count()"
500
```

Let's break the code down. We first load the OAuth token to authenticate with the GitHub API. The token is stored as an environment variable, `GHTOKEN`. The `token` variable is a lazy `val`, so the token is loaded only when we formulate the first request to the API. We have already used this pattern in *Chapter 7, Web APIs*.

We then define two methods to transform from classes in the domain model to `DBObject` instances:

```
def repoToDBObject(repo:Repo):DBObject = ...
def userToDBObject(user:User):DBObject = ...
```

Armed with these two methods, we can add users to our MongoDB collection easily:

```
def insertUsers(coll:MongoCollection)(users:Iterable[User]) {
  users.foreach { user => coll += userToDBObject(user) }
}
```

We used currying to split the arguments of `insertUsers`. This lets us use `insertUsers` as a function factory:

```
val inserter = insertUsers(coll)_
```

This creates a new method, `inserter`, with signature `Iterable[User] => Unit` that inserts users into `coll`. To see how this might come in useful, let's write a function to wrap the whole data ingestion process. This is how a first attempt at this function could look:

```
def ingestUsers(nusers:Int)(inserter:Iterable[User] => Unit) {
  val it = new GitHubUserIterator(token)
  val users = it.take(nusers).toList
  inserter(users)
}
```

Notice how `ingestUsers` takes a method that specifies how the list of users is inserted into the database as its second argument. This function encapsulates the entire code specific to insertion into a MongoDB collection. If we decide, at some later date, that we hate MongoDB and must insert the documents into a SQL database or write them to a flat file, all we need to do is pass a different `inserter` function to `ingestUsers`. The rest of the code remains the same. This demonstrates the increased flexibility afforded by using higher-order functions: we can easily build a framework and let the client code plug in the components that it needs.

The `ingestUsers` method, as defined previously, has one problem: if the `nusers` value is large, it will consume a lot of memory in constructing the entire list of users. A better solution would be to break it down into batches: we fetch a batch of users from the API, insert them into the database, and move on to the next batch. This allows us to control memory usage by changing the batch size. It is also more fault tolerant: if the program crashes, we can just restart from the last successfully inserted batch.

The `.grouped` method, available on all iterables, is useful for batching. It returns an iterator over fragments of the original iterable:

```
scala> val it = (0 to 10)
it: Range.Inclusive = Range(0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10)

scala> it.grouped(3).foreach { println } // In batches of 3
Vector(0, 1, 2)
Vector(3, 4, 5)
Vector(6, 7, 8)
Vector(9, 10)
```

Let's rewrite our `ingestUsers` method to use batches. We will also add a progress report after each batch in order to give the user some feedback:

```
/** Fetch users from GitHub and pass them to `inserter` */
def ingestUsers(nusers:Int)(inserter:Iterable[User] => Unit) {
```

```
val batchSize = 100
val it = new GitHubUserIterator(token)
print("Inserted #users: ")
it.take(nusers).grouped(batchSize).zipWithIndex.foreach {
  case (users, batchNumber) =>
    print(s"${batchNumber*batchSize} ")
    inserter(users)
}
println()
}
```

Let's look at the highlighted line more closely. We start from the user iterator, `it`. We then take the first `nusers`. This returns an `Iterator[User]` that, instead of happily churning through every user in the GitHub database, will terminate after `nusers`. We then group this iterator into batches of 100 users. The `.grouped` method returns `Iterator[Iterator[User]]`. We then zip each batch with its index so that we know which batch we are currently processing (we use this in the `print` statement). The `.zipWithIndex` method returns `Iterator[(Iterator[User], Int)]`. We unpack this tuple in the loop using a case statement that binds `users` to `Iterator[User]` and `batchNumber` to the index. Let's run this through SBT:

```
$ GHOKEN="2502761..." sbt
> runMain InsertUsers
[info] Running InsertUsers
Inserted #users: 0 100 200 300 400
[success] Total time: 215 s, completed 01-Nov-2015 18:44:30
```

Extracting objects from the database

We now have a database populated with a few users. Let's query this database from the REPL:

```
scala> import com.mongodb.casbah.Imports._
import com.mongodb.casbah.Imports._

scala> val collection = MongoClient("github")("users")
MongoCollection = users

scala> val maybeUser = collection.findOne
Option[collection.T] = Some({ "_id" : { "$oid" :
"562e922546f953739c43df02"} , "github_id" : 1 , "login" : "mojombo" ,
"repos" : ...
```

The `findOne` method returns a single `DBObject` object wrapped in an option, unless the collection is empty, in which case it returns `None`. We must therefore use the `get` method to extract the object:

```
scala> val user = maybeUser.get
collection.T = { "_id" : { "$oid" : "562e922546f953739c43df02" } ,
"github_id" : 1 , "login" : "mojombo" , "repos" : ...
```

As you learned earlier in this chapter, `DBObject` is a map-like object with keys of type `String` and values of type `AnyRef`:

```
scala> user("login")
AnyRef =mojombo
```

In general, we want to restore compile-time type information as early as possible when importing objects from the database: we do not want to pass `AnyRefs` around when we can be more specific. We can use the `getAs` method to extract a field and cast it to a specific type:

```
scala> user.getAs[String]("login")
Option[String] = Some(mojombo)
```

If the field is missing in the document or if the value cannot be cast, `getAs` will return `None`:

```
scala> user.getAs[Int]("login")
Option[Int] = None
```

The astute reader may note that the interface provided by `getAs[T]` is similar to the `read[T]` method that we defined on a JDBC result set in *Chapter 5, Scala and SQL through JDBC*.

If `getAs` fails (for instance, because the field is missing), we can use the `orElse` partial function to recover:

```
scala> val loginName = user.getAs[String]("login") orElse {
  println("No login field found. Falling back to 'name'")
  user.getAs[String]("name")
}
loginName: Option[String] = Some(mojombo)
```

The `getAsOrElse` method allows us to substitute a default value if the cast fails:

```
scala> user.getAsOrElse[Int]("id", 5)
Int = 1392879
```

Note that we can also use `getAsOrElse` to throw an exception:

```
scala> user.getAsOrElse[String]("name",
  throw new IllegalArgumentException(
    "Missing value for name")
)
java.lang.IllegalArgumentException: Missing value for name
...
```

Arrays embedded in documents can be cast to `List[T]` objects, where `T` is the type of elements in the array:

```
scala> user.getAsOrElse[List[DBObject]]("repos",
  List.empty[DBObject])
List[DBObject] = List({ "github_id" : 26899533 , "name" :
"30daysoflaptops.github.io" ...
```

Retrieving a single document at a time is not very useful. To retrieve all the documents in a collection, use the `.find` method:

```
scala> val userIterator = collection.find()
userIterator: collection.CursorType = non-empty iterator
```

This returns an iterator of `DBObject`s. To actually fetch the documents from the database, you need to materialize the iterator by transforming it into a collection, using, for instance, `.toList`:

```
scala> val userList = userIterator.toList
List[DBObject] = List({ "_id" : { "$oid": ...
```

Let's bring all of this together. We will write a toy program that prints the average number of repositories per user in our collection. The code works by fetching every document in the collection, extracting the number of repositories from each document, and then averaging over these:

```
// RepoNumber.scala

import com.mongodb.casbah.Imports._

object RepoNumber {

  /** Extract the number of repos from a DBObject
   * representing a user.
   */
  def extractNumber(obj:DBObject):Option[Int] = {
```

```
    val repos = obj.getAs[List[DBObject]]("repos") orElse {
      println("Could not find or parse 'repos' field")
      None
    }
    repos.map { _.size }
  }

val collection = MongoClient().("github").("users")

def main(args:Array[String]) {
  val userIterator = collection.find()

  // Convert from documents to Option[Int]
  val repoNumbers = userIterator.map { extractNumber }

  // Convert from Option[Int] to Int
  val wellFormattedNumbers = repoNumbers.collect {
    case Some(v) => v
  }.toList

  // Calculate summary statistics
  val sum = wellFormattedNumbers.reduce { _ + _ }
  val count = wellFormattedNumbers.size

  if (count == 0) {
    println("No repos found")
  }
  else {
    val mean = sum.toDouble / count.toDouble
    println(s"Total number of users with repos: $count")
    println(s"Total number of repos: $sum")
    println(s"Mean number of repos: $mean")
  }
}
}
```

Let's run this through SBT:

```
> runMain RepoNumber
Total number of users with repos: 500
Total number of repos: 9649
Mean number of repos: 19.298
```

The code starts with the `extractNumber` function, which extracts the number of repositories from each `DBObject`. The return value is `None` if the document does not contain the `repos` field.

The main body of the code starts by creating an iterator over `DBObjects` in the collection. This iterator is then mapped through the `extractNumber` function, which transforms it into an iterator of `Option[Int]`. We then run `.collect` on this iterator to collect all the values that are not `None`, converting from `Option[Int]` to `Int` in the process. Only then do we materialize the iterator to a list using `.toList`. The resulting list, `wellFormattedNumbers`, has the `List[Int]` type. We then just take the mean of this list and print it to screen.

Note that, besides the `extractNumber` function, none of this program deals with Casbah-specific types: the iterator returned by `.find()` is just a Scala iterator. This makes Casbah straightforward to use: the only data type that you need to familiarize yourself with is `DBObject` (compare this with JDBC's `ResultSet`, which we had to explicitly wrap in a stream, for instance).

Complex queries

We now know how to convert `DBObject` instances to custom Scala classes. In this section, you will learn how to construct queries that only return a subset of the documents in the collection.

In the previous section, you learned to retrieve all the documents in a collection as follows:

```
scala> val objs = collection.find().toList
List[DBObject] = List({ "_id" : { "$oid" : "56365cec46f9534fae8ffd7f" }
, ...
```

The `collection.find()` method returns an iterator over all the documents in the collection. By calling `.toList` on this iterator, we materialize it to a list.

We can customize which documents are returned by passing a query document to the `.find` method. For instance, we can retrieve documents for a specific login name:

```
scala> val query = DBObject("login" -> "mojombo")
query: DBObject = { "login" : "mojombo" }

scala> val objs = collection.find(query).toList
List[DBObject] = List({ "_id" : { "$oid" : "562e922546f953739c43df02" } ,
"login" : "mojombo", ...
```

MongoDB queries are expressed as `DBObject` instances. Keys in the `DBObject` correspond to fields in the collection's documents, and the values are expressions controlling the allowed values of this field. Thus, `DBObject("login" -> "mojombo")` will select all the documents for which the `login` field is `mojombo`. Using a `DBObject` instance to represent a query might seem a little obscure, but it will quickly make sense if you read the MongoDB documentation (<https://docs.mongodb.org/manual/core/crud-introduction/>): queries are themselves just JSON objects in MongoDB. Thus, the fact that the query in Casbah is represented as a `DBObject` is consistent with other MongoDB client implementations. It also allows someone familiar with MongoDB to start writing Casbah queries in no time.

MongoDB supports more complex queries. For instance, to query everyone with `"github_id"` between 20 and 30, we can write the following query:

```
scala> val query = DBObject("github_id" ->
  DBObject("$gte" -> 20, "$lt" -> 30))
query: DBObject = { "github_id" : { "$gte" : 20 , "$lt" : 30}}

scala> collection.find(query).toList
List[com.mongodb.casbah.Imports.DBObject] = List({ "_id" : { "$oid" :
"562e922546f953739c43df0f"} , "github_id" : 23 , "login" : "takeo" , ...
```

We limit the range of values that `github_id` can take with `DBObject("$gte" -> 20, "$lt" -> 30)`. The `"$gte"` string indicates that `github_id` must be greater or equal to 20. Similarly, `"$lt"` denotes the *less than* operator. To get a full list of operators that you can use when querying, consult the MongoDB reference documentation (<http://docs.mongodb.org/manual/reference/operator/query/>).

So far, we have only looked at queries on top-level fields. Casbah also lets us query fields in subdocuments and arrays using the *dot* notation. In the context of array values, this will return all the documents for which at least one value in the array matches the query. For instance, to retrieve all users who have a repository whose main language is Scala:

```
scala> val query = DBObject("repos.language" -> "Scala")
query: DBObject = { "repos.language" : "Scala"}

scala> collection.find(query).toList
List[DBObject] = List({ "_id" : { "$oid" : "5635da4446f953234ca634df"},
"login" : "kevinclark"...
```


Casbah query DSL

Using `DBObject` instances to express queries can be very verbose and somewhat difficult to read. Casbah provides a DSL to express queries much more succinctly. For instance, to get all the documents with the `github_id` field between 20 and 30, we would write the following:

```
scala> collection.find("github_id" $gte 20 $lt 30).toList
List[com.mongodb.casbah.Imports.DBObject] = List({ "_id" : { "$oid" :
"562e922546f953739c43df0f" } , "github_id" : 23 , "login" : "takeo" ,
"repos" : ...
```

The operators provided by the DSL will automatically construct `DBObject` instances. Using the DSL operators as much as possible generally leads to much more readable and maintainable code.

Going into the full details of the query DSL is beyond the scope of this chapter. You should find it quite easy to use. For a full list of the operators supported by the DSL, refer to the Casbah documentation at http://mongodb.github.io/casbah/3.0/reference/query_dsl/. We summarize the most important operators here:

Operators	Description
"login" \$eq "mojombo"	This selects documents whose login field is exactlymojombo
"login" \$ne "mojombo"	This selects documents whose login field is notmojombo
"github_id" \$gt 1 \$lt 20	This selects documents with github_id greater than 1 and less than 20
"github_id" \$gte 1 \$lte 20	This selects documents with github_id greater than or equal to 1 and less than or equal to 20
"login" \$in ("mojombo", "defunkt")	The login field is eithermojombo or defunkt
"login" \$nin ("mojombo", "defunkt")	The login field is notmojombo or defunkt
"login" \$regex "^moj.*"	The login field matches the particular regular expression
"login" \$exists true	The login field exists
\$or("login" \$eq "mojombo", "github_id" \$gte 22)	Either the login field ismojombo or the github_id field is greater or equal to 22
\$and("login" \$eq "mojombo", "github_id" \$gte 22)	The login field ismojombo and the github_id field is greater or equal to 22

We can also use the *dot* notation to query arrays and subdocuments. For instance, the following query will count all the users who have a repository in Scala:

```
scala> collection.find("repos.language" $eq "Scala").size
Int = 30
```

Custom type serialization

So far, we have only tried to serialize and deserialize simple types. What if we wanted to decode the language field in the repository array to an enumeration rather than a string? We might, for instance, define the following enumeration:

```
scala> object Language extends Enumeration {
  val Scala, Java, JavaScript = Value
}
defined object Language
```

Casbah lets us define custom serializers tied to a specific Scala type: we can inform Casbah that whenever it encounters an instance of the `Language.Value` type in a `DBObject`, the instance should be passed through a custom transformer that will convert it to, for instance, a string, before writing it to the database.

To define a custom serializer, we need to define a class that extends the `Transformer` trait. This trait exposes a single method, `transform(o:AnyRef):AnyRef`. Let's define a `LanguageTransformer` trait that transforms from `Language.Value` to `String`:

```
scala> import org.bson.{BSON, Transformer}
import org.bson.{BSON, Transformer}

scala> trait LanguageTransformer extends Transformer {
  def transform(o:AnyRef):AnyRef = o match {
    case l:Language.Value => l.toString
    case _ => o
  }
}
defined trait LanguageTransformer
```

We now need to register the trait to be used whenever an instance of type `Language.Value` needs to be decoded. We can do this using the `addEncodingHook` method:

```
scala> BSON.addEncodingHook(
  classOf[Language.Value], new LanguageTransformer {})
```

We can now construct `DBObject` instances containing values of the `Language` enumeration:

```
scala> val repoObj = DBObject(
  "github_id" -> 1234L,
  "language" -> Language.Scala
)
repoObj: DBObject = { "github_id" : 1234 , "language" : "Scala" }
```

What about the reverse? How do we tell Casbah to read the "language" field as `Language.Value`? This is not possible with custom deserializers: "Scala" is now stored as a string in the database. Thus, when it comes to deserialization, "Scala" is no different from, say, "mojombo". We thus lose type information when "Scala" is serialized.

Thus, while custom encoding hooks are useful for serialization, they are much less useful when deserializing. A cleaner, more consistent alternative to customize both serialization and deserialization is to use *type classes*. We have already covered how to use these extensively in *Chapter 5, Scala and SQL through JDBC*, in the context of serializing to and from SQL. The procedure here would be very similar:

1. Define a `MongoReader [T]` type class with a `read (v:Any):T` method.
2. Define concrete implementations of `MongoReader` in the `MongoReader` companion object for all types of interest, such as `String`, `Language.Value`.
3. Enrich `DBObject` with a `read [T:MongoReader]` method using the *pimp my library* pattern.

For instance, the implementation of `MongoReader` for `Language.Value` would be as follows:

```
implicit object LanguageReader extends MongoReader [Language.Value] {
  def read (v:Any):Language.Value = v match {
    case s:String => Language.withName (s)
  }
}
```

We could then do the same with a `MongoWriter` type class. Using type classes is an idiomatic and extensible approach to custom serialization and deserialization.

We provide a complete example of type classes in the code examples associated with this chapter (in the `typeclass` directory).

Beyond Casbah

We have only considered Casbah in this chapter. There are, however, other drivers for MongoDB.

ReactiveMongo is a driver that focusses on asynchronous read and writes to and from the database. All queries return a future, forcing asynchronous behavior. This fits in well with data streams or web applications.

Salat sits at a higher level than Casbah and aims to provide easy serialization and deserialization of case classes.

A full list of drivers is available at <https://docs.mongodb.org/ecosystem/drivers/scala/>.

Summary

In this chapter, you learned how to interact with a MongoDB database. By weaving the constructs learned in the previous chapter – pulling information from a web API – with those learned in this chapter, we can now build a concurrent, reactive program for data ingestion.

In the next chapter, you will learn to build distributed, concurrent structures with greater flexibility using Akka actors.

References

MongoDB: The Definitive Guide, by Kristina Chodorow, is a good introduction to MongoDB. It does not cover interacting with MongoDB in Scala at all, but Casbah is intuitive enough for anyone familiar with MongoDB.

Similarly, the MongoDB documentation (<https://docs.mongodb.org/manual/>) provides an in-depth discussion of MongoDB.

Casbah itself is well-documented (<http://mongodb.github.io/casbah/3.0/>). There is a *Getting Started* guide that is somewhat similar to this chapter and a complete reference guide that will fill in the gaps left by this chapter.

This gist, <https://gist.github.com/switzer/4218526>, implements type classes to serialize and deserialize objects in the domain model to `DBObject`s. The premise is a little different from the suggested usage of type classes in this chapter: we are converting from Scala types to `AnyRef` to be used as values in `DBObject`. However, the two approaches are complementary: one could imagine a set of type classes to convert from `User` or `Repo` to `DBObject` and another to convert from `Language.Value` to `AnyRef`.

9

Concurrency with Akka

Much of this book focusses on taking advantage of multicore and distributed architectures. In *Chapter 4, Parallel Collections and Futures*, you learned how to use parallel collections to distribute batch processing problems over several threads and how to perform asynchronous computations using futures. In *Chapter 7, Web APIs*, we applied this knowledge to query the GitHub API with several concurrent threads.

Concurrency abstractions such as futures and parallel collections simplify the enormous complexity of concurrent programming by limiting what you can do. Parallel collections, for instance, force you to phrase your parallelization problem as a sequence of pure functions on collections.

Actors offer a different way of thinking about concurrency. Actors are very good at encapsulating *state*. Managing state shared between different threads of execution is probably the most challenging part of developing concurrent applications, and, as we will discover in this chapter, actors make it manageable.

GitHub follower graph

In the previous two chapters, we explored the GitHub API, learning how to query the API and parse the results using *json-4s*.

Let's imagine that we want to extract the GitHub follower graph: we want a program that will start from a particular user, extract this user followers, and then extract their followers until we tell it to stop. The catch is that we don't know ahead of time what URLs we need to fetch: when we download the login names of a particular user's followers, we need to verify whether we have fetched these users previously. If not, we add them to a queue of users whose followers we need to fetch. Algorithm aficionados might recognize this as *breadth-first search*.

Let's outline how we might write this in a single-threaded way. The central components are a set of visited users and queue of future users to visit:

```
val seedUser = "odersky" // the origin of the network

// Users whose URLs need to be fetched
val queue = mutable.Queue(seedUser)

// set of users that we have already fetched
// (to avoid re-fetching them)
val fetchedUsers = mutable.Set.empty[String]

while (queue.nonEmpty) {
  val user = queue.dequeue
  if (!fetchedUsers(user)) {
    val followers = fetchFollowersForUser(user)
    followers foreach { follower =>
      // add the follower to queue of people whose
      // followers we want to find.
      queue += follower
    }
    fetchedUsers += user
  }
}
```

Here, the `fetchFollowersForUser` method has signature `String => Iterable[String]` and is responsible for taking a login name, transforming it into a URL in the GitHub API, querying the API, and extracting a list of followers from the response. We will not implement it here, but you can find a complete example in the `chap09/single_threaded` directory of the code examples for this book (<https://github.com/pbugnion/s4ds>). You should have all the tools to implement this yourself if you have read *Chapter 7, Web APIs*.

While this works, it will be painfully slow. The bottleneck is clearly the `fetchFollowersForUser` method, in particular, the part that queries the GitHub API. This program does not lend itself to the concurrency constructs that we have seen earlier in the book because we need to protect the state of the program, embodied by the user queue and set of fetched users, from race conditions. Note that it is not just a matter of making the queue and set thread-safe. We must also keep the two synchronized.

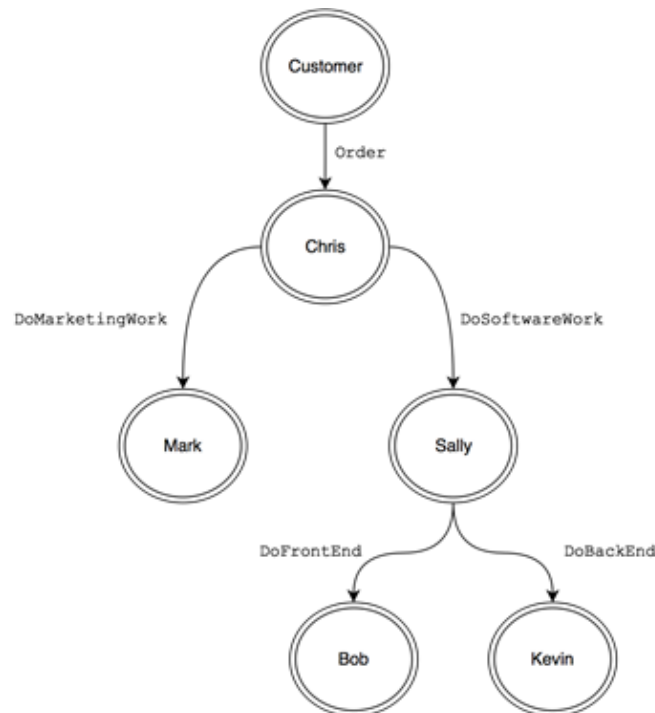
Actors offer an elegant abstraction to encapsulate state. They are lightweight objects that each perform a single task (possibly repeatedly) and communicate with each other by passing messages. The internal state of an actor can only be changed from within the actor itself. Importantly, actors only process messages one at a time, effectively preventing race conditions.

By hiding program state inside actors, we can reason about the program more effectively: if a bug is introduced that makes this state inconsistent, the culprit will be localized entirely in that actor.

Actors as people

In the previous section, you learned that an actor encapsulates state, interacting with the outside world through messages. Actors make concurrent programming more intuitive because they behave a little bit like an ideal workforce.

Let's think of an actor system representing a start-up with five people. There's Chris, the CEO, and Mark, who's in charge of marketing. Then there's Sally, who heads the engineering team. Sally has two minions, Bob and Kevin. As every good organization needs an organizational chart, refer to the following diagram:



Let's say that Chris receives an order. He will look at the order, decide whether it is something that he can process himself, and if not, he will forward it to Mark or Sally. Let's assume that the order asks for a small program so Bob forwards the order to Sally. Sally is very busy working on a backlog of orders so she cannot process the order message straightaway, and it will just sit in her mailbox for a short while. When she finally gets round to processing the order, she might decide to split the order into several parts, some of which she will give to Kevin and some to Bob.

As Bob and Kevin complete items, they will send messages back to Sally to inform her. When every part of the order is fulfilled, Sally will aggregate the parts together and message either the customer directly or Chris with the results.

The task of keeping track of which jobs must be fulfilled to complete the order rests with Sally. When she receives messages from Bob and Kevin, she must update her list of tasks in progress and check whether every task related to this order is complete. This sort of coordination would be more challenging with traditional *synchronize* blocks: every access to the list of tasks in progress and to the list of completed tasks would need to be synchronized. By embedding this logic in Sally, who can only process a single message at a time, we can be sure that there will not be race conditions.

Our start-up works well because each person is responsible for doing a single thing: Chris either delegates to Mark or Sally, Sally breaks up orders into several parts and assigns them to Bob and Kevin, and Bob and Kevin fulfill each part. You might think "hold on, all the logic is embedded in Bob and Kevin, the employees at the bottom of the ladder who do all the actual work". Actors, unlike employees, are cheap, so if the logic embedded in an actor gets too complicated, it is easy to introduce additional layers of delegation until tasks get simple enough.

The employees in our start-up refuse to multitask. When they get a piece of work, they process it completely and then move on to the next task. This means that they cannot get muddled by the complexities of multitasking. Actors, by processing a single message at a time, greatly reduce the scope for introducing concurrency errors such as race conditions.

More importantly, by offering an abstraction that programmers can intuitively understand – that of human workers – Akka makes reasoning about concurrency easier.

Hello world with Akka

Let's install Akka. We add it as a dependency to our `build.sbt` file:

```
scalaVersion := "2.11.7"

libraryDependencies += "com.typesafe.akka" %% "akka-actor" %
  "2.4.0"
```

We can now import Akka as follows:

```
import akka.actor._
```

For our first foray into the world of actors, we will build an actor that echoes every message it receives. The code examples for this section are in a directory called `chap09/hello_akka` in the sample code provided with this book (<https://github.com/pbugnion/s4ds>):

```
// EchoActor.scala
import akka.actor._

class EchoActor extends Actor with ActorLogging {
  def receive = {
    case msg:String =>
      Thread.sleep(500)
      log.info(s"Received '$msg'")
  }
}
```

Let's pick this example apart, starting with the constructor. Our actor class must extend `Actor`. We also add `ActorLogging`, a utility trait that adds the `log` attribute.

The `Echo` actor exposes a single method, `receive`. This is the actor's only way of communicating with the external world. To be useful, all actors must expose a `receive` method. The `receive` method is a partial function, typically implemented with multiple `case` statements. When an actor starts processing a message, it will match it against every `case` statement until it finds one that matches. It will then execute the corresponding block.

Our echo actor accepts a single type of message, a plain string. When this message gets processed, the actor waits for half a second and then echoes the message to the log file.

Let's instantiate a couple of Echo actors and send them messages:

```
// HelloAkka.scala

import akka.actor._

object HelloAkka extends App {

  // We need an actor system before we can
  // instantiate actors
  val system = ActorSystem("HelloActors")

  // instantiate our two actors
  val echo1 = system.actorOf(Props[EchoActor], name="echo1")
  val echo2 = system.actorOf(Props[EchoActor], name="echo2")

  // Send them messages. We do this using the "!" operator
  echo1 ! "hello echo1"
  echo2 ! "hello echo2"
  echo1 ! "bye bye"

  // Give the actors time to process their messages,
  // then shut the system down to terminate the program
  Thread.sleep(500)
  system.shutdown
}
```

Running this gives us the following output:

```
[INFO] [07/19/2015 17:15:23.954] [HelloActor-akka.actor.default-
dispatcher-2] [akka://HelloActor/user/echo1] Received 'hello echo1'
[INFO] [07/19/2015 17:15:23.954] [HelloActor-akka.actor.default-
dispatcher-3] [akka://HelloActor/user/echo2] Received 'hello echo2'
[INFO] [07/19/2015 17:15:24.955] [HelloActor-akka.actor.default-
dispatcher-2] [akka://HelloActor/user/echo1] Received 'bye bye'
```

Note that the `echo1` and `echo2` actors are clearly acting concurrently: `hello echo1` and `hello echo2` are logged at the same time. The second message, passed to `echo1`, gets processed after the actor has finished processing `hello echo1`.

There are a few different things to note:

- To start instantiating actors, we must first create an actor system. There is typically a single actor system per application.
- The way in which we instantiate actors looks a little strange. Instead of calling the constructor, we create an actor properties object, `Props [T]`. We then ask the actor system to create an actor with these properties. In fact, we never instantiate actors with `new`: they are either created by calling the `actorOf` method in the actor system or a similar method from within another actor (more on this later).

We never call an actor's methods from outside that actor. The only way to interact with the actor is to send messages to it. We do this using the *tell* operator, `!`. There is thus no way to mess with an actor's internals from outside that actor (or at least, Akka makes it difficult to mess with an actor's internals).

Case classes as messages

In our "hello world" example, we constructed an actor that is expected to receive a string as message. **Any object can be passed as a message, provided it is immutable.** It is very common to use case classes to represent messages. This is better than using strings because of the additional type safety: the compiler will catch a typo in a case class but not in a string.

Let's rewrite our `EchoActor` to accept instances of case classes as messages. We will make it accept two different messages: `EchoMessage (message)` and `EchoHello`, which just echoes a default message. The examples for this section and the next are in the `chap09/hello_akka_case_classes` directory in the sample code provided with this book (<https://github.com/pbugnion/s4ds>).

A common Akka pattern is to define the messages that an actor can receive in the actor's companion object:

```
// EchoActor.scala

object EchoActor {
  case object EchoHello
  case class EchoMessage(msg:String)
}
```

Let's change the actor definition to accept these messages:

```
class EchoActor extends Actor with ActorLogging {
  import EchoActor._ // import the message definitions
  def receive = {
    case EchoHello => log.info("hello")
    case EchoMessage(s) => log.info(s)
  }
}
```

We can now send `EchoHello` and `EchoMessage` to our actors:

```
echo1 ! EchoActor.EchoHello
echo2 ! EchoActor.EchoMessage("We're learning Akka.")
```

Actor construction

Actor construction is a common source of difficulty for people new to Akka. Unlike (most) ordinary objects, you never instantiate actors explicitly. You would never write, for instance, `val echo = new EchoActor`. In fact, if you try this, Akka raises an exception.

Creating actors in Akka is a two-step process: you first create a `Props` object, which encapsulates the properties needed to construct an actor. The way to construct a `Props` object differs depending on whether the actor takes constructor arguments. If the constructor takes no arguments, we simply pass the actor class as a type parameter to `Props`:

```
val echoProps = Props[EchoActor]
```

If we have an actor whose constructor does take arguments, we must pass these as additional arguments when defining the `Props` object. Let's consider the following actor, for instance:

```
class TestActor(a:String, b:Int) extends Actor { ... }
```

We pass the constructor arguments to the `Props` object as follows:

```
val testProps = Props(classOf[TestActor], "hello", 2)
```

The `Props` instance just embodies the configuration for creating an actor. It does not actually create anything. To create an actor, we pass the `Props` instance to the `system.actorOf` method, defined on the `ActorSystem` instance:

```
val system = ActorSystem("HelloActors")
val echo1 = system.actorOf(echoProps, name="hello-1")
```

The `name` parameter is optional but is useful for logging and error messages. The value returned by `.actorOf` is not the actor itself: it is a *reference* to the actor (it helps to think of it as an address that the actor lives at) and has the `ActorRef` type. `ActorRef` is immutable, but it can be serialized and duplicated without affecting the underlying actor.

There is another way to create actors besides calling `actorOf` on the actor system: each actor exposes a `context.actorOf` method that takes a `Props` instance as its argument. The context is only accessible from within the actor:

```
class TestParentActor extends Actor {
  val echoChild = context.actorOf(echoProps, name="hello-child")
  ...
}
```

The difference between an actor created from the actor system and an actor created from another actor's context lies in the actor hierarchy: each actor has a parent. Any actor created within another actor's context will have that actor as its parent. An actor created by the actor system has a predefined actor, called the *user guardian*, as its parent. We will understand the importance of the actor hierarchy when we study the actor lifecycle at the end of this chapter.

A very common idiom is to define a `props` method in an actor's companion object that acts as a factory method for `Props` instances for that actor. Let's amend the `EchoActor` companion object:

```
object EchoActor {
  def props:Props = Props[EchoActor]

  // message case class definitions here
}
```

We can then instantiate the actor as follows:

```
val echoActor = system.actorOf(EchoActor.props)
```

Anatomy of an actor

Before diving into a full-blown application, let's look at the different components of the actor framework and how they fit together:

- **Mailbox:** A mailbox is basically a queue. Each actor has its own mailbox. When you send a message to an actor, the message lands in its mailbox and does nothing until the actor takes it off the queue and passes it through its `receive` method.

- **Messages:** Messages make synchronization between actors possible. A message can have any type with the sole requirement that it should be immutable. In general, it is better to use case classes or case objects to gain the compiler's help in checking message types.
- **Actor reference:** When we create an actor using `val echo1 = system.actorOf(Props[EchoActor])`, `echo1` has type `ActorRef`. An `ActorRef` is a proxy for an actor and is what the rest of the world interacts with: when you send a message, you send it to the `ActorRef`, not to the actor directly. In fact, you can never obtain a handle to an actor directly in Akka. An actor can obtain an `ActorRef` for itself using the `.self` method.
- **Actor context:** Each actor has a `context` attribute through which you can access methods to create or access other actors and find information about the outside world. We have already seen how to create new actors with `context.actorOf(props)`. We can also obtain a reference to an actor's parent through `context.parent`. An actor can also stop another actor with `context.stop(actorRef)`, where `actorRef` is a reference to the actor that we want to stop.
- **Dispatcher:** The dispatcher is the machine that actually executes the code in an actor. The default dispatcher uses a fork/join thread pool. Akka lets us use different dispatchers for different actors. Tweaking the dispatcher can be useful to optimize the performance and give priority to certain actors. The dispatcher that an actor runs on is accessible through `context.dispatcher`. Dispatchers implement the `ExecutionContext` interface so they can be used to run futures.

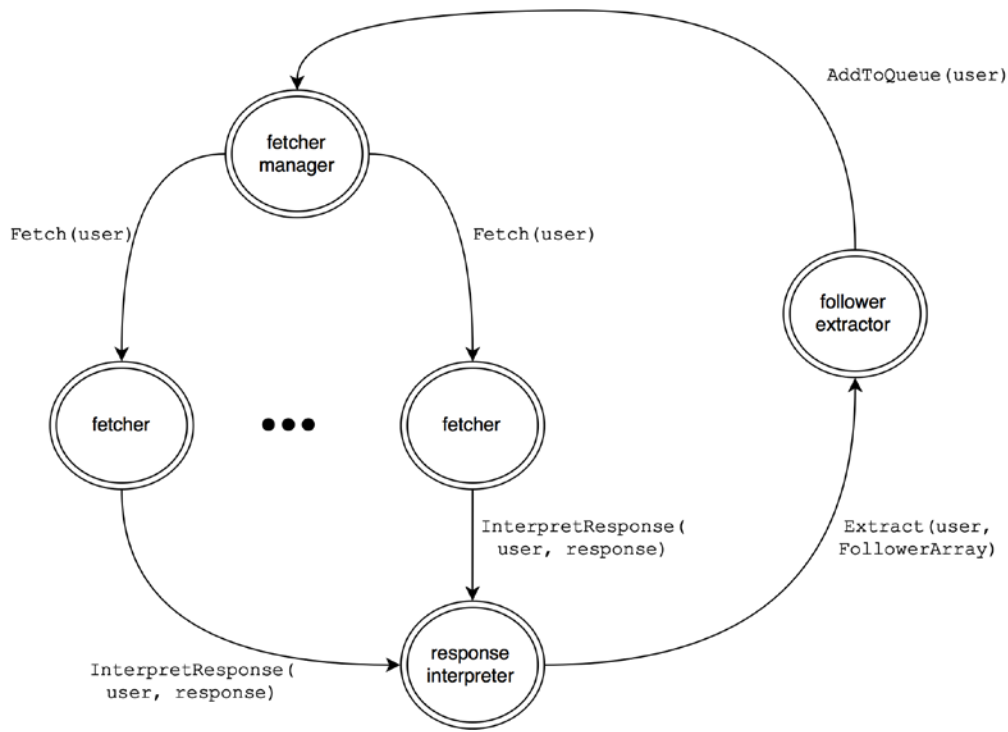
Follower network crawler

The end game for this chapter is to build a crawler to explore GitHub's follower graph. We have already outlined how we can do this in a single-threaded manner earlier in this chapter. Let's design an actor system to do this concurrently.

The moving parts in the code are the data structures managing which users have been fetched or are being fetched. These need to be encapsulated in an actor to avoid race conditions arising from multiple actors trying to change them concurrently. We will therefore create a *fetcher manager* actor whose job is to keep track of which users have been fetched and which users we are going to fetch next.

The part of the code that is likely to be a bottleneck is querying the GitHub API. We therefore want to be able to scale the number of workers doing this concurrently. We will create a pool of *fetchers*, actors responsible for querying the API for the followers of a particular user. Finally, we will create an actor whose responsibility is to interpret the API's response. This actor will forward its interpretation of the response to another actor who will extract the followers and give them to the fetcher manager.

This is what the architecture of the program will look like:



Actor system for our GitHub API crawler

Each actor in our program performs a single task: fetchers just query the GitHub API and the queue manager just distributes work to the fetchers. Akka best practice dictates giving actors as narrow an area of responsibility as possible. This enables better granularity when scaling out (for instance, by adding more fetcher actors, we just parallelize the bottleneck) and better resilience: if an actor fails, it will only affect his area of responsibility. We will explore actor failure later on in this chapter.

We will build the app in several steps, exploring the Akka toolkit as we write the program. Let's start with the `build.sbt` file. Besides Akka, we will mark `scalaj-http` and `json4s` as dependencies:

```
// build.sbt
scalaVersion := "2.11.7"

libraryDependencies += Seq(
  "org.json4s" %% "json4s-native" % "3.2.10",
  "org.scalaj" %% "scalaj-http" % "1.1.4",
  "com.typesafe.akka" %% "akka-actor" % "2.3.12"
)
```

Fetcher actors

The workhorse of our application is the fetcher, the actor responsible for fetching the follower details from GitHub. In the first instance, our actor will accept a single message, `Fetch(user)`. It will fetch the followers corresponding to `user` and log the response to screen. We will use the recipes developed in *Chapter 7, Web APIs*, to query the GitHub API with an OAuth token. We will inject the token through the actor constructor.

Let's start with the companion object. This will contain the definition of the `Fetch(user)` message and two factory methods to create the `Props` instances. You can find the code examples for this section in the `chap09/fetchers_alone` directory in the sample code provided with this book (<https://github.com/pbugnion/s4ds>):

```
// Fetcher.scala
import akka.actor._
import scalaj.http._
import scala.concurrent.Future

object Fetcher {
  // message definitions
  case class Fetch(login:String)

  // Props factory definitions
  def props(token:Option[String]):Props =
    Props(classOf[Fetcher], token)
  def props():Props = Props(classOf[Fetcher], None)
}
```

Let's now define the fetcher itself. We will wrap the call to the GitHub API in a future. This avoids a single slow request blocking the actor. When our actor receives a `Fetch` request, it wraps this request into a future, sends it off, and can then process the next message. Let's go ahead and implement our actor:

```
// Fetcher.scala
class Fetcher(val token:Option[String])
  extends Actor with ActorLogging {
  import Fetcher._ // import message definition

  // We will need an execution context for the future.
  // Recall that the dispatcher doubles up as execution
  // context.
  import context.dispatcher

  def receive = {
    case Fetch(login) => fetchUrl(login)
  }

  private def fetchUrl(login:String) {
    val unauthorizedRequest = Http(
      s"https://api.github.com/users/$login/followers")
    val authorizedRequest = token.map { t =>
      unauthorizedRequest.header("Authorization", s"token $t")
    }

    // Prepare the request: try to use the authorized request
    // if a token was given, and fall back on an unauthorized
    // request
    val request = authorizedRequest.getOrElse(unauthorizedRequest)

    // Fetch from github
    val response = Future { request.asString }
    response.onComplete { r =>
      log.info(s"Response from $login: $r")
    }
  }
}
```

Let's instantiate an actor system and four fetchers to check whether our actor is working as expected. We will read the GitHub token from the environment, as described in *Chapter 7, Web APIs*, then create four actors and ask each one to fetch the followers of a particular GitHub user. We wait five seconds for the requests to get completed, and then shut the system down:

```
// FetcherDemo.scala
import akka.actor._

object FetcherDemo extends App {
  import Fetcher._ // Import the messages

  val system = ActorSystem("fetchers")

  // Read the github token if present.
  val token = sys.env.get("GHTOKEN")

  val fetchers = (0 until 4).map { i =>
    system.actorOf(Fetcher.props(token))
  }

  fetchers(0) ! Fetch("odersky")
  fetchers(1) ! Fetch("derekwyatt")
  fetchers(2) ! Fetch("rkuhn")
  fetchers(3) ! Fetch("tototoshi")

  Thread.sleep(5000) // Wait for API calls to finish
  system.shutdown // Shut system down
}
```

Let's run the code through SBT:

```
$ GHTOKEN="2502761..." sbt run
[INFO] [11/08/2015 16:28:06.500] [fetchers-akka.actor.default-
dispatcher-2] [akka://fetchers/user/$d] Response from tototoshi: Success
(HttpResponse([{"login":"akr4","id":10892,"avatar_url":"https://avatars.
githubusercontent.com/u/10892?v=3","gravatar_id":""...)
```

Notice how we explicitly need to shut the actor system down using `system.shutdown`. The program hangs until the system is shut down. However, shutting down the system will stop all the actors, so we need to make sure that they have finished working. We do this by inserting a call to `Thread.sleep`.

Using `Thread.sleep` to wait until the API calls have finished to shut down the actor system is a little crude. A better approach could be to let the actors signal back to the system that they have completed their task. We will see examples of this pattern later when we implement the *fetcher manager* actor.

Akka includes a feature-rich *scheduler* to schedule events. We can use the scheduler to replace the call to `Thread.sleep` by scheduling a system shutdown five seconds in the future. This is preferable as the scheduler does not block the calling thread, unlike `Thread.sleep`. To use the scheduler, we need to import a global execution context and the duration module:

```
// FetcherDemoWithScheduler.scala

import scala.concurrent.ExecutionContext.Implicits.global
import scala.concurrent.duration._
```

We can then schedule a system shutdown by replacing our call to `Thread.sleep` with the following:

```
system.scheduler.scheduleOnce(5.seconds) { system.shutdown }
```

Besides `scheduleOnce`, the scheduler also exposes a `schedule` method that lets you schedule events to happen regularly (every two seconds, for instance). This is useful for heartbeat checks or monitoring systems. For more information, read the API documentation on the scheduler available at <http://doc.akka.io/docs/akka/snapshot/scala/scheduler.html>.

Note that we are actually cheating a little bit here by not fetching every follower. The response to the follower's query is actually paginated, so we would need to fetch several pages to fetch all the followers. Adding logic to the actor to do this is not terribly complicated. We will ignore this for now and assume that users are capped at 100 followers each.

Routing

In the previous example, we created four fetchers and dispatched messages to them, one after the other. We have a pool of identical actors among which we distribute tasks. Manually routing the messages to the right actor to maximize the utilization of our pool is painful and error-prone. Fortunately, Akka provides us with several routing strategies that we can use to distribute work among our pool of actors. Let's rewrite the previous example with automatic routing. You can find the code examples for this section in the `chap09/fetchers_routing` directory in the sample code provided with this book (<https://github.com/pbugnion/s4ds>). We will reuse the same definition of `Fetchers` and its companion object as we did in the previous section.

Let's start by importing the routing package:

```
// FetcherDemo.scala
import akka.routing._
```

A *router* is an actor that forwards the messages that it receives to its children. The easiest way to define a pool of actors is to tell Akka to create a router and pass it a `Props` object for its children. The router will then manage the creation of the workers directly. In our example (we will only comment on the parts that differ from the previous example in the text, but you can find the full code in the `fetchers_routing` directory with the examples for this chapter), we replace the custom `Fetcher` creation code with the following:

```
// FetcherDemo.scala

// Create a router with 4 workers of props Fetcher.props()
val router = system.actorOf(
  RoundRobinPool(4).props(Fetcher.props(token))
)
```

We can then send the `fetch` messages directly to the router. The router will route the messages to the children in a round-robin manner:

```
List("odersky", "derekwyatt", "rkuhn", "tototoshi").foreach {
  login => router ! Fetch(login)
}
```

We used a round-robin router in this example. Akka offers many different types of routers, including routers with dynamic pool size, to cater to different types of load balancing. Head over to the Akka documentation for a list of all the available routers, at <http://doc.akka.io/docs/akka/snapshot/scala/routing.html>.

Message passing between actors

Merely logging the API response is not very useful. To traverse the follower graph, we must perform the following:

- Check the return code of the response to make sure that the GitHub API was happy with our request
- Parse the response as JSON
- Extract the login names of the followers and, if we have not fetched them already, push them into the queue

You learned how to do all these things in *Chapter 7, Web APIs*, but not in the context of actors.

We could just add the additional processing steps to the `receive` method of our `Fetcher` actor: we could add further transformations to the API response by future composition. However, having actors do several different things, and possibly failing in several different ways, is an anti-pattern: when we learn about managing the actor life cycle, we will see that it becomes much more difficult to reason about our actor systems if the actors contain several bits of logic.

We will therefore use a pipeline of three different actors:

- The fetchers, which we have already encountered, are responsible just for fetching a URL from GitHub. They will fail if the URL is badly formatted or they cannot access the GitHub API.
- The response interpreter is responsible for taking the response from the GitHub API and parsing it to JSON. If it fails at any step, it will just log the error (in a real application, we might take different corrective actions depending on the type of failure). If it manages to extract JSON successfully, it will pass the JSON array to the follower extractor.
- The follower extractor will extract the followers from the JSON array and pass them on to the queue of users whose followers we need to fetch.

We have already built the fetchers, though we will need to modify them to forward the API response to the response interpreter rather than just logging it.

You can find the code examples for this section in the `chap09/all_workers` directory in the sample code provided with this book (<https://github.com/pbugnion/s4ds>). The first step is to modify the fetchers so that, instead of logging the response, they forward the response to the response interpreter. To be able to forward the response to the response interpreter, the fetchers will need a reference to this actor. We will just pass the reference to the response interpreter through the fetcher constructor, which is now:

```
// Fetcher.scala
class Fetcher(
  val token:Option[String],
  val responseInterpreter:ActorRef)
extends Actor with ActorLogging {
  ...
}
```

We must also modify the `Props` factory method in the companion object:

```
// Fetcher.scala
def props(
  token:Option[String], responseInterpreter:ActorRef)
:Props = Props(classOf[Fetcher], token, responseInterpreter)
```

We must also modify the `receive` method to forward the HTTP response to the interpreter rather than just logging it:

```
// Fetcher.scala
class Fetcher(...) extends Actor with ActorLogging {
  ...
  def receive = {
    case Fetch(login) => fetchFollowers(login)
  }

  private def fetchFollowers(login:String) {
    val unauthorizedRequest = Http(
      s"https://api.github.com/users/$login/followers")
    val authorizedRequest = token.map { t =>
      unauthorizedRequest.header("Authorization", s"token $t")
    }

    val request = authorizedRequest.getOrElse(unauthorizedRequest)
    val response = Future { request.asString }

    // Wrap the response in an InterpretResponse message and
    // forward it to the interpreter.
  }
}
```

```

        response.onComplete { r =>
            responseInterpreter !
                ResponseInterpreter.InterpretResponse(login, r)
        }
    }
}

```

The *response interpreter* takes the response, decides if it is valid, parses it to JSON, and forwards it to a follower extractor. The response interpreter will need a reference to the follower extractor, which we will pass in the constructor.

Let's start by defining the `ResponseInterpreter` companion. It will just contain the definition of the messages that the response interpreter can receive and a factory to create a `Props` object to help with instantiation:

```

// ResponseInterpreter.scala
import akka.actor._
import scala.util._

import scalaj.http._
import org.json4s._
import org.json4s.native.JsonMethods._

object ResponseInterpreter {

    // Messages
    case class InterpretResponse(
        login:String, response:Try[HttpResponse[String]]
    )

    // Props factory
    def props(followerExtractor:ActorRef) =
        Props(classOf[ResponseInterpreter], followerExtractor)
}

```

The body of `ResponseInterpreter` should feel familiar: when the actor receives a message giving it a response to interpret, it parses it to JSON using the techniques that you learned in *Chapter 7, Web APIs*. If we parse the response successfully, we forward the parsed JSON to the follower extractor. If we fail to parse the response (possibly because it was badly formatted), we just log the error. We could recover from this in other ways, for instance, by re-adding this login to the queue manager to be fetched again:

```

// ResponseInterpreter.scala
class ResponseInterpreter(followerExtractor:ActorRef)

```



```
extends Actor with ActorLogging {
  // Import the message definitions
  import ResponseInterpreter._

  def receive = {
    case InterpretResponse(login, r) => interpret(login, r)
  }

  // If the query was successful, extract the JSON response
  // and pass it onto the follower extractor.
  // If the query failed, or is badly formatted, throw an error
  // We should also be checking error codes here.
  private def interpret(
    login:String, response:Try[HttpResponse[String]]
  ) = response match {
    case Success(r) => responseToJson(r.body) match {
      case Success(jsonResponse) =>
        followerExtractor ! FollowerExtractor.Extract(
          login, jsonResponse)
      case Failure(e) =>
        log.error(
          s"Error parsing response to JSON for $login: $e")
    }
    case Failure(e) => log.error(
      s"Error fetching URL for $login: $e")
  }

  // Try and parse the response body as JSON.
  // If successful, coerce the `JValue` to a `JArray`.
  private def responseToJson(responseBody:String):Try[JArray] = {
    val jvalue = Try { parse(responseBody) }
    jvalue.flatMap {
      case a:JArray => Success(a)
      case _ => Failure(new IllegalStateException(
        "Incorrectly formatted JSON: not an array"))
    }
  }
}
```

We now have two-thirds of our worker actors. The last link is the follower extractor. This actor's job is simple: it takes the `JArray` passed to it by the response interpreter and converts it to a list of followers. For now, we will just log this list, but when we build our fetcher manager, the follower extractor will send messages asking the manager to add the followers to its queue of logins to fetch.

As before, the companion just defines the messages that this actor can receive and a Props factory method:

```
// FollowerExtractor.scala
import akka.actor._

import org.json4s._
import org.json4s.native.JsonMethods._

object FollowerExtractor {

  // Messages
  case class Extract(login:String, jsonResponse:JArray)

  // Props factory method
  def props = Props[FollowerExtractor]
}
```

The FollowerExtractor class receives Extract messages containing a JArray of information representing a follower. It extracts the login field and logs it:

```
class FollowerExtractor extends Actor with ActorLogging {
  import FollowerExtractor._
  def receive = {
    case Extract(login, followerArray) => {
      val followers = extractFollowers(followerArray)
      log.info(s"$login -> ${followers.mkString(", ")")
    }
  }

  def extractFollowers(followerArray:JArray) = for {
    JObject(follower) <- followerArray
    JField("login", JString(login)) <- follower
  } yield login
}
```

Let's write a new main method to exercise all our actors:

```
// FetchNetwork.scala

import akka.actor._
import akka.routing._
import scala.concurrent.ExecutionContext.Implicits.global
```

```
import scala.concurrent.duration._

object FetchNetwork extends App {

  import Fetcher._ // Import messages and factory method

  // Get token if exists
  val token = sys.env.get("GHTOKEN")

  val system = ActorSystem("fetchers")

  // Instantiate actors
  val followerExtractor = system.actorOf(FollowerExtractor.props)
  val responseInterpreter =
    system.actorOf(ResponseInterpreter.props(followerExtractor))

  val router = system.actorOf(RoundRobinPool(4).props(
    Fetcher.props(token, responseInterpreter)
  ))

  List("odersky", "derekwyatt", "rkuhn", "tototoshi") foreach {
    login => router ! Fetch(login)
  }

  // schedule a shutdown
  system.scheduler.scheduleOnce(5.seconds) { system.shutdown }

}
```

Let's run this through SBT:

```
$ GHTOKEN="2502761d..." sbt run
[INFO] [11/05/2015 20:09:37.048] [fetchers-akka.actor.default-
dispatcher-3] [akka://fetchers/user/$a] derekwyatt -> adulteratedjedi,
joonas, Psycojoker, trapd00r, tyru, ...
[INFO] [11/05/2015 20:09:37.050] [fetchers-akka.actor.default-
dispatcher-3] [akka://fetchers/user/$a] tototoshi -> akr4, yuroyoro,
seratch, yyuu, ...
[INFO] [11/05/2015 20:09:37.051] [fetchers-akka.actor.default-
dispatcher-3] [akka://fetchers/user/$a] odersky -> misto, gkossakowski,
mushtaq, ...
[INFO] [11/05/2015 20:09:37.052] [fetchers-akka.actor.default-
dispatcher-3] [akka://fetchers/user/$a] rkuhn -> arnbak, uzoice, jond3k,
TimothyKlim, reirod, ...
```

Queue control and the pull pattern

We have now defined the three worker actors in our crawler application. The next step is to define the manager. The *fetcher manager* is responsible for keeping a queue of logins to fetch as well as a set of login names that we have already seen in order to avoid fetching the same logins more than once.

A first attempt might involve building an actor that keeps a set of users that we have already seen and just dispatches it to a round-robin router for fetchers when it is given a new user to fetch. The problem with this approach is that the number of messages in the fetchers' mailboxes would accumulate quickly: for each API query, we are likely to get tens of followers, each of which is likely to make it back to a fetcher's inbox. This gives us very little control over the amount of work piling up.

The first problem that this is likely to cause involves the GitHub API rate limit: even with authentication, we are limited to 5,000 requests per hour. It would be useful to stop queries as soon as we hit this threshold. We cannot be responsive if each fetcher has a backlog of hundreds of users that they need to fetch.

A better alternative is to use a *pull* system: the fetchers request work from a central queue when they find themselves idle. Pull systems are common in Akka when we have a producer that produces work faster than consumers can process it (refer to <http://www.michaelpollmeier.com/akka-work-pulling-pattern/>).

Conversations between the manager and fetchers will proceed as follows:

- If the manager goes from a state of having no work to having work, it sends a `WorkAvailable` message to all the fetchers.
- Whenever a fetcher receives a `WorkAvailable` message or when it completes an item of work, it sends a `GiveMeWork` message to the queue manager.
- When the queue manager receives a `GiveMeWork` message, it ignores the request if no work is available or it is throttled. If it has work, it sends a `Fetch(user)` message to the actor.

Let's start by modifying our fetcher. You can find the code examples for this section in the `chap09/ghub_crawler` directory in the sample code provided with this book (<https://github.com/pbugnion/s4ds>). We will pass a reference to the fetcher manager through the constructor. We need to change the companion object to add the `WorkAvailable` message and the `props` factory to include the reference to the manager:

```
// Fetcher.scala
object Fetcher {
  case class Fetch(url:String)
```

```
case object WorkAvailable

def props(
  token:Option[String],
  fetcherManager:ActorRef,
  responseInterpreter:ActorRef):Props =
  Props(classOf[Fetcher],
        token, fetcherManager, responseInterpreter)
}
```

We also need to change the `receive` method so that it queries the `FetcherManager` asking for more work once it's done processing a request or when it receives a `WorkAvailable` message.

This is the final version of the fetchers:

```
class Fetcher(
  val token:Option[String],
  val fetcherManager:ActorRef,
  val responseInterpreter:ActorRef)
extends Actor with ActorLogging {
  import Fetcher._
  import context.dispatcher

  def receive = {
    case Fetch(login) => fetchFollowers(login)
    case WorkAvailable =>
      fetcherManager ! FetcherManager.GiveMeWork
  }

  private def fetchFollowers(login:String) {
    val unauthorizedRequest = Http(
      s"https://api.github.com/users/$login/followers")
    val authorizedRequest = token.map { t =>
      unauthorizedRequest.header("Authorization", s"token $t")
    }
    val request = authorizedRequest.getOrElse(unauthorizedRequest)
    val response = Future { request.asString }

    response.onComplete { r =>
      responseInterpreter !
        ResponseInterpreter.InterpretResponse(login, r)
      fetcherManager ! FetcherManager.GiveMeWork
    }
  }
}
```

Now that we have a working definition of the fetchers, let's build the `FetcherManager`. This is the most complex actor that we have built so far, and, before we dive into building it, we need to learn a bit more about the components of the Akka toolkit.

Accessing the sender of a message

When our fetcher manager receives a `GiveMeWork` request, we will need to send work back to the correct fetcher. We can access the actor who sent a message using the `sender` method, which is a method of `Actor` that returns the `ActorRef` corresponding to the actor who sent the message currently being processed. The case statement corresponding to `GiveMeWork` in the fetcher manager is therefore:

```
def receive = {
  case GiveMeWork =>
    login = // get next login to fetch
    sender ! Fetcher.Fetch(login)
    ...
}
```

As `sender` is a *method*, its return value will change for every new incoming message. It should therefore only be used synchronously with the `receive` method. In particular, using it in a future is dangerous:

```
def receive = {
  case DoSomeWork =>
    val work = Future { Thread.sleep(20000) ; 5 }
    work.onComplete { result =>
      sender ! Complete(result) // NO!
    }
}
```

The problem is that when the future is completed 20 seconds after the message is processed, the actor will, in all likelihood, be processing a different message so the return value of `sender` will have changed. We will thus send the `Complete` message to a completely different actor.

If you need to reply to a message outside of the `receive` method, such as when a future completes, you should bind the value of the current sender to a variable:

```
def receive = {
  case DoSomeWork =>
    // bind the current value of sender to a val
    val requestor = sender
    val work = Future { Thread.sleep(20000) ; 5 }
    work.onComplete { result => requestor ! Complete(result) }
}
```

Stateful actors

The behavior of the fetcher manager depends on whether it has work to give out to the fetchers:

- If it has work to give, it needs to respond to `GiveMeWork` messages with a `Fetcher.Fetch` message
- If it does not have work, it must ignore the `GiveMeWork` messages and, if work gets added, it must send a `WorkAvailable` message to the fetchers

Encoding the notion of state is straightforward in Akka. We specify different receive methods and switch from one to the other depending on the state. We will define the following receive methods for our fetcher manager, corresponding to each of the states:

```
// receive method when the queue is empty
def receiveWhileEmpty: Receive = {
  ...
}

// receive method when the queue is not empty
def receiveWhileNotEmpty: Receive = {
  ...
}
```

Note that we must define the return type of the receive methods as `Receive`. To switch the actor from one method to the other, we can use `context.become(methodName)`. Thus, for instance, when the last login name is popped off the queue, we can transition to using the `receiveWhileEmpty` method with `context.become(receiveWhileEmpty)`. We set the initial state by assigning `receiveWhileEmpty` to the `receive` method:

```
def receive = receiveWhileEmpty
```

Follower network crawler

We are now ready to code up the remaining pieces of our network crawler. The largest missing piece is the fetcher manager. Let's start with the companion object. As with the worker actors, this just contains the definitions of the messages that the actor can receive and a factory to create the `Props` instance:

```
// FetcherManager.scala
import scala.collection.mutable
import akka.actor._

object FetcherManager {
  case class AddToQueue(login:String)
  case object GiveMeWork

  def props(token:Option[String], nFetchers:Int) =
    Props(classOf[FetcherManager], token, nFetchers)
}
```

The manager can receive two messages: `AddToQueue`, which tells it to add a username to the queue of users whose followers need to be fetched, and `GiveMeWork`, emitted by the fetchers when they are unemployed.

The manager will be responsible for launching the fetchers, response interpreter, and follower extractor, as well as maintaining an internal queue of usernames and a set of usernames that we have seen:

```
// FetcherManager.scala

class FetcherManager(val token:Option[String], val nFetchers:Int)
  extends Actor with ActorLogging {

  import FetcherManager._

  // queue of usernames whose followers we need to fetch
  val fetchQueue = mutable.Queue.empty[String]

  // set of users we have already fetched.
  val fetchedUsers = mutable.Set.empty[String]

  // Instantiate worker actors
  val followerExtractor = context.actorOf(
    FollowerExtractor.props(self))
  val responseInterpreter = context.actorOf(
    ResponseInterpreter.props(followerExtractor))
```



```
val fetchers = (0 until nFetchers).map { i =>
  context.actorOf(
    Fetcher.props(token, self, responseInterpreter))
}

// receive method when the actor has work:
// If we receive additional work, we just push it onto the
// queue.
// If we receive a request for work from a Fetcher,
// we pop an item off the queue. If that leaves the
// queue empty, we transition to the 'receiveWhileEmpty'
// method.
def receiveWhileNotEmpty:Receive = {
  case AddToQueue(login) => queueIfNotFetched(login)
  case GiveMeWork =>
    val login = fetchQueue.dequeue
    // send a Fetch message back to the sender.
    // we can use the `sender` method to reply to a message
    sender ! Fetcher.Fetch(login)
    if (fetchQueue.isEmpty) {
      context.become(receiveWhileEmpty)
    }
}

// receive method when the actor has no work:
// if we receive work, we add it onto the queue, transition
// to a state where we have work, and notify the fetchers
// that work is available.
def receiveWhileEmpty:Receive = {
  case AddToQueue(login) =>
    queueIfNotFetched(login)
    context.become(receiveWhileNotEmpty)
    fetchers.foreach { _ ! Fetcher.WorkAvailable }
  case GiveMeWork => // do nothing
}

// Start with an empty queue.
def receive = receiveWhileEmpty

def queueIfNotFetched(login:String) {
  if (! fetchedUsers(login)) {
    log.info(s"Pushing $login onto queue")
    // or do something useful...
    fetchQueue += login
  }
}
```

```

        fetchedUsers += login
    }
}
}

```

We now have a fetcher manager. The rest of the code can remain the same, apart from the follower extractor. Instead of logging followers names, it must send `AddToQueue` messages to the manager. We will pass a reference to the manager at construction time:

```

// FollowerExtractor.scala
import akka.actor._
import org.json4s._
import org.json4s.native.JsonMethods._

object FollowerExtractor {

  // messages
  case class Extract(login:String, jsonResponse:JArray)

  // props factory method
  def props(manager:ActorRef) =
    Props(classOf[FollowerExtractor], manager)
}

class FollowerExtractor(manager:ActorRef)
extends Actor with ActorLogging {
  import FollowerExtractor._

  def receive = {
    case Extract(login, followerArray) =>
      val followers = extractFollowers(followerArray)
      followers foreach { f =>
        manager ! FetcherManager.AddToQueue(f)
      }
  }

  def extractFollowers(followerArray:JArray) = for {
    JObject(follower) <- followerArray
    JField("login", JString(login)) <- follower
  } yield login
}

```

The main method running all this is remarkably simple as all the code to instantiate actors has been moved to the `FetcherManager`. We just need to instantiate the manager and give it the first node in the network, and it will do the rest:

```
// FetchNetwork.scala
import akka.actor._

object FetchNetwork extends App {

  // Get token if exists
  val token = sys.env.get("GHTOKEN")

  val system = ActorSystem("GithubFetcher")
  val manager = system.actorOf(FetcherManager.props(token, 2))
  manager ! FetcherManager.AddToQueue("odersky")

}
```

Notice how we do not attempt to shut down the actor system anymore. We will just let it run, crawling the network, until we stop it or hit the authentication limit. Let's run this through SBT:

```
$ GHTOKEN="2502761d..." sbt "runMain FetchNetwork"
[INFO] [11/06/2015 06:31:04.614] [GithubFetcher-akka.actor.default-
dispatcher-2] [akka://GithubFetcher/user/$a] Pushing odersky onto queue
[INFO] [11/06/2015 06:31:05.563] [GithubFetcher-akka.actor.default-
dispatcher-4] [akka://GithubFetcher/user/$a] Pushing misto onto
queueINFO [11/06/2015 06:31:05.563] [GithubFetcher-akka.actor.default-
dispatcher-4] [akka://GithubFetcher/user/$a] Pushing gkossakowski onto
queue
^c
```

Our program does not actually do anything useful with the followers that it retrieves besides logging them. We could replace the `log.info` call to, for instance, store the nodes in a database or draw the graph to screen.

Fault tolerance

Real programs fail, and they fail in unpredictable ways. Akka, and the Scala community in general, favors planning explicitly for failure rather than trying to write infallible applications. A *fault tolerant* system is a system that can continue to operate when one or more of its components fails. The failure of an individual subsystem does not necessarily mean the failure of the application. How does this apply to Akka?

The actor model provides a natural unit to encapsulate failure: the actor. When an actor throws an exception while processing a message, the default behavior is for the actor to restart, but the exception does not leak out and affect the rest of the system. For instance, let's introduce an arbitrary failure in the response interpreter. We will modify the `receive` method to throw an exception when it is asked to interpret the response for `misto`, one of Martin Odersky's followers:

```
// ResponseInterpreter.scala
def receive = {
  case InterpretResponse("misto", r) =>
    throw new IllegalStateException("custom error")
  case InterpretResponse(login, r) => interpret(login, r)
}
```

If you rerun the code through SBT, you will notice that an error gets logged. The program does not crash, however. It just continues as normal:

```
[ERROR] [11/07/2015 12:05:58.938] [GithubFetcher-akka.actor.default-
dispatcher-2] [akka://GithubFetcher/user/$a/$b] custom error
java.lang.IllegalStateException: custom error
  at ResponseInterpreter$
  ...
[INFO] [11/07/2015 12:05:59.117] [GithubFetcher-akka.actor.default-
dispatcher-2] [akka://GithubFetcher/user/$a] Pushing samfoo onto queue
```

None of the followers of `misto` will get added to the queue: he never made it past the `ResponseInterpreter` stage. Let's step through what happens when the exception gets thrown:

- The interpreter is sent the `InterpretResponse("misto", ...)` message. This causes it to throw an exception and it dies. None of the other actors are affected by the exception.
- A fresh instance of the response interpreter is created with the same `Props` instance as the recently deceased actor.
- When the response interpreter has finished initializing, it gets bound to the same `ActorRef` as the deceased actor. This means that, as far as the rest of the system is concerned, nothing has changed.
- The mailbox is tied to `ActorRef` rather than the actor, so the new response interpreter will have the same mailbox as its predecessor, without the offending message.

Thus, if, for whatever reason, our crawler crashes when fetching or parsing the response for a user, the application will be minimally affected – we will just not fetch this user's followers.

Any internal state that an actor carries is lost when it restarts. Thus, if, for instance, the fetcher manager died, we would lose the current value of the queue and visited users. The risks associated with losing the internal state can be mitigated by the following:

- Adopting a different strategy for failure: we can, for instance, carry on processing messages without restarting the actor in the event of failure. Of course, this is of little use if the actor died because its internal state is inconsistent. In the next section, we will discuss how to change the failure recovery strategy.
- Backing up the internal state by writing it to disk periodically and loading from the backup on restart.
- Protecting actors that carry critical state by ensuring that all "risky" operations are delegated to other actors. In our crawler example, all the interactions with external services, such as querying the GitHub API and parsing the response, happen with actors that carry no internal state. As we saw in the previous example, if one of these actors dies, the application is minimally affected. By contrast, the precious fetcher manager is only allowed to interact with sanitized inputs. This is called the *error kernel* pattern: code likely to cause errors is delegated to kamikaze actors.

Custom supervisor strategies

The default strategy of restarting an actor on failure is not always what we want. In particular, for actors that carry a lot of data, we might want to resume processing after an exception rather than restarting the actor. Akka lets us customize this behavior by setting a *supervisor strategy* in the actor's supervisor.

Recall that all actors have parents, including the top-level actors, who are children of a special actor called the *user guardian*. By default, an actor's supervisor is his parent, and it is the supervisor who decides what happens to the actor on failure.

Thus, to change how an actor reacts to failure, you must set its parent's supervisor strategy. You do this by setting the `supervisorStrategy` attribute. The default strategy is equivalent to the following:

```
val supervisorStrategy = OneForOneStrategy() {
  case _:ActorInitializationException => Stop
  case _:ActorKilledException => Stop
  case _:DeathPactException => Stop
  case _:Exception => Restart
}
```

There are two components to a supervisor strategy:

- `OneForOneStrategy` determines that the strategy applies only to the actor that failed. By contrast, we can use `AllForOneStrategy`, which applies the same strategy to all the supervisees. If a single child fails, all the children will be restarted (or stopped or resumed).
- A partial function mapping `Throwables` to a `Directive`, which is an instruction on what to do in response to a failure. The default strategy, for instance, maps `ActorInitializationException` (which happens if the constructor fails) to the `Stop` directive and (almost all) other exceptions to `Restart`.

There are four directives:

- `Restart`: This destroys the faulty actor and restarts it, binding the newborn actor to the old `ActorRef`. This clears the internal state of the actor, which may be a good thing (the actor might have failed because of some internal inconsistency).
- `Resume`: The actor just moves on to processing the next message in its inbox.
- `Stop`: The actor stops and is not restarted. This is useful in throwaway actors that you use to complete a single operation: if this operation fails, the actor is not needed any more.
- `Escalate`: The supervisor itself rethrows the exception, hoping that its supervisor will know what to do with it.

A supervisor does not have access to which of its children failed. Thus, if an actor has children that might require different recovery strategies, it is best to create a set of intermediate supervisor actors to supervise the different groups of children.

As an example of setting the supervisor strategy, let's tweak the `FetcherManager` supervisor strategy to adopt an all-for-one strategy and stop its children when one of them fails. We start with the relevant imports:

```
import akka.actor.SupervisorStrategy._
```

Then, we just need to set the `supervisorStrategy` attribute in the `FetcherManager` definition:

```
class FetcherManager(...) extends Actor with ActorLogging {  
  ...  
  
  override val supervisorStrategy = AllForOneStrategy() {  
    case _:ActorInitializationException => Stop  
    case _:ActorKilledException => Stop  
    case _:Exception => Stop  
  }  
  ...  
}
```

If you run this through SBT, you will notice that when the code comes across the custom exception thrown by the response interpreter, the system halts. This is because all the actors apart from the fetcher manager are now defunct.

Life-cycle hooks

Akka lets us specify code that runs in response to specific events in an actor's life, through *life-cycle hooks*. Akka defines the following hooks:

- `preStart():` This runs after the actor's constructor has finished but before it starts processing messages. This is useful to run initialization code that depends on the actor being fully constructed.
- `postStop():` This runs when the actor dies after it has stopped processing messages. This is useful to run cleanup code before terminating the actor.
- `preRestart(reason: Throwable, message: Option[Any]):` This is called just after an actor receives an order to restart. The `preRestart` method has access to the exception that was thrown and to the offending message, allowing for corrective action. The default behavior of `preRestart` is to stop each child and then call `postStop`.
- `postRestart(reason: Throwable):` This is called after an actor has restarted. The default behavior is to call `preStart()`.

Let's use system hooks to persist the state of `FetcherManager` between runs of the programs. You can find the code examples for this section in the `chap09/ghub_crawler_fault_tolerant` directory in the sample code provided with this book (<https://github.com/pbugnion/s4ds>). This will make the fetcher manager fault-tolerant. We will use `postStop` to write the current queue and set of visited users to text files and `preStart` to read these text files from the disk. Let's start by importing the libraries necessary to read and write files:

```
// FetcherManager.scala

import scala.io.Source
import scala.util._
import java.io._
```

We will store the names of the two text files in which we persist the state in the `FetcherManager` companion object (a better approach would be to store them in a configuration file):

```
// FetcherManager.scala
object FetcherManager {
  ...
  val fetchedUsersFileName = "fetched-users.txt"
  val fetchQueueFileName = "fetch-queue.txt"
}
```

In the `preStart` method, we load both the set of fetched users and the backlog of users to fetch from the text files, and in the `postStop` method, we overwrite these files with the new values of these data structures:

```
class FetcherManager(
  val token:Option[String], val nFetchers:Int
) extends Actor with ActorLogging {
  ...

  /** pre-start method: load saved state from text files */
  override def preStart {
    log.info("Running pre-start on fetcher manager")

    loadFetchedUsers
    log.info(
      s"Read ${fetchedUsers.size} visited users from source"
    )

    loadFetchQueue
```



```
    log.info(
      s"Read ${fetchQueue.size} users in queue from source"
    )

    // If the saved state contains a non-empty queue,
    // alert the fetchers so they can start working.
    if (fetchQueue.nonEmpty) {
      context.become(receiveWhileNotEmpty)
      fetchers.foreach { _ ! Fetcher.WorkAvailable }
    }
  }

  /** Dump the current state of the manager */
  override def postStop {
    log.info("Running post-stop on fetcher manager")
    saveFetchedUsers
    saveFetchQueue
  }

  /* Helper methods to load from and write to files */
  def loadFetchedUsers {
    val fetchedUsersSource = Try {
      Source.fromFile(fetchedUsersFileName)
    }
    fetchedUsersSource.foreach { s =>
      try s.getLines.foreach { l => fetchedUsers += l }
      finally s.close
    }
  }

  def loadFetchQueue {
    val fetchQueueSource = Try {
      Source.fromFile(fetchQueueFileName)
    }
    fetchQueueSource.foreach { s =>
      try s.getLines.foreach { l => fetchQueue += l }
      finally s.close
    }
  }

  def saveFetchedUsers {
    val fetchedUsersFile = new File(fetchedUsersFileName)
    val writer = new BufferedWriter(
```

```

        new FileWriter(fetchedUsersFile))
    fetchedUsers.foreach { user => writer.write(user + "\n") }
    writer.close()
}

def saveFetchQueue {
    val queueUsersFile = new File(fetchQueueFileName)
    val writer = new BufferedWriter(
        new FileWriter(queueUsersFile))
    fetchQueue.foreach { user => writer.write(user + "\n") }
    writer.close()
}

...
}

```

Now that we save the state of the crawler when it shuts down, we can put a better termination condition for the program than simply interrupting the program once we get bored. In production, we might halt the crawler when we have enough names in a database, for instance. In this example, we will simply let the crawler run for 30 seconds and then shut it down.

Let's modify the main method:

```

// FetchNetwork.scala
import akka.actor._
import scala.concurrent.ExecutionContext.Implicits.global
import scala.concurrent.duration._

object FetchNetwork extends App {

    // Get token if exists
    val token = sys.env.get("GHTOKEN")

    val system = ActorSystem("GithubFetcher")
    val manager = system.actorOf(FetcherManager.props(token, 2))

    manager ! FetcherManager.AddToQueue("odersky")

    system.scheduler.scheduleOnce(30.seconds) { system.shutdown }

}

```

After 30 seconds, we just call `system.shutdown`, which stops all the actors recursively. This will stop the fetcher manager, calling the `postStop` life cycle hook. After one run of the program, I have 2,164 names in the `fetchd-users.txt` file. Running it again increases this number to 3,728 users.

We could improve fault tolerance further by making the fetcher manager dump the data structures at regular intervals while the code runs. As writing to the disk (or to a database) carries a certain element of risk (What if the database server goes down or the disk is full?) it would be better to delegate writing the data structures to a custom actor rather than endangering the manager.

Our crawler has one minor problem: when the fetcher manager stops, it stops the fetcher actors, response interpreter, and follower extractor. However, none of the users currently going through these actors are stored. This also results in a small number of undelivered messages at the end of the code: if the response interpreter stops before a fetcher, the fetcher will try to deliver to a non-existent actor. This only accounts for a small number of users. To recover these login names, we can create a reaper actor whose job is to coordinate the killing of all the worker actors in the correct order and harvest their internal state. This pattern is documented in a blog post by *Derek Wyatt* (<http://letitcrash.com/post/30165507578/shutdown-patterns-in-akka-2>).

What we have not talked about

Akka is a very rich ecosystem, far too rich to do it justice in a single chapter. There are some important parts of the toolkit that you will need, but we have not covered them here. We will give brief descriptions, but you can refer to the Akka documentation for more details:

- The ask operator, `?`, offers an alternative to the tell operator, `!`, that we have used to send messages to actors. Unlike "tell", which just fires a message to an actor, the ask operator expects a response. This is useful when we need to ask actors questions rather than just telling them what to do. The ask pattern is documented at http://doc.akka.io/docs/akka/snapshot/scala/actors.html#Ask__Send-And-Receive-Future.
- Deathwatch allows actors to watch another actor and receive a message when it dies. This is useful for actors that might depend on another actor but not be its direct supervisor. This is documented at http://doc.akka.io/docs/akka/snapshot/scala/actors.html#Lifecycle_Monitoring_aka_DeathWatch.

- In our crawler, we passed references to actors explicitly through the constructor. We can also look up actors using the actor hierarchy with a syntax reminiscent of files in a filesystem at http://doc.akka.io/docs/akka/snapshot/scala/actors.html#Identifying_Actors_via_Actor_Selection.
- We briefly explored how to implement stateful actors with different receive methods and using `context.become` to switch between them. Akka offers a more powerful alternative, based on finite state machines, to encode a more complex set of states and transitions: <http://doc.akka.io/docs/akka/snapshot/scala/fsm.html>.
- We have not discussed distributing actor systems across several nodes in this chapter. The message passing architecture works well with distributed setups: <http://doc.akka.io/docs/akka/2.4.0/common/cluster.html>.

Summary

In this chapter, you learned how to weave actors together to tackle a difficult concurrent problem. More importantly, we saw how Akka's actor framework encourages us to think about concurrent problems in terms of many separate chunks of encapsulated mutable data, synchronized through message passing. Akka makes concurrent programming easier to reason about and more fun.

References

Derek Wyatt's book, *Akka Concurrency*, is a fantastic introduction to Akka. It should definitely be the first stop for anyone wanting to do serious Akka programming.

The **LET IT CRASH** blog (<http://letitcrash.com>) is the official Akka blog, and contains many examples of idioms and patterns to solve common issues.

10

Distributed Batch Processing with Spark

In *Chapter 4, Parallel Collections and Futures*, we discovered how to use parallel collections for "embarrassingly" parallel problems: problems that can be broken down into a series of tasks that require no (or very little) communication between the tasks.

Apache Spark provides behavior similar to Scala parallel collections (and much more), but, instead of distributing tasks across different CPUs on the same computer, it allows the tasks to be distributed across a computer cluster. This provides arbitrary horizontal scalability, since we can simply add more computers to the cluster.

In this chapter, we will learn the basics of Apache Spark and use it to explore a set of emails, extracting features with the view of building a spam filter. We will explore several ways of actually building a spam filter in *Chapter 12, Distributed Machine Learning with MLlib*.

Installing Spark

In previous chapters, we included dependencies by specifying them in a `build.sbt` file, and relying on SBT to fetch them from the Maven Central repositories. For Apache Spark, downloading the source code or pre-built binaries explicitly is more common, since Spark ships with many command line scripts that greatly facilitate launching jobs and interacting with a cluster.

Head over to <http://spark.apache.org/downloads.html> and download Spark 1.5.2, choosing the "pre-built for Hadoop 2.6 or later" package. You can also build Spark from source if you need customizations, but we will stick to the pre-built version since it requires no configuration.

Clicking **Download** will download a tarball, which you can unpack with the following command:

```
$ tar xzf spark-1.5.2-bin-hadoop2.6.tgz
```

This will create a `spark-1.5.2-bin-hadoop2.6` directory. To verify that Spark works correctly, navigate to `spark-1.5.2-bin-hadoop2.6/bin` and launch the Spark shell using `./spark-shell`. This is just a Scala shell with the Spark libraries loaded.

You may want to add the `bin/` directory to your system path. This will let you call the scripts in that directory from anywhere on your system, without having to reference the full path. On Linux or Mac OS, you can add variables to the system path by entering the following line in your shell configuration file (`.bash_profile` on Mac OS, and `.bashrc` or `.bash_profile` on Linux):

```
export PATH=/path/to/spark/bin:$PATH
```

The changes will take effect in new shell sessions. On Windows (if you use PowerShell), you need to enter this line in the `profile.ps1` file in the `WindowsPowerShell` folder in Documents:

```
$env:Path += ";C:\Program Files\GnuWin32\bin"
```

If this worked correctly, you should be able to open a Spark shell in any directory on your system by just typing `spark-shell` in a terminal.

Acquiring the example data

In this chapter, we will explore the Ling-Spam email dataset (The original dataset is described at <http://csmining.org/index.php/ling-spam-datasets.html>). Download the dataset from <http://data.scala4datascience.com/ling-spam.tar.gz> (or `ling-spam.zip`, depending on your preferred mode of compression), and unpack the contents to the directory containing the code examples for this chapter. The archive contains two directories, `spam/` and `ham/`, containing the spam and legitimate emails, respectively.

Resilient distributed datasets

Spark expresses all computations as a sequence of transformations and actions on distributed collections, called **Resilient Distributed Datasets (RDD)**. Let's explore how RDDs work with the Spark shell. Navigate to the examples directory and open a Spark shell as follows:

```
$ spark-shell
scala>
```

Let's start by loading an email in an RDD:

```
scala> val email = sc.textFile("ham/9-463msg1.txt")
email: rdd.RDD[String] = MapPartitionsRDD[1] at textFile
```

`email` is an RDD, with each element corresponding to a line in the input file. Notice how we created the RDD by calling the `textFile` method on an object called `sc`:

```
scala> sc
spark.SparkContext = org.apache.spark.SparkContext@459bf87c
```

`sc` is a `SparkContext` instance, an object representing the entry point to the Spark cluster (for now, just our local machine). When we start a Spark shell, a context is created and bound to the variable `sc` automatically.

Let's split the email into words using `flatMap`:

```
scala> val words = email.flatMap { line => line.split("\\s") }
words: rdd.RDD[String] = MapPartitionsRDD[2] at flatMap
```

This will feel natural if you are familiar with collections in Scala: the `email` RDD behaves just like a list of strings. Here, we split using the regular expression `\s`, denoting white space characters. Instead of using `flatMap` explicitly, we can also manipulate RDDs using Scala's syntactic sugar:

```
scala> val words = for {
  line <- email
  word <- line.split("\\s")
} yield word
words: rdd.RDD[String] = MapPartitionsRDD[3] at flatMap
```


Let's inspect the results. We can use `.take(n)` to extract the first n elements of an RDD:

```
scala> words.take(5)
Array[String] = Array(Subject:, tsd98, workshop, -, -)
```

We can also use `.count` to get the number of elements in an RDD:

```
scala> words.count
Long = 939
```

RDDs support many of the operations supported by collections. Let's use `filter` to remove punctuation from our email. We will remove all words that contain any non-alphanumeric character. We can do this by filtering out elements that match this *regular expression* anywhere in the word: `[^a-zA-Z0-9]`.

```
scala> val nonAlphaNumericPattern = "[^a-zA-Z0-9]".r
nonAlphaNumericPattern: Regex = [^a-zA-Z0-9]
```

```
scala> val filteredWords = words.filter {
  word => nonAlphaNumericPattern.findFirstIn(word) == None
}
filteredWords: rdd.RDD[String] = MapPartitionsRDD[4] at filter
```

```
scala> filteredWords.take(5)
Array[String] = Array(tsd98, workshop, 2nd, call, paper)
```

```
scala> filteredWords.count
Long = 627
```

In this example, we created an RDD from a text file. We can also create RDDs from Scala iterables using the `sc.parallelize` method available on a Spark context:

```
scala> val words = "the quick brown fox jumped over the dog".split(" ")
words: Array[String] = Array(the, quick, brown, fox, ...)
```

```
scala> val wordsRDD = sc.parallelize(words)
wordsRDD: RDD[String] = ParallelCollectionRDD[1] at parallelize at
<console>:23
```

This is useful for debugging and for trialling behavior in the shell. The counterpart to `parallelize` is the `.collect` method, which converts an RDD to a Scala array:

```
scala> val wordLengths = wordsRDD.map { _.length }
wordLengths: RDD[Int] = MapPartitionsRDD[2] at map at <console>:25

scala> wordLengths.collect
Array[Int] = Array(3, 5, 5, 3, 6, 4, 3, 3)
```

The `.collect` method requires the entire RDD to fit in memory on the master node. It is thus either used for debugging with a reduced dataset, or at the end of a pipeline that trims down a dataset.

As you can see, RDDs offer an API much like Scala iterables. The critical difference is that RDDs are *distributed* and *resilient*. Let's explore what this means in practice.

RDDs are immutable

You cannot change an RDD once it is created. All operations on RDDs either create new RDDs or other Scala objects.

RDDs are lazy

When you execute operations like `map` and `filter` on a Scala collection in the interactive shell, the REPL prints the values of the new collection to screen. The same isn't true of Spark RDDs. This is because operations on RDDs are lazy: they are only evaluated when needed.

Thus, when we write:

```
val email = sc.textFile(...)
val words = email.flatMap { line => line.split("\\s") }
```

We are creating an RDD, `words` that knows how to build itself from its parent RDD, `email`, which, in turn, knows that it needs to read a text file and split it into lines. However, none of the commands actually happen until we force the evaluation of the RDDs by calling an *action* to return a Scala object. This is most evident if we try to read from a non-existent text file:

```
scala> val inp = sc.textFile("nonexistent")
inp: rdd.RDD[String] = MapPartitionsRDD[5] at textFile
```

We can create the RDD without a hitch. We can even define further transformations on the RDD. The program crashes only when these transformations are finally evaluated:

```
scala> inp.count // number of lines
org.apache.hadoop.mapred.InvalidInputException: Input path does not
exist: file:/Users/pascal/...
```

The action `.count` is expected to return the number of elements in our RDD as an integer. Spark has no choice but to evaluate `inp`, which results in an exception.

Thus, it is probably more appropriate to think of an RDD as a pipeline of operations, rather than a more traditional collection.

RDDs know their lineage

RDDs can only be constructed from stable storage (for instance, by loading data from a file that is present on every node in the Spark cluster), or through a set of transformations based on other RDDs. Since RDDs are lazy, they need to know how to build themselves when needed. They do this by knowing who their parent RDD is, and what operation they need to apply to the parent. This is a well-defined process since the parent RDD is immutable.

The `toDebugString` method provides a diagram of how an RDD is constructed:

```
scala> filteredWords.toDebugString
(2) MapPartitionsRDD[6] at filter at <console>:27 []
  | MapPartitionsRDD[3] at flatMap at <console>:23 []
  | MapPartitionsRDD[1] at textFile at <console>:21 []
  | ham/9-463msg1.txt HadoopRDD[0] at textFile at <console>:21 []
```

RDDs are resilient

If you run an application on a single computer, you generally don't need to worry about hardware failure in your application: if the computer fails, your application is doomed anyway.

Distributed architectures should, by contrast, be fault-tolerant: the failure of a single machine should not crash the entire application. Spark RDDs are built with fault tolerance in mind. Let's imagine that one of the worker nodes fails, causing the destruction of some of the data associated with an RDD. Since the Spark RDD knows how to build itself from its parent, there is no permanent data loss: the elements that were lost can just be re-computed when needed on another computer.

RDDs are distributed

When you construct an RDD, for instance from a text file, Spark will split the RDD into a number of partitions. Each partition will be entirely localized on a single machine (though there is, in general, more than one partition per machine).

Many transformations on RDDs can be executed on each partition independently. For instance, when performing a `.map` operation, a given element in the output RDD depends on a single element in the parent: data does not need to be moved between partitions. The same is true of `.flatMap` and `.filter` operations. This means that the partition in the RDD produced by one of these operations depends on a single partition in the parent RDD.

On the other hand, a `.distinct` transformation, which removes all duplicate elements from an RDD, requires the data in a given partition to be compared to the data in every other partition. This requires *shuffling* the data across the nodes. Shuffling, especially for large datasets, is an expensive operation and should be avoided if possible.

Transformations and actions on RDDs

The set of operations supported by an RDD can be split into two categories:

- **Transformations** create a new RDD from the current one. Transformations are lazy: they are not evaluated immediately.
- **Actions** force the evaluation of an RDD, and normally return a Scala object, rather than an RDD, or have some form of side-effect. Actions are evaluated immediately, triggering the execution of all the transformations that make up this RDD.

In the tables below, we give some examples of useful transformations and actions. For a full, up-to-date list, consult the Spark documentation (<http://spark.apache.org/docs/latest/programming-guide.html#rdd-operations>).

For the examples in these tables, we assume that you have created an RDD with:

```
scala> val rdd = sc.parallelize(List("quick", "brown", "quick", "dog"))
```

The following table lists common transformations on an RDD. Recall that transformations always generate a new RDD, and that they are lazy operations:

Transformation	Notes	Example (assuming rdd is { "quick", "brown", "quick", "dog" })
<code>rdd.map(func)</code>		<code>rdd.map { _.size } // => { 5, 5, 5, 3 }</code>
<code>rdd.filter(pred)</code>		<code>rdd.filter { _.length < 4 } // => { "dog" }</code>
<code>rdd.flatMap(func)</code>		<code>rdd.flatMap { _.toCharArray } // => { 'q', 'u', 'i', 'c', 'k', 'b', 'r', 'o' ... }</code>
<code>rdd.distinct()</code>	Remove duplicate elements in RDD.	<code>rdd.distinct // => { "dog", "brown", "quick" }</code>
<code>rdd.pipe(command, [envVars])</code>	Pipe through an external program. RDD elements are written, line-by-line, to the process's <code>stdin</code> . The output is read from <code>stdout</code> .	<code>rdd.pipe("tr a-z A-Z") // => { "QUICK", "BROWN", "QUICK", "DOG" }</code>

The following table describes common actions on RDDs. Recall that actions always generate a Scala type or cause a side-effect, rather than creating a new RDD. Actions force the evaluation of the RDD, triggering the execution of the transformations underpinning the RDD.

Action	Notes	Example (assuming rdd is { "quick", "brown", "quick", "dog" })
<code>rdd.first</code>	First element in the RDD.	<code>rdd.first // => quick</code>
<code>rdd.collect</code>	Transform the RDD to an array (the array must be able to fit in memory on the master node).	<code>rdd.collect // => Array[String] ("quick", "brown", "quick", "dog")</code>
<code>rdd.count</code>	Number of elements in the RDD.	<code>rdd.count // => 4</code>

Action	Nodes	Example (assuming rdd is { "quick", "brown", "quick", "dog" })
rdd.countByValue	Map of element to the number of times this element occurs. The map must fit on the master node.	<pre>rdd.countByValue // => Map(quick -> 2, brown -> 1, dog -> 1)</pre>
rdd.take(n)	Return an array of the first <i>n</i> elements in the RDD.	<pre>rdd.take(2) // => Array(quick, brown)</pre>
<pre>rdd. takeOrdered(n:Int) (implicit ordering: Ordering[T])</pre>	<p>Top <i>n</i> elements in the RDD according to the element's default ordering, or the ordering passed as second argument. See the Scala docs for Ordering for how to define custom comparison functions (http://www.scala-lang.org/api/current/index.html#scala.math.Ordering).</p>	<pre>rdd.takeOrdered(2) // => Array(brown, dog) rdd.takeOrdered(2) (Ordering.by { _.size }) // => Array[String] = Array(dog, quick)</pre>
rdd.reduce(func)	Reduce the RDD according to the specified function. Uses the first element in the RDD as the base. func should be commutative and associative.	<pre>rdd.map { _.size }.reduce { _ + _ } // => 18</pre>

Action	Nodes	Example (assuming rdd is { "quick", "brown", "quick", "dog" })
rdd. aggregate(zeroValue) (seqOp, combOp)	Reduction for cases where the reduction function returns a value of type different to the RDD's type. In this case, we need to provide a function for reducing within a single partition (seqOp) and a function for combining the value of two partitions (combOp).	rdd.aggregate(0) (_ + _.size, _ + _) // => 18

Persisting RDDs

We have learned that RDDs only retain the sequence of operations needed to construct the elements, rather than the values themselves. This, of course, drastically reduces memory usage since we do not need to keep intermediate versions of our RDDs in memory. For instance, let's assume we want to trawl through transaction logs to identify all the transactions that occurred on a particular account:

```
val allTransactions = sc.textFile("transaction.log")
val interestingTransactions = allTransactions.filter {
  _.contains("Account: 123456")
}
```

The set of all transactions will be large, while the set of transactions on the account of interest will be much smaller. Spark's policy of remembering *how* to construct a dataset, rather than the dataset itself, means that we never have all the lines of our input file in memory at any one time.

There are two situations in which we may want to avoid re-computing the elements of an RDD every time we use it:

- For interactive use: we might have detected fraudulent behavior on account "123456", and we want to investigate how this might have arisen. We will probably want to perform many different exploratory calculations on this RDD, without having to re-read the entire log file every time. It therefore makes sense to persist `interestingTransactions`.

- When an algorithm re-uses an intermediate result, or a dataset. A canonical example is logistic regression. In logistic regression, we normally use an iterative algorithm to find the 'optimal' coefficients that minimize the loss function. At every step in our iterative algorithm, we must calculate the loss function and its gradient from the training set. We should avoid re-computing the training set (or re-loading it from an input file) if at all possible.

Spark provides a `.persist` method on RDDs to achieve this. By calling `.persist` on an RDD, we tell Spark to keep the dataset in memory next time it is computed.

```
scala> words.persist
rdd.RDD[String] = MapPartitionsRDD[3] at filter
```

Spark supports different levels of persistence, which you can tune by passing arguments to `.persist`:

```
scala> import org.apache.spark.storage.StorageLevel
import org.apache.spark.storage.StorageLevel
```

```
scala> interestingTransactions.persist(
  StorageLevel.MEMORY_AND_DISK)
rdd.RDD[String] = MapPartitionsRDD[3] at filter
```

Spark provides several persistence levels, including:

- `MEMORY_ONLY`: the default storage level. The RDD is stored in RAM. If the RDD is too big to fit in memory, parts of it will not persist, and will need to be re-computed on the fly.
- `MEMORY_AND_DISK`: As much of the RDD is stored in memory as possible. If the RDD is too big, it will spill over to disk. This is only worthwhile if the RDD is expensive to compute. Otherwise, re-computing it may be faster than reading from the disk.

If you persist several RDDs and run out of memory, Spark will clear the least recently used out of memory (either discarding them or saving them to disk, depending on the chosen persistence level). RDDs also expose an `unpersist` method to explicitly tell Spark that an RDD is not needed any more.

Persisting RDDs can have a drastic impact on performance. What and how to persist therefore becomes very important when tuning a Spark application. Finding the best persistence level generally requires some tinkering, benchmarking and experimentation. The Spark documentation provides guidelines on when to use which persistence level (<http://spark.apache.org/docs/latest/programming-guide.html#rdd-persistence>), as well as general tips on tuning memory usage (<http://spark.apache.org/docs/latest/tuning.html>).

Importantly, the `persist` method does not force the evaluation of the RDD. It just notifies the Spark engine that, next time the values in this RDD are computed, they should be saved rather than discarded.

Key-value RDDs

So far, we have only considered RDDs of Scala value types. RDDs of more complex data types support additional operations. Spark adds many operations for *key-value RDDs*: RDDs whose type parameter is a tuple (κ, ν) , for any type κ and ν .

Let's go back to our sample email:

```
scala> val email = sc.textFile("ham/9-463msg1.txt")
email: rdd.RDD[String] = MapPartitionsRDD[1] at textFile
```

```
scala> val words = email.flatMap { line => line.split("\\s") }
words: rdd.RDD[String] = MapPartitionsRDD[2] at flatMap
```

Let's persist the `words` RDD in memory to avoid having to re-read the `email` file from disk repeatedly:

```
scala> words.persist
```

To access key-value operations, we just need to apply a transformation to our RDD that creates key-value pairs. Let's use the `words` as keys. For now, we will just use 1 for every value:

```
scala> val wordsKeyValue = words.map { _ -> 1 }
wordsKeyValue: rdd.RDD[(String, Int)] = MapPartitionsRDD[32] at map
```

```
scala> wordsKeyValue.first
(String, Int) = (Subject:,1)
```

Key-value RDDs support several operations besides the core RDD operations. These are added through an implicit conversion, using the "pimp my library" pattern that we explored in *Chapter 5, Scala and SQL through JDBC*. These additional transformations fall into two broad categories: *by-key* transformations and *joins* between RDDs.

By-key transformations are operations that aggregate the values corresponding to the same key. For instance, we can count the number of times each word appears in our email using `reduceByKey`. This method takes all the values that belong to the same key and combines them using a user-supplied function:

```
scala> val wordCounts = wordsKeyValue.reduceByKey { _ + _ }
wordCounts: rdd.RDD[(String, Int)] = ShuffledRDD[35] at reduceByKey

scala> wordCounts.take(5).foreach { println }
(university,6)
(under,1)
(call,3)
(paper,2)
(chasm,2)
```

Note that `reduceByKey` requires (in general) shuffling the RDD, since not every occurrence of a given key will be in the same partition:

```
scala> wordCounts.toDebugString
(2) ShuffledRDD[36] at reduceByKey at <console>:30 []
+- (2) MapPartitionsRDD[32] at map at <console>:28 []
    | MapPartitionsRDD[7] at flatMap at <console>:23 []
    |   CachedPartitions: 2; MemorySize: 50.3 KB;
ExternalBlockStoreSize: 0.0 B; DiskSize: 0.0 B
    | MapPartitionsRDD[3] at textFile at <console>:21 []
    |   CachedPartitions: 2; MemorySize: 5.1 KB;
ExternalBlockStoreSize: 0.0 B; DiskSize: 0.0 B
    |   ham/9-463msg1.txt HadoopRDD[2] at textFile at <console>:21 []
```

Note that key-value RDDs are not like Scala Maps: the same key can occur multiple times, and they do not support $O(1)$ lookup. A key-value RDD can be transformed to a Scala map using the `.collectAsMap` action:

```
scala> wordCounts.collectAsMap
scala.collection.Map[String,Int] = Map(follow -> 2, famous -> 1...
```

This requires pulling the entire RDD onto the main Spark node. You therefore need to have enough memory on the main node to house the map. This is often the last stage in a pipeline that filters a large RDD to just the information that we need.

There are many by-key operations, which we describe in the table below. For the examples in the table, we assume that `rdd` is created as follows:

```
scala> val words = sc.parallelize(List("quick", "brown", "quick", "dog"))
words: RDD[String] = ParallelCollectionRDD[25] at parallelize at
<console>:21
```

```
scala> val rdd = words.map { word => (word -> word.size) }
rdd: RDD[(String, Int)] = MapPartitionsRDD[26] at map at <console>:23
```

```
scala> rdd.collect
Array[(String, Int)] = Array((quick,5), (brown,5), (quick,5), (dog,3))
```

Transformation	Notes	Example (assumes rdd is { quick -> 5, brown -> 5, quick -> 5, dog -> 3 })
<code>rdd.mapValues</code>	Apply an operation to the values.	<code>rdd.mapValues { _ * 2 } // => { quick -> 10, brown -> 10, quick -> 10, dog -> 6 }</code>
<code>rdd.groupByKey</code>	Return a key-value RDD in which values corresponding to the same key are grouped into iterables.	<code>rdd.groupByKey // => { quick -> Iterable(5, 5), brown -> Iterable(5), dog -> Iterable(3) }</code>
<code>rdd.reduceByKey(func)</code>	Return a key-value RDD in which values corresponding to the same key are combined using a user-supplied function.	<code>rdd.reduceByKey { _ + _ } // => { quick -> 10, brown -> 5, dog -> 3 }</code>
<code>rdd.keys</code>	Return an RDD of the keys.	<code>rdd.keys // => { quick, brown, quick, dog }</code>
<code>rdd.values</code>	Return an RDD of the values.	<code>rdd.values // => { 5, 5, 5, 3 }</code>

The second category of operations on key-value RDDs involves joining different RDDs together by key. This is somewhat similar to SQL joins, where the keys are the column being joined on. Let's load a spam email and apply the same transformations we applied to our ham email:

```
scala> val spamEmail = sc.textFile("spam/spmsgb17.txt")
spamEmail: org.apache.spark.rdd.RDD[String] = MapPartitionsRDD[52] at
textFile at <console>:24

scala> val spamWords = spamEmail.flatMap { _.split("\\s") }
spamWords: org.apache.spark.rdd.RDD[String] = MapPartitionsRDD[53] at
flatMap at <console>:26

scala> val spamWordCounts = spamWords.map {
  _ -> 1 }.reduceByKey { _ + _ }
spamWordsCount: org.apache.spark.rdd.RDD[(String, Int)] = ShuffledRDD[55]
at reduceByKey at <console>:30

scala> spamWordCounts.take(5).foreach { println }
(banner,3)
(package,14)
(call,1)
(country,2)
(offer,1)
```

Both `spamWordCounts` and `wordCounts` are key-value RDDs for which the keys correspond to unique words in the message, and the values are the number of times that word occurs. There will be some overlap in keys between `spamWordCounts` and `wordCounts`, since the emails will share many of the same words. Let's do an *inner join* between those two RDDs to get the words that occur in both emails:

```
scala> val commonWordCounts = wordCounts.join(spamWordCounts)
res93: rdd.RDD[(String, (Int, Int))] = MapPartitionsRDD[58] at join at
<console>:41

scala> commonWordCounts.take(5).foreach { println }
(call, (3,1))
(include, (6,2))
(minute, (2,1))
(form, (1,7))
(, (36,5))
```

The values in the RDD resulting from an inner join will be pairs. The first element in the pair is the value for that key in the first RDD, and the second element is the value for that key in the second RDD. Thus, the word *call* occurs three times in the legitimate email and once in the spam email.

Spark supports all four join types. For instance, let's perform a left join:

```
scala> val leftWordCounts = wordCounts.leftOuterJoin(spamWordCounts)
leftWordCounts: rdd.RDD[(String, (Int, Option[Int]))] =
MapPartitionsRDD[64] at leftOuterJoin at <console>:40
```

```
scala> leftWordCounts.take(5).foreach { println }
(call, (3, Some(1)))
(paper, (2, None))
(chasm, (2, None))
(antonio, (1, None))
(event, (3, None))
```

Notice that the second element in our pair has type `Option[Int]`, to accommodate keys absent in `spamWordCounts`. The word *paper*, for instance, occurs twice in the legitimate email and never in the spam email. In this case, it is more useful to have zeros to indicate absence, rather than `None`. Replacing `None` with a default value is simple with `getOrElse`:

```
scala> val defaultWordCounts = leftWordCounts.mapValues {
  case (leftValue, rightValue) => (leftValue, rightValue.getOrElse(0))
}
org.apache.spark.rdd.RDD[(String, (Int, Option[Int]))] =
MapPartitionsRDD[64] at leftOuterJoin at <console>:40
```

```
scala> defaultwordCounts.take(5).foreach { println }
(call, (3, 1))
(paper, (2, 0))
(chasm, (2, 0))
(antonio, (1, 0))
(event, (3, 0))
```

The table below lists the most common joins on key-value RDDs:

Transformation	Result (assuming rdd1 is { quick -> 1, brown -> 2, quick -> 3, dog -> 4 } and rdd2 is { quick -> 78, brown -> 79, fox -> 80 })
rdd1.join(rdd2)	{ quick -> (1, 78), quick -> (3, 78), brown -> (2, 79) }
rdd1. leftOuterJoin(rdd2)	{ dog -> (4, None), quick -> (1, Some(78)), quick -> (3, Some(78)), brown -> (2, Some(79)) }
rdd1. rightOuterJoin(rdd2)	{ quick -> (Some(1), 78), quick -> (Some(3), 78), brown -> (Some(2), 79), fox -> (None, 80) }
rdd1. fullOuterJoin(rdd2)	{ dog -> (Some(4), None), quick -> (Some(1), Some(78)), quick -> (Some(3), Some(78)), brown -> (Some(2), Some(79)), fox -> (None, Some(80)) }

For a complete list of transformations, consult the API documentation for PairRDDFunctions, <http://spark.apache.org/docs/latest/api/scala/index.html#org.apache.spark.rdd.PairRDDFunctions>.

Double RDDs

In the previous section, we saw that Spark adds functionality to key-value RDDs through an implicit conversion. Similarly, Spark adds statistics functionality to RDDs of doubles. Let's extract the word frequencies for the ham message, and convert the values from integers to doubles:

```
scala> val counts = wordCounts.values.map { _.toDouble }
counts: rdd.RDD[Double] = MapPartitionsRDD[9] at map
```

We can then get summary statistics using the `.stats` action:

```
scala> counts.stats
org.apache.spark.util.StatCounter = (count: 397, mean: 2.365239, stdev: 5.740843, max: 72.000000, min: 1.000000)
```

Thus, the most common word appears 72 times. We can also use the `.histogram` action to get an idea of the distribution of values:

```
scala> counts.histogram(5)
(Array(1.0, 15.2, 29.4, 43.6, 57.8, 72.0), Array(391, 1, 3, 1, 1))
```

The `.histogram` method returns a pair of arrays. The first array indicates the bounds of the histogram bins, and the second is the count of elements in that bin. Thus, there are 391 words that appear less than 15.2 times. The distribution of words is very skewed, such that a histogram with regular-sized bin is not really appropriate. We can, instead, pass in custom bins by passing an array of bin edges to the `histogram` method. For instance, we might distribute the bins logarithmically:

```
scala> counts.histogram(Array(1.0, 2.0, 4.0, 8.0, 16.0, 32.0, 64.0,
128.0))
res13: Array[Long] = Array(264, 94, 22, 11, 1, 4, 1)
```

Building and running standalone programs

So far, we have interacted exclusively with Spark through the Spark shell. In the section that follows, we will build a standalone application and launch a Spark program either locally or on an EC2 cluster.

Running Spark applications locally

The first step is to write the `build.sbt` file, as you would if you were running a standard Scala script. The Spark binary that we downloaded needs to be run against Scala 2.10 (You need to compile Spark from source to run against Scala 2.11. This is not difficult to do, just follow the instructions on <http://spark.apache.org/docs/latest/building-spark.html#building-for-scala-211>).

```
// build.sbt file

name := "spam_mi"

scalaVersion := "2.10.5"

libraryDependencies ++= Seq(
  "org.apache.spark" %% "spark-core" % "1.4.1"
)
```

We then run `sbt package` to compile and build a jar of our program. The jar will be built in `target/scala-2.10/`, and called `spam_mi_2.10-0.1-SNAPSHOT.jar`. You can try this with the example code provided for this chapter.

We can then run the jar locally using the `spark-submit` shell script, available in the `bin/` folder in the Spark installation directory:

```
$ spark-submit target/scala-2.10/spam_mi_2.10-0.1-SNAPSHOT.jar
... runs the program
```

The resources allocated to Spark can be controlled by passing arguments to `spark-submit`. Use `spark-submit --help` to see the full list of arguments.

If the Spark programs has dependencies (for instance, on other Maven packages), it is easiest to bundle them into the application jar using the *SBT assembly* plugin. Let's imagine that our application depends on `breeze-viz`. The `build.sbt` file now looks like:

```
// build.sbt

name := "spam_mi"

scalaVersion := "2.10.5"

libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % "1.5.2" % "provided",
  "org.scalanlp" %% "breeze" % "0.11.2",
  "org.scalanlp" %% "breeze-viz" % "0.11.2",
  "org.scalanlp" %% "breeze-natives" % "0.11.2"
)
```

SBT *assembly* is an SBT plugin that builds *fat* jars: jars that contain not only the program itself, but all the dependencies for the program.

Note that we marked Spark as "provided" in the list of dependencies, which means that Spark itself will not be included in the jar (it is provided by the Spark environment anyway). To include the SBT *assembly* plugin, create a file called `assembly.sbt` in the `project/` directory, with the following line:

```
addSbtPlugin("com.eed3si9n" % "sbt-assembly" % "0.14.0")
```

You will need to re-start SBT for the changes to take effect. You can then create the assembly jar using the `assembly` command in SBT. This will create a jar called `spam_mi-assembly-0.1-SNAPSHOT.jar` in the `target/scala-2.10` directory. You can run this jar using `spark-submit`.

Reducing logging output and Spark configuration

Spark is, by default, very verbose. The default log-level is set to `INFO`. To avoid missing important messages, it is useful to change the log settings to `WARN`. To change the default log level system-wide, go into the `conf` directory in the directory in which you installed Spark. You should find a file called `log4j.properties.template`. Rename this file to `log4j.properties` and look for the following line:

```
log4j.rootCategory=INFO, console
```

Change this line to:

```
log4j.rootCategory=WARN, console
```

There are several other configuration files in that directory that you can use to alter Spark's default behavior. For a full list of configuration options, head over to <http://spark.apache.org/docs/latest/configuration.html>.

Running Spark applications on EC2

Running Spark locally is useful for testing, but the whole point of using a distributed framework is to run programs harnessing the power of several different computers. We can set Spark up on any set of computers that can communicate with each other using HTTP. In general, we also need to set up a distributed file system like HDFS, so that we can share input files across the cluster. For the purpose of this example, we will set Spark up on an Amazon EC2 cluster.

Spark comes with a shell script, `ec2/spark-ec2`, for setting up an EC2 cluster and installing Spark. It will also install HDFS. You will need an account with Amazon Web Services (AWS) to follow these examples (<https://aws.amazon.com>). You will need the AWS access key and secret key, which you can access through the **Account / Security Credentials / Access Credentials** menu in the AWS web console. You need to make these available to the `spark-ec2` script through environment variables. Inject them into your current session as follows:

```
$ export AWS_ACCESS_KEY_ID=ABCDEF...
$ export AWS_SECRET_ACCESS_KEY=2dEf...
```

You can also write these lines into the configuration script for your shell (your `.bashrc` file, or equivalent), to avoid having to re-enter them every time you run the `setup-ec2` script. We discussed environment variables in *Chapter 6, Slick – A Functional Interface for SQL*.

You will also need to create a key pair by clicking on **Key Pairs** in the EC2 web console, creating a new key pair and downloading the certificate file. I will assume you named the key pair `test_ec2` and the certificate file `test_ec2.pem`. Make sure that the key pair is created in the *N. Virginia* region (by choosing the correct region in the upper right corner of the EC2 Management console), to avoid having to specify the region explicitly in the rest of this chapter. You will need to set access permissions on the certificate file to user-readable only:

```
$ chmod 400 test_ec2.pem
```

We are now ready to launch the cluster. Navigate to the `ec2` directory and run:

```
$ ./spark-ec2 -k test_ec2 -i ~/path/to/certificate/test_ec2.pem -s 2
  launch test_cluster
```

This will create a cluster called `test_cluster` with a master and two slaves. The number of slaves is set through the `-s` command line argument. The cluster will take a while to start up, but you can verify that the instances are launching correctly by looking at the **Instances** window in the EC2 Management Console.

The setup script supports many options for customizing the type of instances, the number of hard drives and so on. You can explore these options by passing the `--help` command line option to `spark-ec2`.

The life cycle of the cluster can be controlled by passing different commands to the `spark-ec2` script, such as:

```
# shut down 'test_cluster'
$ ./spark-ec2 stop test_cluster

# start 'test_cluster'
$ ./spark-ec2 -i test_ec2.pem start test_cluster

# destroy 'test_cluster'
$ ./spark-ec2 destroy test_cluster
```

For more detail on using Spark on EC2, consult the official documentation at <http://spark.apache.org/docs/latest/ec2-scripts.html#running-applications>.

Spam filtering

Let's put all we've learned to good use and do some data exploration for our spam filter. We will use the Ling-Spam email dataset: <http://csmining.org/index.php/ling-spam-datasets.html>. The dataset contains 2412 ham emails and 481 spam emails, all of which were received by a mailing list on linguistics. We will extract the words that are most informative of whether an email is spam or ham.

The first steps in any natural language processing workflow are to remove stop words and lemmatization. Removing stop words involves filtering very common words such as *the*, *this* and so on. Lemmatization involves replacing different forms of the same word with a canonical form: both *colors* and *color* would be mapped to *color*, and *organize*, *organizing* and *organizes* would be mapped to *organize*. Removing stop words and lemmatization is very challenging, and beyond the scope of this book (if you do need to remove stop words and lemmatize a dataset, your go-to tool should be the Stanford NLP toolkit: <http://nlp.stanford.edu/software/corenlp.shtml>). Fortunately, the Ling-Spam e-mail dataset has been cleaned and lemmatized already (which is why the text in the emails looks strange).


When we do build the spam filter, we will use the presence of a particular word in an email as the feature for our model. We will use a *bag-of-words* approach: we consider which words appear in an email, but not the word order.

Intuitively, some words will be more important than others when deciding whether an email is spam. For instance, an email that contains *language* is likely to be ham, since the mailing list was for linguistics discussions, and *language* is a word unlikely to be used by spammers. Conversely, words which are common to both message types, for instance *hello*, are unlikely to be much use.

One way of quantifying the importance of a word in determining whether a message is spam is through the **Mutual Information (MI)**. The mutual information is the gain in information about whether a message is ham or spam if we know that it contains a particular word. For instance, the presence of *language* in a particular email is very informative as to whether that email is spam or ham. Similarly, the presence of the word *dollar* is informative since it appears often in spam messages and only infrequently in ham messages. By contrast, the presence of the word *morning* is uninformative, since it is approximately equally common in both spam and ham messages. The formula for the mutual information between the presence of a particular word in an email, and whether that email is spam or ham is:

$$MI(\text{word}) = \sum_{\substack{\text{wordPresent} \in \{\text{true}, \text{false}\} \\ \text{class} \in \{\text{spam}, \text{ham}\}}} P(\text{wordPresent}, \text{class}) \cdot \log_2 \frac{P(\text{wordPresent}, \text{class})}{P(\text{wordPresent})P(\text{class})}$$

where $P(\text{wordPresent}, \text{class})$ is the joint probability of an email containing a particular word and being of that class (either ham or spam), $P(\text{wordPresent})$ is the probability that a particular word is present in an email, and $P(\text{class})$ is the probability that any email is of that class. The MI is commonly used in decision trees.

 The derivation of the expression for the mutual information is beyond the scope of this book. The interested reader is directed to David MacKay's excellent *Information Theory, Inference, and Learning Algorithms*, especially the chapter *Dependent Random Variables*.

A key component of our MI calculation is evaluating the probability that a word occurs in spam or ham messages. The best approximation to this probability, given our data set, is the fraction of messages a word appears in. Thus, for instance, if *language* appears in 40% of messages, we will assume that the probability $P(\text{languagePresent})$ of language being present in any message is 0.4. Similarly, if 40% of the messages are ham, and *language* appears in 50% of those, we will assume that the probability of language being present in an email, and that email being ham is $P(\text{languagePresent}, \text{ham}) = 0.5 \times 0.4 = 0.2$.

Let's write a `wordFractionInFiles` function to calculate the fraction of messages in which each word appears, for all the words in a given corpus. Our function will take, as argument, a path with a shell wildcard identifying a set of files, such as `ham/*`, and it will return a key-value RDD, where the keys are words and the values are the probability that that word occurs in any of those files. We will put the function in an object called `MutualInformation`.

We first give the entire code listing for this function. Don't worry if this doesn't all make sense straight-away: we explain the tricky parts in more detail just after the code. You may find it useful to type some of these commands in the shell, replacing `fileGlob` with, for instance `"ham/*"`:

```
// MutualInformation.scala
import org.apache.spark.{ SparkConf, SparkContext }
import org.apache.spark.spark.SparkContext._
import org.apache.spark.rdd.RDD

object MutualInformation extends App {

  def wordFractionInFiles(sc:SparkContext)(fileGlob:String)
  : (RDD[(String, Double)], Long) = {

    // A set of punctuation words that need to be filtered out.
    val wordsToOmit = Set[String](
      "", ".", ",", ":", "-", "\"", "'", ")",
```

```
    ("", "@", "/", "Subject:"
    )

    val messages = sc.wholeTextFiles(fileGlob)
    // wholeTextFiles generates a key-value RDD of
    // file name -> file content

    val nMessages = messages.count()

    // Split the content of each message into a Set of unique
    // words in that message, and generate a new RDD mapping:
    // message -> word
    val message2Word = messages.flatMapValues {
      mailBody => mailBody.split("\\s").toSet
    }

    val message2FilteredWords = message2Word.filter {
      case(email, word) => ! wordsToOmit(word)
    }

    val word2Message = message2FilteredWords.map { _.swap }

    // word -> number of messages it appears in.
    val word2NumberMessages = word2Message.mapValues {
      _ => 1
    }.reduceByKey { _ + _ }

    // word -> fraction of messages it appears in
    val pPresent = word2NumberMessages.mapValues {
      _ / nMessages.toDouble
    }

    (pPresent, nMessages)
  }
}
```

Let's play with this function in the Spark shell. To be able to access this function from the shell, we need to create a jar with the `MutualInformation` object. Write a `build.sbt` file similar to the one presented in the previous section and package the code into a jar using `sbt package`. Then, open a Spark shell with:

```
$ spark-shell --jars=target/scala-2.10/spam_mi_2.10-0.1-SNAPSHOT.jar
```

This will open a Spark shell with our newly created jar on the classpath. Let's run our `wordFractionInFiles` method on the ham emails:

```
scala> import MutualInformation._
import MutualInformation._

scala> val (fractions, nMessages) = wordFractionInFiles(sc)("ham/*")
fractions: org.apache.spark.rdd.RDD[(String, Double)] =
MapPartitionsRDD[13] at mapValues
nMessages: Long = 2412
```

Let's get a snapshot of the `fractions` RDD:

```
scala> fractions.take(5)
Array[(String, Double)] = Array((rule-base,0.002902155887230514), (re
union,4.1459369817578774E-4), (embarrassingly,4.1459369817578774E-4),
(mller,8.291873963515755E-4), (sapore,4.1459369817578774E-4))
```

It would be nice to see the words that come up most often in ham messages. We can use the `.takeOrdered` action to take the top values of an RDD, with a custom ordering. `.takeOrdered` expects, as its second argument, an instance of the type class `Ordering[T]`, where `T` is the type parameter of our RDD: `(String, Double)` in this case. `Ordering[T]` is a trait with a single `compare(a:T, b:T)` method describing how to compare `a` and `b`. The easiest way of creating an `Ordering[T]` is through the companion object's `by` method, which defines a key by which to compare the elements of our RDD.

We want to order the elements in our key-value RDD by the value and, since we want the most common words, rather than the least, we need to reverse that ordering:

```
scala> fractions.takeOrdered(5)(Ordering.by { - _. _2 })
res0: Array[(String, Double)] = Array((language,0.6737147595356551),
(university,0.6048922056384743), (linguistic,0.5149253731343284),
(information,0.45480928689883915), ('s,0.4369817578772803))
```

Unsurprisingly, `language` is present in 67% of ham emails, `university` in 60% of ham emails and so on. A similar investigation on spam messages reveals that the exclamation mark character `!` is present in 83% of spam emails, `our` is present in 61% and `free` in 57%.

We are now in a position to start writing the body of our application to calculate the mutual information between each word and whether a message is spam or ham. We will put the body of the code in the `MutualInformation` object, which already contains the `wordFractionInFiles` method.

The first step is to create a Spark context:

```
// MutualInformation.scala
import org.apache.spark.{ SparkConf, SparkContext }
import org.apache.spark.SparkContext._
import org.apache.spark.rdd.RDD

object MutualInformation extends App {

  def wordFractionInFiles(sc:SparkContext)(fileGlob:String)
  : (RDD[(String, Double)], Long) = {
    ...
  }

  val conf = new SparkConf().setAppName("lingSpam")
  val sc = new SparkContext(conf)
```

Note that we did not need to do this when we were using the Spark shell because the shell comes with a pre-built context bound to the variable `sc`.

We can now calculate the conditional probabilities of a message containing a particular word given that it is *spam*, $P(\text{wordPresent} | \text{spam})$. This is just the fraction of messages containing that word in the *spam* corpus. This, in turn, lets us infer the joint probability of a message containing a certain word and being *spam* $P(\text{wordPresent}, \text{spam}) = P(\text{wordPresent} | \text{spam}) \times P(\text{spam})$. We will do this for all four combinations of classes: whether any given word is present or absent in a message, and whether that message is spam or ham:

```
/* Conditional probabilities RDD:
   word -> P(present | spam)
*/
val (pPresentGivenSpam, nSpam) = wordFractionInFiles(sc)("spam/*")
val pAbsentGivenSpam = pPresentGivenSpam.mapValues { 1.0 - _ }
val (pPresentGivenHam, nHam) = wordFractionInFiles(sc)("ham/*")
val pAbsentGivenHam = pPresentGivenHam.mapValues { 1.0 - _ }

// pSpam is the fraction of spam messages
val nMessages = nSpam + nHam
val pSpam = nSpam / nMessages.toDouble

// pHam is the fraction of ham messages
```

```

val pHam = 1.0 - pSpam

/* pPresentAndSpam is a key-value RDD of joint probabilities
   word -> P(word present, spam)
*/
val pPresentAndSpam = pPresentGivenSpam.mapValues {
  _ * pSpam
}
val pPresentAndHam = pPresentGivenHam.mapValues { _ * pHam }
val pAbsentAndSpam = pAbsentGivenSpam.mapValues { _ * pSpam }
val pAbsentAndHam = pAbsentGivenHam.mapValues { _ * pHam }

```

We will re-use these RDDs in several places in the calculation, so let's tell Spark to keep them in memory to avoid having to re-calculate them:

```

pPresentAndSpam.persist
pPresentAndHam.persist
pAbsentAndSpam.persist
pAbsentAndHam.persist

```

We now need to calculate the probabilities of words being present, $P(\text{wordPresent})$. This is just the sum of `pPresentAndSpam` and `pPresentAndHam`, for each word. The tricky part is that not all words are present in both the ham and spam messages. We must therefore do a full outer join of those RDDs. This will give an RDD mapping each word to a pair of `Option[Double]` values. For words absent in either the ham or spam messages, we must use a default value. A sensible default is $P(\text{wordPresent} | \text{spam}) = (0.5 / n\text{Spam}) \times P(\text{spam})$ for spam messages (a more rigorous approach would be to use *additive smoothing*). This implies that the word would appear once if the corpus was twice as large.

```

val pJoined = pPresentAndSpam.fullOuterJoin(pPresentAndHam)
val pJoinedDefault = pJoined.mapValues {
  case (presentAndSpam, presentAndHam) =>
    (presentAndSpam.getOrElse(0.5/nSpam * pSpam),
     presentAndHam.getOrElse(0.5/nHam * pHam))
}

```

Note that we could also have chosen 0 as the default value. This complicates the information gain calculation somewhat, since we cannot just take the log of a zero value, and it seems unlikely that a particular word has exactly zero probability of occurring in an email.

We can now construct an RDD mapping words to $P(\text{wordPresent})$, the probability that a word exists in either a spam or a ham message:

```
val pPresent = pJoinedDefault.mapValues {
  case (presentAndHam, presentAndSpam) =>
    presentAndHam + presentAndSpam
}
pPresent.persist

val pAbsent = pPresent.mapValues { 1.0 - _ }
pAbsent.persist
```

We now have all the RDDs that we need to calculate the mutual information between the presence of a word in a message and whether it is ham or spam. We need to bring them all together using the equation for the mutual information outlined earlier.

We will start by defining a helper method that, given an RDD of joint probabilities $P(X, Y)$ and marginal probabilities $P(X)$ and $P(Y)$, calculates $P(X, Y) \times \log\left(\frac{P(X, Y)}{P(X)P(Y)}\right)$. Here, $P(X)$ could, for instance, be the probability of a word being present in a message $P(\text{wordPresent})$ and $P(Y)$ would be the probability that that message is spam, $P(\text{spam})$:

```
def miTerm(
  pXYs: RDD[(String, Double)],
  pXs: RDD[(String, Double)],
  pY: Double,
  default: Double // for words absent in PXY
): RDD[(String, Double)] =
  pXs.leftOuterJoin(pXYs).mapValues {
    case (pX, Some(pXY)) => pXY * math.log(pXY / (pX * pY))
    case (pX, None) => default * math.log(default / (pX * pY))
  }
```

We can use our function to calculate the four terms in the mutual information sum:

```
val miTerms = List(
  miTerm(pPresentAndSpam, pPresent, pSpam, 0.5/nSpam * pSpam),
  miTerm(pPresentAndHam, pPresent, pHam, 0.5/nHam * pHam),
  miTerm(pAbsentAndSpam, pAbsent, pSpam, 0.5/nSpam * pSpam),
  miTerm(pAbsentAndHam, pAbsent, pHam, 0.5/nHam * pHam)
)
```

Finally, we just need to sum those four terms together:

```
val mutualInformation = miTerms.reduce {
  (term1, term2) => term1.join(term2).mapValues {
    case (l, r) => l + r
  }
}
```

The RDD `mutualInformation` is a key-value RDD mapping each word to a measure of how informative the presence of that word is in discerning whether a message is spam or ham. Let's print out the twenty words that are most informative of whether a message is ham or spam:

```
mutualInformation.takeOrdered(20)(Ordering.by { -_._2 })
  .foreach { println }
```

Let's run this using `spark-submit`:

```
$ sbt package
$ spark-submit target/scala-2.10/spam_mi_2.10-0.1-SNAPSHOT.jar
(!,0.1479941771292119)
(language,0.14574624861510874)
(remove,0.11380645864246142)
(free,0.1073496947123657)
(university,0.10695975885487692)
(money,0.07531772498093084)
(click,0.06887598051593441)
(our,0.058950906866052394)
(today,0.05485248095680509)
(sell,0.05385519653184113)
(english,0.053509319455430575)
(business,0.05299311289740539)
(market,0.05248394151802276)
(product,0.05096229706182162)
(million,0.050233193237964546)
(linguistics,0.04990172586630499)
(internet,0.04974101556655623)
(company,0.04941817269989519)
(%,0.04890193809823071)
(save,0.04861393414892205)
```

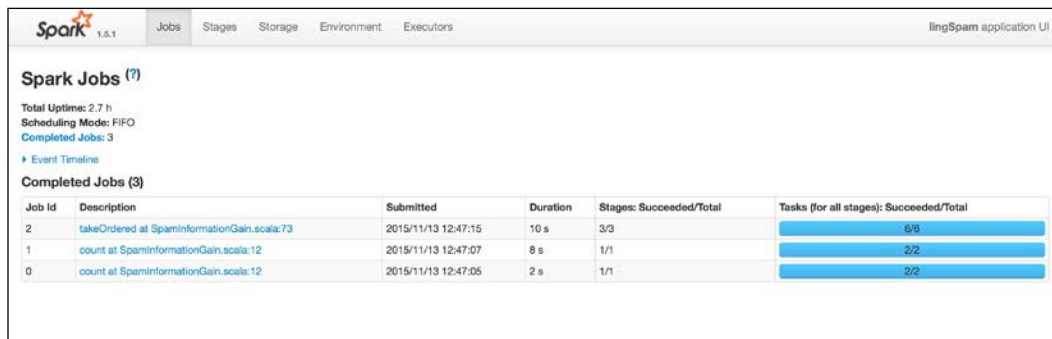
Thus, we find that the presence of words like `language` or `free` or `!` carry the most information, because they are almost exclusively present in either just spam messages or just ham messages. A very simple classification algorithm could just take the top 10 (by mutual information) spam words, and the top 10 ham words and see whether a message contains more spam words or ham words. We will explore machine learning algorithms for classification in more depth in *Chapter 12, Distributed Machine Learning with MLlib*.

Lifting the hood

In the last section of this chapter, we will discuss, very briefly, how Spark works internally. For a more detailed discussion, see the *References* section at the end of the chapter.

When you open a Spark context, either explicitly or by launching the Spark shell, Spark starts a web UI with details of how the current task and past tasks have executed. Let's see this in action for the example mutual information program we wrote in the last section. To prevent the context from shutting down when the program completes, you can insert a call to `readLine` as the last line of the `main` method (after the call to `takeOrdered`). This expects input from the user, and will therefore pause program execution until you press *enter*.

To access the UI, point your browser to `127.0.0.1:4040`. If you have other instances of the Spark shell running, the port may be `4041`, or `4042` and so on.



The screenshot shows the Spark Jobs UI for a 'lingSpam application UI'. It displays a table of completed jobs with the following data:

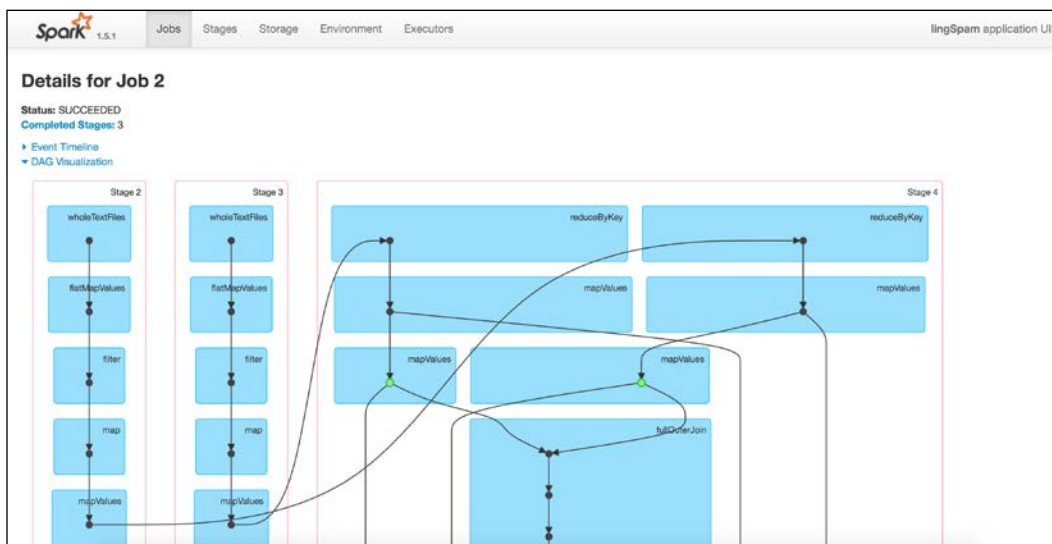
Job Id	Description	Submitted	Duration	Stages: Succeeded/Total	Tasks (for all stages): Succeeded/Total
2	takeOrdered at SpamInformationGain.scala:73	2015/11/13 12:47:15	10 s	3/3	6/6
1	count at SpamInformationGain.scala:12	2015/11/13 12:47:07	8 s	1/1	2/2
0	count at SpamInformationGain.scala:12	2015/11/13 12:47:05	2 s	1/1	2/2

The first page of the UI tells us that our application contains three *jobs*. A job occurs as the result of an action. There are, indeed, three actions in our application: the first two are called within the `wordFractionInFiles` function:

```
val nMessages = messages.count()
```

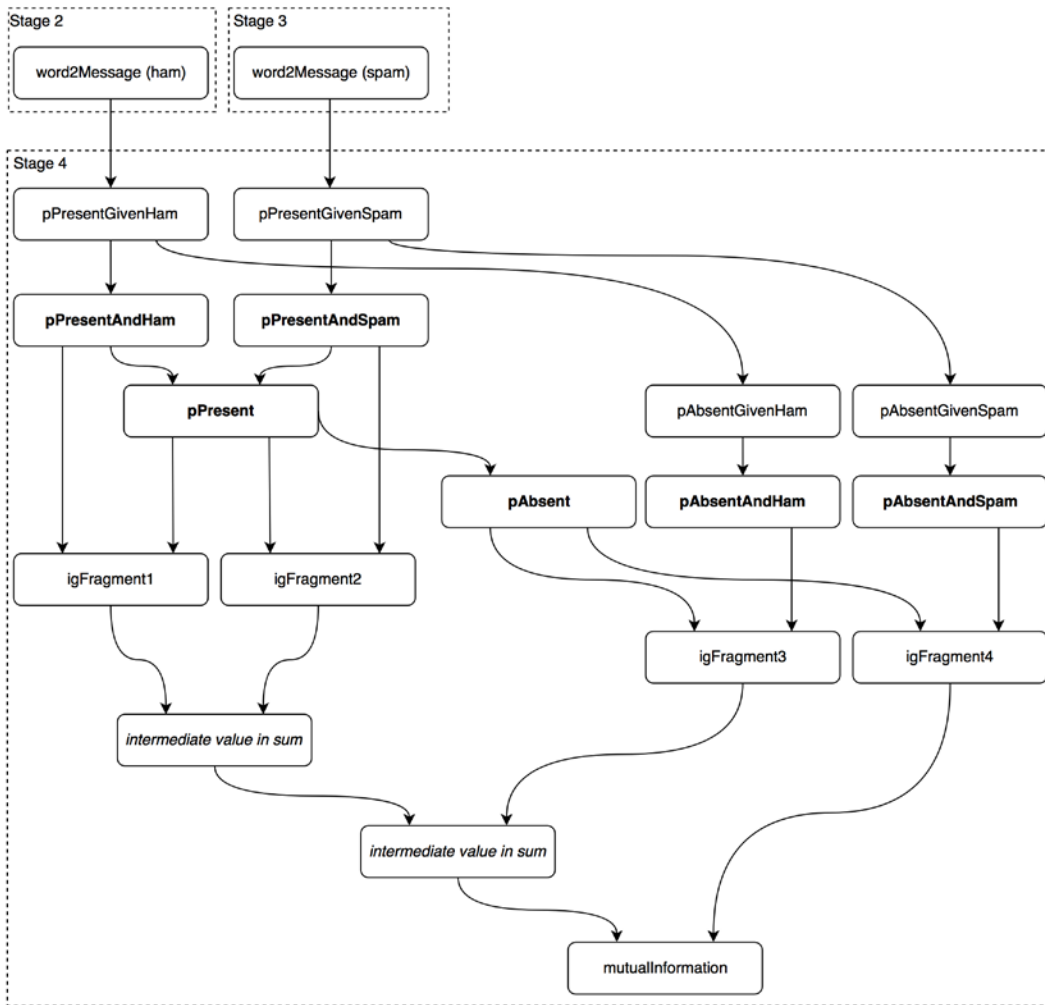
The last job results from the call to `takeOrdered`, which forces the execution of the entire pipeline of RDD transformations that calculate the mutual information.

The web UI lets us delve deeper into each job. Click on the `takeOrdered` job in the job table. You will get taken to a page that describes the job in more detail:



Of particular interest is the **DAG visualization** entry. This is a graph of the execution plan to fulfill the action, and provides a glimpse of the inner workings of Spark.

When you define a job by calling an action on an RDD, Spark looks at the RDD's lineage and constructs a graph mapping the dependencies: each RDD in the lineage is represented by a node, with directed edges going from this RDD's parent to itself. This type of graph is called a **directed acyclic graph (DAG)**, and is a data structure useful for dependency resolution. Let's explore the DAG for the `takeOrdered` job in our program using the web UI. The graph is quite complex, and it is therefore easy to get lost, so here is a simplified reproduction that only lists the RDDs bound to variable names in the program.



As you can see, at the bottom of the graph, we have the `mutualInformation` RDD. This is the RDD that we need to construct for our action. This RDD depends on the intermediate elements in the `sum`, `igFragment1`, `igFragment2`, and so on. We can work our way back through the list of dependencies until we reach the other end of the graph: RDDs that do not depend on other RDDs, only on external sources.

Once the graph is built, the Spark engine formulates a plan to execute the job. The plan starts with the RDDs that only have external dependencies (such as RDDs built by loading files from disk or fetching from a database) or RDDs that already have cached data. Each arrow along the graph is translated to a set of *tasks*, with each task applying a transformation to a partition of the data.

Tasks are grouped into *stages*. A stage consists of a set of tasks that can all be performed without needing an intermediate shuffle.

Data shuffling and partitions

To understand data shuffling in Spark, we first need to understand how data is partitioned in RDDs. When we create an RDD by, for instance, loading a file from HDFS, or reading a file in local storage, Spark has no control over what bits of data are distributed in which partitions. This becomes a problem for key-value RDDs: these often require knowing where occurrences of a particular key are, for instance to perform a join. If the key can occur anywhere in the RDD, we have to look through every partition to find the key.

To prevent this, Spark allows the definition of a *partitioner* on key-value RDDs. A partitioner is an attribute of the RDD that determines which partition a particular key lands in. When an RDD has a partitioner set, the location of a key is entirely determined by the partitioner, and not by the RDD's history, or the number of keys. Two different RDDs with the same partitioner will map the same key to the same partition.

Partitions impact performance through their effect on transformations. There are two types of transformations on key-value RDDs:

- Narrow transformations, like `mapValues`. In narrow transformations, the data to compute a partition in the child RDD resides on a single partition in the parent. The data processing for a narrow transformation can therefore be performed entirely locally, without needing to communicate data between nodes.
- Wide transformations, like `reduceByKey`. In wide transformations, the data to compute any single partition can reside on all the partitions in the parent. The RDD resulting from a wide transformation will, in general, have a partitioner set. For instance, the output of a `reduceByKey` transformation are hash-partitioned by default: the partition that a particular key ends up in is determined by `hash(key) % numPartitions`.

Thus, in our mutual information example, the RDDs `pPresentAndSpam` and `pPresentAndHam` will have the same partition structure since they both have the default hash partitioner. All descendent RDDs retain the same keys, all the way down to `mutualInformation`. The word `language`, for instance, will be in the same partition for each RDD.

Why does all this matter? If an RDD has a partitioner set, this partitioner is retained through all subsequent narrow transformations originating from this RDD. Let's go back to our mutual information example. The RDDs `pPresentGivenHam` and `pPresentGivenSpam` both originate from `reduceByKey` operations, and they both have string keys. They will therefore both have the same hash-partitioner (unless we explicitly set a different partitioner). This partitioner is retained as we construct `pPresentAndSpam` and `pPresentAndHam`. When we construct `pPresent`, we perform a full outer join of `pPresentAndSpam` and `pPresentAndHam`. Since both these RDDs have the same partitioner, the child RDD `pPresent` has narrow dependencies: we can just join the first partition of `pPresentAndSpam` with the first partition of `pPresentAndHam`, the second partition of `pPresentAndSpam` with the second partition of `pPresentAndHam` and so on, since any string key will be hashed to the same partition in both RDDs. By contrast, without partitioner, we would have to join the data in each partition of `pPresentAndSpam` with every partition of `pPresentAndHam`. This would require sending data across the network to all the nodes holding `pPresentAndSpam`, a time-consuming exercise.

This process of having to send the data to construct a child RDD across the network, as a result of wide dependencies, is called *shuffling*. Much of the art of optimizing a Spark program involves reducing shuffling and, when shuffling is necessary, reducing the amount of shuffling.

Summary

In this chapter, we explored the basics of Spark and learned how to construct and manipulate RDDs. In the next chapter, we will learn about Spark SQL and DataFrames, a set of implicit conversions that allow us to manipulate RDDs in a manner similar to pandas DataFrames, and how to interact with different data sources using Spark.

Reference

- *Learning Spark*, by Holden Karau, Andy Konwinski, Patrick Wendell, and Matei Zaharia, O'Reilly, provides a much more complete introduction to Spark that this chapter can provide. I thoroughly recommend it.
- If you are interested in learning more about information theory, I recommend David MacKay's book *Information Theory, Inference, and Learning Algorithms*.
- *Information Retrieval*, by Manning, Raghavan, and Schütze, describes how to analyze textual data (including lemmatization and stemming). An online
- On the Ling-Spam dataset, and how to analyze it: http://www.aueb.gr/users/ion/docs/ir_memory_based_antispam_filtering.pdf.
- This blog post delves into the Spark Web UI in more detail. <https://databricks.com/blog/2015/06/22/understanding-your-spark-application-through-visualization.html>.
- This blog post, by Sandy Ryza, is the first in a two-part series discussing Spark internals, and how to leverage them to improve performance: <http://blog.cloudera.com/blog/2015/03/how-to-tune-your-apache-spark-jobs-part-1/>.

11

Spark SQL and DataFrames

In the previous chapter, we learned how to build a simple distributed application using Spark. The data that we used took the form of a set of e-mails stored as text files.

We learned that Spark was built around the concept of **resilient distributed datasets (RDDs)**. We explored several types of RDDs: simple RDDs of strings, key-value RDDs, and RDDs of doubles. In the case of key-value RDDs and RDDs of doubles, Spark added functionality beyond that of the simple RDDs through implicit conversions. There is one important type of RDD that we have not explored yet: **DataFrames** (previously called **SchemaRDD**). DataFrames allow the manipulation of objects significantly more complex than those we have explored to date.

A DataFrame is a distributed tabular data structure, and is therefore very useful for representing and manipulating structured data. In this chapter, we will first investigate DataFrames through the Spark shell, and then use the Ling-spam e-mail dataset, presented in the previous chapter, to see how DataFrames can be integrated in a machine learning pipeline.

DataFrames – a whirlwind introduction

Let's start by opening a Spark shell:

```
$ spark-shell
```

Let's imagine that we are interested in running analytics on a set of patients to estimate their overall health level. We have measured, for each patient, their height, weight, age, and whether they smoke.

We might represent the readings for each patient as a case class (you might wish to write some of this in a text editor and paste it into the Scala shell using `:paste`):

```
scala> case class PatientReadings(  
  val patientId: Int,  
  val heightCm: Int,  
  val weightKg: Int,  
  val age: Int,  
  val isSmoker: Boolean  
)  
defined class PatientReadings
```

We would, typically, have many thousands of patients, possibly stored in a database or a CSV file. We will worry about how to interact with external sources later in this chapter. For now, let's just hard-code a few readings directly in the shell:

```
scala> val readings = List(  
  PatientReadings(1, 175, 72, 43, false),  
  PatientReadings(2, 182, 78, 28, true),  
  PatientReadings(3, 164, 61, 41, false),  
  PatientReadings(4, 161, 62, 43, true)  
)  
List[PatientReadings] = List(...
```

We can convert readings to an RDD by using `sc.parallelize`:

```
scala> val readingsRDD = sc.parallelize(readings)  
readingsRDD: RDD[PatientReadings] = ParallelCollectionRDD[0] at  
parallelize at <console>:25
```

Note that the type parameter of our RDD is `PatientReadings`. Let's convert the RDD to a DataFrame using the `.toDF` method:

```
scala> val readingsDF = readingsRDD.toDF  
readingsDF: sql.DataFrame = [patientId: int, heightCm: int, weightKg:  
int, age: int, isSmoker: boolean]
```

We have created a DataFrame where each row corresponds to the readings for a specific patient, and the columns correspond to the different features:

```
scala> readingsDF.show
+-----+-----+-----+----+-----+
|patientId|heightCm|weightKg|age|isSmoker|
+-----+-----+-----+----+-----+
|      1 |    175 |     72 | 43 |   false |
|      2 |    182 |     78 | 28 |    true |
|      3 |    164 |     61 | 41 |   false |
|      4 |    161 |     62 | 43 |    true |
+-----+-----+-----+----+-----+
```

The easiest way to create a DataFrame is to use the `toDF` method on an RDD. We can convert any `RDD[T]`, where `T` is a case class or a tuple, to a DataFrame. Spark will map each attribute of the case class to a column of the appropriate type in the DataFrame. It uses reflection to discover the names and types of the attributes. There are several other ways of constructing DataFrames, both from RDDs and from external sources, which we will explore later in this chapter.

DataFrames support many operations for manipulating the rows and columns. For instance, let's add a column for the **Body Mass Index (BMI)**. The BMI is a common way of aggregating *height* and *weight* to decide if someone is overweight or underweight. The formula for the BMI is:

$$BMI = weight(kg) / height(m)^2$$

Let's start by creating a column of the height in meters:

```
scala> val heightM = readingsDF("heightCm") / 100.0
heightM: sql.Column = (heightCm / 100.0)
```

`heightM` has data type `Column`, representing a column of data in a DataFrame. Columns support many arithmetic and comparison operators that apply element-wise across the column (similarly to Breeze vectors encountered in *Chapter 2, Manipulating Data with Breeze*). Operations on columns are lazy: the `heightM` column is not actually computed when defined. Let's now define a BMI column:

```
scala> val bmi = readingsDF("weightKg") / (heightM*heightM)
bmi: sql.Column = (weightKg / ((heightCm / 100.0) * (heightCm / 100.0)))
```

It would be useful to add the `bmi` column to our `readings` DataFrame. Since DataFrames, like RDDs, are immutable, we must define a new DataFrame that is identical to `readingsDF`, but with an additional column for the BMI. We can do this using the `withColumn` method, which takes, as its arguments, the name of the new column and a `Column` instance:

```
scala> val readingsWithBmiDF = readingsDF.withColumn("BMI", bmi)
readingsWithBmiDF: sql.DataFrame = [heightCm: int, weightKg: int, age: int, isSmoker: boolean, BMI: double]
```

All the operations we have seen so far are *transformations*: they define a pipeline of operations that create new DataFrames. These transformations are executed when we call an **action**, such as `show`:

```
scala> readingsWithBmiDF.show
+-----+-----+-----+-----+-----+-----+
|patientId|heightCm|weightKg|age|isSmoker|          BMI|
+-----+-----+-----+-----+-----+-----+
|         1|      175|       72| 43|   false|23.510204081632654|
|         2|      182|       78| 28|    true| 23.54788069073783|
|         3|      164|       61| 41|   false|22.679952409280194|
|         4|      161|       62| 43|    true| 23.9188302920412|
+-----+-----+-----+-----+-----+-----+
```

Besides creating additional columns, DataFrames also support filtering rows that satisfy a certain predicate. For instance, we can select all smokers:

```
scala> readingsWithBmiDF.filter {
  readingsWithBmiDF("isSmoker")
}.show
+-----+-----+-----+-----+-----+-----+
|patientId|heightCm|weightKg|age|isSmoker|          BMI|
+-----+-----+-----+-----+-----+-----+
|         2|      182|       78| 28|    true|23.54788069073783|
|         4|      161|       62| 43|    true| 23.9188302920412|
+-----+-----+-----+-----+-----+-----+
```

Or, to select everyone who weighs more than 70 kgs:

```
scala> readingsWithBmiDF.filter {
  readingsWithBmiDF("weightKg") > 70
}.show
```

patientId	heightCm	weightKg	age	isSmoker	BMI
1	175	72	43	false	23.510204081632654
2	182	78	28	true	23.54788069073783

It can become cumbersome to keep repeating the DataFrame name in an expression. Spark defines the operator `$` to refer to a column in the current DataFrame. Thus, the filter expression above could have been written more succinctly using:

```
scala> readingsWithBmiDF.filter { $"weightKg" > 70 }.show
```

patientId	heightCm	weightKg	age	isSmoker	BMI
1	175	72	43	false	23.510204081632654
2	182	78	28	true	23.54788069073783

The `.filter` method is overloaded. It accepts either a column of Boolean values, as above, or a string identifying a Boolean column in the current DataFrame. Thus, to filter our `readingsWithBmiDF` DataFrame to sub-select smokers, we could also have used the following:

```
scala> readingsWithBmiDF.filter("isSmoker").show
```

patientId	heightCm	weightKg	age	isSmoker	BMI
2	182	78	28	true	23.54788069073783
4	161	62	43	true	23.9188302920412

When comparing for equality, you must compare columns with the special *triple-equals* operator:

```
scala> readingsWithBmiDF.filter { $"age" === 28 }.show
+-----+-----+-----+---+-----+-----+
|patientId|heightCm|weightKg|age|isSmoker|          BMI|
+-----+-----+-----+---+-----+-----+
|         2|      182|       78| 28|    true|23.54788069073783|
+-----+-----+-----+---+-----+-----+
```

Similarly, you must use `!==` to select rows that are not equal to a value:

```
scala> readingsWithBmiDF.filter { $"age" !== 28 }.show
+-----+-----+-----+---+-----+-----+
|patientId|heightCm|weightKg|age|isSmoker|          BMI|
+-----+-----+-----+---+-----+-----+
|         1|      175|       72| 43|   false|23.510204081632654|
|         3|      164|       61| 41|   false|22.679952409280194|
|         4|      161|       62| 43|    true| 23.9188302920412|
+-----+-----+-----+---+-----+-----+
```

Aggregation operations

We have seen how to apply an operation to every row in a DataFrame to create a new column, and we have seen how to use filters to build new DataFrames with a sub-set of rows from the original DataFrame. The last set of operations on DataFrames is grouping operations, equivalent to the `GROUP BY` statement in SQL. Let's calculate the average BMI for smokers and non-smokers. We must first tell Spark to group the DataFrame by a column (the `isSmoker` column, in this case), and then apply an aggregation operation (averaging, in this case) to reduce each group:

```
scala> val smokingDF = readingsWithBmiDF.groupBy(
  "isSmoker").agg(avg("BMI"))
smokingDF: org.apache.spark.sql.DataFrame = [isSmoker: boolean, AVG(BMI): double]
```

This has created a new DataFrame with two columns: the grouping column and the column over which we aggregated. Let's show this DataFrame:

```
scala> smokingDF.show
+-----+-----+
| isSmoker |      AVG(BMI) |
+-----+-----+
|    true | 23.733355491389517 |
|    false | 23.095078245456424 |
+-----+-----+
```

Besides averaging, there are several operators for performing the aggregation across each group. We outline some of the more important ones in the table below, but, for a full list, consult the *Aggregate functions* section of [http://spark.apache.org/docs/latest/api/scala/index.html#org.apache.spark.sql.functions\\$](http://spark.apache.org/docs/latest/api/scala/index.html#org.apache.spark.sql.functions$):

Operator	Notes
<code>avg(column)</code>	Group averages of the values in the specified column.
<code>count(column)</code>	Number of elements in each group in the specified column.
<code>countDistinct(column, ...)</code>	Number of distinct elements in each group. This can also accept multiple columns to return the count of unique elements across several columns.
<code>first(column), last(column)</code>	First/last element in each group
<code>max(column), min(column)</code>	Largest/smallest element in each group
<code>sum(column)</code>	Sum of the values in each group

Each aggregation operator takes either the name of a column, as a string, or an expression of type `Column`. The latter allows aggregation of compound expressions. If we wanted the average height, in meters, of the smokers and non-smokers in our sample, we could use:

```
scala> readingsDF.groupBy("isSmoker").agg {
  avg($"heightCm"/100.0)
}.show
+-----+-----+
| isSmoker | AVG((heightCm / 100.0)) |
+-----+-----+
```



```
| true | 1.715 |
| false | 1.6949999999999998 |
+-----+
```

We can also use compound expressions to define the column on which to group. For instance, to count the number of patients in each age group, increasing by decade, we can use:

```
scala> readingsDF.groupBy(floor($"age"/10)).agg(count("*")).show
+-----+
| FLOOR((age / 10)) | count(1) |
+-----+
| 4.0 | 3 |
| 2.0 | 1 |
+-----+
```

We have used the short-hand "*" to indicate a count over every column.

Joining DataFrames together

So far, we have only considered operations on a single DataFrame. Spark also offers SQL-like joins to combine DataFrames. Let's assume that we have another DataFrame mapping the patient id to a (systolic) blood pressure measurement. We will assume we have the data as a list of pairs mapping patient IDs to blood pressures:

```
scala> val bloodPressures = List((1 -> 110), (3 -> 100), (4 -> 125))
bloodPressures: List[(Int, Int)] = List((1,110), (3,100), (4,125))

scala> val bloodPressureRDD = sc.parallelize(bloodPressures)
res16: rdd.RDD[(Int, Int)] = ParallelCollectionRDD[74] at parallelize at
<console>:24
```

We can construct a DataFrame from this RDD of tuples. However, unlike when constructing DataFrames from RDDs of case classes, Spark cannot infer column names. We must therefore pass these explicitly to `.toDF`:

```
scala> val bloodPressureDF = bloodPressureRDD.toDF(
  "patientId", "bloodPressure")
bloodPressureDF: DataFrame = [patientId: int, bloodPressure: int]

scala> bloodPressureDF.show
```

```

+-----+-----+
|patientId|bloodPressure|
+-----+-----+
|      1 |      110 |
|      3 |      100 |
|      4 |      125 |
+-----+-----+

```

Let's join `bloodPressureDF` with `readingsDF`, using the patient ID as the join key:

```

scala> readingsDF.join(bloodPressureDF,
  readingsDF("patientId") === bloodPressureDF("patientId")
).show

```

```

+-----+-----+-----+-----+-----+-----+-----+
|patientId|heightCm|weightKg|age|isSmoker|patientId|bloodPressure|
+-----+-----+-----+-----+-----+-----+-----+
|      1 |    175 |    72 | 43 |  false |      1 |      110 |
|      3 |    164 |    61 | 41 |  false |      3 |      100 |
|      4 |    161 |    62 | 43 |   true |      4 |      125 |
+-----+-----+-----+-----+-----+-----+-----+

```

This performs an *inner join*: only patient IDs present in both DataFrames are included in the result. The type of join can be passed as an extra argument to `join`. For instance, we can perform a *left join*:

```

scala> readingsDF.join(bloodPressureDF,
  readingsDF("patientId") === bloodPressureDF("patientId"),
  "leftouter"
).show

```

```

+-----+-----+-----+-----+-----+-----+-----+
|patientId|heightCm|weightKg|age|isSmoker|patientId|bloodPressure|
+-----+-----+-----+-----+-----+-----+-----+
|      1 |    175 |    72 | 43 |  false |      1 |      110 |
|      2 |    182 |    78 | 28 |   true |    null |     null |
|      3 |    164 |    61 | 41 |  false |      3 |      100 |
|      4 |    161 |    62 | 43 |   true |      4 |      125 |
+-----+-----+-----+-----+-----+-----+-----+

```

Possible join types are `inner`, `outer`, `leftouter`, `rightouter`, or `leftsemi`. These should all be familiar, apart from `leftsemi`, which corresponds to a *left semi join*. This is the same as an inner join, but only the columns on the left-hand side are retained after the join. It is thus a way to filter a DataFrame for rows which are present in another DataFrame.

Custom functions on DataFrames

So far, we have only used built-in functions to operate on DataFrame columns. While these are often sufficient, we sometimes need greater flexibility. Spark lets us apply custom transformations to every row through **user-defined functions (UDFs)**. Let's assume that we want to use the equation that we derived in *Chapter 2, Manipulating Data with Breeze*, for the probability of a person being male, given their height and weight. We calculated that the decision boundary was given by:

$$f = -0.75 + 2.48 \times \text{rescaledHeight} + 2.23 \times \text{rescaledWeight}$$

Any person with $f > 0$ is more likely to be male than female, given their height and weight and the training set used for *Chapter 2, Manipulating Data with Breeze* (which was based on students, so is unlikely to be representative of the population as a whole). To convert from a height in centimeters to the normalized height, `rescaledHeight`, we can use this formula:

$$\text{rescaledHeight} = \frac{\text{height} - \langle \text{height} \rangle}{\sigma_{\text{height}}} = \frac{\text{height} - 171}{8.95}$$

Similarly, to convert a weight (in kilograms) to the normalized weight, `rescaledWeight`, we can use:

$$\text{rescaledWeight} = \frac{\text{weight} - \langle \text{weight} \rangle}{\sigma_{\text{weight}}} = \frac{\text{weight} - 65.7}{13.4}$$

The average and standard deviation of the `height` and `weight` are calculated from the training set. Let's write a Scala function that returns whether a person is more likely to be male, given their height and weight:

```
scala> def likelyMale(height:Int, weight:Int):Boolean = {  
  val rescaledHeight = (height - 171.0) / 8.95
```

```

val rescaledWeight = (weight - 65.7)/13.4
-0.75 + 2.48*rescaledHeight + 2.23*rescaledWeight > 0
}

```

To use this function on Spark DataFrames, we need to register it as a **user-defined function (UDF)**. This transforms our function, which accepts integer arguments, into one that accepts column arguments:

```

scala> val likelyMaleUdf = sqlContext.udf.register(
  "likelyMaleUdf", likelyMale _)
likelyMaleUdf: org.apache.spark.sql.UserDefinedFunction = UserDefinedFunc
tion(<function2>,BooleanType,List())

```

To register a UDF, we must have access to a `sqlContext` instance. The SQL context provides the entry point for DataFrame operations. The Spark shell creates a SQL context at startup, bound to the variable `sqlContext`, and destroys it when the shell session is closed.

The first argument passed to the `register` function is the name of the UDF (we will use the UDF name later when we write SQL statements on the DataFrame, but you can ignore it for now). We can then use the UDF just like the built-in transformations included in Spark:

```

scala> val likelyMaleColumn = likelyMaleUdf(
  readingsDF("heightCm"), readingsDF("weightKg"))
likelyMaleColumn: org.apache.spark.sql.Column = UDF(heightCm,weightKg)

```

```

scala> readingsDF.withColumn("likelyMale", likelyMaleColumn).show

```

```

+-----+-----+-----+-----+-----+
|patientId|heightCm|weightKg|age|isSmoker|likelyMale|
+-----+-----+-----+-----+-----+
|      1 |    175 |     72 | 43 |   false |      true |
|      2 |    182 |     78 | 28 |    true |      true |
|      3 |    164 |     61 | 41 |   false |   false |
|      4 |    161 |     62 | 43 |    true |   false |
+-----+-----+-----+-----+-----+

```

As you can see, Spark applies the function underlying the UDF to every row in the DataFrame. We are not limited to using UDFs to create new columns. We can also use them in `filter` expressions. For instance, to select rows likely to correspond to women:

```
scala> readingsDF.filter(
  ! likelyMaleUdf($"heightCm", $"weightKg")
).show
```

patientId	heightCm	weightKg	age	isSmoker
3	164	61	41	false
4	161	62	43	true

Using UDFs lets us define arbitrary Scala functions to transform rows, giving tremendous additional power for data manipulation.

DataFrame immutability and persistence

DataFrames, like RDDs, are immutable. When you define a transformation on a DataFrame, this always creates a new DataFrame. The original DataFrame cannot be modified in place (this is notably different to pandas DataFrames, for instance).

Operations on DataFrames can be grouped into two: *transformations*, which result in the creation of a new DataFrame, and *actions*, which usually return a Scala type or have a side-effect. Methods like `filter` or `withColumn` are transformations, while methods like `show` or `head` are actions.

Transformations are lazy, much like transformations on RDDs. When you generate a new DataFrame by transforming an existing DataFrame, this results in the elaboration of an execution plan for creating the new DataFrame, but the data itself is not transformed immediately. You can access the execution plan with the `queryExecution` method.

When you call an action on a DataFrame, Spark processes the action as if it were a regular RDD: it implicitly builds a direct acyclic graph to resolve dependencies, processing the transformations needed to build the DataFrame on which the action was called.

Much like RDDs, we can persist DataFrames in memory or on disk:

```
scala> readingsDF.persist
readingsDF.type = [patientId: int, heightCm: int,...]
```

This works in the same way as persisting RDDs: next time the RDD is calculated, it will be kept in memory (provided there is enough space), rather than discarded. The level of persistence can also be set:

```
scala> import org.apache.spark.storage.StorageLevel
import org.apache.spark.storage.StorageLevel
```

```
scala> readingsDF.persist(StorageLevel.MEMORY_AND_DISK)
readingsDF.type = [patientId: int, heightCm: int, ...]
```

SQL statements on DataFrames

By now, you will have noticed that many operations on DataFrames are inspired by SQL operations. Additionally, Spark allows us to register DataFrames as tables and query them with SQL statements directly. We can therefore build a temporary database as part of the program flow.

Let's register `readingsDF` as a temporary table:

```
scala> readingsDF.registerTempTable("readings")
```

This registers a temporary table that can be used in SQL queries. Registering a temporary table relies on the presence of a SQL context. The temporary tables are destroyed when the SQL context is destroyed (when we close the shell, for instance).

Let's explore what we can do with our temporary tables and the SQL context. We can first get a list of all the tables currently registered with the context:

```
scala> sqlContext.tables
DataFrame = [tableName: string, isTemporary: boolean]
```

This returns a DataFrame. In general, all operations on a SQL context that return data return DataFrames:

```
scala> sqlContext.tables.show
+-----+-----+
| tableName | isTemporary |
+-----+-----+
| readings | true |
+-----+-----+
```

We can query this table by passing SQL statements to the SQL context:

```
scala> sqlContext.sql("SELECT * FROM readings").show
```

```
+-----+-----+-----+---+-----+
|patientId|heightCm|weightKg|age|isSmoker|
+-----+-----+-----+---+-----+
|         1|      175|       72| 43|   false|
|         2|      182|       78| 28|    true|
|         3|      164|       61| 41|   false|
|         4|      161|       62| 43|    true|
+-----+-----+-----+---+-----+
```

Any UDFs registered with the `sqlContext` are available through the name given to them when they were registered. We can therefore use them in SQL queries:

```
scala> sqlContext.sql("""
SELECT
  patientId,
  likelyMaleUdf(heightCm, weightKg) AS likelyMale
FROM readings
""").show
```

```
+-----+-----+
|patientId|likelyMale|
+-----+-----+
|         1|      true|
|         2|      true|
|         3|   false|
|         4|   false|
+-----+-----+
```

You might wonder why one would want to register DataFrames as temporary tables and run SQL queries on those tables, when the same functionality is available directly on DataFrames. The main reason is for interacting with external tools. Spark can run a SQL engine that exposes a JDBC interface, meaning that programs that know how to interact with a SQL database will be able to make use of the temporary tables.

We don't have the space to cover how to set up a distributed SQL engine in this book, but you can find details in the Spark documentation (<http://spark.apache.org/docs/latest/sql-programming-guide.html#distributed-sql-engine>).

Complex data types – arrays, maps, and structs

So far, all the elements in our DataFrames were simple types. DataFrames support three additional collection types: arrays, maps, and structs.

Structs

The first compound type that we will look at is the **struct**. A struct is similar to a case class: it stores a set of key-value pairs, with a fixed set of keys. If we convert an RDD of a case class containing nested case classes to a DataFrame, Spark will convert the nested objects to a struct.

Let's imagine that we want to serialize Lords of the Ring characters. We might use the following object model:

```
case class Weapon(name:String, weaponType:String)
case class LotrCharacter(name:String, val weapon:Weapon)
```

We want to create a DataFrame of LotrCharacter instances. Let's create some dummy data:

```
scala> val characters = List(
  LotrCharacter("Gandalf", Weapon("Glamdring", "sword")),
  LotrCharacter("Frodo", Weapon("Sting", "dagger")),
  LotrCharacter("Aragorn", Weapon("Anduril", "sword"))
)
characters: List[LotrCharacter] = List(LotrCharacter...

scala> val charactersDF = sc.parallelize(characters).toDF
charactersDF: DataFrame = [name: string, weapon: struct<name:string,weaponType:string>]
```

```
scala> charactersDF.printSchema
root
 |-- name: string (nullable = true)
 |-- weapon: struct (nullable = true)
 |    |-- name: string (nullable = true)
```



```
| | -- weaponType: string (nullable = true)
```

```
scala> charactersDF.show
+-----+-----+
| name | weapon |
+-----+-----+
| Gandalf | [Glamdring, sword] |
| Frodo | [Sting, dagger] |
| Aragorn | [Anduril, sword] |
+-----+-----+
```

The `weapon` attribute in the case class was converted to a struct column in the DataFrame. To extract sub-fields from a struct, we can pass the field name to the column's `.apply` method:

```
scala> val weaponTypeColumn = charactersDF("weapon").apply("weaponType")
weaponTypeColumn: org.apache.spark.sql.Column = weapon[weaponType]
```

We can use this derived column just as we would any other column. For instance, let's filter our DataFrame to only contain characters who wield a sword:

```
scala> charactersDF.filter { weaponTypeColumn === "sword" }.show
+-----+-----+
| name | weapon |
+-----+-----+
| Gandalf | [Glamdring, sword] |
| Aragorn | [Anduril, sword] |
+-----+-----+
```

Arrays

Let's return to the earlier example, and assume that, besides height, weight, and age measurements, we also have phone numbers for our patients. Each patient might have zero, one, or more phone numbers. We will define a new case class and new dummy data:

```
scala> case class PatientNumbers(
  patientId: Int, phoneNumbers: List[String])
```

```
defined class PatientNumbers

scala> val numbers = List(
  PatientNumbers(1, List("07929123456")),
  PatientNumbers(2, List("07929432167", "07929234578")),
  PatientNumbers(3, List.empty),
  PatientNumbers(4, List("07927357862"))
)
```

```
scala> val numbersDF = sc.parallelize(numbers).toDF
numbersDF: org.apache.spark.sql.DataFrame = [patientId: int,
phoneNumbers: array<string>]
```

The `List[String]` array in our case class gets translated to an `array<string>` data type:

```
scala> numbersDF.printSchema
root
 |-- patientId: integer (nullable = false)
 |-- phoneNumbers: array (nullable = true)
 |   |-- element: string (containsNull = true)
```

As with structs, we can construct a column for a specific index the array. For instance, we can select the first element in each array:

```
scala> val bestNumberColumn = numbersDF("phoneNumbers")(0)
bestNumberColumn: org.apache.spark.sql.Column = phoneNumbers[0]
```

```
scala> numbersDF.withColumn("bestNumber", bestNumberColumn).show
+-----+-----+-----+
|patientId|    phoneNumbers| bestNumber|
+-----+-----+-----+
|      1| List(07929123456)| 07929123456|
|      2| List(07929432167,...| 07929432167|
|      3|           List()|         null|
|      4| List(07927357862)| 07927357862|
+-----+-----+-----+
```

Maps

The last compound data type is the map. Maps are similar to structs inasmuch as they store key-value pairs, but the set of keys is not fixed when the DataFrame is created. They can thus store arbitrary key-value pairs.

Scala maps will be converted to DataFrame maps when the DataFrame is constructed. They can then be queried in a manner similar to structs.

Interacting with data sources

A major challenge in data science or engineering is dealing with the wealth of input and output formats for persisting data. We might receive or send data as CSV files, JSON files, or through a SQL database, to name a few.

Spark provides a unified API for serializing and de-serializing DataFrames to and from different data sources.

JSON files

Spark supports loading data from JSON files, provided that each line in the JSON file corresponds to a single JSON object. Each object will be mapped to a DataFrame row. JSON arrays are mapped to arrays, and embedded objects are mapped to structs.

This section would be a little dry without some data, so let's generate some from the GitHub API. Unfortunately, the GitHub API does not return JSON formatted as a single object per line. The code repository for this chapter contains a script, `FetchData.scala` which will download and format JSON entries for Martin Odersky's repositories, saving the objects to a file named `odersky_repos.json` (go ahead and change the GitHub user in `FetchData.scala` if you want). You can also download a pre-constructed data file from data.scala4datascience.com/odersky_repos.json.

Let's dive into the Spark shell and load this data into a DataFrame. Reading from a JSON file is as simple as passing the file name to the `sqlContext.read.json` method:

```
scala> val df = sqlContext.read.json("odersky_repos.json")
df: DataFrame = [archive_url: string, assignees_url: ...]
```

Reading from a JSON file loads data as a DataFrame. Spark automatically infers the schema from the JSON documents. There are many columns in our DataFrame. Let's sub-select a few to get a more manageable DataFrame:

```
scala> val reposDF = df.select("name", "language", "fork", "owner")
reposDF: DataFrame = [name: string, language: string, ...]
```

```
scala> reposDF.show
```

```
+-----+-----+-----+-----+
|          name| language| fork|          owner|
+-----+-----+-----+-----+
|          dotty|     Scala| true| [https://avatars....|
|        frontend|JavaScript| true| [https://avatars....|
|          scala|     Scala| true| [https://avatars....|
|    scala-dist|     Scala| true| [https://avatars....|
|scala.github.com|JavaScript| true| [https://avatars....|
|          scalax|     Scala| false| [https://avatars....|
|          sips|      CSS| false| [https://avatars....|
+-----+-----+-----+-----+
```

Let's save the DataFrame back to JSON:

```
scala> reposDF.write.json("repos_short.json")
```

If you look at the files present in the directory in which you are running the Spark shell, you will notice a `repos_short.json` directory. Inside it, you will see files named `part-000000`, `part-000001`, and so on. When serializing JSON, each partition of the DataFrame is serialized independently. If you are running this on several machines, you will find parts of the serialized output on each computer.

You may, optionally, pass a mode argument to control how Spark deals with the case of an existing `repos_short.json` file:

```
scala> import org.apache.spark.sql.SaveMode
import org.apache.spark.sql.SaveMode
```

```
scala> reposDF.write.mode(
  SaveMode.Overwrite).json("repos_short.json")
```

Available save modes are `ErrorIfExists`, `Append` (only available for Parquet files), `Overwrite`, and `Ignore` (do not save if the file exists already).

Parquet files

Apache Parquet is a popular file format well-suited for storing tabular data. It is often used for serialization in the Hadoop ecosystem, since it allows for efficient extraction of specific columns and rows without having to read the entire file.

Serialization and deserialization of Parquet files is identical to JSON, with the substitution of `json` with `parquet`:

```
scala> reposDF.write.parquet("repos_short.parquet")
```

```
scala> val newDF = sqlContext.read.parquet("repos_short.parquet")
newDF: DataFrame = [name: string, language: string, fo...]
```

```
scala> newDF.show
```

```
+-----+-----+-----+-----+
|          name| language| fork|          owner|
+-----+-----+-----+-----+
|          dotty|      Scala| true| [https://avatars....|
|          frontend| JavaScript| true| [https://avatars....|
|          scala|      Scala| true| [https://avatars....|
|          scala-dist|      Scala| true| [https://avatars....|
| scala.github.com| JavaScript| true| [https://avatars....|
|          scalax|      Scala| false| [https://avatars....|
|          sips|      CSS| false| [https://avatars....|
+-----+-----+-----+-----+
```

In general, Parquet will be more space-efficient than JSON for storing large collections of objects. Parquet is also much more efficient at retrieving specific columns or rows, if the partition can be inferred from the row. Parquet is thus advantageous over JSON unless you need the output to be human-readable, or de-serializable by an external program.

Standalone programs

So far, we have been using Spark SQL and DataFrames through the Spark shell. To use it in standalone programs, you will need to create it explicitly, from a Spark context:

```
val conf = new SparkConf().setAppName("applicationName")
val sc = new SparkContext(conf)
val sqlContext = new org.apache.spark.sql.SQLContext(sc)
```

Additionally, importing the `implicits` object nested in `sqlContext` allows the conversions of RDDs to DataFrames:

```
import sqlContext.implicits._
```

We will use DataFrames extensively in the next chapter to manipulate data to get it ready for use with MLlib.

Summary

In this chapter, we explored Spark SQL and DataFrames. DataFrames add a rich layer of abstraction on top of Spark's core engine, greatly facilitating the manipulation of tabular data. Additionally, the source API allows the serialization and de-serialization of DataFrames from a rich variety of data files.

In the next chapter, we will build on our knowledge of Spark and DataFrames to build a spam filter using MLlib.

References

DataFrames are a relatively recent addition to Spark. There is thus still a dearth of literature and documentation. The first port of call should be the Scala docs, available at: <http://spark.apache.org/docs/latest/api/scala/index.html#org.apache.spark.sql.DataFrame>.

The Scaladocs for operations available on the `DataFrame Column` type can be found at: <http://spark.apache.org/docs/latest/api/scala/#org.apache.spark.sql.Column>.

There is also extensive documentation on the Parquet file format: <https://parquet.apache.org>.

12

Distributed Machine Learning with MLlib

Machine learning describes the construction of algorithms that make predictions from data. It is a core component of most data science pipelines, and is often seen to be the component adding the most value: the accuracy of the machine learning algorithm determines the success of the data science endeavor. It is also, arguably, the section of the data science pipeline that requires the most knowledge from fields beyond software engineering: a machine learning expert will be familiar, not just with algorithms, but also with statistics and with the business domain.

Choosing and tuning a machine learning algorithm to solve a particular problem involves significant exploratory analysis to try and determine which features are relevant, how features are correlated, whether there are outliers in the dataset, and so on. Designing suitable machine learning pipelines is difficult. Add on an additional layer of complexity resulting from the size of datasets and the need for scalability, and you have a real challenge.

MLlib helps mitigate this difficulty. MLlib is a component of Spark that provides machine learning algorithms on top of the core Spark libraries. It offers a set of learning algorithms that parallelize well over distributed datasets.

MLlib has evolved into two separate layers. MLlib itself contains the core algorithms, and **ml**, also called the *pipeline API*, defines an API for gluing algorithms together and provides a higher level of abstraction. The two libraries differ in the data types on which they operate: the original MLlib predates the introduction of DataFrames, and acts mainly on RDDs of feature vectors. The pipeline API operates on DataFrames.

In this chapter, we will study the newer pipeline API, diving into MLlib only when the functionality is missing from the pipeline API.

This chapter does not try to teach the machine learning fundamentals behind the algorithms that we present. We assume that the reader has a good enough grasp of machine learning tools and techniques to understand, at least superficially, what the algorithms presented here do, and we defer to better authors for in-depth explanations of the mechanics of statistical learning (we present several references at the end of the chapter).

MLlib is a rich library that is evolving rapidly. This chapter does not aim to give a complete overview of the library. We will work through the construction of a machine learning pipeline to train a spam filter, learning about the parts of MLlib that we need along the way. Having read this chapter, you will have an understanding of how the different parts of the library fit together, and can use the online documentation, or a more specialized book (see references at the end of this chapter) to learn about the parts of MLlib not covered here.

Introducing MLlib – Spam classification

Let's introduce MLlib with a concrete example. We will look at spam classification using the Ling-Spam dataset that we used in the *Chapter 10, Distributed Batch Processing with Spark*. We will create a spam filter that uses logistic regression to estimate the probability that a given message is spam.

We will run through examples using the Spark shell, but you will find an analogous program in `LogisticRegressionDemo.scala` among the examples for this chapter. If you have not installed Spark, refer to *Chapter 10, Distributed Batch Processing with Spark*, for installation instructions.

Let's start by loading the e-mails in the Ling-Spam dataset. If you have not done this for *Chapter 10, Distributed Batch Processing with Spark*, download the data from `data.scala4datascience.com/ling-spam.tar.gz` or `data.scala4datascience.com/ling-spam.zip`, depending on whether you want a `tar.gz` file or a `zip` file, and unpack the archive. This will create a `spam` directory and a `ham` directory containing spam and ham messages, respectively.

Let's use the `wholeTextFiles` method to load spam and ham e-mails:

```
scala> val spamText = sc.wholeTextFiles("spam/*")
spamText: RDD[(String, String)] = spam/...
```

```
scala> val hamText = sc.wholeTextFiles("ham/*")
hamText: RDD[(String, String)] = ham/...
```

The `wholeTextFiles` method creates a key-value RDD where the keys are the file names and the values are the contents of the files:

```
scala> spamText.first
(String, String) =
(file:spam/spmsgal.txt,"Subject: great part-time summer job! ...")
```

```
scala> spamText.count
Long = 481
```

The algorithms in the pipeline API work on DataFrames. We must therefore convert our key-value RDDs to DataFrames. We define a new case class, `LabelledDocument`, which contains a message text and a category label identifying whether a message is spam or ham:

```
scala> case class LabelledDocument(
  fileName:String,
  text:String,
  category:String
)
defined class LabelledDocument

scala> val spamDocuments = spamText.map {
  case (fileName, text) =>
    LabelledDocument(fileName, text, "spam")
}
spamDocuments: RDD[LabelledDocument] = MapPartitionsRDD[2] at map

scala> val hamDocuments = hamText.map {
  case (fileName, text) =>
    LabelledDocument(fileName, text, "ham")
}
hamDocuments: RDD[LabelledDocument] = MapPartitionsRDD[3] at map
```

To create models, we will need all the documents in a single DataFrame. Let's therefore take the union of our two `LabelledDocument` RDDs, and transform that to a DataFrame. The union method concatenates RDDs together:

```
scala> val allDocuments = spamDocuments.union(hamDocuments)
allDocuments: RDD[LabelledDocument] = UnionRDD[4] at union
```

```
scala> val documentsDF = allDocuments.toDF
documentsDF: DataFrame = [fileName: string, text: string, category:
string]
```

Let's do some basic checks to verify that we have loaded all the documents. We start by persisting the DataFrame in memory to avoid having to re-create it from the raw text files.

```
scala> documentsDF.persist
documentsDF.type = [fileName: string, text: string, category: string]
```

```
scala> documentsDF.show
```

```
+-----+-----+-----+
|          fileName|          text|category|
+-----+-----+-----+
|file:/Users/pasca...|Subject: great pa...|   spam|
|file:/Users/pasca...|Subject: auto ins...|   spam|
|file:/Users/pasca...|Subject: want bes...|   spam|
|file:/Users/pasca...|Subject: email 57...|   spam|
|file:/Users/pasca...|Subject: n't miss...|   spam|
|file:/Users/pasca...|Subject: amaze wo...|   spam|
|file:/Users/pasca...|Subject: help loa...|   spam|
|file:/Users/pasca...|Subject: beat irs...|   spam|
|file:/Users/pasca...|Subject: email 57...|   spam|
|file:/Users/pasca...|Subject: best , b...|   spam|
|...|
+-----+-----+-----+
```

```
scala> documentsDF.groupBy("category").agg(count("*")).show
```

```
+-----+-----+
|category|COUNT(1)|
+-----+-----+
```

```
| spam | 481 |
| ham | 2412 |
+-----+
```

Let's now split the DataFrame into a training set and a test set. We will use the test set to validate the model that we build. For now, we will just use a single split, training the model on 70% of the data and testing it on the remaining 30%. In the next section, we will look at cross-validation, which provides more rigorous way to check the accuracy of our models.

We can achieve this 70-30 split using the DataFrame's `.randomSplit` method:

```
scala> val Array(trainDF, testDF) = documentsDF.randomSplit(
  Array(0.7, 0.3))
trainDF: DataFrame = [fileName: string, text: string, category: string]
testDF: DataFrame = [fileName: string, text: string, category: string]
```

The `.randomSplit` method takes an array of weights and returns an array of DataFrames, of approximately the size specified by the weights. For instance, we passed weights `0.7` and `0.3`, indicating that any given row has a 70% chance of ending up in `trainDF`, and a 30% chance of ending up in `testDF`. Note that this means the split DataFrames are not of fixed size: `trainDF` is approximately, but not exactly, 70% the size of `documentsDF`:

```
scala> trainDF.count / documentsDF.count.toDouble
Double = 0.7013480815762184
```

If you need a fixed size sample, use the DataFrame's `.sample` method to obtain `trainDF` and filter `documentDF` for rows not in `trainDF`.

We are now in a position to start using MLlib. Our attempt at classification will involve performing logistic regression on *term-frequency vectors*: we will count how often each word appears in each message, and use the frequency of occurrence as a feature. Before jumping into the code, let's take a step back and discuss the structure of machine learning pipelines.

Pipeline components

Pipelines consist of a set of components joined together such that the DataFrame produced by one component is used as input for the next component. The components available are split into two classes: *transformers* and *estimators*.

Transformers

Transformers transform one DataFrame into another, normally by appending one or more columns.

The first step in our spam classification algorithm is to split each message into an array of words. This is called **tokenization**. We can use the `Tokenizer` transformer, provided by MLlib:

```
scala> import org.apache.spark.ml.feature._
import org.apache.spark.ml.feature._

scala> val tokenizer = new Tokenizer()
tokenizer: org.apache.spark.ml.feature.Tokenizer = tok_75559f60e8cf
```

The behavior of transformers can be customized through getters and setters. The easiest way of obtaining a list of the parameters available is to call the `.explainParams` method:

```
scala> println(tokenizer.explainParams)
inputCol: input column name (undefined)
outputCol: output column name (default: tok_75559f60e8cf__output)
```

We see that the behavior of a `Tokenizer` instance can be customized using two parameters: `inputCol` and `outputCol`, describing the header of the column containing the input (the string to be tokenized) and the output (the array of words), respectively. We can set these parameters using the `setInputCol` and `setOutputCol` methods.

We set `inputCol` to "text", since that is what the column is called in our training and test DataFrames. We will set `outputCol` to "words":

```
scala> tokenizer.setInputCol("text").setOutputCol("words")
org.apache.spark.ml.feature.Tokenizer = tok_75559f60e8cf
```

In due course, we will integrate `tokenizer` into a pipeline, but, for now, let's just use it to transform the training DataFrame, to verify that it works correctly.

```
scala> val tokenizedDF = tokenizer.transform(trainDF)
tokenizedDF: DataFrame = [fileName: string, text: string, category:
string, words: array<string>]

scala> tokenizedDF.show
```

```

+-----+-----+-----+-----+
|   fileName |      text | category |   words |
+-----+-----+-----+-----+
| file:/Users... | Subject: auto... | spam | [subject:, auto, ... |
| file:/Users... | Subject: want... | spam | [subject:, want, ... |
| file:/Users... | Subject: n't ... | spam | [subject:, n't, m... |
| file:/Users... | Subject: amaz... | spam | [subject:, amaze,... |
| file:/Users... | Subject: help... | spam | [subject:, help, ... |
| file:/Users... | Subject: beat... | spam | [subject:, beat, ... |
| ... |
+-----+-----+-----+-----+

```

The `tokenizer` transformer produces a new `DataFrame` with an additional column, `words`, containing an array of the words in the `text` column.

Clearly, we can use our `tokenizer` to transform any `DataFrame` with the correct schema. We could, for instance, use it on the test set. Much of machine learning involves calling the same (or a very similar) pipeline on different data sets. By providing the pipeline abstraction, `Mlib` facilitates reasoning about complex machine learning algorithms consisting of many cleaning, transformation, and modeling components.

The next step in our pipeline is to calculate the frequency of occurrence of each word in each message. We will eventually use these frequencies as features in our algorithm. We will use the `HashingTF` transformer to transform from arrays of words to word frequency vectors for each message.

The `HashingTF` transformer constructs a sparse vector of word frequencies from input iterables. Each element in the word array gets transformed to a hash code. This hash code is truncated to a value between 0 and a large number n , the total number of elements in the output vector. The term frequency vector is just the number of occurrences of the truncated hash.

Let's run through an example manually to understand how this works. We will calculate the term frequency vector for `Array("the", "dog", "jumped", "over", "the")`. Let's set n , the number of elements in the sparse output vector, to 16 for this example. The first step is to calculate the hash code for each element in our array. We can use the built-in `##` method, which calculates a hash code for any object:

```
scala> val words = Array("the", "dog", "jumped", "over", "the")
words: Array[String] = Array(the, dog, jumped, over, the)
```

```
scala> val hashCodes = words.map { _.## }
hashCodes: Array[Int] = Array(114801, 99644, -1148867251, 3423444,
114801)
```

To transform the hash codes into valid vector indices, we take the modulo of each hash by the size of the vector (16, in this case):

```
scala> val indices = hashCodes.map { code => Math.abs(code % 16) }
indices: Array[Int] = Array(1, 12, 3, 4, 1)
```

We can then create a mapping from indices to the number of times that index appears:

```
scala> val indexFrequency = indices.groupBy(identity).mapValues {
  _.size.toDouble
}
indexFrequency: Map[Int,Double] = Map(4 -> 1.0, 1 -> 2.0, 3 -> 1.0, 12 ->
1.0)
```

Finally, we can convert this map to a sparse vector, where the value at each element in the vector is the frequency with which this particular index occurs:

```
scala> import org.apache.spark.mllib.linalg._
import org.apache.spark.mllib.linalg._

scala> val termFrequencies = Vectors.sparse(16, indexFrequency.toSeq)
termFrequencies: linalg.Vector = (16, [1,3,4,12], [2.0,1.0,1.0,1.0])
```

Note that the `.toString` output for a sparse vector consists of three elements: the total size of the vector, followed by two lists: the first is a series of indices, and the second is a series of values at those indices.

Using a sparse vector provides a compact and efficient way of representing the frequency of occurrence of words in the message, and is exactly how `HashingTF` works under the hood. The disadvantage is that the mapping from words to indices is not necessarily unique: truncating hash codes by the length of the vector will map different strings to the same index. This is known as a *collision*. The solution is to make n large enough that the frequency of collisions is minimized.



`HashingTF` is similar to building a hash table (for example, a Scala map) whose keys are words and whose values are the number of times that word occurs in the message, with one important difference: it does not attempt to deal with hash collisions. Thus, if two words map to the same hash, they will have the wrong frequency. There are two advantages to using this algorithm over just constructing a hash table:

- We do not have to maintain a list of distinct words in memory.
- Each e-mail can be transformed to a vector independently of all others: we do not have to reduce over different partitions to get the set of keys in the map. This greatly eases applying this algorithm to each e-mail in a distributed manner, since we can apply the `HashingTF` transformation on each partition independently.

The main disadvantage is that we must use machine learning algorithms that can take advantage of the sparse representation efficiently. This is the case with logistic regression, which we will use here.

As you might expect, the `HashingTF` transformer takes, as parameters, the input and output columns. It also takes a parameter defining the number of distinct hash buckets in the vector. Increasing the number of buckets decreases the number of collisions. In practice, a value between $2^{18} = 262144$ and $2^{20} = 1048576$ is recommended.

```
scala> val hashingTF = (new HashingTF()
  .setInputCol("words")
  .setOutputCol("features")
  .setNumFeatures(1048576))
hashingTF: org.apache.spark.ml.feature.HashingTF = hashingTF_3b78eca9595c

scala> val hashedDF = hashingTF.transform(tokenizedDF)
```



```
hashedDF: DataFrame = [fileName: string, text: string, category: string,  
words: array<string>, features: vector]
```

```
scala> hashedDF.select("features").show
```

```
+-----+  
|           features|  
+-----+  
|(1048576, [0,33,36...|  
|(1048576, [0,36,40...|  
|(1048576, [0,33,34...|  
|(1048576, [0,33,36...|  
|(1048576, [0,33,34...|  
|(1048576, [0,33,34...|  
+-----+
```

Each element in the `features` column is a sparse vector:

```
scala> import org.apache.spark.sql.Row  
import org.apache.spark.sql.Row
```

```
scala> val firstRow = hashedDF.select("features").first  
firstRow: org.apache.spark.sql.Row = ...
```

```
scala> val Row(v:Vector) = firstRow  
v: Vector = (1048576, [0,33,36,37,...], [1.0,3.0,4.0,1.0,...])
```

We can thus interpret our vector as: the word that hashes to element 33 occurs three times, the word that hashes to element 36 occurs four times etc.

Estimators

We now have the features ready for logistic regression. The last step prior to running logistic regression is to create the target variable. We will transform the category column in our DataFrame to a binary 0/1 target column. Spark provides a `StringIndexer` class that replaces a set of strings in a column with doubles. A `StringIndexer` is not a transformer: it must first be 'fitted' to a set of categories to calculate the mapping from string to numeric value. This introduces the second class of components in the pipeline API: *estimators*.

Unlike a transformer, which works "out of the box", an estimator must be fitted to a DataFrame. For our string indexer, the fitting process involves obtaining the list of unique strings ("spam" and "ham") and mapping each of these to a double. The fitting process outputs a transformer which can be used on subsequent DataFrames.

```
scala> val indexer = (new StringIndexer()
  .setInputCol("category")
  .setOutputCol("label"))
indexer: org.apache.spark.ml.feature.StringIndexer = strIdx_16db03fd0546
```

```
scala> val indexTransform = indexer.fit(trainDF)
indexTransform: StringIndexerModel = strIdx_16db03fd0546
```

The transformer produced by the fitting process has a `labels` attribute describing the mapping it applies:

```
scala> indexTransform.labels
Array[String] = Array(ham, spam)
```

Each label will get mapped to its index in the array: thus, our transformer maps `ham` to 0 and `spam` to 1:

```
scala> val labelledDF = indexTransform.transform(hashDF)
labelledDF: org.apache.spark.sql.DataFrame = [fileName: string, text:
string, category: string, words: array<string>, features: vector, label:
double]
```

```
scala> labelledDF.select("category", "label").distinct.show
```

```
+-----+-----+
|category|label|
+-----+-----+
|    ham |  0.0 |
|    spam|  1.0 |
+-----+-----+
```

We now have the feature vectors and classification labels in the correct format for logistic regression. The component for performing logistic regression is an estimator: it is fitted to a training DataFrame to create a trained model. The model can then be used to transform test DataFrames.

```
scala> import org.apache.spark.ml.classification.LogisticRegression
import org.apache.spark.ml.classification.LogisticRegression
```

```
scala> val classifier = new LogisticRegression().setMaxIter(50)
classifier: LogisticRegression = logreg_a5e921e7c1a1
```

The `LogisticRegression` estimator expects the feature column to be named "features" and the label column (the target) to be named "label", by default. There is no need to set these explicitly, since they match the column names set by `hashingTF` and `indexer`. There are several parameters that can be set to control how logistic regression works:

```
scala> println(classifier.explainParams)
elasticNetParam: the ElasticNet mixing parameter, in range [0, 1]. For
alpha = 0, the penalty is an L2 penalty. For alpha = 1, it is an L1
penalty. (default: 0.0)
fitIntercept: whether to fit an intercept term (default: true)
labelCol: label column name (default: label)
maxIter: maximum number of iterations (>= 0) (default: 100, current: 50)
regParam: regularization parameter (>= 0) (default: 0.0)
threshold: threshold in binary classification prediction, in range [0, 1]
(default: 0.5)
tol: the convergence tolerance for iterative algorithms (default: 1.0E-6)
...
```

For now, we just set the `maxIter` parameter. We will look at the effect of other parameters, such as regularization, later on. Let's now fit the classifier to `labelledDF`:

```
scala> val trainedClassifier = classifier.fit(labelledDF)
trainedClassifier: LogisticRegressionModel = logreg_353d18f6a5f0
```

This produces a transformer that we can use on a DataFrame with a features column. The transformer appends a prediction column and a probability column. We can, for instance use `trainedClassifier` to transform `labelledDF`, the training set itself:

```
scala> val labelledDFWithPredictions = trainedClassifier.transform(
  labelledDF)
labelledDFWithPredictions: DataFrame = [fileName: string, ...

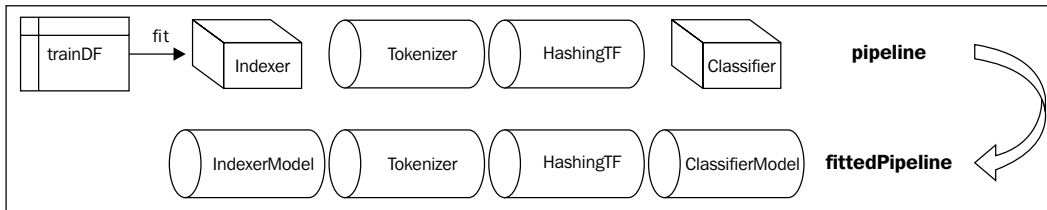
scala> labelledDFWithPredictions.select($"label", $"prediction").show
+-----+-----+
|label|prediction|
+-----+-----+
| 1.0|      1.0|
| 1.0|      1.0|
| 1.0|      1.0|
| 1.0|      1.0|
| 1.0|      1.0|
| 1.0|      1.0|
| 1.0|      1.0|
| 1.0|      1.0|
+-----+-----+
```

A quick way of checking the performance of our model is to just count the number of misclassified messages:

```
scala> labelledDFWithPredictions.filter {
  $"label" != $"prediction"
}.count
Long = 1
```

In this case, logistic regression managed to correctly classify every message but one in the training set. This is perhaps unsurprising, given the large number of features and the relatively clear demarcation between the words used in spam and legitimate e-mails.

Of course, the real test of a model is not how well it performs on the training set, but how well it performs on a test set. To test this, we could just push the test DataFrame through the same stages that we used to train the model, replacing estimators with the fitted transformer that they produced. MLLib provides the *pipeline* abstraction to facilitate this: we wrap an ordered list of transformers and estimators in a pipeline. This pipeline is then fitted to a DataFrame corresponding to the training set. The fitting produces a `PipelineModel` instance, equivalent to the pipeline but with estimators replaced by transformers, as shown in this diagram:



Let's construct the pipeline for our logistic regression spam filter:

```
scala> import org.apache.spark.ml.Pipeline
import org.apache.spark.ml.Pipeline

scala> val pipeline = new Pipeline().setStages(
  Array(indexer, tokenizer, hashingTF, classifier)
)
pipeline: Pipeline = pipeline_7488113e284d
```

Once the pipeline is defined, we fit it to the DataFrame holding the training set:

```
scala> val fittedPipeline = pipeline.fit(trainDF)
fittedPipeline: org.apache.spark.ml.PipelineModel = pipeline_089525c6f100
```

When fitting a pipeline to a DataFrame, estimators and transformers are treated differently:

- Transformers are applied to the DataFrame and copied, as is, into the pipeline model.
- Estimators are fitted to the DataFrame, producing a transformer. The transformer is then applied to the DataFrame, and appended to the pipeline model.

We can now apply the pipeline model to the test set:

```
scala> val testDFWithPredictions = fittedPipeline.transform(testDF)
testDFWithPredictions: DataFrame = [fileName: string, ...
```

This has added a `prediction` column to the DataFrame with the predictions of our logistic regression model. To measure the performance of our algorithm, we calculate the classification error on the test set:

```
scala> testDFWithPredictions.filter {
  $"label" !== $"prediction"
}.count
Long = 20
```

Thus, our naive logistic regression algorithm, with no model selection, or regularization, mis-classifies 2.3% of e-mails. You may, of course, get slightly different results, since the train-test split was random.

Let's save the training and test DataFrames, with predictions, as parquet files:

```
scala> import org.apache.spark.sql.SaveMode
import org.apache.spark.sql.SaveMode

scala> (labelledDFWithPredictions
  .select("fileName", "label", "prediction", "probability")
  .write.mode(SaveMode.Overwrite)
  .parquet("transformedTrain.parquet"))

scala> (testDFWithPredictions
  .select("fileName", "label", "prediction", "probability")
  .write.mode(SaveMode.Overwrite)
  .parquet("transformedTest.parquet"))
```



In spam classification, a false positive is considerably worse than a false negative: it is much worse to classify a legitimate message as spam, than it is to let a spam message through. To account for this, we could increase the threshold for classification: only messages that score, for instance, 0.7 or above would get classified as spam. This raises the obvious question of choosing the right threshold. One way to do this would be to investigate the false positive rate incurred in the test set for different thresholds, and choosing the lowest threshold to give us an acceptable false positive rate. A good way of visualizing this is to use ROC curves, which we will investigate in the next section.

Evaluation

Unfortunately, the functionality for evaluating model quality in the pipeline API remains limited, as of version 1.5.2. Logistic regression does output a summary containing several evaluation metrics (available through the `summary` attribute on the trained model), but these are calculated on the training set. In general, we want to evaluate the performance of the model both on the training set and on a separate test set. We will therefore dive down to the underlying MLlib layer to access evaluation metrics.

MLlib provides a module, `org.apache.spark.mllib.evaluation`, with a set of classes for assessing the quality of a model. We will use the `BinaryClassificationMetrics` class here, since spam classification is a binary classification problem. Other evaluation classes provide metrics for multi-class models, regression models and ranking models.

As in the previous section, we will illustrate the concepts in the shell, but you will find analogous code in the `ROC.scala` script in the code examples for this chapter. We will use *breeze-viz* to plot curves, so, when starting the shell, we must ensure that the relevant libraries are on the classpath. We will use SBT assembly, as described in *Chapter 10, Distributed Batch Processing with Spark* (specifically, the *Building and running standalone programs* section), to create a JAR with the required dependencies. We will then pass this JAR to the Spark shell, allowing us to import *breeze-viz*. Let's write a `build.sbt` file that declares a dependency on *breeze-viz*:

```
// build.sbt
name := "spam_filter"

scalaVersion := "2.10.5"

libraryDependencies ++= Seq(
```

```

    "org.apache.spark" %% "spark-core" % "1.5.2" % "provided",
    "org.apache.spark" %% "spark-mllib" % "1.5.2" % "provided",
    "org.scalanlp" %% "breeze" % "0.11.2",
    "org.scalanlp" %% "breeze-viz" % "0.11.2",
    "org.scalanlp" %% "breeze-natives" % "0.11.2"
  )

```

Package the dependencies into a jar with:

```
$ sbt assembly
```

This will create a jar called `spam_filter-assembly-0.1-SNAPSHOT.jar` in the `target/scala-2.10/` directory. To include this jar in the Spark shell, re-start the shell with the `--jars` command line argument:

```
$ spark-shell --jars=target/scala-2.10/spam_filter-assembly-0.1-SNAPSHOT.jar
```

To verify that the packaging worked correctly, try to import `breeze.plot`:

```
scala> import breeze.plot._
import breeze.plot._
```

Let's load the test set, with predictions, which we created in the previous section and saved as a parquet file:

```
scala> val testDFWithPredictions = sqlContext.read.parquet(
  "transformedTest.parquet")
testDFWithPredictions: org.apache.spark.sql.DataFrame = [fileName:
string, label: double, prediction: double, probability: vector]
```

The `BinaryClassificationMetrics` object expects an `RDD[(Double, Double)]` object of pairs of scores (the probability assigned by the classifier that a particular e-mail is spam) and labels (whether an e-mail is actually spam). We can extract this RDD from our DataFrame:

```
scala> import org.apache.spark.mllib.linalg.Vector
import org.apache.spark.mllib.linalg.Vector

scala> import org.apache.spark.sql.Row
import org.apache.spark.sql.Row

scala> val scoresLabels = testDFWithPredictions.select(
```



```
"probability", "label").map {
  case Row(probability:Vector, label:Double) =>
    (probability(1), label)
}
org.apache.spark.rdd.RDD[(Double, Double)] = MapPartitionsRDD[3] at map
at <console>:23
```

```
scala> scoresLabels.take(5).foreach(println)
(0.9999999967713409,1.0)
(0.9999983827108793,1.0)
(0.9982059900606365,1.0)
(0.9999790713978142,1.0)
(0.9999999999999272,1.0)
```

We can now construct the `BinaryClassificationMetrics` instance:

```
scala> import org.apache.spark.mllib.evaluation.
BinaryClassificationMetrics
import mllib.evaluation.BinaryClassificationMetrics

scala> val bm = new BinaryClassificationMetrics(scoresLabels)
bm: BinaryClassificationMetrics = mllib.evaluation.BinaryClassificationMe
trics@254ed9ba
```

The `BinaryClassificationMetrics` objects contain many useful metrics for evaluating the performance of a classification model. We will look at the **receiver operating characteristic (ROC) curve**.

ROC Curves

Imagine gradually decreasing, from 1.0, the probability threshold at which we assume a particular e-mail is spam. Clearly, when the threshold is set to 1.0, no e-mails will get classified as spam. This means that there will be no **false positives** (ham messages which we incorrectly classify as spam), but it also means that there will be no **true positives** (spam messages that we correctly identify as spam): all spam e-mails will be incorrectly identified as ham.

As we gradually lower the probability threshold at which we assume a particular e-mail is spam, our spam filter will, hopefully, start identifying a large fraction of e-mails as spam. The vast majority of these will, if our algorithm is well-designed, be real spam. Thus, our rate of true positives increases. As we gradually lower the threshold, we start classifying messages about which we are less sure of as spam. This will increase the number of messages correctly identified as spam, but it will also increase the number of false positives.

The ROC curve plots, for each threshold value, the fraction of true positives against the fraction of false positives. In the best case, the curve is always 1: this happens when all spam messages are given a score of 1.0, and all ham messages are given a score of 0.0. By contrast, the worst case happens when the curve is a diagonal $P(\text{true positive}) = P(\text{false positive})$, which occurs when our algorithm does no better than random. In general, ROC curves fall somewhere in between, forming a convex shell above the diagonal. The deeper this shell, the better our algorithm.



(left) ROC curve for a model performing much better than random: the curve reaches very high true positive rates for a low false positive rate.

(middle) ROC curve for a model performing significantly better than random.

(right) ROC curve for a model performing only marginally better than random: the true positive rate is only marginally larger than the rate of false positives, for any given threshold, meaning that nearly half the examples are misclassified.

We can calculate an array of points on the ROC curve using the `.roc` method on our `BinaryClassificationMetrics` instance. This returns an `RDD[(Double, Double)]` of (*false positive, true positive*) fractions for each threshold value. We can collect this as an array:

```
scala> val rocArray = bm.roc.collect
rocArray: Array[(Double, Double)] = Array((0.0,0.0),
(0.0,0.16793893129770993), ...
```

Of course, an array of numbers is not very enlightening, so let's plot the ROC curve with `breeze-viz`. We start by transforming our array of pairs into two arrays, one of false positives and one of true positives:

```
scala> val falsePositives = rocArray.map { _._1 }
falsePositives: Array[Double] = Array(0.0, 0.0, 0.0, 0.0, 0.0, ...
```

```
scala> val truePositives = rocArray.map { _._2 }
truePositives: Array[Double] = Array(0.0, 0.16793893129770993,
0.19083969465...
```

Let's plot these two arrays:

```
scala> import breeze.plot._
import breeze.plot.

scala> val f = Figure()
f: breeze.plot.Figure = breeze.plot.Figure@3aa746cd

scala> val p = f.subplot(0)
p: breeze.plot.Plot = breeze.plot.Plot@5ed1438a

scala> p += plot(falsePositives, truePositives)
p += plot(falsePositives, truePositives)

scala> p.xlabel = "false positives"
p.xlabel: String = false positives

scala> p.ylabel = "true positives"
p.ylabel: String = true positives

scala> p.title = "ROC"
```

```
p.title: String = ROC
```

```
scala> f.refresh
```

The ROC curve hits 1.0 for a small value of x: that is, we retrieve all true positives at the cost of relatively few false positives. To visualize the curve more accurately, it is instructive to limit the range on the x-axis from 0 to 0.1.

```
scala> p.xlim = (0.0, 0.1)
```

```
p.xlim: (Double, Double) = (0.0,0.1)
```

We also need to tell breeze-viz to use appropriate tick spacing, which requires going down to the JFreeChart layer underlying breeze-viz:

```
scala> import org.jfree.chart.axis.NumberTickUnit
```

```
import org.jfree.chart.axis.NumberTickUnit
```

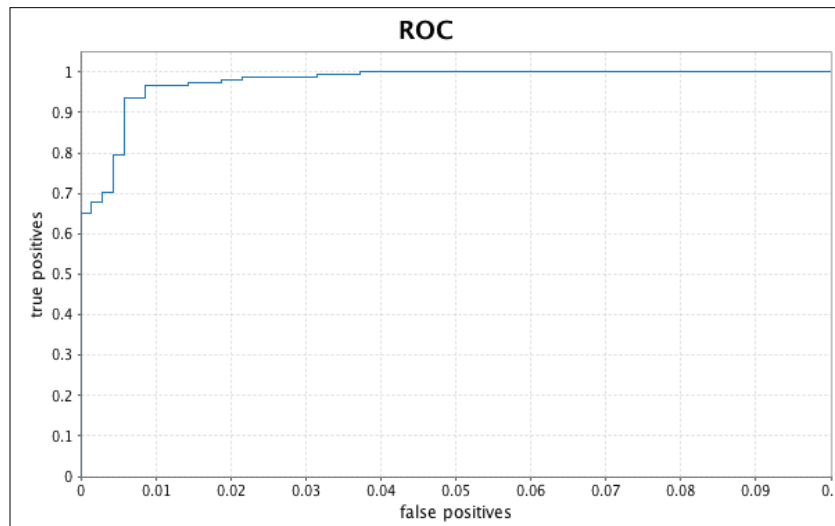
```
scala> p.xaxis.setTickUnit(new NumberTickUnit(0.01))
```

```
scala> p.yaxis.setTickUnit(new NumberTickUnit(0.1))
```

We can now save the graph:

```
scala> f.saveas("roc.png")
```

This produces the following graph, stored in roc.png:



ROC curve for spam classification with logistic regression.
Note that we have limited the false positive axis at 0.1

By looking at the graph, we see that we can filter out 85% of spam without a single **false positive**. Of course, we would need a larger test set to really validate this assumption.

A graph is useful to really understand the behavior of a model. Sometimes, however, we just want to have a single measure of the quality of a model. The area under the ROC curve can be a good such metric:

```
scala> bm.areaUnderROC
res21: Double = 0.9983061235861147
```

This can be interpreted as follows: given any two messages randomly drawn from the test set, one of which is ham, and one of which is spam, there is a 99.8% probability that the model assigned a greater likelihood of spam to the spam message than to the ham message.

Other useful measures of model quality are the precision and recall for particular thresholds, or the F1 score. All of these are provided by the `BinaryClassificationMetrics` instance. The API documentation lists the methods available: <https://spark.apache.org/docs/latest/api/scala/index.html#org.apache.spark.mllib.evaluation.BinaryClassificationMetrics>.

Regularization in logistic regression

One of the dangers of machine learning is over-fitting: the algorithm captures not only the signal in the training set, but also the statistical noise that results from the finite size of the training set.

A way to mitigate over-fitting in logistic regression is to use regularization: we impose a penalty for large values of the parameters when optimizing. We can do this by adding a penalty to the cost function that is proportional to the magnitude of the parameters. Formally, we re-write the logistic regression cost function (described in *Chapter 2, Manipulating Data with Breeze*) as:

$$Cost(params) = Cost_{LR}(params) + \lambda \|params\|_n$$

where $Cost_{LR}$ is the normal logistic regression cost function:

$$Cost_{LR}(params) = \sum_i target_i \times (params \cdot training_i) - \log[\exp(params \cdot training_i) + 1]$$

Here, $params$ is the vector of parameters, $training_i$ is the vector of features for the i th training example, and $target_i$ is 1 if the i th training example is spam, and 0 otherwise. This is identical to the logistic regression cost-function introduced in *Chapter 2, Manipulating data with Breeze*, apart from the addition of the regularization term $\lambda \|params\|_n$, the L_n norm of the parameter vector. The most common value of n is 2, in which case $\|params\|_2$ is just the magnitude of the parameter vector:

$$\|params\|_2 = \sqrt{\sum_i params_i^2}$$

The additional regularization term drives the algorithm to reduce the magnitude of the parameter vector. When using regularization, features must all have comparable magnitude. This is commonly achieved by normalizing the features. The logistic regression estimator provided by MLlib normalizes all features by default. This can be turned off with the `setStandardization` parameter.

Spark has two hyperparameters that can be tweaked to control regularization:

- The type of regularization, set with the `elasticNetParam` parameter. A value of 0 indicates L_2 regularization.
- The degree of regularization (λ in the cost function), set with the `regParam` parameter. A high value of the regularization parameter indicates a strong regularization. In general, the greater the danger of over-fitting, the larger the regularization parameter ought to be.

Let's create a new logistic regression instance that uses regularization:

```
scala> val lrWithRegularization = (new LogisticRegression()
  .setMaxIter(50))
lrWithRegularization: LogisticRegression = logreg_16b65b325526

scala> lrWithRegularization.setElasticNetParam(0)
lrWithRegularization.type = logreg_1e3584a59b3a
```

To choose the appropriate value of λ , we fit the pipeline to the training set and calculate the classification error on the test set for several values of λ . Further on in the chapter, we will learn about cross-validation in MLlib, which provides a much more rigorous way of choosing hyper-parameters.

```
scala> val lambdas = Array(0.0, 1.0E-12, 1.0E-10, 1.0E-8)
lambdas: Array[Double] = Array(0.0, 1.0E-12, 1.0E-10, 1.0E-8)

scala> lambdas foreach { lambda =>
  lrWithRegularization.setRegParam(lambda)
  val pipeline = new Pipeline().setStages(
    Array(indexer, tokenizer, hashingTF, lrWithRegularization))
  val model = pipeline.fit(trainDF)
  val transformedTest = model.transform(testDF)
  val classificationError = transformedTest.filter {
    $"prediction" != $"label"
  }.count
  println(s"$lambda => $classificationError")
}
0 => 20
1.0E-12 => 20
1.0E-10 => 20
1.0E-8 => 23
```

For our example, we see that any attempt to add L_2 regularization leads to a decrease in classification accuracy.

Cross-validation and model selection

In the previous example, we validated our approach by withholding 30% of the data when training, and testing on this subset. This approach is not particularly rigorous: the exact result changes depending on the random train-test split. Furthermore, if we wanted to test several different hyperparameters (or different models) to choose the best one, we would, unwittingly, choose the model that best reflects the specific rows in our test set, rather than the population as a whole.

This can be overcome with *cross-validation*. We have already encountered cross-validation in *Chapter 4, Parallel Collections and Futures*. In that chapter, we used random subsample cross-validation, where we created the train-test split randomly.

In this chapter, we will use **k-fold cross-validation**: we split the training set into k parts (where, typically, k is 10 or 3) and use $k-1$ parts as the training set and the last as the test set. The train/test cycle is repeated k times, keeping a different part as test set each time.

Cross-validation is commonly used to choose the best set of hyperparameters for a model. To illustrate choosing suitable hyperparameters, we will go back to our regularized logistic regression example. Instead of intuiting the hyper-parameters ourselves, we will choose the hyper-parameters that give us the best cross-validation score.

We will explore setting both the regularization type (through `elasticNetParam`) and the degree of regularization (through `regParam`). A crude, but effective way to find good values of the parameters is to perform a grid search: we calculate the cross-validation score for every pair of values of the regularization parameters of interest.

We can build a grid of parameters using MLlib's `ParamGridBuilder`.

```
scala> import org.apache.spark.ml.tuning.{ParamGridBuilder,
CrossValidator}
import org.apache.spark.ml.tuning.{ParamGridBuilder, CrossValidator}
```

```
scala> val paramGridBuilder = new ParamGridBuilder()
paramGridBuilder: ParamGridBuilder = ParamGridBuilder@1dd694d0
```

To add hyper-parameters over which to optimize to the grid, we use the `addGrid` method:

```
scala> val lambdas = Array(0.0, 1.0E-12, 1.0E-10, 1.0E-8)
Array[Double] = Array(0.0, 1.0E-12, 1.0E-10, 1.0E-8)
```

```
scala> val elasticNetParams = Array(0.0, 1.0)
elasticNetParams: Array[Double] = Array(0.0, 1.0)
```

```
scala> paramGridBuilder.addGrid(
  lrWithRegularization.regParam, lambdas).addGrid(
  lrWithRegularization.elasticNetParam, elasticNetParams)
paramGridBuilder.type = ParamGridBuilder@1dd694d0
```


Once all the dimensions are added, we can just call the `build` method on the builder to build the grid:

```
scala> val paramGrid = paramGridBuilder.build
paramGrid: Array[org.apache.spark.ml.param.ParamMap] =
Array({
  logreg_f7dfb27bed7d-elasticNetParam: 0.0,
  logreg_f7dfb27bed7d-regParam: 0.0
}, {
  logreg_f7dfb27bed7d-elasticNetParam: 1.0,
  logreg_f7dfb27bed7d-regParam: 0.0
} ...)
```

```
scala> paramGrid.length
Int = 8
```

As we can see, the grid is just a one-dimensional array of sets of parameters to pass to the logistic regression model prior to fitting.

The next step in setting up the cross-validation pipeline is to define a metric for comparing model performance. Earlier in the chapter, we saw how to use `BinaryClassificationMetrics` to estimate the quality of a model. Unfortunately, the `BinaryClassificationMetrics` class is part of the core MLlib API, rather than the new pipeline API, and is thus not (easily) compatible. The pipeline API offers a `BinaryClassificationEvaluator` class instead. This class works directly on `DataFrames`, and thus fits perfectly into the pipeline API flow:

```
scala> import org.apache.spark.ml.evaluation.
BinaryClassificationEvaluator
import org.apache.spark.ml.evaluation.BinaryClassificationEvaluator

scala> val evaluator = new BinaryClassificationEvaluator()
evaluator: BinaryClassificationEvaluator = binEval_64b08538f1a2

scala> println(evaluator.explainParams)
labelCol: label column name (default: label)
metricName: metric name in evaluation (areaUnderROC|areaUnderPR)
(default: areaUnderROC)
rawPredictionCol: raw prediction (a.k.a. confidence) column name
(default: rawPrediction)
```

From the parameter list, we see that the `BinaryClassificationEvaluator` class supports two metrics: the area under the ROC curve, and the area under the precision-recall curve. It expects, as input, a `DataFrame` containing a `label` column (the model truth) and a `rawPrediction` column (the column containing the probability that an e-mail is spam or ham).

We now have all the parameters we need to run cross-validation. We first build the pipeline, and then pass the pipeline, the evaluator and the array of parameters over which to run the cross-validation to an instance of `CrossValidator`:

```
scala> val pipeline = new Pipeline().setStages(
  Array(indexer, tokenizer, hashingTF, lrWithRegularization))
pipeline: Pipeline = pipeline_3ed29f72a4cc
```

```
scala> val crossval = (new CrossValidator()
  .setEstimator(pipeline)
  .setEvaluator(evaluator)
  .setEstimatorParamMaps(paramGrid)
  .setNumFolds(3))
crossval: CrossValidator = cv_5ebfa1143a9d
```

We will now fit `crossval` to `trainDF`:

```
scala> val cvModel = crossval.fit(trainDF)
cvModel: CrossValidatorModel = cv_5ebfa1143a9d
```

This step can take a fairly long time (over an hour on a single machine). This creates a transformer, `cvModel`, corresponding to the logistic regression object with the parameters that best represent `trainDF`. We can use it to predict the classification error on the test `DataFrame`:

```
scala> cvModel.transform(testDF).filter {
  $"prediction" != $"label"
}.count
Long = 20
```

Cross-validation has therefore resulted in a model that performs identically to the original, naive logistic regression model with no hyper-parameters. `cvModel` also contains a list of the evaluation score for each set of parameter in the parameter grid:

```
scala> cvModel.avgMetrics
Array[Double] = Array(0.996427805316161, ...)
```

The easiest way to relate this to the hyper-parameters is to zip it with `cvModel.getEstimatorParamMaps`. This gives us a list of (*hyperparameter values, cross-validation score*) pairs:

```
scala> val params2score = cvModel.getEstimatorParamMaps.zip(
  cvModel.avgMetrics)
Array[(ml.param.ParamMap,Double)] = Array(({
  logreg_8f107aabb304-elasticNetParam: 0.0,
  logreg_8f107aabb304-regParam: 0.0
},0.996427805316161),...)

scala> params2score.foreach {
  case (params, score) =>
    val lambda = params(lrWithRegularization.regParam)
    val elasticNetParam = params(
      lrWithRegularization.elasticNetParam)
    val l2Orl1 = if(elasticNetParam == 0.0) "L2" else "L1"
    println(s"$l2Orl1, $lambda => $score")
}
L2, 0.0 => 0.996427805316161
L1, 0.0 => 0.996427805316161
L2, 1.0E-12 => 0.9964278053175655
L1, 1.0E-12 => 0.9961429402772803
L2, 1.0E-10 => 0.9964382546369551
L1, 1.0E-10 => 0.9962223090037103
L2, 1.0E-8 => 0.9964159754613495
L1, 1.0E-8 => 0.9891008277659763
```

The best set of hyper-parameters correspond to L_2 regularization with a regularization parameter of $1E-10$, though this only corresponds to a tiny improvement in AUC.

This completes our spam filter example. We have successfully trained a spam filter for this particular Ling-Spam dataset. To obtain better results, one could experiment with better feature extraction: we could remove stop words or use TF-IDF vectors, rather than just term frequency vectors as features, and we could add additional features like the length of messages, or even *n-grams*. We could also experiment with non-linear algorithms, such as random forest. All of these steps would be straightforward to add to the pipeline.

Beyond logistic regression

We have concentrated on logistic regression in this chapter, but MLlib offers many alternative algorithms that will capture non-linearity in the data more effectively. The consistency of the pipeline API makes it easy to try out different algorithms and see how they perform. The pipeline API offers decision trees, random forest and gradient boosted trees for classification, as well as a simple feed-forward neural network, which is still experimental. It offers lasso and ridge regression and decision trees for regression, as well as PCA for dimensionality reduction.

The lower level MLlib API also offers principal component analysis for dimensionality reduction, several clustering methods including *k*-means and latent Dirichlet allocation and recommender systems using alternating least squares.

Summary

MLlib tackles the challenge of devising scalable machine learning algorithms head-on. In this chapter, we used it to train a simple scalable spam filter. MLlib is a vast, rapidly evolving library. The best way to learn more about what it can offer is to try and port code that you might have written using another library (such as scikit-learn).

In the next chapter, we will look at how to build web APIs and interactive visualizations to share our results with the rest of the world.

References

The best reference is the online documentation, including:

- The pipeline API: <http://spark.apache.org/docs/latest/ml-features.html>
- A full list of transformers: <http://spark.apache.org/docs/latest/ml-lib-guide.html#sparkml-high-level-apis-for-ml-pipelines>

Advanced Analytics with Spark, by Sandy Ryza, Uri Laserson, Sean Owen and Josh Wills provides a detailed and up-to-date introduction to machine learning with Spark.

There are several books that introduce machine learning in more detail than we can here. We have mentioned *The Elements of Statistical Learning*, by Friedman, Tibshirani and Hastie several times in this book. It is one of the most complete introductions to the mathematical underpinnings of machine learning currently available.

Andrew Ng's Machine Learning course on <https://www.coursera.org/> provides a good introduction to machine learning. It uses Octave/MATLAB as the programming language, but should be straightforward to adapt to Breeze and Scala.

13

Web APIs with Play

In the first 12 chapters of this book, we introduced basic tools and libraries for anyone wanting to build data science applications: we learned how to interact with SQL and MongoDB databases, how to build fast batch processing applications using Spark, how to apply state-of-the-art machine learning algorithms using MLlib, and how to build modular concurrent applications in Akka.

In the last chapters of this book, we will branch out to look at a web framework: *Play*. You might wonder why a web framework would feature in a data science book; surely such topics are best left to software engineers or web developers. Data scientists, however, rarely exist in a vacuum. They often need to communicate results or insights to stakeholders. As compelling as an ROC curve may be to someone well versed in statistics, it may not carry as much weight with less technical people. Indeed, it can be much easier to sell insights when they are accompanied by an engaging visualization.

Many modern interactive data visualization applications are web applications running in a web browser. Often, these involve **D3.js**, a JavaScript library for building data-driven web pages. In this chapter and the next, we will look at integrating D3 with Scala.

Writing a web application is a complex endeavor. We will split this task over this chapter and the next. In this chapter, we will learn how to write a REST API that we can use as backend for our application, or query in its own right. In the next chapter, we will look at integrating front-end code with Play to query the API exposed by the backend and display it using D3. We assume at least a basic familiarity with HTTP in this chapter: you should have read *Chapter 7, Web APIs*, at least.

Many data scientists or aspiring data scientists are unlikely to be familiar with the inner workings of web technologies. Learning how to build complex websites or web APIs can be daunting. This chapter therefore starts with a general discussion of dynamic websites and the architecture of web applications. If you are already familiar with server-side programming and with web frameworks, you can easily skip over the first few sections.

Client-server applications

A website works through the interaction between two computers: the client and the server. If you enter the URL `www.github.com/pbugnion/s4ds/graphs` in a web browser, your browser queries one of the GitHub servers. The server will look through its database for information concerning the repository that you are interested in. It will serve this information as HTML, CSS, and JavaScript to your computer. Your browser is then responsible for interpreting this response in the correct way.

If you look at the URL in question, you will notice that there are several graphs on that page. Unplug your internet connection and you can still interact with the graphs. All the information necessary for interacting with the graphs was transferred, as JavaScript, when you loaded that webpage. When you play with the graphs, the CPU cycles necessary to make those changes happen are spent on *your* computer, not a GitHub server. The code is executed *client-side*. Conversely, when you request information about a new repository, that request is handled by a GitHub server. It is said to be handled *server-side*.

A web framework like Play can be used on the server. For client-side code, we can only use a language that the client browser will understand: HTML for the layout, CSS for the styling and JavaScript, or languages that can compile to JavaScript, for the logic.

Introduction to web frameworks

This section is a brief introduction to how modern web applications are designed. Go ahead and skip it if you already feel comfortable writing backend code.

Loosely, a web framework is a set of tools and code libraries for building web applications. To understand what a web framework provides, let's take a step back and think about what you would need to do if you did not have one.

You want to write a program that listens on port 80 and sends HTML (or JSON or XML) back to clients that request it. This is simple if you are serving the same file back to every client: just load the HTML from file when you start the server, and send it to clients who request it.

So far, so good. But what if you now want to customize the HTML based on the client request? You might choose to respond differently based on part of the URL that the client put in his browser, or based on specific elements in the HTTP request. For instance, the product page on `amazon.com` is different to the payment page. You need to write code to parse the URL and the request, and then route the request to the relevant handler.

You might now want to customize the HTML returned dynamically, based on specific elements of the request. The page for every product on `amazon.com` follows the same outline, but specific elements are different. It would be wasteful to store the entire HTML content for every product. A better way is to store the details for each product in a database and inject them into an HTML template when a client requests information on that product. You can do this with a *template processor*. Of course, writing a good template processor is difficult.

You might deploy your web framework and realize that it cannot handle the traffic directed to it. You decide that handlers responding to client requests should run asynchronously. You now have to deal with concurrency.

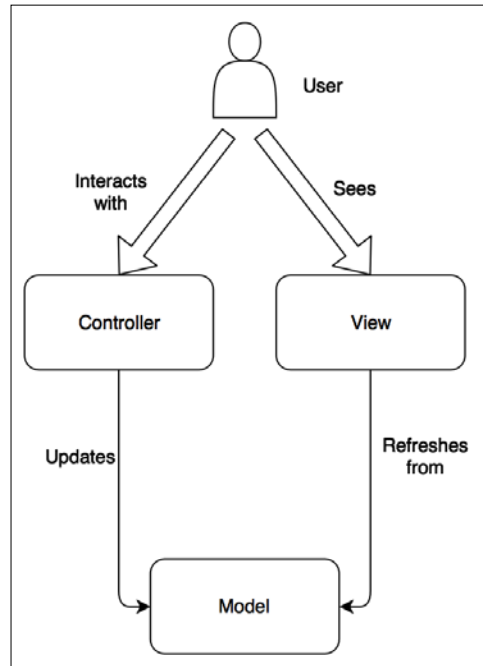
A web framework essentially provides the wires to bind everything together. Besides bundling an HTTP server, most frameworks will have a router that automatically routes a request, based on the URL, to the correct handler. In most cases, the handler will run asynchronously, giving you much better scalability. Many frameworks have a template processor that lets you write HTML (or sometimes JSON or XML) templates intuitively. Some web frameworks also provide functionality for accessing a database, for parsing JSON or XML, for formulating HTTP requests and for localization and internationalization.

Model-View-Controller architecture

Many web frameworks impose program architectures: it is difficult to provide wires to bind disparate components together without making some assumptions about what those components are. The **Model-View-Controller (MVC)** architecture is particularly popular on the Web, and it is the architecture the Play framework assumes. Let's look at each component in turn:

- The model is the data underlying the application. For example, I expect the application underlying GitHub has models for users, repositories, organizations, pull requests and so on. In the Play framework, a model is often an instance of a case class. The core responsibility of the model is to remember the current state of the application.
- Views are representations of a model or a set of models on the screen.

- The controller handles client interactions, possibly changing the model. For instance, if you *star* a project on GitHub, the controller will update the relevant models. Controllers normally carry very little application state: remembering things is the job of the models.



MVC architecture: the state of the application is provided by the model. The view provides a visual representation of the model to the user, and the controller handles logic: what to do when the user presses a button or submits a form.

The MVC framework works well because it decouples the user interface from the underlying data and structures the flow of actions: a controller can update the model state or the view, a model can send signals to the view to tell it to update, and the view merely displays that information. The model carries no information related to the user interface. This separation of concerns results in an easier mental model of information flow, better encapsulation and greater testability.

Single page applications

The client-server duality adds a degree of complication to the elegant MVC architecture. Where should the model reside? What about the controller? Traditionally, the model and the controller ran almost entirely on the server, which just pushed the relevant HTML view to the client.

The growth in client-side JavaScript frameworks, such as AngularJS, has resulted in a gradual shift to putting more code in the client. Both the controller and a temporary version of the model typically run client-side. The server just functions as a web API: if, for instance, the user updates the model, the controller will send an HTTP request to the server informing it of the change.

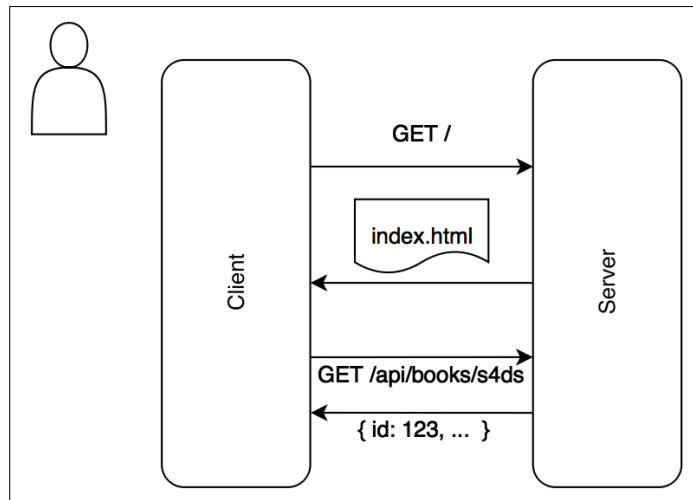
It then makes sense to think of the program running server-side and the one running client-side as two separate applications: the server persists data in databases, for instance, and provides a programmatic interface to this data, usually as a web service returning JSON or XML data. The client-side program maintains its own model and controller, and polls the server whenever it needs a new model, or whenever it needs to inform the server that the persistent view of the model should be changed.

Taken to the extreme, this results in **Single-Page Applications**. In a single-page application, the first time the client requests a page from the server, he receives the HTML and the JavaScript necessary to build the framework for the entire application. If the client needs further data from the server, he will poll the server's API. This data is returned as JSON or XML.

This might seem a little complicated in the abstract, so let's think how the Amazon website might be structured as a single-page application. We will just concern ourselves with the products page here, since that's complicated enough. Let's imagine that you are on the home page, and you hit a link for a particular product. The application running on your computer knows how to display products, for instance through an HTML template. The JavaScript also has a prototype for the model, such as:

```
{
  product_id: undefined,
  product_name: undefined,
  product_price: undefined,
  ...
}
```

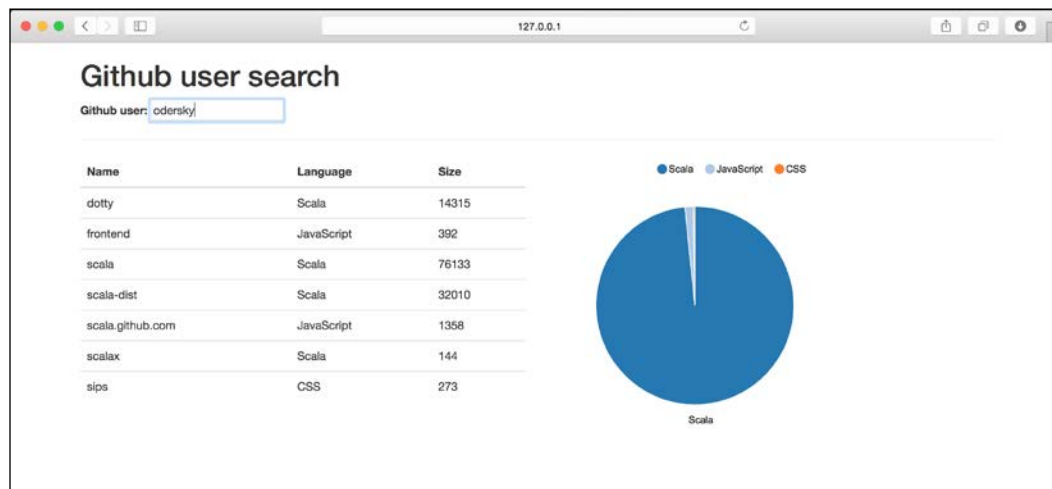
What it's currently missing is knowledge of what data to put in those fields for the product you have just selected: there is no way that information could have been sent to your computer when the website loaded, since there was no way to know what product you might click on (and sending information about every product would be prohibitively costly). So the Amazon client sends a request to the server for information on that product. The Amazon server replies with a JSON object (or maybe XML). The client then updates its model with that information. When the update is complete, an event is fired to update the view:



Client-server communications in a single-page application: when the client first accesses the website, it receives HTML, CSS and JavaScript files that contain the entire logic for the application. From then on, the client only uses the server as an API when it requests additional data. The application running in the user's web browser and the one running on the server are nearly independent. The only coupling is through the structure of the API exposed by the server.

Building an application

In this chapter and the next, we will build a single-page application that relies on an API written in Play. We will build a webpage that looks like this:



The user enters the name of someone on GitHub and can view a list of their repositories and a chart summarizing what language they use. You can find the application deployed at app.scala4datascience.com. Go ahead and give it a whirl.

To get a glimpse of the innards, type `app.scala4datascience.com/api/repos/odersky`. This returns a JSON object like:

```
[{"name": "dotty", "language": "Scala", "is_fork": true, "size": 14653},
{"name": "frontend", "language": "JavaScript", "is_fork": true, "size": 392},
{"name": "legacy-svn-scala", "language": "Scala", "is_fork": true, "size": 296706},
...]
```

We will build the API in this chapter, and write the front-end code in the next chapter.

The Play framework

The Play framework is a web framework built on top of Akka. It has a proven track record in industry, and is thus a reliable choice for building scalable web applications.

Play is an *opinionated* web framework: it expects you to follow the MVC architecture, and it has a strong opinion about the tools you should be using. It comes bundled with its own JSON and XML parsers, with its own tools for accessing external APIs, and with recommendations for how to access databases.

Web applications are much more complex than the command line scripts we have been developing in this book, because there are many more components: the backend code, routing information, HTML templates, JavaScript files, images, and so on. The Play framework makes strong assumptions about the directory structure for your project. Building that structure from scratch is both mind-numbingly boring and easy to get wrong. Fortunately, we can use **Typesafe activators** to bootstrap the project (you can also download the code from the Git repository in <https://github.com/pbugnion/s4ds> but I encourage you to start the project from a basic activator structure and code along instead, using the finished version as an example).

Typesafe activator is a custom version of SBT that includes templates to get Scala programmers up and running quickly. To install activator, you can either download a JAR from <https://www.typesafe.com/activator/download>, or, on Mac OS, via homebrew:

```
$ brew install typesafe-activator
```

You can then launch the activator console from the terminal. If you downloaded activator:

```
$ ./path/to/activator/activator new
```

Or, if you installed via Homebrew:

```
$ activator new
```

This starts a new project in the current directory. It starts by asking what template you want to start with. Choose `play-scala`. It then asks for a name for your application. I chose `ghub-display`, but go ahead and be creative!

Let's explore the newly created project structure (I have only retained the most important files):

```
|— app
|   |— controllers
|   |   └─ Application.scala
```

```

|   └─ views
|       └─ main.scala.html
|       └─ index.scala.html
└─ build.sbt
└─ conf
    └─ application.conf
    └─ routes
└─ project
    └─ build.properties
    └─ plugins.sbt
└─ public
    └─ images
        └─ favicon.png
    └─ javascripts
        └─ hello.js
    └─ stylesheets
        └─ main.css
└─ test
    └─ ApplicationSpec.scala
    └─ IntegrationSpec.scala

```

Let's run the app:

```

$ ./activator
[ghub-display] $ run

```

Head over to your browser and navigate to the URL `127.0.0.1:9000/`. The page may take a few seconds to load. Once it is loaded, you should see a default page that says **Your application is ready**.

Before we modify anything, let's walk through how this happens. When you ask your browser to take you to `127.0.0.1:9000/`, your browser sends an HTTP request to the server listening at that address (in this case, the Netty server bundled with Play). The request is a GET request for the route `/`. The Play framework looks in `conf/routes` to see if it has a route satisfying `/`:

```

$ cat conf/routes
# Home page
GET      /                               controllers.Application.index
...

```

We see that the `conf/routes` file does contain the route `/` for GET requests. The second part of that line, `controllers.Application.index`, is the name of a Scala function to handle that route (more on that in a moment). Let's experiment. Change the route end-point to `/hello`. Refresh your browser without changing the URL. This will trigger recompilation of the application. You should now see an error page:



The error page tells you that the app does not have an action for the route `/` any more. If you navigate to `127.0.0.1:9000/hello`, you should see the landing page again.

Besides learning a little of how routing works, we have also learned two things about developing Play applications:

- In development mode, code gets recompiled when you refresh your browser and there have been code changes
- Compilation and runtime errors get propagated to the web page

Let's change the route back to `/`. There is a lot more to say on routing, but it can wait till we start building our application.

The `conf/routes` file tells the Play framework to use the method `controllers.Application.index` to handle requests to `/`. Let's look at the `Application.scala` file in `app/controllers`, where the `index` method is defined:

```
// app/controllers/Application.scala
package controllers

import play.api._
import play.api.mvc._

class Application extends Controller {

  def index = Action {
    Ok(views.html.index("Your new application is ready."))
  }

}
```

We see that `controllers.Application.index` refers to the method `index` in the class `Application`. This method has return type `Action`. An `Action` is just a function that maps HTTP requests to responses. Before explaining this in more detail, let's change the action to:

```
def index = Action {
  Ok("hello, world")
}
```

Refresh your browser and you should see the landing page replaced with "hello world". By having our action return `Ok("hello, world")`, we are asking Play to return an HTTP response with status code 200 (indicating that the request was successful) and the body "hello world".

Let's go back to the original content of `index`:

```
Action {
  Ok(views.html.index("Your new application is ready. "))
}
```

We can see that this calls the method `views.html.index`. This might appear strange, because there is no `views` package anywhere. However, if you look at the `app/views` directory, you will notice two files: `index.scala.html` and `main.scala.html`. These are templates, which, at compile time, get transformed into Scala functions. Let's have a look at `main.scala.html`:

```
// app/views/main.scala.html
@(title: String)(content: Html)

<!DOCTYPE html>

<html lang="en">
  <head>
    <title>@title</title>
    <!-- not so important stuff -->
  </head>
  <body>
    @content
  </body>
</html>
```


At compile time, this template is compiled to a function `main(title:String)(content:Html)` in the package `views.html`. Notice that the function package and name comes from the template file name, and the function arguments come from the first line of the template. The template contains embedded `@title` and `@content` values, which get filled in by the arguments to the function. Let's experiment with this in a Scala console:

```
$ activator console
scala> import views.html._
import views.html._

scala> val title = "hello"
title: String = hello

scala> val content = new play.twirl.api.Html("<b>World</b>")
content: play.twirl.api.Html = <b>World</b>

scala> main(title)(content)
res8: play.twirl.api.HtmlFormat.Appendable =
<!DOCTYPE html>

<html lang="en">
  <head>
    <title>hello</title>
    <!-- not so important stuff -->
  </head>
  <body>
    <b>World</b>
  </body>
</html>
```

We can call `views.html.main`, just like we would call a normal Scala function. The arguments we pass in get embedded in the correct place, as defined by the template in `views/main.scala.html`.

This concludes our introductory tour of Play. Let's briefly go over what we have learnt: when a request reaches the Play server, the server reads the URL and the HTTP verb and checks that these exist in its `conf/routes` file. It will then pass the request to the `Action` defined by the controller for that route. This `Action` returns an HTTP response that gets fed back to the browser. In constructing the response, the `Action` may make use of a template, which, as far as it is concerned is just a function `(arguments list) => String` or `(arguments list) => HTML`.

Dynamic routing

Routing, as we saw, is the mapping of HTTP requests to Scala handlers. Routes are stored in `conf/routes`. A route is defined by an HTTP verb, followed by the end-point, followed by a Scala function:

```
// verb    // end-point          // Scala handler
GET       /                       controllers.Application.index
```

We learnt to add new routes by just adding lines to the `routes` file. We are not limited to static routes, however. The Play framework lets us include wild cards in routes. The value of the wild card can be passed as an argument to the controller. To see how this works, let's create a controller that takes the name of a person as argument. In the `Application` object in `app.controllers`, add:

```
// app/controllers/Application.scala

class Application extends Controller {

  ...

  def hello(name:String) = Action {
    Ok(s"hello, $name")
  }
}
```

We can now define a route handled by this controller:

```
// conf/routes
GET /hello/:name          controllers.Application.hello(name)
```

If you now point your browser to `127.0.0.1:9000/hello/Jim`, you will see **hello, Jim** appear on the screen.

Any string between `:` and the following `/` is treated as a wild card: it will match any combination of characters. The value of the wild card can be passed to the controller. Note that the wild card can appear anywhere in the URL, and there can be more than one wild card. The following are all valid route definitions, for instance:

```
GET /hello/person-:name      controllers.Application.hello(name)
// ... matches /hello/person-Jim

GET /hello/:name/picture    controllers.Application.pictureFor(name)
// ... matches /hello/Jim/picture

GET /hello/:first/:last     controllers.Application.hello(first, last)
// ... matches /hello/john/doe
```

There are many other options for selecting routes and passing arguments to the controller. Consult the documentation for the Play framework for a full discussion on the routing possibilities: <https://www.playframework.com/documentation/2.4.x/ScalaRouting>.



URL design

It is generally considered best practice to leave the URL as simple as possible. The URL should reflect the hierarchical structure of the information of the website, rather than the underlying implementation. GitHub is a very good example of this: its URLs make intuitive sense. For instance, the URL for the repository for this book is:

```
https://github.com/pbugnion/s4ds
```

To access the issues page for that repository, add `/issues` to the route. To access the first issue, add `/1` to that route. These are called **semantic URLs** (https://en.wikipedia.org/wiki/Semantic_URL).

Actions

We have talked about routes, and how to pass parameters to controllers. Let's now talk about what we can do with the controller.

The method defined in the route must return a `play.api.mvc.Action` instance. The `Action` type is a thin wrapper around the type `Request[A] => Result`, where `Request[A]` identifies an HTTP request and `Result` is an HTTP response.

Composing the response

An HTTP response, as we saw in *Chapter 7, Web APIs*, is composed of:

- the status code (such as 200 for a successful response, or 404 for a missing page)
- the response headers, a key-value list indicating metadata related to the response
- The response body. This can be HTML for web pages, or JSON, XML or plain text (or many other formats). This is generally the bit that we are really interested in.

The Play framework defines a `play.api.mvc.Result` object that symbolizes a response. The object contains a `header` attribute with the status code and the headers, and a `body` attribute containing the body.

The simplest way to generate a `Result` is to use one of the factory methods in `play.api.mvc.Results`. We have already seen the `Ok` method, which generates a response with status code 200:

```
def hello(name:String) = Action {  
  Ok("hello, $name")  
}
```

Let's take a step back and open a Scala console so we can understand how this works:

```
$ activator console  
scala> import play.api.mvc._  
import play.api.mvc._  
  
scala> val res = Results.Ok("hello, world")  
res: play.api.mvc.Result = Result(200, Map(Content-Type -> text/plain;  
charset=utf-8))  
  
scala> res.header.status  
Int = 200  
  
scala> res.header.headers  
Map[String,String] = Map(Content-Type -> text/plain; charset=utf-8)  
  
scala> res.body  
play.api.libs.iteratee.Enumerator[Array[Byte]] = play.api.libs.iteratee.  
Enumerator$$anon$18@5fb83873
```

We can see how the `Results.Ok(...)` creates a `Result` object with status 200 and (in this case), a single header denoting the content type. The body is a bit more complicated: it is an enumerator that can be pushed onto the output stream when needed. The enumerator contains the argument passed to `Ok`: "hello, world", in this case.

There are many factory methods in `Results` for returning different status codes. Some of the more relevant ones are:

- `Action { Results.NotFound }`
- `Action { Results.BadRequest("bad request") }`
- `Action { Results.InternalServerError("error") }`
- `Action { Results.Forbidden }`
- `Action { Results.Redirect("/home") }`

For a full list of `Result` factories, consult the API documentation for `Results` (<https://www.playframework.com/documentation/2.4.x/api/scala/index.html#play.api.mvc.Results>).

We have, so far, been limiting ourselves to passing strings as the content of the `Ok` result: `Ok("hello, world")`. We are not, however, limited to passing strings. We can pass a JSON object:

```
scala> import play.api.libs.json._
import play.api.libs.json._

scala> val jsonObj = Json.obj("hello" -> "world")
jsonObj: play.api.libs.json.JsObject = {"hello":"world"}

scala> Results.Ok(jsonObj)
play.api.mvc.Result = Result(200, Map(Content-Type -> application/json; charset=utf-8))
```

We will cover interacting with JSON in more detail when we start building the API. We can also pass HTML as the content. This is most commonly the case when returning a view:

```
scala> val htmlObj = views.html.index("hello")
htmlObj: play.twirl.api.HTMLFormat.Appendable =

<!DOCTYPE html>
```

```

<html lang="en">
  <head>
  ...

scala> Results.Ok(htmlObj)
play.api.mvc.Result = Result(200, Map(Content-Type -> text/html;
charset=utf-8))

```

Note how the `Content-Type` header is set based on the type of content passed to `Ok`. The `Ok` factory uses the `Writeable` type class to convert its argument to the body of the response. Thus, any content type for which a `Writeable` type class exists can be used as argument to `Ok`. If you are unfamiliar with type classes, you might want to read the *Looser coupling with type classes* section in *Chapter 5, Scala and SQL through JDBC*.

Understanding and parsing the request

We now know how to formulate (basic) responses. The other half of the equation is the HTTP request. Recall that an `Action` is just a function mapping `Request => Result`. We can access the request using:

```

def hello(name:String) = Action { request =>
  ...
}

```

One of the reasons for needing a reference to the request is to access parameters in the query string. Let's modify the `Hello`, `<name>` example that we wrote earlier to, optionally, include a title in the query string. Thus, a URL could be formatted as `/hello/Jim?title=Dr`. The `request` instance exposes the `getQueryString` method for accessing specific keys in the query string. This method returns `Some[String]` if the key is present in the query, or `None` otherwise. We can re-write our `hello` controller as:

```

def hello(name:String) = Action { request =>
  val title = request.getQueryString("title")
  val titleString = title.map { _ + " " }.getOrElse("")
  Ok(s"Hello, $titleString$name")
}

```

Try this out by accessing the URL `127.0.0.1:9000/hello/Odersky?title=Dr` in your browser. The browser should display `Hello, Dr Odersky`.

We have, so far, been concentrating on GET requests. These do not have a body. Other types of HTTP request, most commonly POST requests, do contain a body. Play lets the user pass *body parsers* when defining the action. The request body will be passed through the body parser, which will convert it from a byte stream to a Scala type. As a very simple example, let's define a new route that accepts POST requests:

```
POST      /hello      controllers.Application.helloPost
```

We will apply the predefined `parse.text` body parser to the incoming request body. This converts the body of the request to a string. The `helloPost` controller looks like:

```
def helloPost = Action(parse.text) { request =>
  Ok("Hello. You told me: " + request.body)
}
```



You cannot test POST requests easily in the browser. You can use cURL instead. cURL is a command line utility for dispatching HTTP requests. It is installed by default on Mac OS and should be available via the package manager on Linux distributions. The following will send a POST request with "I think that Scala is great" in the body:

```
$ curl --data "I think that Scala is great" --header
  "Content-type:text/plain" 127.0.0.1:9000/hello
```

This prints the following line to the terminal:

```
Hello. You told me: I think that Scala is great
```

There are several types of built-in body parsers:

- `parse.file(new File("filename.txt"))` will save the body to a file.
- `parse.json` will parse the body as JSON (we will learn more about interacting with JSON in the next section).
- `parse.xml` will parse the body as XML.
- `parse.urlFormEncoded` will parse the body as returned by submitting an HTML form. The `request.body` attribute is a Scala map from `String` to `Seq[String]`, mapping each form element to its value(s).

For a full list of body parsers, the best source is the Scala API documentation for `play.api.mvc.BodyParsers.parse` available at: [https://www.playframework.com/documentation/2.5.x/api/scala/index.html#play.api.mvc.BodyParsers\\$.parse\\$](https://www.playframework.com/documentation/2.5.x/api/scala/index.html#play.api.mvc.BodyParsers$.parse$).

Interacting with JSON

JSON, as we discovered in previous chapters, is becoming the de-facto language for communicating structured data over HTTP. If you develop a web application or a web API, it is likely that you will have to consume or emit JSON, or both.

In *Chapter 7, Web APIs*, we learned how to parse JSON through `json4s`. The Play framework includes its own JSON parser and emitter. Fortunately, it behaves in much the same way as `json4s`.

Let's imagine that we are building an API that summarizes information about GitHub repositories. Our API will emit a JSON array listing a user's repositories when queried about a specific user (much like the GitHub API, but with just a subset of fields).

Let's start by defining a model for the repository. In Play applications, models are normally stored in the folder `app/models`, in the `models` package:

```
// app/models/Repo.scala

package models

case class Repo (
  val name:String,
  val language:String,
  val isFork: Boolean,
  val size: Long
)
```

Let's add a route to our application that serves arrays of repos for a particular user. In `conf/routes`, add the following line:

```
// conf/routes
GET    /api/repos/:username      controllers.Api.repos(username)
```

Let's now implement the framework for the controller. We will create a new controller for our API, imaginatively called `Api`. For now, we will just have the controller return dummy data. This is what the code looks like (we will explain the details shortly):

```
// app/controllers/Api.scala
package controllers
import play.api._
import play.api.mvc._
```



```
import play.api.libs.json._

import models.Repo

class Api extends Controller {

  // Some dummy data.
  val data = List[Repo](
    Repo("dotty", "Scala", true, 14315),
    Repo("frontend", "JavaScript", true, 392)
  )

  // Typeclass for converting Repo -> JSON
  implicit val writesRepos = new Writes[Repo] {
    def writes(repo:Repo) = Json.obj(
      "name" -> repo.name,
      "language" -> repo.language,
      "is_fork" -> repo.isFork,
      "size" -> repo.size
    )
  }

  // The controller
  def repos(username:String) = Action {

    val repoArray = Json.toJson(data)
    // toJson(data) relies on existence of
    // `Writes[List[Repo]]` type class in scope

    Ok(repoArray)
  }
}
```

If you point your web browser to `127.0.0.1:9000/api/repos/odersky`, you should now see the following JSON object:

```
[{"name":"dotty","language":"Scala","is_fork":true,"size":14315}, {"name":"frontend","language":"JavaScript","is_fork":true,"size":392}]
```

The only tricky part of this code is the conversion from `Repo` to JSON. We call `Json.toJson` on `data`, an instance of type `List[Repo]`. The `toJson` method relies on the existence of a type class `Writes[T]` for the type `T` passed to it.

The Play framework makes extensive use of type classes to define how to convert models to specific formats. Recall that we learnt how to write type classes in the context of SQL and MongoDB. The Play framework's expectations are very similar: for the `Json.toJson` method to work on an instance of type `Repo`, there must be a `Writes[Repo]` implementation available that specifies how to transform `Repo` objects to JSON.

In the Play framework, the `Writes[T]` type class defines a single method:

```
trait Writes[T] {  
  def writes(obj:T):Json  
}
```

`Writes` methods for built-in simple types and for collections are already built into the Play framework, so we do not need to worry about defining `Writes[Boolean]`, for instance.

The `Writes[Repo]` instance is commonly defined either directly in the controller, if it is just used for that controller, or in the `Repo` companion object, where it can be used across several controllers. For simplicity, we just embedded it in the controller.

Note how type-classes allow for separation of concerns. The model just defines the `Repo` type, without attaching any behavior. The `Writes[Repo]` type class just knows how to convert from a `Repo` instance to JSON, but knows nothing of the context in which it is used. Finally, the controller just knows how to create a JSON HTTP response.

Congratulations, you have just defined a web API that returns JSON! In the next section, we will learn how to fetch data from the GitHub web API to avoid constantly returning the same array.

Querying external APIs and consuming JSON

So far, we have learnt how to provide the user with a dummy JSON array of repositories in response to a request to `/api/repos/:username`. In this section, we will replace the dummy data with the user's actual repositories, downloaded from GitHub.

In *Chapter 7, Web APIs*, we learned how to query the GitHub API using Scala's `Source.fromURL` method and `scalaj-http`. It should come as no surprise that the Play framework implements its own library for interacting with external web services.

Let's edit the `Api` controller to fetch information about a user's repositories from GitHub, rather than using dummy data. When called with a username as argument, the controller will:

1. Send a GET request to the GitHub API for that user's repositories.
2. Interpret the response, converting the body from a JSON object to a `List[Repo]`.
3. Convert from the `List[Repo]` to a JSON array, forming the response.

We start by giving the full code listing before explaining the thornier parts in detail:

```
// app/controllers/Api.scala

package controllers

import play.api._
import play.api.mvc._
import play.api.libs.ws.WS // query external APIs
import play.api.Play.current
import play.api.libs.json._ // parsing JSON
import play.api.libs.functional.syntax._
import play.api.libs.concurrent.Execution.Implicits.defaultContext

import models.Repo

class Api extends Controller {

  // type class for Repo -> Json conversion
  implicit val writesRepo = new Writes[Repo] {
    def writes(repo:Repo) = Json.obj(
      "name" -> repo.name,
      "language" -> repo.language,
      "is_fork" -> repo.isFork,
      "size" -> repo.size
    )
  }

  // type class for Github Json -> Repo conversion
  implicit val readsRepoFromGithub: Reads[Repo] = (
    (JsPath \ "name").read[String] and
    (JsPath \ "language").read[String] and
    (JsPath \ "fork").read[Boolean] and
  )
```

```

    (JsPath \ "size").read[Long]
  )(Repo.apply _)

// controller
def repos(username:String) = Action.async {

  // GitHub URL
  val url = s"https://api.github.com/users/$username/repos"
  val response = WS.url(url).get() // compose get request

  // "response" is a Future
  response.map { r =>
    // executed when the request completes
    if (r.status == 200) {

      // extract a list of repos from the response body
      val reposOpt = Json.parse(r.body).validate[List[Repo]]
      reposOpt match {
        // if the extraction was successful:
        case JsSuccess(repos, _) => Ok(Json.toJson(repos))

        // If there was an error during the extraction
        case _ => InternalServerError
      }
    }
    else {
      // GitHub returned something other than 200
      NotFound
    }
  }
}
}

```

If you have written all this, point your browser to, for instance, `127.0.0.1:9000/api/repos/odersky` to see the list of repositories owned by Martin Odersky:

```
[{"name":"dotty","language":"Scala","is_fork":true,"size":14653}, {"name":"frontend","language":"JavaScript","is_fork":true,"size":392}, ...
```

This code sample is a lot to take in, so let's break it down.

Calling external web services

The first step in querying external APIs is to import the `WS` object, which defines factory methods for creating HTTP requests. These factory methods rely on a reference to an implicit Play application in the namespace. The easiest way to ensure this is the case is to import `play.api.Play.current`, a reference to the current application.

Let's ignore the `readsRepoFromGithub` type class for now and jump straight to the controller body. The URL that we want to hit with a GET request is `"https://api.github.com/users/$username/repos"`, with the appropriate value for `$username`. We create a GET request with `WS.url(url).get()`. We can also add headers to an existing request. For instance, to specify the content type, we could have written:

```
WS.url(url).withHeaders("Content-Type" ->
  "application/json").get()
```

We can use headers to pass a GitHub OAuth token using:

```
val token = "2502761d..."
WS.url(url).withHeaders("Authorization" -> s"token $token").get()
```

To formulate a POST request, rather than a GET request, replace the final `.get()` with `.post(data)`. Here, `data` can be JSON, XML or a string.

Adding `.get` or `.post` fires the request, returning a `Future[WSResponse]`. You should, by now, be familiar with futures. By writing `response.map { r => ... }`, we specify a transformation to be executed on the future result, when it returns. The transformation verifies the response's status, returning `NotFound` if the status code of the response is anything but 200.

Parsing JSON

If the status code is 200, the callback parses the response body to JSON and converts the parsed JSON to a `List[Repo]` instance. We already know how to convert from a `Repo` object to JSON using the `Writes[Repo]` type class. The converse, going from JSON to a `Repo` object, is a little more challenging, because we have to account for incorrectly formatted JSON. To this effect, the Play framework provides the `.validate[T]` method on JSON objects. This method tries to convert the JSON to an instance of type `T`, returning `JsSuccess` if the JSON is well-formatted, or `JsError` otherwise (similar to Scala's `Try` object). The `.validate` method relies on the existence of a type class `Reads[Repo]`. Let's experiment with a Scala console:

```
$ activator console
```

```
scala> import play.api.libs.json._
```

```
import play.api.libs.json._

scala> val s = """
  { "name": "dotty", "size": 150, "language": "Scala", "fork": true }
  """
s: String = "
  { "name": "dotty", "size": 150, "language": "Scala", "fork": true }
  "

scala> val parsedJson = Json.parse(s)
parsedJson: play.api.libs.json.JsValue = {"name":"dotty","size":150,"language":"Scala","fork":true}
```

Using `Json.parse` converts a string to an instance of `JsValue`, the super-type for JSON instances. We can access specific fields in `parsedJson` using XPath-like syntax (if you are not familiar with XPath-like syntax, you might want to read *Chapter 6, Slick – A Functional Interface for SQL*):

```
scala> parsedJson \ "name"
play.api.libs.json.JsLookupResult = JsDefined("dotty")
```

XPath-like lookups return an instance with type `JsLookupResult`. This takes two values: either `JsDefined`, if the path is valid, or `JsUndefined` if it is not:

```
scala> parsedJson \ "age"
play.api.libs.json.JsLookupResult = JsUndefined('age' is undefined on
object: {"name":"dotty","size":150,"language":"Scala","fork":true})
```

To go from a `JsLookupResult` instance to a `String` in a type-safe way, we can use the `.validate[String]` method:

```
scala> (parsedJson \ "name").validate[String]
play.api.libs.json.JsResult[String] = JsSuccess(dotty,)
```

The `.validate[T]` method returns either `JsSuccess` if the `JsDefined` instance could be successfully cast to `T`, or `JsError` otherwise. To illustrate the latter, let's try validating this as an `Int`:

```
scala> (parsedJson \ "name").validate[Int]
dplay.api.libs.json.JsResult[Int] = JsError(List((),List(ValidationError(List(error.expected.jsnumber),WrappedArray())))))
```

Calling `.validate` on an instance of type `JsUndefined` also returns in a `JsError`:

```
scala> (parsedJson \ "age").validate[Int]
play.api.libs.json.JsResult[Int] = JsError(List((),List(ValidationError(List('age' is undefined on object: {"name":"dotty","size":150,"language":"Scala","fork":true}),WrappedArray()))))
```

To convert from an instance of `JsResult [T]` to an instance of type `T`, we can use pattern matching:

```
scala> val name = (parsedJson \ "name").validate[String] match {
  case JsSuccess(n, _) => n
  case JsError(e) => throw new IllegalStateException(
    s"Error extracting name: $e")
}
name: String = dotty
```

We can now use `.validate` to cast JSON to simple types in a type-safe manner. But, in the code example, we used `.validate [Repo]`. This works provided a `Reads [Repo]` type class is implicitly available in the namespace.

The most common way of defining `Reads [T]` type classes is through a DSL provided in `import play.api.libs.functional.syntax._`. The DSL works by chaining operations returning either `JsSuccess` or `JsError` together. Discussing exactly how this DSL works is outside the scope of this chapter (see, for instance, the Play framework documentation page on JSON combinators: <https://www.playframework.com/documentation/2.4.x/ScalaJsonCombinators>). We will stick to discussing the syntax.

```
scala> import play.api.libs.functional.syntax._
import play.api.libs.functional.syntax._

scala> import models.Repo
import models.Repo

scala> implicit val readsRepoFromGithub:Reads[Repo] = (
  (JsPath \ "name").read[String] and
  (JsPath \ "language").read[String] and
  (JsPath \ "fork").read[Boolean] and
```

```

    (JsPath \ "size").read[Long]
  )(Repo.apply _)
readsRepoFromGithub: play.api.libs.json.Reads[models.Repo] = play.api.
libs.json.Reads$$anon$8@a198ddb

```

The Reads type class is defined in two stages. The first chains together `read[T]` methods with `and`, combining successes and errors. The second uses the `apply` method of the companion object of a case class (or `Tuple` instance) to construct the object, provided the first stage completed successfully. Now that we have defined the type class, we can call `validate[Repo]` on a `JsValue` object:

```

scala> val repoOpt = parsedJson.validate[Repo]
play.api.libs.json.JsResult[models.Repo] = JsSuccess(Repo(dotty,Scala,true,150),)

```

We can then use pattern matching to extract the `Repo` object from the `JsSuccess` instance:

```

scala> val JsSuccess(repo, _) = repoOpt
repo: models.Repo = Repo(dotty,Scala,true,150)

```

We have, so far, only talked about validating single repos. The Play framework defines type classes for collection types, so, provided `Reads[Repo]` is defined, `Reads[List[Repo]]` will also be defined.

Now that we understand how to extract Scala objects from JSON, let's get back to the code. If we manage to successfully convert the repositories to a `List[Repo]`, we emit it again as JSON. Of course, converting from GitHub's JSON representation of a repository to a Scala object, and from that Scala object directly to our JSON representation of the object, might seem convoluted. However, if this were a real application, we would have additional logic. We could, for instance, store repos in a cache, and try and fetch from that cache instead of querying the GitHub API. Converting from JSON to Scala objects as early as possible decouples the code that we write from the way GitHub returns repositories.

Asynchronous actions

The last bit of the code sample that is new is the call to `Action.async`, rather than just `Action`. Recall that an `Action` instance is a thin wrapper around a `Request => Result` method. Our code, however, returns a `Future[Result]`, rather than a `Result`. When that is the case, use the `Action.async` to construct the action, rather than `Action` directly. Using `Action.async` tells the Play framework that the code creating the `Action` is asynchronous.

Creating APIs with Play: a summary

In the last section, we deployed an API that responds to GET requests. Since this is a lot to take in, let's summarize how to go about API creation:

1. Define appropriate routes in `/conf/routes`, using wildcards in the URL as needed.
2. Create Scala case classes in `/app/models` to represent the models used by the API.
3. Create `write[T]` methods to write models to JSON or XML so that they can be returned by the API.
4. Bind the routes to controllers. If the controllers need to do more than a trivial amount of work, wrap the work in a future to avoid blocking the server.

There are many more useful components of the Play framework that you are likely to need, such as, for instance, how to use Slick to access SQL databases. We do not, unfortunately, have time to cover these in this introduction. The Play framework has extensive, well-written documentation that will fill the gaping holes in this tutorial.

Rest APIs: best practice

As the Internet matures, REST (representational state transfer) APIs are emerging as the most reliable design pattern for web APIs. An API is described as *RESTful* if it follows these guiding principles:

- The API is designed as a set of resources. For instance, the GitHub API provides information about users, repositories, followers, etc. Each user, or repository, is a specific resource. Each resource can be addressed through a different HTTP end-point.
- The URLs should be simple and should identify the resource clearly. For instance, `api.github.com/users/odersky` is simple and tells us clearly that we should expect information about the user Martin Odersky.
- There is no *world resource* that contains all the information about the system. Instead, top-level resources contain links to more specialized resources. For instance, the user resource in the GitHub API contains links to that user's repositories and that user's followers, rather than having all that information embedded in the user resource directly.

- The API should be discoverable. The response to a request for a specific resource should contain URLs for related resources. When you query the user resource on GitHub, the response contains the URL for accessing that user's followers, repositories etc. The client should use the URLs provided by the API, rather than attempting to construct them client-side. This makes the client less brittle to changes in the API.
- There should be as little state maintained on the server as possible. For instance, when querying the GitHub API, we must pass the authentication token with every request, rather than expecting our authentication status to be *remembered* on the server. Having each interaction be independent of the history provides much better scalability: if any interaction can be handled by any server, load balancing is much easier.

Summary

In this chapter, we introduced the Play framework as a tool for building web APIs. We built an API that returns a JSON array of a user's GitHub repositories. In the next chapter, we will build on this API and construct a single-page application to represent this data graphically.

References

- This Wikipedia page gives information on semantic URLs:
https://en.wikipedia.org/wiki/Semantic_URL and
<http://apiux.com/2013/04/03/url-design-restful-web-services/>.
- For a much more in depth discussion of the Play framework, I suggest *Play Framework Essentials* by Julien Richard-Foy.
- *REST in Practice: Hypermedia and Systems Architecture*, by Jim Webber, Savvas Parastatidis and Ian Robinson describes how to architect REST APIs.

14

Visualization with D3 and the Play Framework

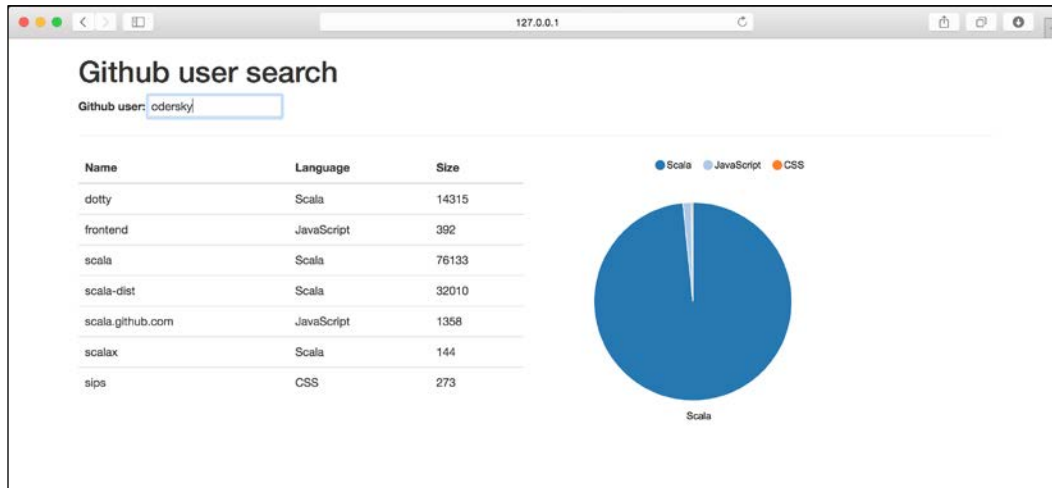
In the previous chapter, we learned about the Play framework, a web framework for Scala. We built an API that returns a JSON array describing a user's GitHub repositories.

In this chapter, we will construct a fully-fledged web application that displays a table and a chart describing a user's repositories. We will learn to integrate **D3.js**, a JavaScript library for building data-driven web pages, with the Play framework. This will set you on the path to building compelling interactive visualizations that showcase results obtained with machine learning.

This chapter assumes that you are familiar with HTML, CSS, and JavaScript. We present references at the end of the chapter. You should also have read the previous chapter.

GitHub user data

We will build a single-page application that uses, as its backend, the API developed in the previous chapter. The application contains a form where the user enters the login name for a GitHub account. The application queries the API to get a list of repositories for that user and displays them on the screen as both a table and a pie chart summarizing programming language use for that user:



To see a live version of the application, head over to <http://app.scala4datascience.com>.

Do I need a backend?

In the previous chapter, we learned about the client-server model that underpins how the internet works: when you enter a website URL in your browser, the server serves HTML, CSS, and JavaScript to your browser, which then renders it in the appropriate manner.

What does this all mean for you? Arguably the second question that you should be asking yourself when building a web application is whether you need to do any server-side processing (right after "is this really going to be worth the effort?"). Could you just create an HTML web-page with some JavaScript?

You can get away without a backend if the data needed to build the whole application is small enough: typically a few megabytes. If your application is larger, you will need a backend to transfer just the data the client currently needs. Surprisingly, you can often build visualizations without a backend: while data science is accustomed to dealing with terabytes of data, the goal of the data science process is often condensing these huge data sets to a few meaningful numbers.

Having a backend also lets you include logic invisible to the client. If you need to validate a password, you clearly cannot send the code to do that to the client computer: it needs to happen out of sight, on the server.

If your application is small enough and you do not need to do any server-side processing, stop reading this chapter, brush up on your JavaScript if you have to, and forget about Scala for now. Not having to worry about building a backend will make your life easier.

Clearly, however, we do not have that freedom for the application that we want to build: the user could enter the name of anyone on GitHub. Finding information about that user requires a backend with access to tremendous storage and querying capacity (which we simulate by just forwarding the request to the GitHub API and re-interpreting the response).

JavaScript dependencies through web-jars

One of the challenges of developing web applications is that we are writing two quasi-separate programs: the server-side program and the client-side program. These generally require different technologies. In particular, for any but the most trivial application, we must keep track of JavaScript libraries, and integrate processing the JavaScript code (for instance, for minification) in the build process.

The Play framework manages JavaScript dependencies through *web-jars*. These are just JavaScript libraries packaged as jars. They are deployed on Maven Central, which means that we can just add them as dependencies to our `build.sbt` file. For this application, we will need the following JavaScript libraries:

- Require.js, a library for writing modular JavaScript
- JQuery
- Bootstrap
- Underscore.js, a library that adds many functional constructs and client-side templating.
- D3, the graph plotting library
- NVD3, a graph library built on top of D3

If you are planning on coding up the examples provided in this chapter, the easiest will be for you to start from the code for the previous chapter (You can download the code for *Chapter 13, Web APIs with Play*, from GitHub: <https://github.com/pbugnion/s4ds/tree/master/chap13>). We will assume this as a starting point here onwards.

Let's include the dependencies on the web-jars in the `build.sbt` file:

```
libraryDependencies += Seq(
  "org.webjars" % "requirejs" % "2.1.22",
  "org.webjars" % "jquery" % "2.1.4",
  "org.webjars" % "underscorejs" % "1.8.3",
  "org.webjars" % "nvd3" % "1.8.1",
  "org.webjars" % "d3js" % "3.5.6",
  "org.webjars" % "bootstrap" % "3.3.6"
)
```

Fetch the modules by running `activator update`. Once you have done this, you will notice the JavaScript libraries in `target/web/public/main/lib`.

Towards a web application: HTML templates

In the previous chapter, we briefly saw how to construct HTML templates by interleaving Scala snippets in an HTML file. We saw that templates are compiled to Scala functions, and we learned how to call these functions from the controllers.

In single-page applications, the majority of the logic governing what is actually displayed in the browser resides in the client-side JavaScript, not in the server. The pages served by the server contain the bare-bones HTML framework.

Let's create the HTML layout for our application. We will save this in `views/index.scala.html`. The template will just contain the layout for the application, but will not contain any information about any user's repositories. To fetch that information, the application will have to query the API developed in the previous chapter. The template does not take any parameters, since all the dynamic HTML generation will happen client-side.

We use the Bootstrap grid layout to control the HTML layout. If you are not familiar with Bootstrap layouts, consult the documentation at <http://getbootstrap.com/css/#grid-example-basic>.

```
// app/views/index.scala.html
<!DOCTYPE html>

<html lang="en">
  <head>
    <title>Github User display</title>
    <link rel="stylesheet" media="screen"
      href="@routes.Assets.versioned("stylesheets/main.css")">
    <link rel="shortcut icon" type="image/png"
      href="@routes.Assets.versioned("images/favicon.png")">
    <link rel="stylesheet" media="screen"
      href=@routes.Assets.versioned("lib/nvd3/nv.d3.css") >
    <link rel="stylesheet" media="screen"
      href=@routes.Assets.versioned(
        "lib/bootstrap/css/bootstrap.css")>
  </head>

  <body>
    <div class="container">

      <!-- Title row -->
      <div class="row">
        <h1>Github user search</h1>
      </div>

      <!-- User search row -->
      <div class="row">
        <label>Github user: </label>
        <input type="text" id="user-selection">
      </div>
    </div>
  </body>
</html>
```



```
        <span id="searching-span"></span>
        <hr />
    </div>

    <!-- Results row -->
    <div id="response" class="row"></div>
</div>
</body>
</html>
```

In the HTML head, we link the CSS stylesheets that we need for the application. Instead of specifying the path explicitly, we use the `@routes.Assets.versioned(...)` function. This resolves to a URI corresponding to the location where the assets are stored post-compilation. The argument passed to the function should be the path from `target/web/public/main` to the asset you need.

We want to serve the compiled version of this view when the user accesses the route `/` on our server. We therefore need to add this route to `conf/routes`:

```
# conf/routes
GET    /           controllers.Application.index
```

The route is served by the `index` function in the `Application` controller. All this controller needs to do is serve the `index` view:

```
// app/controllers/Application.scala
package controllers

import play.api._
import play.api.mvc._

class Application extends Controller {

  def index = Action {
    Ok(views.html.index())
  }
}
```

Start the Play framework by running `activator run` in the root directory of the application and point your web browser to `127.0.0.1:9000/`. You should see the framework for our web application. Of course, the application does not do anything yet, since we have not written any of the JavaScript logic yet.



Modular JavaScript through RequireJS

The simplest way of injecting JavaScript libraries into the namespace is to add them to the HTML framework via `<script>...</script>` tags in the HTML header. For instance, to add JQuery, we would add the following line to the head of the document:

```
<script src=@routes.Assets.versioned("lib/jquery/jquery.js")
  type="text/javascript"></script>
```

While this works, it does not scale well to large applications, since every library gets imported into the global namespace. Modern client-side JavaScript frameworks such as AngularJS provide an alternative way of defining and loading modules that preserve encapsulation.

We will use RequireJS. In a nutshell, RequireJS lets us encapsulate JavaScript modules through functions. For instance, if we wanted to write a module `example` that contains a function for hiding a `div`, we would define the module as follows:

```
// example.js
define(["jquery", "underscore"], function($, _) {

  // hide a div
  function hide(div_name) {
    $(div_name).hide() ;
  }

  // what the module exports.
  return { "hide": hide }

}) ;
```

We encapsulate our module as a callback in a function called `define`. The `define` function takes two arguments: a list of dependencies, and a function definition. The `define` function binds the dependencies to the arguments list of the callback: in this case, functions in JQuery will be bound to `$` and functions in Underscore will be bound to `_`. This creates a module which exposes whatever the callback function returns. In this case, we export the `hide` function, binding it to the name "hide". Our example module thus exposes the `hide` function.

To load this module, we pass it as a dependency to the module in which we want to use it:

```
define(["example"], function(example) {

  function hide_all() {
```

```
    example.hide("#top") ;
    example.hide("#bottom") ;
  }

  return { "hide_all": hide_all } ;
});
```

Notice how the functions in `example` are encapsulated, rather than existing in the global namespace. We call them through `example.<function-name>`. Furthermore, any functions or variables defined internally to the `example` module remain private.

Sometimes, we want JavaScript code to exist outside of modules. This is often the case for the script that bootstraps the application. For these, replace `define` with `require`:

```
require(["jquery", "example"], function($, example) {
  $(document).ready(function() {
    example.hide("#header") ;
  });
});
```

Now that we have an overview of RequireJS, how do we use it in the Play framework? The first step is to add the dependency on the RequireJS web jar, which we have done. The Play framework also adds a RequireJS SBT plugin (<https://github.com/sbt/sbt-rjs>), which should be installed by default if you used the `play-scala` activator. If this is missing, it can be added with the following line in `plugins.sbt`:

```
// project/plugins.sbt

addSbtPlugin("com.typesafe.sbt" % "sbt-rjs" % "1.0.7")
```

We also need to add the plugin to the list of stages. This allows the plugin to manipulate the JavaScript assets when packaging the application as a jar. Add the following line to `build.sbt`:

```
pipelineStages := Seq(rjs)
```

You will need to restart the activator for the changes to take effect.

We are now ready to use RequireJS in our application. We can use it by adding the following line in the head section of our view:

```
// index.scala.html

<html>
  <head>
```

```
...  
  
    <script  
      type="text/javascript"  
      src=@routes.Assets.versioned("lib/requirejs/require.js").url  
      data-main=@routes.Assets.versioned("javascripts/main.js").url>  
    </script>  
  
  </head>  
  ...  
</html>
```

When the view is compiled, this is resolved to tags like:

```
<script type="text/javascript"  
  data-main="/assets/javascripts/main.js"  
  src="/assets/lib/requirejs/require.min.js">  
</script>
```

The argument passed to `data-main` is the entry point for our application. When RequireJS loads, it will execute `main.js`. That script must therefore bootstrap our application. In particular, it should contain a configuration object for RequireJS, to make it aware of where all the libraries are.

Bootstrapping the applications

When we linked `require.js` to our application, we told it to use `main.js` as our entry point. To test that this works, let's start by entering a dummy `main.js`. JavaScript files in Play applications go in `/public/javascripts`:

```
// public/javascripts/main.js  
  
require([], function() {  
  console.log("hello, JavaScript");  
});
```

To verify that this worked, head to `127.0.0.1:9000` and open the browser console. You should see `"hello, JavaScript"` in the console.

Let's now write a more useful `main.js`. We will start by configuring RequireJS, giving it the location of modules we will use in our application. Unfortunately, NVD3, the graph library that we use, does not play very well with RequireJS so we have to use an ugly hack to make it work. This complicates our `main.js` file somewhat:

```
// public/javascripts/main.js

(function (requirejs) {
  'use strict';

  // -- RequireJS config --
  requirejs.config({
    // path to the web jars. These definitions allow us
    // to use "jquery", rather than "../lib/jquery/jquery",
    // when defining module dependencies.
    paths: {
      "jquery": "../lib/jquery/jquery",
      "underscore": "../lib/underscorejs/underscore",
      "d3": "../lib/d3js/d3",
      "nvd3": "../lib/nvd3/nv.d3",
      "bootstrap": "../lib/bootstrap/js/bootstrap"
    },

    shim: {
      // hack to get nvd3 to work with requirejs.
      // see this so question:
      // http://stackoverflow.com/questions/13157704/how-to-integrate-
      // d3-with-require-js#comment32647365_13171592
      nvd3: {
        deps: ["d3.global"],
        exports: "nv"
      },
      bootstrap : { deps : ['jquery'] }
    }
  });
})(requirejs);

// hack to get nvd3 to work with requirejs.
// see this so question on Stack Overflow:
```

```
// http://stackoverflow.com/questions/13157704/how-to-integrate-d3-  
with-require-js#comment32647365_13171592  
define("d3.global", ["d3"], function(d3global) {  
    d3 = d3global;  
});  
  
require([], function() {  
    // Our application  
    console.log("hello, JavaScript");  
}) ;
```

Now that we have the configuration in place, we can dig into the JavaScript part of the application.

Client-side program architecture

The basic idea is simple: the user searches for the name of someone on GitHub in the input box. When he enters a name, we fire a request to the API designed earlier in this chapter. When the response from the API returns, the program binds that response to a model and emits an event notifying that the model has been changed. The views listen for this event and refresh from the model in response.

Designing the model

Let's start by defining the client-side model. The model holds information regarding the repos of the user currently displayed. It gets filled in after the first search.

```
// public/javascripts/model.js  
  
define([], function(){  
    return {  
        ghubUser: "", // last name that was searched for  
        exists: true, // does that person exist on github?  
        repos: [] // list of repos  
    } ;  
});
```

To see a populated value of the model, head to the complete application example on `app.scala4datascience.com`, open a JavaScript console in your browser, search for a user (for example, `odersky`) in the application and type the following in the console:

```
> require(["model"], function(model) { console.log(model) ; })
{ghubUser: "odersky", exists: true, repos: Array}

> require(["model"], function(model) {
  console.log(model.repos[0]);
})
{name: "dotty", language: "Scala", is_fork: true, size: 14653}
```

These import the "model" module, bind it to the variable `model`, and then print information to the console.

The event bus

We need a mechanism for informing the views when the model is updated, since the views need to refresh from the new model. This is commonly handled through *events* in web applications. JQuery lets us bind callbacks to specific events. The callback is executed when that event occurs.

For instance, to bind a callback to the event "custom-event", enter the following in a JavaScript console:

```
> $(window).on("custom-event", function() {
  console.log("custom event received") ;
});
```

We can fire the event using:

```
> $(window).trigger("custom-event");
custom event received
```

Events in JQuery require an *event* bus, a DOM element on which the event is registered. In this case, we used the window DOM element as our event bus, but any JQuery element would have served. Centralizing event definitions to a single module is helpful. We will, therefore, create an `events` module containing two functions: `trigger`, which triggers an event (specified by a string) and `on`, which binds a callback to a specific event:

```
// public/javascripts/events.js

define(["jquery"], function($) {

    var bus = $(window) ; // widget to use as an event bus

    function trigger(eventType) {
        $(bus).trigger(eventType) ;
    }

    function on(eventType, f) {
        $(bus).on(eventType, f) ;
    }

    return {
        "trigger": trigger,
        "on": on
    } ;
});
```

We can now emit and receive events using the `events` module. You can test this out in a JavaScript console on the live version of the application (at app.scala4datascience.com). Let's start by registering a listener:

```
> require(["events"], function(events) {
    // register event listener
    events.on("hello_event", function() {
        console.log("Received event") ;
    }) ;
});
```

If we now trigger the event `"hello_event"`, the listener prints `"Received event"`:

```
> require(["events"], function(events) {
    // trigger the event
    events.trigger("hello_event") ;
});
```


Using events allows us to decouple the controller from the views. The controller does not need to know anything about the views, and vice-versa. The controller just needs to emit a "model_updated" event when the model is updated, and the views need to refresh from the model when they receive that event.

AJAX calls through JQuery

We can now write the controller for our application. When the user enters a name in the text input, we query the API, update the model and trigger a `model_updated` event.

We use JQuery's `$.getJSON` function to query our API. This function takes a URL as its first argument, and a callback as its second argument. The API call is asynchronous: `$.getJSON` returns immediately after execution. All request processing must, therefore, be done in the callback. The callback is called if the request is successful, but we can define additional handlers that are always called, or called on failure. Let's try this out in the browser console (either your own, if you are running the API developed in the previous chapter, or on `app.scala4datascience.com`). Recall that the API is listening to the end-point `/api/repos/:user`:

```
> $.getJSON("/api/repos/odersky", function(data) {
  console.log("API response:");
  console.log(data);
  console.log(data[0]);
}) ;
{readyState: 1, getResponseHeader: function, ...}
```

API response:

```
[Object, Object, Object, Object, Object, ...]
{name: "dotty", language: "Scala", is_fork: true, size: 14653}
```

`getJSON` returns immediately. A few tenths of a second later, the API responds, at which point the response gets fed through the callback.

The callback only gets executed on success. It takes, as its argument, the JSON object returned by the API. To bind a callback that is executed when the API request fails, call the `.fail` method on the return value of `getJSON`:

```
> $.getJSON("/api/repos/junk123456", function(data) {
  console.log("called on success");
}).fail(function() {
  console.log("called on failure") ;
}) ;
```

```

}) ;
{readyState: 1, getResponseHeader: function, ...}

```

called on failure

We can also use the `.always` method on the return value of `getJSON` to specify a callback that is executed, whether the API query was successful or not.

Now that we know how to use `$.getJSON` to query our API, we can write the controller. The controller listens for changes to the `#user-selection` input field. When a change occurs, it fires an AJAX request to the API for information on that user. It binds a callback which updates the model when the API replies with a list of repositories. We will define a controller module that exports a single function, `initialize`, that creates the event listeners:

```

// public/javascripts/controller.js
define(["jquery", "events", "model"], function($, events, model) {

  function initialize() {
    $("#user-selection").change(function() {

      var user = $("#user-selection").val() ;
      console.log("Fetching information for " + user) ;

      // Change cursor to a 'wait' symbol
      // while we wait for the API to respond
      $("*").css({"cursor": "wait"}) ;

      $.getJSON("/api/repos/" + user, function(data) {
        // Executed on success
        model.exists = true ;
        model.repos = data ;
      }).fail(function() {
        // Executed on failure
        model.exists = false ;
        model.repos = [] ;
      }).always(function() {
        // Always executed
        model.githubUser = user ;

        // Restore cursor
        $("*").css({"cursor": "initial"}) ;

        // Tell the rest of the application

```

```
        // that the model has been updated.
        events.trigger("model_updated") ;
    });
  });
} ;

return { "initialize": initialize };

});
```

Our controller module just exposes the `initialize` method. Once the initialization is performed, the controller interacts with the rest of the application through event listeners. We will call the controller's `initialize` method in `main.js`. Currently, the last lines of that file are just an empty `require` block. Let's import our controller and initialize it:

```
// public/javascripts/main.js

require(["controller"], function(controller) {
  controller.initialize();
});
```

To test that this works, we can bind a dummy listener to the `"model_updated"` event. For instance, we could log the current model to the browser JavaScript console with the following snippet (which you can write directly in the JavaScript console):

```
> require(["events", "model"],
function(events, model) {
  events.on("model_updated", function () {
    console.log("model_updated event received");
    console.log(model);
  });
});
```

If you then search for a user, the model will be printed to the console. We now have the controller in place. The last step is writing the views.

Response views

If the request fails, we just display **Not found** in the response div. This part is the easiest to code up, so let's do that first. We define an `initialize` method that generates the view. The view then listens for the `"model_updated"` event, which is fired by the controller after it updates the model. Once the initialization is complete, the only way to interact with the response view is through `"model_updated"` events:

```
// public/javascripts/responseView.js

define(["jquery", "model", "events"],
function($, model, events) {

    var failedResponseHtml =
        "<div class='col-md-12'>Not found</div>" ;

    function initialize() {
        events.on("model_updated", function() {
            if (model.exists) {
                // success - we will fill this in later.
                console.log("model exists")
            }
            else {
                // failure - the user entered
                // is not a valid GitHub login
                $("#response").html(failedResponseHtml) ;
            }
        }) ;
    }

    return { "initialize": initialize } ;

});
```

To bootstrap the view, we must call the `initialize` function from `main.js`. Just add a dependency on `responseView` in the `require` block, and call `responseView.initialize()`. With these modifications, the final `require` block in `main.js` is:

```
// public/javascripts/main.js

require(["controller", "responseView"],
function(controller, responseView) {
    controller.initialize();
    responseView.initialize() ;
});
```

You can check that this all works by entering junk in the user input to deliberately cause the API request to fail.

When the user enters a valid GitHub login name and the API returns a list of repos, we must display those on the screen. We display a table and a pie chart that aggregates the repository sizes by language. We will define the pie chart and the table in two separate modules, called `repoGraph.js` and `repoTable.js`. Let's assume those exist for now and that they expose a `build` method that accepts a `model` and the name of a `div` in which to appear.

Let's update the code for `responseView` to accommodate the user entering a valid GitHub user name:

```
// public/javascripts/responseView.js

define(["jquery", "model", "events", "repoTable", "repoGraph"],
function($, model, events, repoTable, repoGraph) {

  // HTML to inject when the model represents a valid user
  var successfulResponseHtml =
    "<div class='col-md-6' id='response-table'></div>" +
    "<div class='col-md-6' id='response-graph'></div>" ;

  // HTML to inject when the model is for a non-existent user
  var failedResponseHtml =
    "<div class='col-md-12'>Not found</div>" ;

  function initialize() {
    events.on("model_updated", function() {
      if (model.exists) {
        $("#response").html(successfulResponseHtml) ;
        repoTable.build(model, "#response-table") ;
        repoGraph.build(model, "#response-graph") ;
      }
      else {
        $("#response").html(failedResponseHtml) ;
      }
    }) ;
  }

  return { "initialize": initialize } ;

});
```

Let's walk through what happens in the event of a successful API call. We inject the following bit of HTML in the #response div:

```
var successfulResponseHtml =
  "<div class='col-md-6' id='response-table'></div>" +
  "<div class='col-md-6' id='response-graph'></div>" ;
```

This adds two HTML divs, one for the table of repositories, and the other for the graph. We use Bootstrap classes to split the response div vertically.

Let's now turn our attention to the table view, which needs to expose a single `build` method, as described in the previous section. We will just display the repositories in an HTML table. We will use *Underscore templates* to build the table dynamically. Underscore templates work much like string interpolation in Scala: we define a template with placeholders. Let's try this in a browser console:

```
> require(["underscore"], function(_) {
  var myTemplate = _.template(
    "Hello, <%= title %> <%= name %>!"
  ) ;
});
```

This creates a `myTemplate` function which accepts an object with attributes `title` and `name`:

```
> require(["underscore"], function(_) {
  var myTemplate = _.template( ... );
  var person = { title: "Dr.", name: "Odersky" } ;
  console.log(myTemplate(person)) ;
});
```

Underscore templates thus provide a convenient mechanism for formatting an object as a string. We will create a template for each row in our table, and pass the model for each repository to the template:

```
// public/javascripts/repoTable.js

define(["underscore", "jquery"], function(_, $) {

  // Underscore template for each row
  var rowTemplate = _.template("<tr>" +
    "<td><%= name %></td>" +
    "<td><%= language %></td>" +
    "<td><%= size %></td>" +
    "</tr>") ;

  // template for the table
```

```
var repoTable = _.template(
  "<table id='repo-table' class='table'>" +
  "<thead>" +
  "<tr>" +
  "<th>Name</th><th>Language</th><th>Size</th>" +
  "</tr>" +
  "</thead>" +
  "<tbody>" +
  "<%= tbody %>" +
  "</tbody>" +
  "</table>") ;

// Builds a table for a model
function build(model, divName) {
  var tbody = "" ;
  _.each(model.repos, function(repo) {
    tbody += rowTemplate(repo) ;
  }) ;
  var table = repoTable({tbody: tbody}) ;
  $(divName).html(table) ;
}

return { "build": build } ;
}) ;
```

Drawing plots with NVD3

D3 is a library that offers low-level components for building interactive visualizations in JavaScript. By offering the low-level components, it gives a huge degree of flexibility to the developer. The learning curve can, however, be quite steep. In this example, we will use NVD3, a library which provides pre-made graphs for D3. This can greatly speed up initial development. We will place the code in the file `repoGraph.js` and expose a single method, `build`, which takes, as arguments, a model and a div and draws a pie chart in that div. The pie chart will aggregate language use across all the user's repositories.

The code for generating a pie chart is nearly identical to the example given in the NVD3 documentation, available at <http://nvd3.org/examples/pie.html>. The data passed to the graph must be available as an array of objects. Each object must contain a `label` field and a `size` field. The `label` field identifies the language, and the `size` field is the total size of all the repositories for that user written in that language. The following would be a valid data array:

```
[
  { label: "Scala", size: 1234 },
  { label: "Python", size: 4567 }
]
```

To get the data in this format, we must aggregate sizes across the repositories written in a particular language in our model. We write the `generateDataFromModel` function to transform the `repos` array in the model to an array suitable for NVD3. The crux of the aggregation is performed by a call to Underscore's `groupBy` method, to group repositories by language. This method works exactly like Scala's `groupBy` method. With this in mind, the `generateDataFromModel` function is:

```
// public/javascripts/repoGraph.js

define(["underscore", "d3", "nvd3"],
function(_, d3, nv) {

  // Aggregate the repo size by language.
  // Returns an array of objects like:
  // [ { label: "Scala", size: 1245},
  //   { label: "Python", size: 432 } ]
  function generateDataFromModel(model) {

    // Build an initial object mapping each
    // language to the repositories written in it
    var language2Repos = _.groupBy(model.repos,
      function(repo) { return repo.language ; } ) ;

    // Map each { "language": [ list of repos ], ...}
    // pairs to a single document { "language": totalSize }
    // where totalSize is the sum of the individual repos.
    var plotObjects = _.map(language2Repos,
      function(repos, language) {
        var sizes = _.map(repos, function(repo) {
          return repo.size;
        });
        // Sum over the sizes using 'reduce'
        var totalSize = _.reduce(sizes,
```



```
        function(memo, size) { return memo + size; },
        0) ;
        return { label: language, size: totalSize } ;
    }) ;

    return plotObjects;
}
```

We can now build the pie chart, using NVD3's addGraph method:

```
// Build the chart.
function build(model, divName) {
    var transformedModel = generateDataFromModel(model) ;
    nv.addGraph(function() {

        var height = 350;
        var width = 350;

        var chart = nv.models.pieChart()
            .x(function (d) { return d.label ; })
            .y(function (d) { return d.size ;})
            .width(width)
            .height(height) ;

        d3.select(divName).append("svg")
            .datum(transformedModel)
            .transition()
            .duration(350)
            .attr('width', width)
            .attr('height', height)
            .call(chart) ;

        return chart ;
    });
}

return { "build" : build } ;

});
```

This was the last component of our application. Point your browser to 127.0.0.1:9000 and you should see the application running.

Congratulations! We have built a fully-functioning single-page web application.

Summary

In this chapter, we learned how to write a fully-featured web application with the Play framework. Congratulations on making it this far. Building web applications are likely to push many data scientists beyond their comfort zone, but knowing enough about the web to build basic applications will allow you to share your results in a compelling, engaging manner, as well as facilitate communications with software engineers and web developers.

This concludes our whistle stop tour of Scala libraries. Over the course of this book, we have learned how to tackle linear algebra and optimization problems efficiently using Breeze, how to insert and query data in SQL databases in a functional manner, and both how to interact with web APIs and how to create them. We have reviewed some of tools available to the data scientist for writing concurrent or parallel applications, from parallel collections and futures to Spark via Akka. We have seen how pervasive these constructs are in Scala libraries, from futures in the Play framework to Akka as the backbone of Spark. If you have read this far, pat yourself on the back.

This book gives you the briefest of introduction to the libraries it covers, hopefully just enough to give you a taste of what each tool is good for, what you could accomplish with it, and how it fits in the wider Scala ecosystem. If you decide to use any of these in your data science pipeline, you will need to read the documentation in more detail, or a more complete reference book. The references listed at the end of each chapter should provide a good starting point.

Both Scala and data science are evolving rapidly. Do not stay wedded to a particular toolkit or concept. Remain on top of current developments and, above all, remain pragmatic: find the right tool for the right job. Scala and the libraries discussed here will often be that tool, but not always: sometimes, a shell command or a short Python script will be more effective. Remember also that programming skills are but one aspect of the data scientist's body of knowledge. Even if you want to specialize in the engineering side of data science, learn about the problem domain and the mathematical underpinnings of machine learning.

Most importantly, if you have taken the time to read this book, it is likely that you view programming and data science as more than a day job. Coding in Scala can be satisfying and rewarding, so have fun and be awesome!

References

There are thousands of HTML and CSS tutorials dotted around the web. A simple Google search will give you a much better idea of the resources available than any list of references I can provide.

Mike Bostock's website has a wealth of beautiful D3 visualizations: <http://bost.ocks.org/mike/>. To understand a bit more about D3, I recommend *Scott Murray's Interactive Data Visualization for the Web*.

You may also wish to consult the references given in the previous chapter for reference books on the Play framework and designing REST APIs.

Pattern Matching and Extractors

Pattern matching is a powerful tool for control flow in Scala. It is often underused and under-estimated by people coming to Scala from imperative languages.

Let's start with a few examples of pattern matching before diving into the theory. We start by defining a tuple:

```
scala> val names = ("Pascal", "Bugnion")
names: (String, String) = (Pascal,Bugnion)
```

We can use pattern matching to extract the elements of this tuple and bind them to variables:

```
scala> val (firstName, lastName) = names
firstName: String = Pascal
lastName: String = Bugnion
```

We just extracted the two elements of the `names` tuple, binding them to the variables `firstName` and `lastName`. Notice how the left-hand side defines a pattern that the right-hand side must match: we are declaring that the variable `names` must be a two-element tuple. To make the pattern more specific, we could also have specified the expected types of the elements in the tuple:

```
scala> val (firstName:String, lastName:String) = names
firstName: String = Pascal
lastName: String = Bugnion
```

What happens if the pattern on the left-hand side does not match the right-hand side?

```
scala> val (firstName, middleName, lastName) = names
<console>:13: error: constructor cannot be instantiated to expected type;
found   : (T1, T2, T3)
required: (String, String)
    val (firstName, middleName, lastName) = names
```

This results in a compile error. Other types of pattern matching failures result in runtime errors.

Pattern matching is very expressive. To achieve the same behavior without pattern matching, you would have to do the following explicitly:

- Verify that the variable `names` is a two-element tuple
- Extract the first element and bind it to `firstName`
- Extract the second element and bind it to `lastName`

If we expect certain elements in the tuple to have specific values, we can verify this as part of the pattern match. For instance, we can verify that the first element of the `names` tuple matches "Pascal":

```
scala> val ("Pascal", lastName) = names
lastName: String = Bugnion
```

Besides tuples, we can also match on Scala collections:

```
scala> val point = Array(1, 2, 3)
point: Array[Int] = Array(1, 2, 3)
```

```
scala> val Array(x, y, z) = point
x: Int = 1
y: Int = 2
z: Int = 3
```

Notice the similarity between this pattern matching and array construction:

```
scala> val point = Array(x, y, z)
point: Array[Int] = Array(1, 2, 3)
```

Syntactically, Scala expresses pattern matching as the reverse process to instance construction. We can think of pattern matching as the deconstruction of an object, binding the object's constituent parts to variables.

When matching against collections, one is sometimes only interested in matching the first element, or the first few elements, and discarding the rest of the collection, whatever its length. The operator `_*` will match against any number of elements:

```
scala> val Array(x, _) = point
x: Int = 1
```

By default, the part of the pattern matched by the `_*` operator is not bound to a variable. We can capture it as follows:

```
scala> val Array(x, xs @ _) = point
x: Int = 1
xs: Seq[Int] = Vector(2, 3)
```

Besides tuples and collections, we can also match against case classes. Let's start by defining a case representing a name:

```
scala> case class Name(first: String, last: String)
defined class Name
```

```
scala> val name = Name("Martin", "Odersky")
name: Name = Name(Martin,Odersky)
```

We can match against instances of `Name` in much the same way we matched against tuples:

```
scala> val Name(firstName, lastName) = name
firstName: String = Martin
lastName: String = Odersky
```

All these patterns can also be used in `match` statements:

```
scala> def greet(name:Name) = name match {
  case Name("Martin", "Odersky") => "An honor to meet you"
  case Name(first, "Bugnion") => "Wow! A family member!"
  case Name(first, last) => s"Hello, $first"
}
greet: (name: Name)String
```

Pattern matching in for comprehensions

Pattern matching is useful in *for* comprehensions for extracting items from a collection that match a specific pattern. Let's build a collection of `Name` instances:

```
scala> val names = List(Name("Martin", "Odersky"),
  Name("Derek", "Wyatt"))
names: List[Name] = List(Name(Martin,Odersky), Name(Derek,Wyatt))
```

We can use pattern matching to extract the internals of the class in a *for*-comprehension:

```
scala> for { Name(first, last) <- names } yield first
List[String] = List(Martin, Derek)
```

So far, nothing terribly ground-breaking. But what if we wanted to extract the surname of everyone whose first name is "Martin"?

```
scala> for { Name("Martin", last) <- names } yield last
List[String] = List(Odersky)
```

Writing `Name("Martin", last) <- names` extracts the elements of names that match the pattern. You might think that this is a contrived example, and it is, but the examples in *Chapter 7, Web APIs* demonstrate the usefulness and versatility of this language pattern, for instance, for extracting specific fields from JSON objects.

Pattern matching internals

If you define a case class, as we saw with `Name`, you get pattern matching against the constructor *for free*. You should be using case classes to represent your data as much as possible, thus reducing the need to implement your own pattern matching. It is nevertheless useful to understand how pattern matching works.

When you create a case class, Scala automatically builds a companion object:

```
scala> case class Name(first: String, last: String)
defined class Name

scala> Name.<tab>
apply  asInstanceOf  curried  isInstanceOf  toString  tupled
unapply
```

The method used (internally) for pattern matching is `unapply`. This method takes, as argument, an object and returns `Option[T]`, where `T` is a tuple of the values of the case class.

```
scala> val name = Name("Martin", "Odersky")
name: Name = Name(Martin,Odersky)

scala> Name.unapply(name)
Option[(String, String)] = Some((Martin,Odersky))
```

The `unapply` method is an *extractor*. It plays the opposite role of the constructor: it takes an object and extracts the list of parameters needed to construct that object. When you write `val Name(firstName, lastName)`, or when you use `Name` as a case in a match statement, Scala calls `Name.unapply` on what you are matching against. A value of `Some[(String, String)]` implies a pattern match, while a value of `None` implies that the pattern fails.

To write custom extractors, you just need an object with an `unapply` method. While `unapply` normally resides in the companion object of a class that you are deconstructing, this need not be the case. In fact, it does not need to correspond to an existing class at all. For instance, let's define a `NonZeroDouble` extractor that matches any non-zero double:

```
scala> object NonZeroDouble {
  def unapply(d:Double):Option[Double] = {
    if (d == 0.0) { None } else { Some(d) }
  }
}
defined object NonZeroDouble

scala> val NonZeroDouble(denominator) = 5.5
denominator: Double = 5.5

scala> val NonZeroDouble(denominator) = 0.0
scala.MatchError: 0.0 (of class java.lang.Double)
... 43 elided
```

We defined an extractor for `NonZeroDouble`, despite the absence of a corresponding `NonZeroDouble` class.

This `NonZeroDouble` extractor would be useful in a match object. For instance, let's define a `safeDivision` function that returns a default value when the denominator is zero:

```
scala> def safeDivision(numerator:Double,
  denominator:Double, fallBack:Double) =
  denominator match {
    case NonZeroDouble(d) => numerator / d
    case _ => fallBack
  }
safeDivision: (numerator: Double, denominator: Double, fallBack: Double)
Double
```

```
scala> safeDivision(5.0, 2.0, 100.0)
Double = 2.5
```

```
scala> safeDivision(5.0, 0.0, 100.0)
Double = 100.0
```

This is a trivial example because the `NonZeroDouble.unapply` method is so simple, but you can hopefully see the usefulness and expressiveness, if we were to define a more complex test. Defining custom extractors lets you define powerful control flow constructs to leverage `match` statements. More importantly, they enable the client using the extractors to think about control flow declaratively: the client can declare that they need a `NonZeroDouble`, rather than instructing the compiler to check whether the value is zero.

Extracting sequences

The previous section explains extraction from case classes, and how to write custom extractors, but it does not explain how extraction works on sequences:

```
scala> val Array(a, b) = Array(1, 2)
a: Int = 1
b: Int = 2
```

Rather than relying on an `unapply` method, sequences rely on an `unapplySeq` method defined in the companion object. This is expected to return an `Option[Seq[A]]`:

```
scala> Array.unapplySeq(Array(1, 2))
Option[IndexedSeq[Int]] = Some(Vector(1, 2))
```

Let's write an example. We will write an extractor for Breeze vectors (which do not currently support pattern matching). To avoid clashing with the `DenseVector` companion object, we will write our `unapplySeq` in a separate object, called `DV`. All our `unapplySeq` method needs to do is convert its argument to a Scala `Vector` instance. To avoid muddying the concepts with generics, we will write this implementation for `[Double]` vectors only:

```
scala> import breeze.linalg._
import breeze.linalg._

scala> object DV {
  // Just need to convert to a Scala vector.
  def unapplySeq(v:DenseVector[Double]) = Some(v.toScalaVector)
}
defined object DV
```

Let's try our new extractor implementation:

```
scala> val vec = DenseVector(1.0, 2.0, 3.0)
vec: breeze.linalg.DenseVector[Double] = DenseVector(1.0, 2.0, 3.0)

scala> val DV(x, y, z) = vec
x: Double = 1.0
y: Double = 2.0
z: Double = 3.0
```

Summary

Pattern matching is a powerful tool for control flow. It encourages the programmer to think declaratively: declare that you expect a variable to match a certain pattern, rather than explicitly tell the computer how to check that it matches this pattern. This can save many lines of code and enhance clarity.

Reference

For an overview of pattern matching in Scala, there is no better reference than *Programming in Scala*, by *Martin Odersky*, *Bill Venners*, and *Lex Spoon*. An online version of the first edition is available at: <https://www.artima.com/pins1ed/case-classes-and-pattern-matching.html>.

Daniel Westheide's blog covers slightly more advanced Scala constructs, and is a very useful read: <http://danielwestheide.com/blog/2012/11/21/the-neophytes-guide-to-scala-part-1-extractors.html>.

Module 2

Scala Data Analysis Cookbook

*Navigate the world of data analysis, visualization, and machine learning
with over 100 hands-on Scala recipes*

1

Getting Started with Breeze

In this chapter, we will cover the following recipes:

- ▶ Getting Breeze—the linear algebra library
- ▶ Working with vectors
- ▶ Working with matrices
- ▶ Vectors and matrices with randomly distributed values
- ▶ Reading and writing CSV files

Introduction

This chapter gives you a quick overview of one of the most popular data analysis libraries in Scala, how to get them, and their most frequently used functions and data structures.

We will be focusing on Breeze in this first chapter, which is one of the most popular and powerful linear algebra libraries. Spark MLlib, which we will be seeing in the subsequent chapters, builds on top of Breeze and Spark, and provides a powerful framework for scalable machine learning.

Getting Breeze – the linear algebra library

In simple terms, Breeze (<http://www.scalanlp.org>) is a Scala library that extends the Scala collection library to provide support for vectors and matrices in addition to providing a whole bunch of functions that support their manipulation. We could safely compare Breeze to NumPy (<http://www.numpy.org/>) in Python terms. Breeze forms the foundation of MLlib—the Machine Learning library in Spark, which we will explore in later chapters.

In this first recipe, we will see how to pull the Breeze libraries into our project using **Scala Build Tool (SBT)**. We will also see a brief history of Breeze to better appreciate why it could be considered as the "go to" linear algebra library in Scala.



For all our recipes, we will be using Scala 2.10.4 along with Java 1.7. I wrote the examples using the Scala IDE, but please feel free to use your favorite IDE.

How to do it...

Let's add the Breeze dependencies into our `build.sbt` so that we can start playing with them in the subsequent recipes. The Breeze dependencies are just two—the `breeze` (core) and the `breeze-native` dependencies.

1. Under a brand new folder (which will be our project root), create a new file called `build.sbt`.
2. Next, add the `breeze` libraries to the project dependencies:

```
organization := "com.packt"

name := "chapter1-breeze"

scalaVersion := "2.10.4"

libraryDependencies ++= Seq(
  "org.scalanlp" %% "breeze" % "0.11.2",
  //Optional - the 'why' is explained in the How it works
  section
  "org.scalanlp" %% "breeze-natives" % "0.11.2"
)
```

3. From that folder, issue a `sbt compile` command in order to fetch all your dependencies.



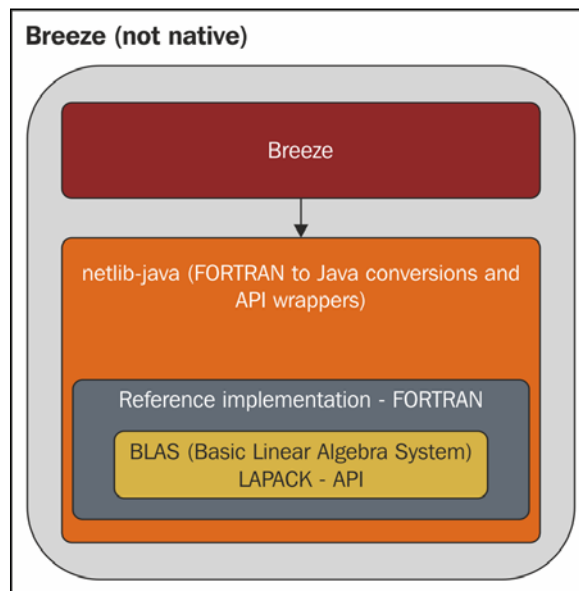
You could import the project into your Eclipse using `sbt eclipse` after installing the `sbteclipse` plugin <https://github.com/typesafehub/sbteclipse/>. For IntelliJ IDEA, you just need to import the project by pointing to the root folder where your `build.sbt` file is.

There's more...

Let's look into the details of what the `breeze` and `breeze-native` library dependencies we added bring to us.

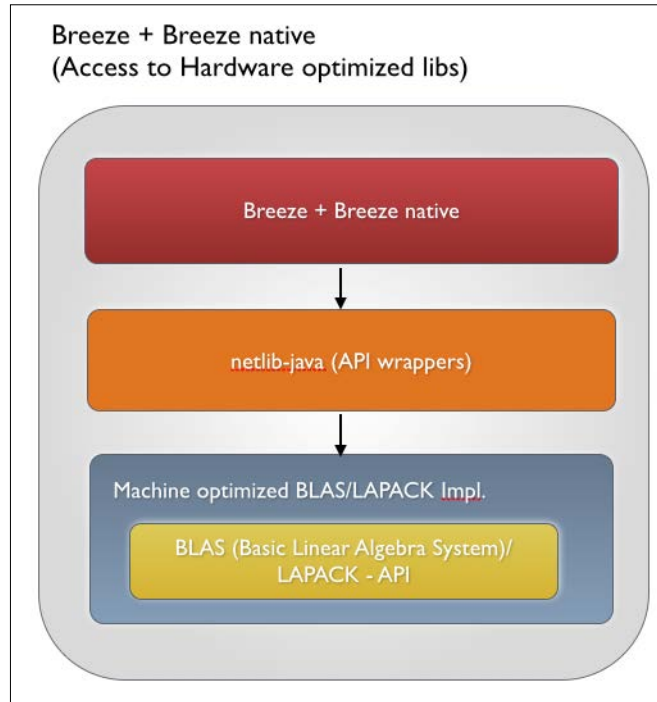
The `org.scalanlp.breeze` dependency

Breeze has a long history in that it isn't written from scratch in Scala. Without the native dependency, Breeze leverages the power of `netlib-java` that has a Java-compiled version of the FORTRAN Reference implementation of BLAS/LAPACK. The `netlib-java` also provides gentle wrappers over the Java compiled library. What this means is that we could still work without the native dependency but the performance won't be great considering the best performance that we could leverage out of this FORTRAN-translated library is the performance of the FORTRAN reference implementation itself. However, for serious number crunching with the best performance, we should add the `breeze-natives` dependency too.



The `org.scalanlp.breeze-natives` package

With its native additive, Breeze looks for the machine-specific implementations of the BLAS/LAPACK libraries. The good news is that there are open source and (vendor provided) commercial implementations for most popular processors and GPUs. The most popular open source implementations include ATLAS (<http://math-atlas.sourceforge.net>) and OpenBLAS (<http://www.openblas.net/>).



If you are running a Mac, you are in luck—Native BLAS libraries come out of the box on Macs. Installing NativeBLAS on Ubuntu / Debian involves just running the following commands:

```
sudo apt-get install libatlas3-base libopenblas-base
sudo update-alternatives --config libblas.so.3
sudo update-alternatives --config liblapack.so.3
```



Downloading the example code

You can download the example code files from your account at <http://www.packtpub.com> for all the Packt Publishing books you have purchased. If you purchased this book elsewhere, you can visit <http://www.packtpub.com/support> and register to have the files e-mailed directly to you.

```

File Edit View Search Terminal Help
arun@arun-VirtualBox:~$ sudo update-alternatives --config libblas.so.3
There are 2 choices for the alternative libblas.so.3 (providing /usr/lib/libblas.so.3).

-----
Selection    Path                                          Priority  Status
-----
* 0          /usr/lib/openblas-base/libblas.so.3        40       auto mode
 1          /usr/lib/atlas-base/atlas/libblas.so.3     35       manual mode
 2          /usr/lib/openblas-base/libblas.so.3        40       manual mode
-----

Press enter to keep the current choice[*], or type selection number: 1
update-alternatives: using /usr/lib/atlas-base/atlas/libblas.so.3 to provide /usr/lib/libblas.so.3 (libblas.so.3) in manual mode
arun@arun-VirtualBox:~$ sudo update-alternatives --config liblapack.so.3
There is only one alternative in link group liblapack.so.3 (providing /usr/lib/liblapack.so.3): /usr/lib/atlas-base/atlas/liblapack.so.3
Nothing to configure.
arun@arun-VirtualBox:~$

```

For Windows, please refer to the installation instructions on <https://github.com/xiany/OpenBLAS/wiki/Installation-Guide>.

Working with vectors

There are subtle yet powerful differences between Breeze vectors and Scala's own `scala.collection.Vector`. As we'll see in this recipe, Breeze vectors have a lot of functions that are linear algebra specific, and the more important thing to note here is that Breeze's vector is a Scala wrapper over `netlib-java` and most calls to the vector's API delegates the call to it.

Vectors are one of the core components in Breeze. They are containers of homogenous data. In this recipe, we'll first see how to create vectors and then move on to various data manipulation functions to modify those vectors.

In this recipe, we will look at various operations on vectors. This recipe has been organized in the form of the following sub-recipes:

- ▶ Creating vectors:
 - ❑ Creating a vector from values
 - ❑ Creating a zero vector
 - ❑ Creating a vector out of a function
 - ❑ Creating a vector of linearly spaced values
 - ❑ Creating a vector with values in a specific range
 - ❑ Creating an entire vector with a single value
 - ❑ Slicing a sub-vector from a bigger vector
 - ❑ Creating a Breeze vector from a Scala vector
- ▶ Vector arithmetic:
 - ❑ Scalar operations
 - ❑ Calculating the dot product of a vector
 - ❑ Creating a new vector by adding two vectors together

- ▶ Appending vectors and converting a vector of one type to another:
 - ❑ Concatenating two vectors
 - ❑ Converting a vector of int to a vector of double
- ▶ Computing basic statistics:
 - ❑ Mean and variance
 - ❑ Standard deviation
 - ❑ Find the largest value
 - ❑ Finding the sum, square root and log of all the values in the vector

Getting ready

In order to run the code, you could either use the Scala or use the Worksheet feature available in the Eclipse Scala plugin (or Scala IDE) or in IntelliJ IDEA. The reason these options are suggested is due to their quick turnaround time.

How to do it...

Let's look at each of the above sub-recipes in detail. For easier reference, the output of the respective command is shown as well. All the classes that are being used in this recipe are from the `breeze.linalg` package. So, an `"import breeze.linalg._"` statement at the top of your file would be perfect.

Creating vectors

Let's look at the various ways we could construct vectors. Most of these construction mechanisms are through the `apply` method of the vector. There are two different flavors of vector—`breeze.linalg.DenseVector` and `breeze.linalg.SparseVector`—the choice of the vector depends on the use case. The general rule of thumb is that if you have data that is at least 20 percent zeroes, you are better off choosing `SparseVector` but then the 20 percent is a variant too.

Constructing a vector from values

- ▶ **Creating a dense vector from values:** Creating a `DenseVector` from values is just a matter of passing the values to the `apply` method:

```
val dense=DenseVector(1,2,3,4,5)
println (dense) //DenseVector(1, 2, 3, 4, 5)
```

- ▶ **Creating a sparse vector from values:** Creating a `SparseVector` from values is also through passing the values to the `apply` method:

```
val sparse=SparseVector(0.0, 1.0, 0.0, 2.0, 0.0)
println (sparse) //SparseVector((0,0.0), (1,1.0), (2,0.0),
(3,2.0), (4,0.0))
```

Notice how the `SparseVector` stores values against the index.

Obviously, there are simpler ways to create a vector instead of just throwing all the data into its `apply` method.

Creating a zero vector

Calling the vector's `zeros` function would create a zero vector. While the numeric types would return a `0`, the object types would return `null` and the Boolean types would return `false`:

```
val denseZeros=DenseVector.zeros[Double] (5) //DenseVector(0.0,
0.0, 0.0, 0.0, 0.0)

val sparseZeros=SparseVector.zeros[Double] (5) //SparseVector()
```

Not surprisingly, the `SparseVector` does not allocate any memory for the contents of the vector. However, the creation of the `SparseVector` object itself is accounted for in the memory.

Creating a vector out of a function

The `tabulate` function in `vector` is an interesting and useful function. It accepts a size argument just like the `zeros` function but it also accepts a function that we could use to populate the values for the vector. The function could be anything ranging from a random number generator to a naïve index based generator, which we have implemented here. Notice how the return value of the function (`Int`) could be converted into a vector of `Double` by using the type parameter:

```
val
denseTabulate=DenseVector.tabulate[Double] (5) (index=>index*index)
//DenseVector(0.0, 1.0, 4.0, 9.0, 16.0)
```

Creating a vector of linearly spaced values

The `linspace` function in `breeze.linalg` creates a new `Vector[Double]` of linearly spaced values between two arbitrary numbers. Not surprisingly, it accepts three arguments—the start, end, and the total number of values that we would like to generate. Please note that the start and the end values are inclusive while being generated:

```
val spaceVector=breeze.linalg.linspace(2, 10, 5)
//DenseVector(2.0, 4.0, 6.0, 8.0, 10.0)
```

Creating a vector with values in a specific range

The `range` function in a vector has two variants. The plain vanilla function accepts a start and end value (start inclusive):

```
val allNosTill10=DenseVector.range(0, 10)
//DenseVector(0, 1, 2, 3, 4, 5, 6, 7, 8, 9)
```

The other variant is an overloaded function that accepts a "step" value:

```
val evenNosTill20=DenseVector.range(0, 20, 2)
// DenseVector(0, 2, 4, 6, 8, 10, 12, 14, 16, 18)
```

Just like the `range` function, which has all the arguments as integers, there is also a `rangeD` function that takes the start, stop, and the step parameters as `Double`:

```
val rangeD=DenseVector.rangeD(0.5, 20, 2.5)
// DenseVector(0.5, 3.0, 5.5, 8.0, 10.5, 13.0, 15.5)
```

Creating an entire vector with a single value

Filling an entire vector with the same value is child's play. We just say HOW BIG is this vector going to be and then WHAT value. That's it.

```
val denseJust2s=DenseVector.fill(10, 2)
// DenseVector(2, 2, 2, 2, 2, 2, 2, 2, 2, 2)
```

Slicing a sub-vector from a bigger vector

Choosing a part of the vector from a previous vector is just a matter of calling the `slice` method on the bigger vector. The parameters to be passed are the start index, end index, and an optional "step" parameter. The step parameter adds the step value for every iteration until it reaches the end index. Note that the end index is excluded in the sub-vector:

```
val allNosTill10=DenseVector.range(0, 10)
//DenseVector(0, 1, 2, 3, 4, 5, 6, 7, 8, 9)
val fourThroughSevenIndexVector= allNosTill10.slice(4, 7)
//DenseVector(4, 5, 6)
val twoThroughNineSkip2IndexVector= allNosTill10.slice(2, 9, 2)
//DenseVector(2, 4, 6)
```

Creating a Breeze Vector from a Scala Vector

A Breeze vector object's `apply` method could even accept a Scala Vector as a parameter and construct a vector out of it:

```
val
vectFromArray=DenseVector(collection.immutable.Vector(1,2,3,4))
// DenseVector(Vector(1, 2, 3, 4))
```

Vector arithmetic

Now let's look at the basic arithmetic that we could do on vectors with scalars and vectors.

Scalar operations

Operations with scalars work just as we would expect, propagating the value to each element in the vector.

Adding a scalar to each element of the vector is done using the `+` function (surprise!):

```
val inPlaceValueAddition=evenNosTill20 +2
//DenseVector(2, 4, 6, 8, 10, 12, 14, 16, 18, 20)
```

Similarly the other basic arithmetic operations—subtraction, multiplication, and division involves calling the respective functions named after the universally accepted symbols (`-`, `*`, and `/`):

```
//Scalar subtraction
val inPlaceValueSubtraction=evenNosTill20 -2
//DenseVector(-2, 0, 2, 4, 6, 8, 10, 12, 14, 16)

//Scalar multiplication
val inPlaceValueMultiplication=evenNosTill20 *2
//DenseVector(0, 4, 8, 12, 16, 20, 24, 28, 32, 36)

//Scalar division
val inPlaceValueDivision=evenNosTill20 /2
//DenseVector(0, 1, 2, 3, 4, 5, 6, 7, 8, 9)
```

Calculating the dot product of two vectors

Each vector object has a function called `dot`, which accepts another vector of the same length as a parameter.

Let's fill in just 2s to a new vector of length 5:

```
val justFive2s=DenseVector.fill(5, 2)
//DenseVector(2, 2, 2, 2, 2)
```

We'll create another vector from 0 to 5 with a step value of 1 (a fancy way of saying 0 through 4):

```
val zeroThrough4=DenseVector.range(0, 5, 1)
//DenseVector(0, 1, 2, 3, 4)
```

Here's the dot function:

```
val dotVector=zeroThrough4.dot(justFive2s)
//Int = 20
```

It is to be expected of the function to complain if we pass in a vector of a different length as a parameter to the dot product - Breeze throws an `IllegalArgumentException` if we do that. The full exception message is:

```
java.lang.IllegalArgumentException: Vectors must be the same
length!
```

Creating a new vector by adding two vectors together

The `+` function is overloaded to accept a vector other than the scalar we saw previously. The operation does a corresponding element-by-element addition and creates a new vector:

```
val evenNosTill20=DenseVector.range(0, 20, 2)
//DenseVector(0, 2, 4, 6, 8, 10, 12, 14, 16, 18)

val denseJust2s=DenseVector.fill(10, 2)
//DenseVector(2, 2, 2, 2, 2, 2, 2, 2, 2, 2)

val additionVector=evenNosTill20 + denseJust2s
// DenseVector(2, 4, 6, 8, 10, 12, 14, 16, 18, 20)
```

There's an interesting behavior encapsulated in the addition though. Assuming you try to add two vectors of different lengths, if the first vector is smaller and the second vector larger, the resulting vector would be the size of the first vector and the rest of the elements in the second vector would be ignored!

```
val fiveLength=DenseVector(1,2,3,4,5)
//DenseVector(1, 2, 3, 4, 5)
val tenLength=DenseVector.fill(10, 20)
//DenseVector(20, 20, 20, 20, 20, 20, 20, 20, 20, 20)

fiveLength+tenLength
//DenseVector(21, 22, 23, 24, 25)
```

On the other hand, if the first vector is larger and the second vector smaller, it would result in an `ArrayIndexOutOfBoundsException`:

```
tenLength+fiveLength
// java.lang.ArrayIndexOutOfBoundsException: 5
```

Appending vectors and converting a vector of one type to another

Let's briefly see how to append two vectors and convert vectors of one numeric type to another.

Concatenating two vectors

There are two variants of concatenation. There is a `vertcat` function that just vertically concatenates an arbitrary number of vectors—the size of the vector just increases to the sum of the sizes of all the vectors combined:

```
val justFive2s=DenseVector.fill(5, 2)
//DenseVector(2, 2, 2, 2, 2)

val zeroThrough4=DenseVector.range(0, 5, 1)
//DenseVector(0, 1, 2, 3, 4)

val concatVector=DenseVector.vertcat(zeroThrough4, justFive2s)
//DenseVector(0, 1, 2, 3, 4, 2, 2, 2, 2, 2)
```

No surprise here. There is also the `horzcat` method that places the second vector horizontally next to the first vector, thus forming a matrix.

```
val concatVector1=DenseVector.horzcat(zeroThrough4, justFive2s)
//breeze.linalg.DenseMatrix[Int]
0 2
1 2
2 2
3 2
4 2
```



While dealing with vectors of different length, the `vertcat` function happily arranges the second vector at the bottom of the first vector. Not surprisingly, the `horzcat` function throws an exception:

`java.lang.IllegalArgumentException`, meaning all vectors must be of the same size!

Converting a vector of Int to a vector of Double

The conversion of one type of vector into another is not automatic in Breeze. However, there is a simple way to achieve this:

```
val evenNosTill20Double=breeze.linalg.convert (evenNosTill20,
Double)
```

Computing basic statistics

Other than the creation and the arithmetic operations that we saw previously, there are some interesting summary statistics operations that are available in the library. Let's look at them now:



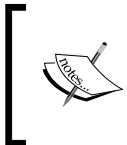
Needs import of `breeze.linalg._` and `breeze.numerics._`. The operations in the Other operations section aim to simulate the NumPy's UFunc or universal functions.

Now, let's briefly look at how to calculate some basic summary statistics for a vector.

Mean and variance

Calculating the mean and variance of a vector could be achieved by calling the `meanAndVariance` universal function in the `breeze.stats` package. Note that this needs a vector of `Double`:

```
meanAndVariance (evenNosTill20Double)
//MeanAndVariance (9.0, 36.666666666666664, 10)
```



As you may have guessed, converting an `Int` vector to a `Double` vector and calculating the mean and variance for that vector could be merged into a one-liner:

```
meanAndVariance (convert (evenNosTill20, Double))
```

Standard deviation

Calling the `stddev` on a `Double` vector could give the standard deviation:

```
stddev (evenNosTill20Double)
//Double = 6.0553007081949835
```

Find the largest value in a vector

The `max` universal function inside the `breeze.linalg` package would help us find the maximum value in a vector:

```
val intMaxOfVectorVals=max (evenNosTill20)
//18
```

Finding the sum, square root and log of all the values in the vector

The same as with `max`, the `sum` universal function inside the `breeze.linalg` package calculates the `sum` of the vector:

```
val intSumOfVectorVals=sum (evenNosTill120)
//90
```

The functions `sqrt`, `log`, and various other universal functions in the `breeze.numerics` package calculate the square root and log values of all the individual elements inside the vector:

The Sqrt function

```
val sqrtOfVectorVals= sqrt (evenNosTill120)
// DenseVector(0.0, 1. 4142135623730951, 2.0, 2.449489742783178,
2.8284271247461903, 3.16227766016 83795, 3.4641016151377544,
3.7416573867739413, 4.0, 4.242640687119285)
```

The Log function

```
val log2VectorVals=log(evenNosTill120)
// DenseVector(-Infinity , 0.6931471805599453, 1.3862943611198906,
1.791759469228055, 2.079441541679 8357, 2.302585092994046,
2.4849066497880004, 2.6390573296152584, 2.77258872 2239781,
2.8903717578961645)
```

Working with matrices

As we discussed in the *Working with vectors* recipe, you could use the Eclipse or IntelliJ IDEA Scala worksheets for a faster turnaround time.

How to do it...

There are a variety of functions that we have in a matrix. In this recipe, we will look at some details around:

- ▶ Creating matrices:
 - Creating a matrix from values
 - Creating a zero matrix
 - Creating a matrix out of a function
 - Creating an identity matrix
 - Creating a matrix from random numbers
 - Creating from a Scala collection

- ▶ Matrix arithmetic:
 - Addition
 - Multiplication (also element-wise)
- ▶ Appending and conversion:
 - Concatenating a matrix vertically
 - Concatenating a matrix horizontally
 - Converting a matrix of Int to a matrix of Double
- ▶ Data manipulation operations:
 - Getting column vectors
 - Getting row vectors
 - Getting values inside the matrix
 - Getting the inverse and transpose of a matrix
- ▶ Computing basic statistics:
 - Mean and variance
 - Standard deviation
 - Finding the largest value
 - Finding the sum, square root and log of all the values in the matrix
 - Calculating the eigenvectors and eigenvalues of a matrix

Creating matrices

Let's first see how to create a matrix.

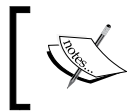
Creating a matrix from values

The simplest way to create a matrix is to pass in the values in a row-wise fashion into the `apply` function of the matrix object:

```
val simpleMatrix=DenseMatrix((1,2,3),(11,12,13),(21,22,23))
//Returns a DenseMatrix[Int]
  1  2  3
11 12 13
21 22 23
```

There's also a Sparse version of the matrix too—the **Compressed Sparse Column Matrix (CSCMatrix)**:

```
val sparseMatrix=CSCMatrix((1,0,0),(11,0,0),(0,0,23))
//Returns a SparseMatrix[Int]
(0,0) 1
(1,0) 11
(2,2) 23
```



Breeze's Sparse matrix is a **Dictionary of Keys (DOK)** representation with (row, column) mapped against the value.

Creating a zero matrix

Creating a zero matrix is just a matter of calling the matrix's `zeros` function. The first integer parameter indicates the rows and the second parameter indicates the columns:

```
val denseZeros=DenseMatrix.zeros[Double](5,4)
//Returns a DenseMatrix[Double]
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
0.0 0.0 0.0 0.0
```

```
val compressedSparseMatrix=CSCMatrix.zeros[Double](5,4)
//Returns a CSCMatrix[Double] = 5 x 4 CSCMatrix
```



Notice how the `SparseMatrix` doesn't allocate any memory for the values in the zero value matrix.

Creating a matrix out of a function

The `tabulate` function in a matrix is very similar to the vector's version. It accepts a row and column size as a tuple (in the example `(5, 4)`). It also accepts a function that we could use to populate the values for the matrix. In our example, we generated the values of the matrix by just multiplying the row and column index:

```
val denseTabulate=DenseMatrix.tabulate[Double](5,4)((firstIdx,secondIdx) =>firstIdx*secondIdx)
```

Returns a `DenseMatrix[Double]` =

```
0.0 0.0 0.0 0.0
0.0 1.0 2.0 3.0
0.0 2.0 4.0 6.0
0.0 3.0 6.0 9.0
0.0 4.0 8.0 12.0
```

The `type` parameter is needed only if you would like to convert the type of the matrix from an `Int` to a `Double`. So, the following call without the parameter would just return an `Int` matrix:

```
val denseTabulate=DenseMatrix.tabulate(5,4)((firstIdx,secondIdx) =>firstIdx*secondIdx)
```

```
0 1 2 3
0 2 4 6
0 3 6 9
0 4 8 12
```

Creating an identity matrix

The `eye` function of the matrix would generate an identity square matrix with the given dimension (in the example's case, 3):

```
val identityMatrix=DenseMatrix.eye[Int](3)
```

Returns a `DenseMatrix[Int]`

```
1 0 0
0 1 0
0 0 1
```

Creating a matrix from random numbers

The `rand` function in the matrix would generate a matrix of a given dimension (4 rows * 4 columns in our case) with random values between 0 and 1. We'll have an in-depth look into random number generated vectors and matrices in a subsequent recipe.

```
val randomMatrix=DenseMatrix.rand(4, 4)
```

Returns `DenseMatrix[Double]`

```
0.09762565779429777    0.01089176285376725    0.2660579009292807
0.19428193961985674
0.9662568115400412    0.718377391997945    0.8230367668470933
0.3957540854393169
0.9080090988364429    0.7697780247035393    0.49887760321635066
0.26722019105654415
3.326843165250004E-4  0.447925644082819    0.8195838733418965
0.7682752255172411
```

Creating from a Scala collection

We could create a matrix out of a Scala array too. The constructor of the matrix accepts three arguments—the rows, the columns, and an array with values for the dimensions. Note that the data from the array is picked up to construct the matrix in the column first order:

```
val vectFromArray=new DenseMatrix(2,2,Array(2,3,4,5))
```

Returns `DenseMatrix[Int]`

```
2  4
3  5
```

If there are more values than the number of values required by the dimensions of the matrix, the rest of the values are ignored. Note how (6, 7) is ignored in the array:

```
val vectFromArray=new DenseMatrix(2,2,Array(2,3,4,5,6,7))
```

Returns `DenseMatrix[Int]`

```
2  4
3  5
```

However, if fewer values are present in the array than what is required by the dimensions of the matrix, then the constructor call would throw an `ArrayIndexOutOfBoundsException`:

```
val vectFromArrayIobe=new DenseMatrix(2,2,Array(2,3,4))
```

```
//throws java.lang.ArrayIndexOutOfBoundsException: 3
```

Matrix arithmetic

Now let's look at the basic arithmetic that we could do using matrices.

Let's consider a simple 3*3 `simpleMatrix` and a corresponding identity matrix:

```
val simpleMatrix=DenseMatrix((1,2,3),(11,12,13),(21,22,23))
//DenseMatrix[Int]
1  2  3
11 12 13
21 22 23
```

```
val identityMatrix=DenseMatrix.eye[Int](3)
//DenseMatrix[Int]
1  0  0
0  1  0
0  0  1
```

Addition

Adding two matrices will result in a matrix whose corresponding elements are summed up.

```
val additionMatrix=identityMatrix + simpleMatrix
// Returns DenseMatrix[Int]
2  2  3
11 13 13
21 22 24
```

Multiplication

Now, as you would expect, multiplying a matrix with its identity should give you the matrix itself:

```
val simpleTimesIdentity=simpleMatrix * identityMatrix
//Returns DenseMatrix[Int]
1  2  3
11 12 13
21 22 23
```

Breeze also has an alternative element-by-element operation that has the format of prefixing the operator with a colon, for example, `:+`, `:-`, `:*`, and so on. Check out what happens when we do an element-wise multiplication of the identity matrix and the simple matrix:

```
val elementWiseMulti=identityMatrix :* simpleMatrix
//DenseMatrix[Int]
1  0  0
0  12 0
0  0  23
```

Appending and conversion

Let's briefly see how to append two matrices and convert matrices of one numeric type to another.

Concatenating matrices – vertically

Similar to vectors, matrix has a `vertcat` function, which vertically concatenates an arbitrary number of matrices—the row size of the matrix just increases to the sum of the row sizes of all matrices combined:

```
val vertConcatMatrix=DenseMatrix.vertcat(identityMatrix, simpleMatrix)

//DenseMatrix[Int]
1  0  0
0  1  0
0  0  1
1  2  3
11 12 13
21 22 23
```

Attempting to concatenate a matrix of different columns would, as expected, throw an `IllegalArgumentException`:

```
java.lang.IllegalArgumentException: requirement failed: Not all
matrices have the same number of columns
```

Concatenating matrices – horizontally

Not surprisingly, the `horzcat` function concatenates the matrix horizontally—the column size of the matrix increases to the sum of the column sizes of all the matrices:

```
val horzConcatMatrix=DenseMatrix.horzcat(identityMatrix, simpleMatrix)
// DenseMatrix[Int]
1  0  0  1  2  3
```



```
0 1 0 11 12 13
0 0 1 21 22 23
```

Similar to the vertical concatenation, attempting to concatenate a matrix of a different row size would throw an `IllegalArgumentException`:

```
java.lang.IllegalArgumentException: requirement failed: Not all
matrices have the same number of rows
```

Converting a matrix of `Int` to a matrix of `Double`

The conversion of one type of matrix to another is not automatic in Breeze. However, there is a simple way to achieve this:

```
import breeze.linalg.convert
val simpleMatrixAsDouble=convert(simpleMatrix, Double)
// DenseMatrix[Double] =
1.0  2.0  3.0
11.0 12.0 13.0
21.0 22.0 23.0
```

Data manipulation operations

Let's create a simple 2*2 matrix that will be used for the rest of this section:

```
val simpleMatrix=DenseMatrix((4.0,7.0),(3.0,-5.0))
//DenseMatrix[Double] =
4.0  7.0
3.0 -5.0
```

Getting column vectors out of the matrix

The first column vector could be retrieved by passing in the column parameter as 0 and using `::` in order to say that we are interested in all the rows.

```
val firstVector=simpleMatrix(:,0)
//DenseVector(4.0, 3.0)
```

Getting the second column vector and so on is achieved by passing the correct zero-indexed column number:

```
val secondVector=simpleMatrix(:,1)
//DenseVector(7.0, -5.0)
```

Alternatively, you could explicitly pass in the columns to be extracted:

```
val firstVectorByCols=simpleMatrix(0 to 1,0)
//DenseVector(4.0, 3.0)
```

While explicitly stating the range (as in 0 to 1), we have to be careful not to exceed the matrix size. For example, the following attempt to select 3 columns (0 through 2) on a 2 * 2 matrix would throw an `ArrayIndexOutOfBoundsException`:

```
val errorTryingToSelect3ColumnsOn2By2Matrix=simpleMatrix(0,0 to 2)
//java.lang.ArrayIndexOutOfBoundsException
```

Getting row vectors out of the matrix

If we would like to get the row vector, all we need to do is play with the row and column parameters again. As expected, it would give a transpose of the column vector, which is simply a row vector.

Like the column vector, we could either explicitly state our columns or pass in a wildcard (`::`) to cover the entire range of columns:

```
val firstRowStatingCols=simpleMatrix(0,0 to 1)
//Transpose(DenseVector(4.0, 7.0))

val firstRowAllCols=simpleMatrix(0,::)
//Transpose(DenseVector(4.0, 7.0))
```

Getting the second row vector is achieved by passing the second row (1) and all the columns (`::`) in that vector:

```
val secondRow=simpleMatrix(1,::)
//Transpose(DenseVector(3.0, -5.0))
```

Getting values inside the matrix

Assuming we are just interested in the values within the matrix, pass in the exact row and the column number of the matrix. In order to get the first row and first column of the matrix, just pass in the row and the column number:

```
val firstRowFirstCol=simpleMatrix(0,0)
//Double = 4.0
```

Getting the inverse and transpose of a matrix

Getting the inverse and the transpose of a matrix is a little counter-intuitive in Breeze. Let's consider the same matrix that we dealt with earlier:

```
val simpleMatrix=DenseMatrix((4.0,7.0),(3.0,-5.0))
```

On the one hand, `transpose` is a function on the matrix object itself, like so:

```
val transpose=simpleMatrix.t
4.0  3.0
7.0 -5.0
```

`inverse`, on the other hand is a universal function under the `breeze.linalg` package:

```
val inverse=inv(simpleMatrix)

0.12195121951219512  0.17073170731707318
0.07317073170731708  -0.0975609756097561
```

Let's do a matrix product to its inverse and confirm whether it is an identity matrix:


```
simpleMatrix * inverse

1.0  0.0
-5.551115123125783E-17  1.0
```

As expected, the result is indeed an identity matrix with rounding errors when doing floating point arithmetic.

Computing basic statistics

Now, just like vectors, let's briefly look at how to calculate some basic summary statistics for a matrix.

 This needs import of `breeze.linalg._`, `breeze.numerics._` and `breeze.stats._`. The operations in the "Other operations" section aims to simulate the NumPy's UFunc or universal functions.

Mean and variance

Calculating the mean and variance of a matrix could be achieved by calling the `meanAndVariance` universal function in the `breeze.stats` package. Note that this needs a matrix of `Double`:

```
meanAndVariance(simpleMatrixAsDouble)
// MeanAndVariance(12.0, 75.75, 9)
```

Alternatively, converting an `Int` matrix to a `Double` matrix and calculating the mean and variance for that `Matrix` could be merged into a one-liner:

```
meanAndVariance(convert(simpleMatrix, Double))
```

Standard deviation

Calling the `stddev` on a `Double` vector could give the standard deviation:

```
stddev(simpleMatrixAsDouble)
//Double = 8.703447592764606
```

Next up, let's look at some basic aggregation operations:

```
val simpleMatrix=DenseMatrix((1,2,3),(11,12,13),(21,22,23))
```

Finding the largest value in a matrix

The (`apply` method of the) `max` object (a universal function) inside the `breeze.linalg` package will help us do that:

```
val intMaxOfMatrixVals=max (simpleMatrix)
//23
```

Finding the sum, square root and log of all the values in the matrix

The same as with `max`, the `sum` object inside the `breeze.linalg` package calculates the sum of all the matrix elements:

```
val intSumOfMatrixVals=sum (simpleMatrix)
//108
```

The functions `sqrt`, `log`, and various other objects (universal functions) in the `breeze.numerics` package calculate the square root and log values of all the individual values inside the matrix.

Sqrt

```
val sqrtOfMatrixVals= sqrt (simpleMatrix)
//DenseMatrix[Double] =
1.0          1.4142135623730951  1.7320508075688772
3.3166247903554  3.4641016151377544  3.605551275463989
4.58257569495584  4.69041575982343  4.795831523312719
```

Log

```
val log2MatrixVals=log(simpleMatrix)
//DenseMatrix[Double]
0.0          0.6931471805599453  1.0986122886681098
2.3978952727983707  2.4849066497880004  2.5649493574615367
3.044522437723423  3.091042453358316  3.1354942159291497
```

Calculating the eigenvectors and eigenvalues of a matrix

Calculating eigenvectors is straightforward in Breeze. Let's consider our `simpleMatrix` from the previous section:

```
val simpleMatrix=DenseMatrix((4.0,7.0),(3.0,-5.0))
```

Calling the `breeze.linalg.eig` universal function on a matrix returns a `breeze.linalg.eig.DenseEig` object that encapsulate eigenvectors and eigenvalues:

```
val denseEig=eig(simpleMatrix)
```

This line of code returns the following:

```
Eig(  
DenseVector(5.922616289332565, -6.922616289332565),  
DenseVector(0.0, 0.0)  
,0.9642892971721949 -0.5395744865143975 0.26485118719604456  
0.8419378679586305)
```

We could extract the eigenvectors and eigenvalues by calling the corresponding functions on the returned `Eig` reference:

```
val eigenVectors=denseEig.eigenvectors  
//DenseMatrix[Double] =  
0.9642892971721949 -0.5395744865143975  
0.26485118719604456 0.8419378679586305
```

The two `eigenValues` corresponding to the two `eigenvectors` could be captured using the `eigenvalues` function on the `Eig` object:

```
val eigenValues=denseEig.eigenvalues  
//DenseVector[Double] = DenseVector(5.922616289332565,  
-6.922616289332565)
```

Let's validate the eigenvalues and the vectors:

1. Let's multiply the matrix with the first eigenvector:

```
val matrixToEigVector=simpleMatrix*denseEig.eigenvectors (::,0)  
//DenseVector(5.7111154990610915, 1.568611955536362)
```

2. Then let's multiply the first eigenvalue with the first eigenvector. The resulting vector will be the same with a marginal error when doing floating point arithmetic:

```
val vectorToEigValue=denseEig.eigenvectors (::,0) *  
denseEig.eigenvalues (0)  
//DenseVector(5.7111154990610915, 1.5686119555363618)
```

How it works...

The same as with vectors, the initialization of the Breeze matrices are achieved by way of the `apply` method or one of the various methods in the matrix's `Object` class. Various other operations are provided by way of polymorphic functions available in the `breeze.numeric`, `breeze.linalg` and `breeze.stats` packages.

Vectors and matrices with randomly distributed values

The `breeze.stats.distributions` package supplements the random number generator that is built into Scala. Scala's default generator just provides the ability to get the random values one by one using the "next" methods. Random number generators in Breeze provide the ability to build vectors and matrices out of these generators. In this recipe, we'll briefly see three of the most common distributions of random numbers.

In this recipe, we will cover at the following sub-recipes:

- ▶ *Creating vectors with uniformly distributed random values*
- ▶ *Creating vectors with normally distributed random values*
- ▶ *Creating vectors with random values that have a Poisson distribution*
- ▶ *Creating a matrix with uniformly random values*
- ▶ *Creating a matrix with normally distributed random values*
- ▶ *Creating a matrix with random values that has a Poisson distribution*

How it works...

Before we delve into how to create the vectors and matrices out of random numbers, let's create instances of the most common random number distribution. All these generators are under the `breeze.stats.distributions` package:

```
//Uniform distribution with low being 0 and high being 10
val uniformDist=Uniform(0,10)

//Gaussian distribution with mean being 5 and Standard deviation
being 1
val gaussianDist=Gaussian(5,1)

//Poisson distribution with mean being 5
val poissonDist=Poisson(5)
```

We could actually directly sample from these generators. Given any distribution we created previously, we could sample either a single value or a sequence of values:

```
//Samples a single value
println (uniformDist.sample())
//eg. 9.151191360491392

//Returns a sample vector of size that is passed in as parameter
println (uniformDist.sample(2))
//eg. Vector(6.001980062275654, 6.210874664967401)
```

Creating vectors with uniformly distributed random values

With no generator parameter, the `DenseVector.rand` method accepts a parameter for the length of the vector to be returned. The result is a vector (of length 10) with uniformly distributed values between 0 and 1:

```
val uniformWithoutSize=DenseVector.rand(10)
println ("uniformWithoutSize \n"+ uniformWithoutSize)
//DenseVector(0.1235038023750481, 0.3120595941786264, 0.3575638744660876,
0.5640844223813524, 0.5336149399548831, 0.1338053814330793,
0.9099684427908603, 0.38690724148973166, 0.22561993631651522,
0.45120359622713657)
```

The `DenseVector.rand` method optionally accepts a distribution object and generates random values using that input distribution. The following line generates a vector of 10 uniformly distributed random values that are within the range 0 and 10:

```
val uniformDist=Uniform(0,10)

val uniformVectInRange=DenseVector.rand(10, uniformDist)
println ("uniformVectInRange \n"+uniformVectInRange)
//DenseVector(1.5545833905907314, 6.172564377264846, 8.45578509265587,
7.683763574965107, 8.018688137742062, 4.5876187984930406,
3.274758584944064, 2.3873947264259954, 2.139988841403757,
8.314112884416943)
```

Creating vectors with normally distributed random values

In the place of the `uniformDist` generator, we could also pass the previously created Gaussian generator, which is configured to yield a distribution that has a mean of 5 and standard deviation of 1:

```
val gaussianVector=DenseVector.rand(10, gaussianDist)
println ("gaussianVector \n"+gaussianVector)
```

```
//DenseVector(4.235655596913547, 5.535011377545014, 6.201428236839494,
6.046289604188366, 4.319709374229152,
4.2379652913447154, 2.957868021601233, 3.96371080427211,
4.351274306757224, 5.445022658876723)
```

Creating vectors with random values that have a Poisson distribution

Similarly, by passing the previously created Poisson random number generator, a vector of values that has a mean of 5 could be generated:

```
val poissonVector=DenseVector.rand(10, poissonDist)
println ("poissonVector \n"+poissonVector)
//DenseVector(5, 5, 7, 11, 7, 6, 6, 6, 6, 6)
```

We saw how easy it is to create a vector of random values. Now, let's proceed to create a matrix of random values. Similar to `DenseVector.rand` to generate vectors with random values, we'll use the `DenseMatrix.rand` function to generate a matrix of random values.

Creating a matrix with uniformly random values

The `DenseMatrix.rand` defaults to the uniform distribution and generates a matrix of random values given the row and the column parameter. However, if we would like to have a distribution within a range, then as in vectors, we could use the optional parameter:

```
//Uniform distribution, Creates a 3 * 3 Matrix with random values from 0
to 1
val uniformMat=DenseMatrix.rand(3, 3)
println ("uniformMat \n"+uniformMat)

0.4492155777289115  0.9098840386699856  0.8203022252988292
0.0888975848853315  0.009677790736892788  0.6058885905934237
0.6201415814136939  0.7017492438727635  0.08404147915159443

//Creates a 3 * 3 Matrix with uniformly distributed random values with
low being 0 and high being 10
val uniformMatrixInRange=DenseMatrix.rand(3,3, uniformDist)
println ("uniformMatrixInRange \n"+uniformMatrixInRange)

7.592014659345548  8.164652560340933  6.966445294464401
8.35949395084735  3.442654641743763  3.6761640240938442
9.42626645215854  0.23658921372298636  7.327120138868571
```


Creating a matrix with normally distributed random values

Just as in vectors, in place of the `uniformDist` generator, we could also pass the previously created Gaussian generator to the `rand` function to generate a matrix of random values that has a mean of 5 and standard deviation of 1:

```
//Creates a 3 * 3 Matrix with normally distributed random values
with mean being 5 and Standard deviation being 1
val gaussianMatrix=DenseMatrix.rand(3, 3,gaussianDist)
println ("gaussianMatrix \n"+gaussianMatrix)
```

```
5.724540885605018    5.647051873430568    5.337906135107098
6.2228893721489875    4.799561665187845    5.12469779489833
5.136960834730864    5.176410360757703    5.262707072950913
```

Creating a matrix with random values that has a Poisson distribution

Similarly, by passing the previously created Poisson random number generator, a matrix of random values that has a mean of 5 could be generated:

```
//Creates a 3 * 3 Matrix with Poisson distribution with mean being 5
val poissonMatrix=DenseMatrix.rand(3, 3,poissonDist)
println ("poissonMatrix \n"+poissonMatrix)
4  11  3
6  6   5
6  4   2
```

Reading and writing CSV files

Reading and writing a CSV file in Breeze is really a breeze. We just have two functions in `breeze.linalg` package to play with. They are very intuitively named `csvread` and `csvwrite`.

In this recipe, you'll see how to:

1. Read a CSV file into a matrix
2. Save selected columns of a matrix into a new matrix
3. Write the newly created matrix into a CSV file
4. Extract a vector out of the matrix
5. Write the vector into a CSV

How it works...

There are just two functions that we need to remember in order to read and write data from and to CSV files. The signatures of the functions are pretty straightforward too:

```
csvread(file, separator, quote, escape, skipLines)
csvwrite(file, mat, separator, quote, escape, skipLines)
```

Let's look at the parameters by order of importance:

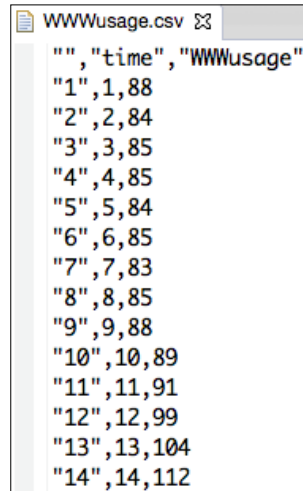
- ▶ `file`: `java.io.File`: Represents the file location.
- ▶ `separator`: Defaults to a comma so as to represent a CSV. Could be overridden when needed.
- ▶ `skipLines`: This is the number of lines to be skipped while reading the file. Generally, if there is a header, we pass a `skipLines=1`.
- ▶ `mat`: While writing, this is the matrix object that is being written.
- ▶ `quote`: This defaults to double quotes. It is a character that implies that the value inside is one single value.
- ▶ `escape`: This defaults to a backspace. It is a character used to escape special characters.

Let's see these in action. For the sake of clarity, I have skipped the `quote` and the `escape` parameter while calling the `csvread` and `csvwrite` functions. For this recipe, we will do three things:

- ▶ Read a CSV file as a matrix
- ▶ Extract a sub-matrix out of the read matrix
- ▶ Write the matrix

Read the CSV as a matrix:

1. Let's use the `csvread` function to read a CSV file into a 100*3 matrix. We'll also skip the header while reading and print 5 rows as a sample:



```
val usageMatrix=csvread(file=new File("WWWusage.csv"),
separator=',', skipLines=1)
//print first five rows
println ("Usage matrix \n"+ usageMatrix(0 to 5,:))
```

Output :

```
1.0  1.0  88.0
2.0  2.0  84.0
3.0  3.0  85.0
4.0  4.0  85.0
5.0  5.0  84.0
6.0  6.0  85.0
```

2. Extract a sub-matrix out of the read matrix:

For the sake of generating a submatrix let's skip the first column and save the second and the third column into a new matrix. Let's call it `firstColumnSkipped`:

```
val firstColumnSkipped= usageMatrix(:, 1 to
usageMatrix.cols-1)

//Sample some data so as to ensure we are fine
```

```
println ("First Column skipped \n"+ firstColumnSkipped(0 to  
5, ::))
```

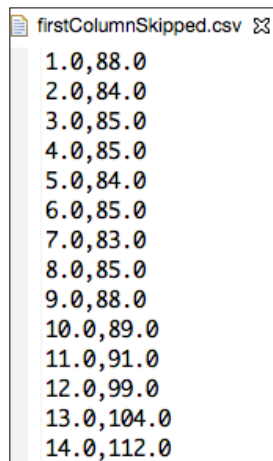
Output :

```
1.0 88.0  
2.0 84.0  
3.0 85.0  
4.0 85.0  
5.0 84.0  
6.0 85.0
```

3. Write the matrix:

As a final step, let's write the `firstColumnSkipped` matrix to a new CSV file named `firstColumnSkipped.csv`:

```
//Write this modified matrix to a file  
csvwrite(file=new File ("firstColumnSkipped.csv"),  
mat=firstColumnSkipped, separator=',')
```



The screenshot shows a text editor window titled "firstColumnSkipped.csv". The content of the file is a CSV list of 14 rows, each with two numerical values separated by a comma. The values are: 1.0,88.0; 2.0,84.0; 3.0,85.0; 4.0,85.0; 5.0,84.0; 6.0,85.0; 7.0,83.0; 8.0,85.0; 9.0,88.0; 10.0,89.0; 11.0,91.0; 12.0,99.0; 13.0,104.0; 14.0,112.0.

2

Getting Started with Apache Spark DataFrames

In this chapter, we will cover the following recipes:

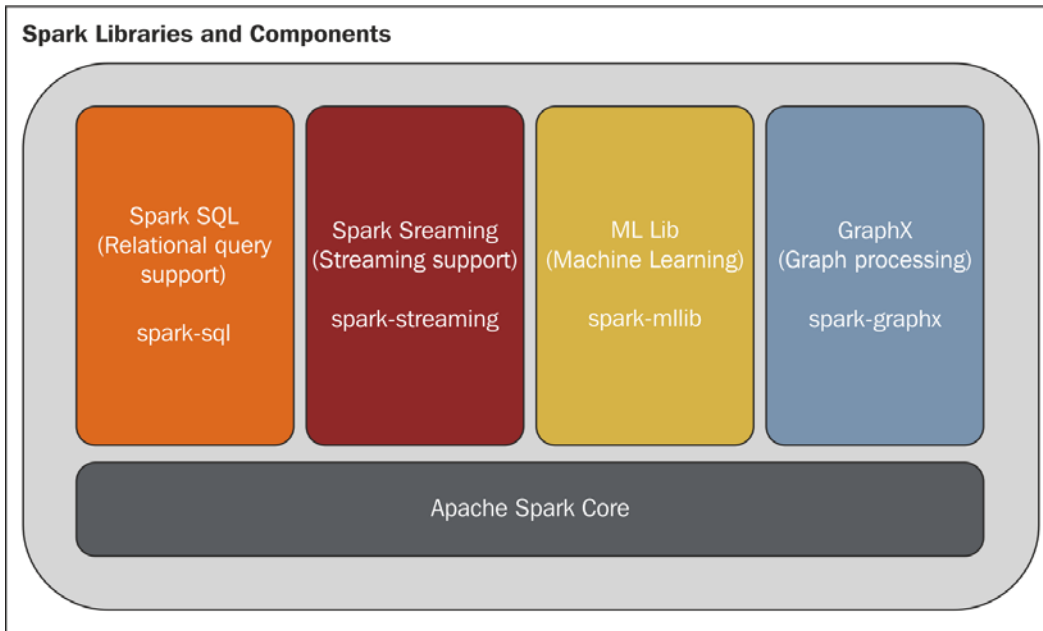
- ▶ Getting Apache Spark
- ▶ Creating a DataFrame from CSV
- ▶ Manipulating DataFrames
- ▶ Creating a DataFrame from Scala case classes

Introduction

Apache Spark is a cluster computing platform that claims to run about 10 times faster than Hadoop. In general terms, we could consider it as a means to run our complex logic over massive amounts of data at a blazingly fast speed. The other good thing about Spark is that the programs that we write are much smaller than the typical MapReduce classes that we write for Hadoop. So, not only do our programs run faster but it also takes less time to write them.

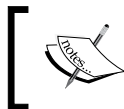
Spark has four major higher level tools built on top of the Spark Core: Spark Streaming, Spark MLlib (machine learning), Spark SQL (an SQL interface for accessing the data), and GraphX (for graph processing). The Spark Core is the heart of Spark. Spark provides higher level abstractions in Scala, Java, and Python for data representation, serialization, scheduling, metrics, and so on.

At the risk of stating the obvious, a DataFrame is one of the primary data structures used in data analysis. They are just like an RDBMS table that organizes all your attributes into columns and all your observations into rows. It's a great way to store and play with heterogeneous data. In this chapter, we'll talk about DataFrames in Spark.



Getting Apache Spark

In this recipe, we'll take a look at how to bring Spark into our project (using **SBT**) and how Spark works internally.



The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter1-spark-csv/build.sbt>.

How to do it...

Let's now throw some Spark dependencies into our `build.sbt` file so that we can start playing with them in subsequent recipes. For now, we'll just focus on three of them: Spark Core, Spark SQL, and Spark MLlib. We'll take a look at a host of other Spark dependencies as we proceed further in this book:

1. Under a brand new folder (which will be your project root), create a new file called `build.sbt`.
2. Next, let's add the Spark libraries to the project dependencies.
3. Note that Spark 1.4.x requires Scala 2.10.x. This becomes the first section of our `build.sbt`:

```
organization := "com.packt"

name := "chapter1-spark-csv"

scalaVersion := "2.10.4"

val sparkVersion="1.4.1"

libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % sparkVersion,
  "org.apache.spark" %% "spark-sql" % sparkVersion,
  "org.apache.spark" %% "spark-mllib" % sparkVersion
)
```

Creating a DataFrame from CSV

In this recipe, we'll look at how to create a new DataFrame from a delimiter-separated values file.



The code for this recipe can be found at <https://github.com/arunma/ScalaDataAnalysisCookbook/blob/master/chapter1-spark-csv/src/main/scala/com/packt/scaladata/spark/csv/DataFrameCSV.scala>.

How to do it...

This recipe involves four steps:

1. Add the `spark-csv` support to our project.
2. Create a Spark Config object that gives information on the environment that we are running Spark in.
3. Create a Spark context that serves as an entry point into Spark. Then, we proceed to create an `SQLContext` from the Spark context.
4. Load the CSV using the `SQLContext`.
5. CSV support isn't first-class in Spark, but it is available through an external library from Databricks. So, let's go ahead and add that to our `build.sbt`.

After adding the `spark-csv` dependency, our complete `build.sbt` looks like this:

```
organization := "com.packt"

name := "chapter1-spark-csv"

scalaVersion := "2.10.4"

val sparkVersion="1.4.1"

libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % sparkVersion,
  "org.apache.spark" %% "spark-sql" % sparkVersion,
  "com.databricks" %% "spark-csv" % "1.0.3"
)
```

6. `SparkConf` holds all of the information required to run this Spark "cluster." For this recipe, we are running locally, and we intend to use only two cores in the machine—`local[2]`. More details about this can be found in the *There's more...* section of this recipe:

```
import org.apache.spark.SparkConf

val conf = new
SparkConf().setAppName("csvDataFrame").setMaster("local[2]")
```



When we say that the master of this run is "local," we mean that we are running Spark on standalone mode. We'll see what "standalone" mode means in the *There's more...* section.

7. Initialize the Spark context with the Spark configuration. This is the core entry point for doing anything with Spark:

```
import org.apache.spark.SparkContext
val sc = new SparkContext(conf)
```

The easiest way to query data in Spark is by using SQL queries:

```
import org.apache.spark.sql.SQLContext
val sqlContext=new SQLContext(sc)
```

8. Now, let's load our pipe-separated file. The `students` is of type `org.apache.spark.sql.DataFrame`:

```
import com.databricks.spark.csv._
val students=sqlContext.csvFile(filePath="StudentData.csv",
useHeader=true, delimiter='|')
```

How it works...

The `csvFile` function of `sqlContext` accepts the full `filePath` of the file to be loaded. If the CSV has a header, then the `useHeader` flag will read the first row as column names. The delimiter flag defaults to a comma, but you can override the character as needed.

Instead of using the `csvFile` function, we could also use the `load` function available in `SQLContext`. The `load` function accepts the format of the file (in our case, it is CSV) and options as `Map`. We can specify the same parameters that we specified earlier using `Map`, like this:

```
val options=Map("header"->"true", "path"->"ModifiedStudent.csv")

val
newStudents=sqlContext.load("com.databricks.spark.csv",options)
```

There's more...

As we saw earlier, we now ran the Spark program in standalone mode. In standalone mode, the **Driver** program (the brain) and the **Worker** nodes all get crammed into a single JVM. In our example, we set `master` to `local[2]`, which means that we intend to run Spark in standalone mode and request it to use only two cores in the machine.

Spark can be run on three different modes:

- ▶ Standalone
- ▶ Standalone cluster, using its in-built cluster manager
- ▶ Using external cluster managers, such as Apache Mesos and YARN

In *Chapter 6, Scaling Up*, we have dedicated explanations and recipes for how to run Spark on inbuilt cluster modes on Mesos and YARN. In a clustered environment, Spark runs a Driver program along with a number of Worker nodes. As the name indicates, the Driver program houses the brain of the program, which is our main program. The Worker nodes have the data and perform various transformations on it.

Manipulating DataFrames

In the previous recipe, we saw how to create a DataFrame. The next natural step, after creating DataFrames, is to play with the data inside them. Other than the numerous functions that help us to do that, we also find other interesting functions that help us sample the data, print the schema of the data, and so on. We'll take a look at them one by one in this recipe.



The code and the sample file for this recipe could be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter1-spark-csv/src/main/scala/com/packt/scaladata/spark/csv/DataFrameCSV.scala>.

How to do it...

Now, let's see how we can manipulate DataFrames using the following subrecipes:

- ▶ Printing the schema of the DataFrame
- ▶ Sampling data in the DataFrame
- ▶ Selecting specific columns in the DataFrame
- ▶ Filtering data by condition
- ▶ Sorting data in the frame
- ▶ Renaming columns
- ▶ Treating the DataFrame as a relational table to execute SQL queries
- ▶ Saving the DataFrame as a file

Printing the schema of the DataFrame

After creating the DataFrame from various sources, we would obviously want to quickly check its schema. The `printSchema` function lets us do just that. It prints our column names and the data types to the default output stream:

1. Let's load a sample DataFrame from the `StudentData.csv` file:

```
//Now, lets load our pipe-separated file
//students is of type org.apache.spark.sql.DataFrame
```

```
val
students=sqlContext.csvFile(filePath="StudentData.csv",
useHeader=true, delimiter='|')
```

- Let's print the schema of this DataFrame:

```
students.printSchema
```

Output

```
root
 |-- id: string (nullable = true)
 |-- studentName: string (nullable = true)
 |-- phone: string (nullable = true)
 |-- email: string (nullable = true)
```

Sampling the data in the DataFrame

The next logical thing that we would like to do is to check whether our data got loaded into the DataFrame correctly. There are a few ways of sampling the data in the newly created DataFrame:

- ▶ Using the `show` method. This is the simplest way. There are two variants of the `show` method, as explained here:
 - One with an integer parameter that specifies the number of rows to be sampled.
 - The second is without the integer parameter. In it, the number of rows defaults to 20.

The distinct quality about the `show` method as compared to the other functions that sample data is that it displays the rows along with the headers and prints the output directly to the default output stream (console):

```
//Sample n records along with headers
students.show (3)
```

```
//Sample 20 records along with headers
students.show ()
```

```
//Output of show(3)
```

```
+--+-----+-----+
|id|studentName|      phone|      email|
```

```
+--+-----+-----+-----+
| 1|      Burke|1-300-746-8446|ullamcorper.velit...|
| 2|      Kamal|1-668-571-5046|pede.Suspendisse...|
| 3|      Olga|1-956-311-1686|Aenean.eget.metus...|
+--+-----+-----+-----+
```

- ▶ Using the `head` method. This method also accepts an integer parameter representing the number of rows to be fetched. The `head` method returns an array of rows. To print these rows, we can pass the `println` method to the `foreach` function of the arrays:

```
//Sample the first 5 records
students.head(5).foreach(println)
```

If you are not a great fan of `head`, you can use the `take` function, which is common across all Scala sequences. The `take` method is just an alias of the `head` method and delegates all its calls to `head`:

```
//Alias of head
students.take(5).foreach(println)
```

```
//Output
```

```
[1,Burke,1-300-746-8446,ullamcorper.velit.in@ametnullaDonec.co.uk]
[2,Kamal,1-668-571-5046,pede.Suspendisse@interdumenim.edu]
[3,Olga,1-956-311-1686,Aenean.eget.metus@dictumcursusNunc.edu]
[4,Belle,1-246-894-6340,vitae.aliquet.nec@neque.co.uk]
[5,Trevor,1-300-527-4967,dapibus.id@acturpisegestas.net]
```

Selecting DataFrame columns

As you have seen, all DataFrame columns have names. The `select` function helps us pick and choose specific columns from a previously existing DataFrame and form a completely new one out of it:

- ▶ Selecting a single column: Let's say that you would like to select only the `email` column from a DataFrame. Since DataFrames are immutable, the selection returns a new DataFrame:

```
val emailDataFrame:DataFrame=students.select("email")
```

Now, we have a new DataFrame called `emailDataFrame`, which has only the e-mail as its contents. Let's sample and check whether that is true:

```
emailDataFrame.show(3)
```

```
//Output
```

```
+-----+
|          email |
+-----+
| ullamcorper.velit... |
| pede.Suspendisse@... |
| Aenean.eget.metus... |
+-----+
```

- ▶ Selecting more than one column: The `select` function actually accepts an arbitrary number of column names, which means that you can easily select more than one column from your source DataFrame:

```
val studentEmailDF=students.select("studentName", "email")
```



The only requirement is that the string parameters that specify must be a valid column name. Otherwise, an `org.apache.spark.sql.AnalysisException` exception is thrown. The `printSchema` function serves as a quick reference for the column names.

Let's sample and check whether we have indeed selected the `studentName` and `email` columns in the new DataFrame:

```
studentEmailDF.show(3)
```

```
Output
```

```
+-----+-----+
| studentName |          email |
+-----+-----+
|      Burke | ullamcorper.velit... |
|      Kamal | pede.Suspendisse@... |
|      Olga | Aenean.eget.metus... |
+-----+-----+
```

Filtering data by condition

Now that we have seen how to select columns from a DataFrame, let's see how to filter the rows of a DataFrame based on conditions. For row-based filtering, we can treat the DataFrame as a normal Scala collection and filter the data based on a condition. In all of these examples, I have added the `show` method at the end for clarity:

1. Filtering based on a column value:

```
//Print the first 5 records that has student id more than 5
students.filter("id > 5").show(7)
```

Output

```
+---+-----+-----+-----+
|id|studentName|      phone|      email|
+---+-----+-----+-----+
| 6|    Laurel|1-691-379-9921|adipiscing@consec...|
| 7|     Sara|1-608-140-1995|Donec.nibh@enimEt...|
| 8|   Kaseem|1-881-586-2689|cursus.et.magna@e...|
| 9|     Lev|1-916-367-5608|Vivamus.nisi@ipsu...|
|10|    Maya|1-271-683-2698|accumsan.convalli...|
|11|     Emi|1-467-270-1337|      est@nunc.com|
|12|    Caleb|1-683-212-0896|Suspendisse@Quisq...|
+---+-----+-----+-----+
```

Notice that even though the `id` field is inferred as a String type, it does the numerical comparison correctly. On the other hand, `students.filter("email > 'c'")` would give back all the e-mail IDs that start with a character greater than 'c'.

2. Filtering based on an empty column value. The following filter selects all students without names:

```
students.filter("studentName = '').show(7)
```

Output

```
+---+-----+-----+-----+
|id|studentName|      phone|      email|
+---+-----+-----+-----+
|21|           |1-598-439-7549|consectetuer.adip...|
|32|           |1-184-895-9602|accumsan.laoreet@...|
```

```
| 45 |          | 1-245-752-0481 | Suspendisse.eleif... |
| 83 |          | 1-858-810-2204 | sociis.natoque@eu... |
| 94 |          | 1-443-410-7878 | Praesent.eu.nulla... |
+---+-----+-----+-----+-----+
```

3. Filtering based on more than one condition. This filter shows all records whose student names are empty or student name field has a NULL string value:

```
students.filter("studentName = '' OR studentName = 'NULL'").show(7)
```

Output

```
+---+-----+-----+-----+-----+
| id | studentName |          phone |          email |
+---+-----+-----+-----+
| 21 |              | 1-598-439-7549 | consecetuer.adip... |
| 32 |              | 1-184-895-9602 | accumsan.laoreet... |
| 33 |          NULL | 1-105-503-0141 | Donec@Inmipede.co.uk |
| 45 |              | 1-245-752-0481 | Suspendisse.eleif... |
| 83 |              | 1-858-810-2204 | sociis.natoque@eu... |
| 94 |              | 1-443-410-7878 | Praesent.eu.nulla... |
+---+-----+-----+-----+-----+
```

We are just limiting the output to seven records using the `show(7)` function.

4. Filtering based on SQL-like conditions.

This filter gets the entries of all students whose names start with the letter 'M'.

```
students.filter("SUBSTR(studentName,0,1) = 'M'").show(7)
```

Output

```
+---+-----+-----+-----+-----+
| id | studentName |          phone |          email |
+---+-----+-----+-----+
| 10 |      Maya | 1-271-683-2698 | accumsan.convalli... |
| 19 |    Malachi | 1-608-637-2772 | Proin.mi.Aliquam... |
| 24 |    Marsden | 1-477-629-7528 | Donec.dignissim.m... |
| 37 |      Maggy | 1-910-887-6777 | facilisi.Sed.nequ... |
| 61 |      Maxine | 1-422-863-3041 | aliquet.molestie... |
| 77 |      Maggy | 1-613-147-4380 | pellentesque@mi.net |
| 97 |    Maxwell | 1-607-205-1273 | metus.In@musAenea... |
+---+-----+-----+-----+-----+
```


Sorting data in the frame

Using the `sort` function, we can order the DataFrame by a particular column:

- Ordering by a column in descending order:

```
students.sort(students("studentName").desc).show(7)
```

Output

```
+---+-----+-----+-----+
|id|studentName|      phone|      email|
+---+-----+-----+-----+
|50|      Yasir|1-282-511-4445|eget.odio.Aliquam...|
|52|      Xena|1-527-990-8606|in.faucibus.orci...|
|86|     Xandra|1-677-708-5691|libero@arcuVestib...|
|43|     Wynter|1-440-544-1851|amet.risus.Donec...|
|31|    Wallace|1-144-220-8159|  lorem.lorem@non.net|
|66|     Vance|1-268-680-0857|pellentesque@netu...|
|41|     Tyrone|1-907-383-5293|non.bibendum.sed...|
| 5|     Trevor|1-300-527-4967|dapibus.id@acturp...|
|65|     Tiger|1-316-930-7880|nec@mollisnoncurs...|
|15|     Tarik|1-398-171-2268|turpis@felisorci.com|
+---+-----+-----+-----+
```

- Ordering by more than one column (ascending):

```
students.sort("studentName", "id").show(10)
```

Output

```
+---+-----+-----+-----+
|id|studentName|      phone|      email|
+---+-----+-----+-----+
|21|           |1-598-439-7549|consectetuer.adip...|
|32|           |1-184-895-9602|accumsan.laoreet...|
|45|           |1-245-752-0481|Suspendisse.eleif...|
|83|           |1-858-810-2204|sociis.natoque@eu...|
|94|           |1-443-410-7878|Praesent.eu.nulla...|
|91|     Abel|1-530-527-7467|  urna@veliteu.edu|
+---+-----+-----+-----+
```

```
| 69 |      Aiko | 1-682-230-7013 | turpis.vitae.puru... |
| 47 |      Alma | 1-747-382-6775 |      nec.enim@non.org |
| 26 |     Amela | 1-526-909-2605 | in@vitaesodales.edu |
| 16 |     Amena | 1-878-250-3129 | lorem.luctus.ut@s... |
+---+-----+-----+-----+-----+
```

Alternatively, the `orderBy` alias of the `sort` function can be used to achieve this. Also, multiple column orders could be specified using the `DataFrame`'s `apply` method:

```
students.sort(students("studentName").desc, students("id").asc).show(10)
```

Renaming columns

If we don't like the column names of the source `DataFrame` and wish to change them to something nice and meaningful, we can do that using the `as` function while selecting the columns.

In this example, we rename the `"studentName"` column to `"name"` and retain the `"email"` column's name as is:

```
val copyOfStudents=students.select(students("studentName").as("name"),
students("email"))
```

```
copyOfStudents.show()
```

Output

```
+-----+-----+
|  name |      email |
+-----+-----+
|  Burke | ullamcorper.velit... |
|  Kamal | pede.Suspendisse@... |
|   Olga | Aenean.eget.metus... |
|  Belle | vitae.aliquet.nec... |
| Trevor | dapibus.id@acturp... |
| Laurel | adipiscing@consec... |
|   Sara | Donec.nibh@enimEt... |
```

Treating the DataFrame as a relational table

The real power of DataFrames lies in the fact that we can treat it like a relational table and use SQL to query. This involves two simple steps:

1. Register the `students` DataFrame as a table with the name "students" (or any other name):

```
students.registerTempTable("students")
```

2. Query it using regular SQL:

```
val dfFilteredBySQL=sqlContext.sql("select * from students where  
studentName!='' order by email desc")
```

```
dfFilteredBySQL.show(7)
```

```
id studentName phone      email  
87 Selma        1-601-330-4409 vulputate.velit@p  
96 Channing    1-984-118-7533 viverra.Donec.tem  
4 Belle        1-246-894-6340 vitae.aliquet.nec  
78 Finn        1-213-781-6969 vestibulum.massa@  
53 Kasper      1-155-575-9346 velit.eget@pedeCu  
63 Dylan       1-417-943-8961 vehicula.aliquet@  
35 Cadman      1-443-642-5919 ut.lacus@adipisci
```



The lifetime of the temporary table is tied to the life of the `SQLContext` that was used to create the DataFrame.

Joining two DataFrames

Now that we have seen how to register a DataFrame as a table, let's see how to perform SQL-like join operations on DataFrames.

Inner join

An inner join is the default join and it just gives those results that are matching on both DataFrames when a condition is given:

```
val students1=sqlContext.csvFile(filePath="StudentPrep1.csv",  
useHeader=true, delimiter='|')
```

```
val students2=sqlContext.csvFile(filePath="StudentPrep2.csv",  
useHeader=true, delimiter='|')
```

```
val studentsJoin=students1.join(students2, students1("id")==students2("id"))
studentsJoin.show(studentsJoin.count.toInt)
```

The output is as follows:

id	studentName	phone	email	id	studentName	phone	email
1	Burke	1-300-746-8446	lullamcorper.velit...	1	BurkeDifferentName	1-300-746-8446	lullamcorper.velit...
2	Kamal	1-668-571-5046	pede.Suspendisse@...	2	KamalDifferentName	1-668-571-5046	pede.Suspendisse@...
3	Olga	1-956-311-1686	Aenean.eget.metus...	3	Olga	1-956-311-1686	Aenean.eget.metus...
4	Belle	1-246-894-6340	vitae.aliquet.nec...	4	BelleDifferentName	1-246-894-6340	vitae.aliquet.nec...
5	Trevor	1-300-527-4967	dapibus.id@acturp...	5	Trevor	1-300-527-4967	dapibusDifferentE...
6	Laurel	1-691-379-9921	adipiscing@consec...	6	LaurelInvalidPhone	00000000	adipiscing@consec...
7	Sara	1-608-140-1995	Donec.nibh@enimEt...	7	Sara	1-608-140-1995	Donec.nibh@enimEt...
8	Kaseem	1-881-586-2689	cursus.et.magna@e...	8	Kaseem	1-881-586-2689	cursus.et.magna@e...
9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...	9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...
10	Maya	1-271-683-2698	accumsan.convalli...	10	Maya	1-271-683-2698	accumsan.convalli...

Right outer join

A right outer join shows all the additional unmatched rows that are available in the right-hand-side DataFrame. We can see from the following output that the entry with ID 999 from the right-hand-side DataFrame is now shown:

```
val studentsRightOuterJoin=students1.join(students2, students1("id")==students2("id"), "right_outer")
studentsRightOuterJoin.show(studentsRightOuterJoin.count.toInt)
```

id	studentName	phone	email	id	studentName	phone	email
1	Burke	1-300-746-8446	lullamcorper.velit...	1	BurkeDifferentName	1-300-746-8446	lullamcorper.velit...
2	Kamal	1-668-571-5046	pede.Suspendisse@...	2	KamalDifferentName	1-668-571-5046	pede.Suspendisse@...
3	Olga	1-956-311-1686	Aenean.eget.metus...	3	Olga	1-956-311-1686	Aenean.eget.metus...
4	Belle	1-246-894-6340	vitae.aliquet.nec...	4	BelleDifferentName	1-246-894-6340	vitae.aliquet.nec...
5	Trevor	1-300-527-4967	dapibus.id@acturp...	5	Trevor	1-300-527-4967	dapibusDifferentE...
6	Laurel	1-691-379-9921	adipiscing@consec...	6	LaurelInvalidPhone	00000000	adipiscing@consec...
7	Sara	1-608-140-1995	Donec.nibh@enimEt...	7	Sara	1-608-140-1995	Donec.nibh@enimEt...
8	Kaseem	1-881-586-2689	cursus.et.magna@e...	8	Kaseem	1-881-586-2689	cursus.et.magna@e...
9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...	9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...
10	Maya	1-271-683-2698	accumsan.convalli...	10	Maya	1-271-683-2698	accumsan.convalli...
null	null	null	null	999	LevUniqueToSecondRDD	1-916-367-5608	Vivamus.nisi@ipsu...

Left outer join

Similar to a right outer join, a left outer join returns not only the matching rows, but also the additional unmatched rows of the left-hand-side DataFrame:

```
val studentsLeftOuterJoin=students1.join(students2, students1("id")==students2("id"), "left_outer")
studentsLeftOuterJoin.show(studentsLeftOuterJoin.count.toInt)
```

Saving the DataFrame as a file

As the next step, let's save a DataFrame in a file store. The `load` function, which we used in an earlier recipe, has a similar-looking counterpart called `save`.

This involves two steps:

1. Create a map containing the various options that you would like the `save` method to use. In this case, we specify the filename and ask it to have a header:

```
val options=Map("header"->"true", "path"->"ModifiedStudent.csv")
```

To keep it interesting, let's choose column names from the source DataFrame. In this example, we pick the `studentName` and `email` columns and change the `studentName` column's name to just `name`.

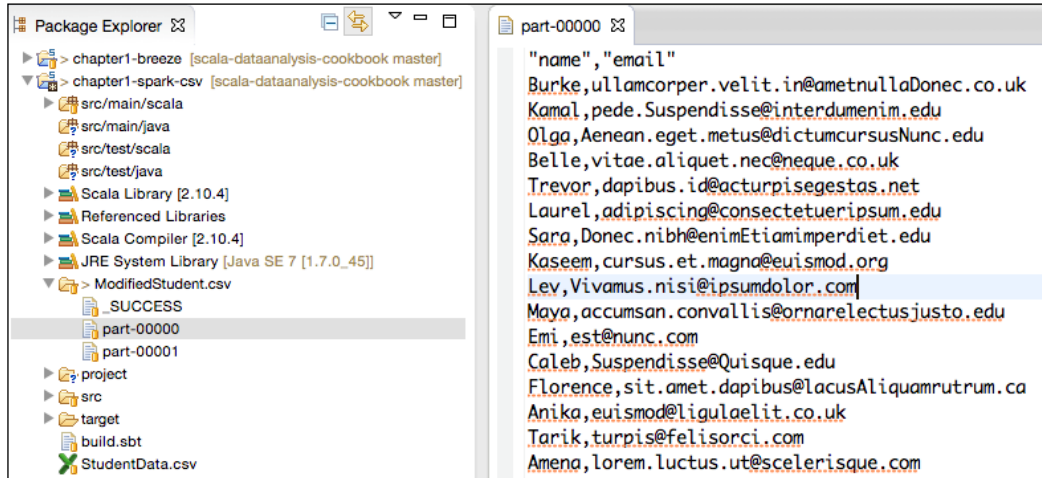
```
val copyOfStudents=students.select(students("studentName").as("name"), students("email"))
```

2. Finally, save this new DataFrame with the headers in a file named `ModifiedStudent.csv`:

```
copyOfStudents.save("com.databricks.spark.csv", SaveMode.Overwrite, options)
```

The second argument is a little interesting. We can choose `Overwrite` (as we did here), `Append`, `Ignore`, or `ErrorIfExists`. `Overwrite`—as the name implies—overwrites the file if it already exists, `Ignore` ignores writing if the file exists, `ErrorIfExists` complains for pre-existence of the file, and `Append` continues writing from the last edit location. Throwing an error is the default behavior.

The output of the `save` method looks like this:



Creating a DataFrame from Scala case classes

In this recipe, we'll see how to create a new DataFrame from Scala case classes.



The code for this recipe can be found at <https://github.com/arunma/ScalaDataAnalysisCookbook/blob/master/chapter1-spark-csv/src/main/scala/com/packt/scaladata/spark/csv/DataFrameFromCaseClasses.scala>.

How to do it...

1. We create a new entity called `Employee` with the `id` and `name` fields, like this:

```
case class Employee(id:Int, name:String)
```

Similar to the previous recipe, we create `SparkContext` and `SQLContext`.

```
val conf = new SparkConf().setAppName("colRowDataFrame").
setMaster("local[2]")
```

```
//Initialize Spark context with Spark configuration. This is the
core entry point to do anything with Spark
```

```
val sc = new SparkContext(conf)
```

```
//The easiest way to query data in Spark is to use SQL queries.  
val sqlContext=new SQLContext(sc)
```

2. We can source these employee objects from a variety of sources, such as an RDBMS data source, but for the sake of this example, we construct a list of employees, as follows:

```
val listOfEmployees =List(Employee(1,"Arun"), Employee(2,  
"Jason"), Employee (3, "Abhi"))
```

3. The next step is to pass the `listOfEmployees` to the `createDataFrame` function of `SQLContext`. That's it! We now have a `DataFrame`. When we try to print the schema using the `printSchema` method of the `DataFrame`, we will see that the `DataFrame` has two columns, with names `id` and `name`, as defined in the `case class`:

```
//Pass in the Employees into the `createDataFrame` function.  
val empFrame=sqlContext.createDataFrame(listOfEmployees)  
empFrame.printSchema
```

Output:

```
root  
|-- id: integer (nullable = false)  
|-- name: string (nullable = true)
```

As you might have guessed, the schema of the `DataFrame` is inferred from the `case class` using reflection.

4. We can get a different name for the `DataFrame`—other than the names specified in the `case class`—using the `withColumnRenamed` function, as shown here:

```
val empFrameWithRenamedColumns=sqlContext.createDataFrame(listOf  
Employees).withColumnRenamed("id", "empId")  
  
empFrameWithRenamedColumns.printSchema
```

Output:

```
root  
|-- empId: integer (nullable = false)  
|-- name: string (nullable = true)
```

5. Let's query the DataFrame using Spark's first-class SQL support. Before that, however, we'll have to register the DataFrame as a table. The `registerTempTable`, as we saw in the previous recipe, helps us achieve this. With the following command, we will have registered the DataFrame as a table by name "employeeTable"

```
"employeeTable"
```

```
empFrameWithRenamedColumns.registerTempTable("employeeTable")
```

6. Now, for the actual query. Let's arrange the DataFrame in descending order of names:

```
val sortedByNameEmployees=sqlContext.sql("select * from
employeeTable order by name desc")
```

```
sortedByNameEmployees.show()
```

Output:

```
+-----+-----+
|empId| name|
+-----+-----+
|    2| Jason|
|    1|  Arun|
|    3|  Abhi|
+-----+-----+
```

How it works...

The `createDataFrame` function accepts a sequence of `scala.Product`. Scala case classes extend from `Product`, and therefore it fits in the budget. That said, we can actually use a sequence of tuples to create a DataFrame, since tuples implement `Product` too:

```
val mobiles=sqlContext.createDataFrame(Seq((1,"Android"), (2, "iPhone")))
mobiles.printSchema
mobiles.show()
```

Output:

```
//Schema
root
|-- _1: integer (nullable = false)
|-- _2: string (nullable = true)
```



```
//Data
+---+-----+
|_1|      _2|
+---+-----+
| 1| Android|
| 2| iPhone|
+---+-----+
```

Of course, you can rename the column using `withColumnRenamed`.

3

Loading and Preparing Data – DataFrame

In this chapter, we will cover the following recipes:

- ▶ Loading more than 22 features into classes
- ▶ Loading JSON into DataFrames
- ▶ Storing data as Parquet files
- ▶ Using the Avro data model in Parquet
- ▶ Loading from RDBMS
- ▶ Preparing data in DataFrames

Introduction

In previous chapters, we saw how to import data from a CSV file to Breeze and Spark DataFrames. However, almost all the time, the source data that is to be analyzed is available in a variety of source formats. Spark, with its DataFrame API, provides a uniform API that can be used to represent any source (or multiple sources). In this chapter, we'll focus on the various input formats that we can load from in Spark. Towards the end of this chapter, we'll also briefly see some data preparation recipes.

Loading more than 22 features into classes

Case classes have an inherent limitation. They can hold only 22 attributes—Catch 22, if you will. While a reasonable percentage of datasets would fit in that budget, in many cases, the limitation of 22 features in a dataset is a huge turnoff. In this recipe, we'll take a sample `Student` dataset (<http://archive.ics.uci.edu/ml/datasets/Student+Performance>), which has 33 features, and we'll see how we can work around this.



The 22-field limit is resolved in Scala version 2.11. However, Spark 1.4 uses Scala 2.10.

How to do it...

Case classes in Scala cannot go beyond encapsulating 22 fields because the companion classes that are generated (during compilation) for these case classes cannot find the matching `FunctionN` and `TupleN` classes. Let's take the example of the `Employee` case class that we created in *Chapter 2, Getting Started with Apache Spark DataFrames*:

```
case class Employee(id:Int, name:String)
```

When we look at its decompiled companion object, we notice that for the two constructor parameters of the case class, the companion class uses `Tuple2` and `AbstractFunction2` in its `unapply` method, the method that gets invoked when we pattern-match against a case class. The problem we face is that the Scala library has objects only until `Tuple22` and `Function22` (probably because outside the data analysis world, having an entity object with 10 fields is not a great idea). However, there is a simple yet powerful workaround, and we will be seeing it in this recipe.

```
Employee$class
package com.packt.scaladata.spark.csv;

import scala.None.;

public final class Employee$ extends AbstractFunction2<Object, String, Employee>
implements Serializable
{
    public static final MODULES;


    static
    {
        new ();
    }


    public final String toString()
    {
        return "Employee";
    }
    public Employee apply(int id, String name) { return new Employee(id, name); }
    public Option<Tuple2<Object, String>> unapply(Employee x$0) { return x$0 == null ? None..MODULES : new Some(new Tuple2(BoxesR
    private Object readResolve() { return MODULES; }
    private Employee$() { MODULES = this; }
}
```

We saw in *Chapter 2, Getting Started with Apache Spark DataFrames* (in the *Creating a DataFrame from CSV* recipe), that the requirement for creating a `DataFrame` using `SQLContext.createDataFrame` from a collection of classes is that the class must extend `scala.Product`. So, what we intend to do is write our own class that extends from `scala.Product`.

This recipe consists of four steps:

1. Creating `SQLContext` from `SparkContext` and `Config`.
2. Creating a `Student` class that extends `Product` and overrides the necessary functions.
3. Constructing an RDD of the `Student` classes from the sample dataset (`student-mat.csv`).
4. Creating a `DataFrame` from the RDD, followed by printing the schema and sampling the data.

 Refer to the *How it works...* section of this recipe for a basic introduction to RDD.

 The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/tree/master/chapter3-data-loading>.


Let's now cover these steps in detail:

1. **Creating `SQLContext`:** As with our recipes from the previous chapter, we construct `SparkContext` from `SparkConfig` and then create an `SQLContext` from `SparkContext`:

```
val conf=new
SparkConf().setAppName("DataWith33Atts").setMaster("local[2]")
val sc=new SparkContext(conf)
val sqlContext=new SQLContext(sc)
```

2. **Creating the `Student` class:** Our next step is to create a simple Scala class that declares its constructor parameters, and make it extend `Product`.

Making a class extend `Product` requires us to override two functions from `scala.Product` and one function from `scala.Equals` (which `scala.Product`, in turn, extends from). The implementation of each of these functions is pretty straightforward.

 Refer to the API docs of `Product` (<http://www.scala-lang.org/api/2.10.4/index.html#scala.Product>) and `Equals` (<http://www.scala-lang.org/api/2.10.4/index.html#scala.Equals>) for more details.

Firstly, let's make our Student class declare its fields and extend Product:

```
class Student (school:String,  
              sex:String,  
              age:Int,  
              address:String,  
              famsize:String,  
              pstatus:String,  
              medu:Int,  
              fedu:Int,  
              mjob:String,  
              fjob:String,  
              reason:String,  
              guardian:String,  
              traveltime:Int,  
              studytime:Int,  
              failures:Int,  
              schoolsup:String,  
              famsup:String,  
              paid:String,  
              activities:String,  
              nursery:String,  
              higher:String,  
              internet:String,  
              romantic:String,  
              famrel:Int,  
              freetime:Int,  
              goout:Int,  
              dalc:Int,  
              walc:Int,  
              health:Int,  
              absences:Int,  
              g1:Int,  
              g2:Int,  
              g3:Int) extends Product{
```

Next, let's implement these three functions after briefly looking at what they are expected to do:

- `productArity() : Int`: This returns the size of the attributes. In our case, it's 33. So, our implementation looks like this:

```
override def productArity: Int = 33
```

- `productElement (n: Int) : Any`: Given an index, this returns the attribute. As protection, we also have a default case, which throws an `IndexOutOfBoundsException` exception:

```
@throws(classOf [IndexOutOfBoundsException])
override def productElement(n: Int): Any = n match {
  case 0 => school
  case 1 => sex
  case 2 => age
  case 3 => address
  case 4 => famsize
  case 5 => pstatus
  case 6 => medu
  case 7 => fedu
  case 8 => mjob
  case 9 => fjob
  case 10 => reason
  case 11 => guardian
  case 12 => traveltime
  case 13 => studytime
  case 14 => failures
  case 15 => schoolsup
  case 16 => famsup
  case 17 => paid
  case 18 => activities
  case 19 => nursery
  case 20 => higher
  case 21 => internet
  case 22 => romantic
  case 23 => famrel
  case 24 => freetime
  case 25 => goout
  case 26 => dalc
  case 27 => walc
  case 28 => health
  case 29 => absences
  case 30 => g1
  case 31 => g2
  case 32 => g3
  case _ => throw new
IndexOutOfBoundsException(n.toString())
}
```

- `canEqual (that: Any): Boolean`: This is the last of the three functions, and it serves as a boundary condition when an equality check is being done against this class:

```
override def canEqual(that: Any): Boolean =
  that.isInstanceOf[Student]
```

3. Constructing an RDD of students from the `student-mat.csv` file: Now that we have our `Student` class ready, let's convert the "student-mat.csv" input file into a `DataFrame`:

```
val rddOfStudents=convertCSVToStudents("student-mat.csv", sc)

def convertCSVToStudents(filePath: String, sc: SparkContext):
RDD[Student] = {
  val rddOfStudents: RDD[Student] = sc.textFile(filePath).
flatMap(eachLine => Student(eachLine))
  rddOfStudents
}
```

As you can see, we have an `apply` method for `Student` that accepts a `String` and returns an `Option[Student]`. We use `flatMap` to filter out `None` thereby resulting in `RDD[Student]`.

Let's look at the `Student` companion object's `apply` function. It's a very simple function that takes a `String`, splits it based on semicolons into an array, and then passes the parameters to the `Student`'s constructor. The method returns `None` if there is an error:

```
object Student {

  def apply(str: String): Option[Student] = {
    val paramArray = str.split(";").map(param =>
param.replaceAll("\"", "")) //Few values have extra double
quotes around it
    Try(
      new Student(paramArray(0),
        paramArray(1),
        paramArray(2).toInt,
        paramArray(3),
        paramArray(4),
        paramArray(5),
        paramArray(6).toInt,
        paramArray(7).toInt,
        paramArray(8),
```

```

paramArray(9),
paramArray(10),
paramArray(11),
paramArray(12).toInt,
paramArray(13).toInt,
paramArray(14).toInt,
paramArray(15),
paramArray(16),
paramArray(17),
paramArray(18),
paramArray(19),
paramArray(20),
paramArray(21),
paramArray(22),
paramArray(23).toInt,
paramArray(24).toInt,
paramArray(25).toInt,
paramArray(26).toInt,
paramArray(27).toInt,
paramArray(28).toInt,
paramArray(29).toInt,
paramArray(30).toInt,
paramArray(31).toInt,
paramArray(32).toInt)) match {
case Success(student) => Some(student)
case Failure(throwable) => {
  println(throwable.getMessage())
  None
}
}
}

```

4. Creating a DataFrame, printing the schema, and sampling: Finally, we create a DataFrame from `RDD[Student]`. Converting an `RDD[T]` to a DataFrame of the same type is just a matter of calling the `toDF()` function. You are required to import `sqlContext.implicitly._`. Optionally, you can use the `createDataFrame` method of `sqlContext` too.



The `toDF()` function is overloaded so as to accept custom column names while converting to a DataFrame.

We then print the schema using the DataFrame's `printSchema()` method and sample data for confirmation using the `show()` method:

```
import sqlContext.implicits._

//Create DataFrame
val studentDataFrame = rddOfStudents.toDF()
  studentDataFrame.printSchema()
  studentDataFrame.show()
```

The following is the output of the preceding code:

```
root
|-- school: string (nullable = true)
|-- sex: string (nullable = true)
|-- age: integer (nullable = false)
|-- address: string (nullable = true)
|-- famsize: string (nullable = true)
|-- pstatus: string (nullable = true)
|-- medu: integer (nullable = false)
|-- fedu: integer (nullable = false)
|-- mjob: string (nullable = true)
|-- fjob: string (nullable = true)
|-- reason: string (nullable = true)
|-- guardian: string (nullable = true)
|-- traveltime: integer (nullable = false)
|-- studytime: integer (nullable = false)
|-- failures: integer (nullable = false)
|-- schoolsup: string (nullable = true)
|-- famsup: string (nullable = true)
|-- paid: string (nullable = true)
|-- activities: string (nullable = true)
|-- nursery: string (nullable = true)
|-- higher: string (nullable = true)
|-- internet: string (nullable = true)
|-- romantic: string (nullable = true)
|-- famrel: integer (nullable = false)
|-- freetime: integer (nullable = false)
|-- goout: integer (nullable = false)
|-- dalc: integer (nullable = false)
|-- walc: integer (nullable = false)
|-- health: integer (nullable = false)
|-- absences: integer (nullable = false)
```

```
|-- g1: integer (nullable = false)
|-- g2: integer (nullable = false)
|-- g3: integer (nullable = false)
```

```
[info] root
[info] |-- school: string (nullable = true)
[info] |-- sex: string (nullable = true)
[info] |-- age: integer (nullable = false)
[info] |-- address: string (nullable = true)
[info] |-- famsize: string (nullable = true)
[info] |-- pstatus: string (nullable = true)
[info] |-- medu: integer (nullable = false)
[info] |-- fedu: integer (nullable = false)
[info] |-- mjob: string (nullable = true)
[info] |-- fjob: string (nullable = true)
[info] |-- reason: string (nullable = true)
[info] |-- guardian: string (nullable = true)
[info] |-- travelttime: integer (nullable = false)
[info] |-- studytime: integer (nullable = false)
[info] |-- failures: integer (nullable = false)
[info] |-- schoolsup: string (nullable = true)
[info] |-- famsup: string (nullable = true)
[info] |-- paid: string (nullable = true)
[info] |-- activities: string (nullable = true)
[info] |-- nursery: string (nullable = true)
[info] |-- higher: string (nullable = true)
[info] |-- internet: string (nullable = true)
[info] |-- romantic: string (nullable = true)
[info] |-- famrel: integer (nullable = false)
[info] |-- freetime: integer (nullable = false)
[info] |-- goout: integer (nullable = false)
[info] |-- dalc: integer (nullable = false)
[info] |-- walc: integer (nullable = false)
[info] |-- health: integer (nullable = false)
[info] |-- absences: integer (nullable = false)
[info] |-- g1: integer (nullable = false)
[info] |-- g2: integer (nullable = false)
[info] |-- g3: integer (nullable = false)
```

How it works...

The foundation of Spark is the **Resilient Distributed Dataset (RDD)**. From a programmer's perspective, the composability of RDDs just like a regular Scala collection is a huge advantage. An RDD wraps three vital (and two subsidiary) pieces of information that help in the reconstruction of data. This enables fault tolerance. The other major advantage is that while RDDs can be composed into hugely complex graphs using RDD operations, the entire flow of data itself is not very difficult to reason with.

Other than optional optimization attributes (such as data location), at its core, RDD just wraps three vital pieces of information:

- ▶ The dependent/parent RDD (empty if not available)
- ▶ The number of partitions
- ▶ The function that needs to be applied to each element of the RDD

In simple words, RDDs are just collections of data elements that can exist in the memory or on the disk. These data elements must be serializable in order to have the capability to be moved across multiple machines (or be serialized on the disk). The number of partitions or blocks of data is primarily determined by the source of the input data (say, if the data is in HDFS, then each block would translate to a single partition), but there are also other ways of playing around with the number of partitions.

So, the number of partitions could be any of these:

- ▶ Dictated by the input data itself, for example, the number of blocks in the case of reading files from HDFS
- ▶ The number set by the `spark.default.parallelism` parameter (set while starting the cluster)
- ▶ The number set by calling `repartition` or `coalesce` on the RDD itself

Note that currently, for all our recipes, we are running our Spark application in the self-contained single JVM mode. While the programs work just fine, we are not yet exploiting the distributed nature of the RDDs. In *Chapter 6, Scaling Up*, we'll explore how to bundle and deploy our Spark application on a variety of cluster managers: YARN, Spark standalone clusters, and Mesos.

There's more...

In the previous chapter, we created a `DataFrame` from a `List of Employee` case classes:

```
val listOfEmployees =List(Employee(1,"Arun"), Employee(2, "Jason"),
Employee (3, "Abhi"))

val empFrame=sqlContext.createDataFrame(listOfEmployees)
```

However, in this recipe, we loaded a file, converted them to `RDD[String]`, transformed them into case classes, and finally converted them into a `DataFrame`.

There are subtle, yet powerful, differences in these approaches. In the first approach (converting a `List` of case classes into a `DataFrame`), we have the entire collection in the memory of the driver (we'll look at drivers and workers in *Chapter 6, Scaling Up*). Except for playing around with Spark, for all practical purposes, we don't have our dataset as a collection of case classes. We generally have it as a text file or read from a database. Also, requiring to hold the entire collection in a single machine before converting it into a distributed dataset (RDD) will unfold itself as a memory issue.

In this recipe, we loaded an HDFS distributed file as an `RDD[String]` that is distributed across a cluster of worker nodes, and then serialized each `String` into a case class, making the `RDD[String]` into an `RDD[Student]`. So, each worker node that holds some partitions of the dataset handles the computation around transforming `RDD[String]` to the case class, while making the resulting dataset conform to a fixed schema enforced by the case class itself. Since the computation and the data itself are distributed, we don't need to worry about a single machine requiring a lot of memory to store the entire dataset.

Loading JSON into DataFrames

JSON has become the most common text-based data representation format these days. In this recipe, we'll see how to load data represented as JSON into our `DataFrame`. To make it more interesting, let's have our JSON in HDFS instead of our local filesystem.

The **Hadoop Distributed File System (HDFS)** is a highly distributed filesystem that is both scalable and fault tolerant. It is a critical part of the Hadoop ecosystem and is inspired by the Google File System paper (<http://research.google.com/archive/gfs.html>). More details about the architecture and communication protocols on HDFS can be found at http://hadoop.apache.org/docs/r1.2.1/hdfs_design.html.

How to do it...

In this recipe, we'll see three subrecipes:

- ▶ How to create a schema-inferenced `DataFrame` from JSON using `sqlContext.jsonFile`
- ▶ Alternatively, if we prefer to preprocess the input file before parsing it into JSON, we'll parse the input file as text and convert it into JSON using `sqlContext.jsonRDD`
- ▶ Finally, we'll take a look at declaring an explicit schema and using it to create a `DataFrame`

Reading a JSON file using `SQLContext.jsonFile`

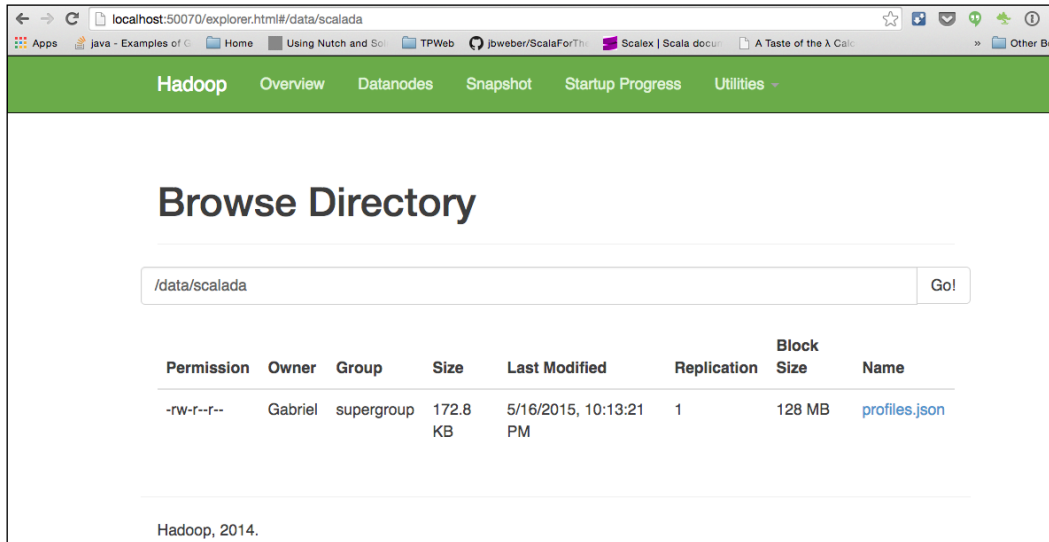
This recipe consists of three steps:

1. Storing our `json` (`profiles.json`) in HDFS: A copy of the data file is added to our project repository, and it can be downloaded from <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter3-data-loading/profiles.json>:

```
hadoop fs -mkdir -p /data/scalada
hadoop fs -put profiles.json /data/scalada/profiles.json
hadoop fs -ls /data/scalada
-rw-r--r--  1 Gabriel supergroup    176948 2015-05-16 22:13 /
data/scalada/profiles.json
```

Loading and Preparing Data – DataFrame

The following screenshot shows the HDFS file explorer available at `http://localhost:50070`, which confirms that our upload is successful:



2. Creating contexts: We do the regular stuff—create `SparkConfig`, `SparkContext`, and then `SQLContext`:

```
val conf = new
SparkConf().setAppName("DataFromJSON").setMaster("local[2]")
val sc = new SparkContext(conf)
val sqlContext = new SQLContext(sc)
```

3. Creating a DataFrame from JSON: In this step, we use the `jsonFile` function of `SQLContext` to create a DataFrame. This is very similar to the `sqlContext.csvFile` function that we used in *Chapter 2, Getting Started with Apache Spark DataFrames*. There's just one thing that we need to watch out here; our `.json` should be formatted as one line per record. It is unusual to store JSON as one line per record considering that it is a structured format, but the `jsonFile` function treats every single line as one record, failing to do which it would throw a `scala.MatchError` error while parsing:

```
val
dFrame=sqlContext.jsonFile("hdfs://localhost:9000/data/scalada/
profiles.json")
```

That's it! We are done! Let's just print the schema and sample the data:

```
dFrame.printSchema()
dFrame.show()
```

The following screenshot shows the schema that is inferred from the JSON file. Note that now the age is resolved as long and tags are resolved as an array of string, as you can see here:

```
[info] root
[info] |-- _id: string (nullable = true)
[info] |-- about: string (nullable = true)
[info] |-- address: string (nullable = true)
[info] |-- age: long (nullable = true)
[info] |-- company: string (nullable = true)
[info] |-- email: string (nullable = true)
[info] |-- eyeColor: string (nullable = true)
[info] |-- favoriteFruit: string (nullable = true)
[info] |-- gender: string (nullable = true)
[info] |-- name: string (nullable = true)
[info] |-- phone: string (nullable = true)
[info] |-- registered: string (nullable = true)
[info] |-- tags: array (nullable = true)
[info] |   |-- element: string (containsNull = true)
```

The next screenshot shows you a sample of the dataset:

_id	about	address	age	company	email	eyeColor	favoriteFruit	gender
155578ccb0cc5b350d...	Eu excepteur esse...	1694 Oriental Cour...	301	ENDIPIN	tracynguyen@endip...	brown	apple	female
155578ccb6975c4e2a...	Proident exercita...	1267 Amber Street...	231	WARETEL	leannagarrett@war...	brown	strawberry	female
155578ccb33399a615...	Aute proident Lor...	1243 Bridgewater S...	241	IMPERIUM	blairwhite@imperi...	brown	banana	male
155578ccb0f1d5ab09...	Officia cillum nu...	1647 Loring Avenue...	241	BEADZZA	andrearay@beadzza...	blue	apple	female
155578ccb591a45d4e...	Sit fugiat mollit...	1721 Bijou Avenue...	271	AUSTECH	penningtongilbert...	green	apple	male
155578ccb9f0cd20c4...	Minim do eiusmod...	1694 Llama Court...	211	PYRAMIA	shelleyburns@pyra...	green	banana	female
155578ccb8d0acc28...	Qui proident ulla...	1498 Perry Terrace...	401	EDECINE	nicolefigueroa@ed...	green	apple	female
155578ccb682cca21...	Labore exercitati...	1243 Stillwell Ave...	321	SINGAVERA	galealvarado@sing...	blue	banana	female
155578ccb0d9025ddd...	Velit cillum Lore...	1649 Beard Street...	361	FURNITECH	melindaparker@fur...	blue	strawberry	female
155578ccb5be70dedd...	Laborum tempor mi...	1972 Marconi Place...	361	DIGIAL	lbyerscarson@digia...	blue	apple	male
155578ccb5a1050a5...	Duis fugiat Lorem...	1483 Hanson Place...	311	ASSURITY	kristiemckinney@a...	green	banana	female
155578ccb07fa02369...	Consequat fugiat...	1540 Woodpoint Roa...	401	MICROLUXE	salazarburks@micr...	brown	strawberry	male
155578ccb809e55bf0...	Lorem culpa Lorem...	1442 Ainslie Stree...	321	VIOCULAR	hopkinspatterson@...	green	apple	male
155578ccb204ff8ee6...	Qui ad cillum mag...	1444 Argyle Road...	231	IMKAN	maysrosario@imkan...	green	apple	male
155578ccb4b062fc61...	Duis ex velit dui...	1571 Sunnyside Ave...	381	HELIXO	atkinshancock@hel...	blue	strawberry	male
155578ccb5ff361a9...	Et magna laboris...	1385 Meeker Avenue...	401	SLOFAST	edwinarobertson@s...	blue	strawberry	female
155578ccb386940ac3...	Labore sit mollit...	1936 Cheever Place...	371	FLEETMIX	elsienioel@fleetm...	blue	apple	female
155578ccbfc41ff7fe...	Consequat eiusmod...	1406 Lake Place, M...	361	EVENTAGE	mirandamarsh@even...	green	apple	female
155578ccbfa6b6c300...	Duis fugiat conse...	1364 Metropolitan...	311	BALOOBA	sharronmcconnell@...	brown	apple	female
155578ccbdd6650d81...	Consequat et magn...	1113 Applegate Cou...	291	EURON	mcdowellwelch@eur...	blue	strawberry	male

Reading a text file and converting it to JSON RDD

In the previous section, we saw how we can directly import a `textFile` containing JSON records as a `DataFrame` using `sqlContext.jsonFile`. Now, we'll see an alternate approach, wherein we construct an `RDD[String]` from the same `profiles.json` file and then convert them into a `DataFrame`. This has a distinct advantage from the previous approach—we can have more control over the schema instead of relying on the one that is inferred:

```
val strRDD=sc.textFile("hdfs://localhost:9000/data/scalada/profiles.json")
val jsonDf=sqlContext.jsonRDD(strRDD)
jsonDf.printSchema()
```

The following is the output of the preceding command:

```
[info] root
[info] |-- _id: string (nullable = true)
[info] |-- about: string (nullable = true)
[info] |-- address: string (nullable = true)
[info] |-- age: long (nullable = true)
[info] |-- company: string (nullable = true)
[info] |-- email: string (nullable = true)
[info] |-- eyeColor: string (nullable = true)
[info] |-- favoriteFruit: string (nullable = true)
[info] |-- gender: string (nullable = true)
[info] |-- name: string (nullable = true)
[info] |-- phone: string (nullable = true)
[info] |-- registered: string (nullable = true)
[info] |-- tags: array (nullable = true)
[info] |   |-- element: string (containsNull = true)
```

Explicitly specifying your schema

Using `jsonRDD` and letting it resolve the schema by itself is clean and simple. However, it gives less control over the types; for example, the `age` field must be `Integer` and not `Long`. Similarly, the `registered` column is inferred as a `String` while it is actually a `TimeStamp`. In order to achieve this, let's go ahead and declare our own schema. The way we do this is by constructing a `StructType` and `StructField`:

```
val profilesSchema = StructType(
  Seq(
    StructField("_id",StringType, true),
    StructField("about",StringType, true),
    StructField("address",StringType, true),
    StructField("age",IntegerType, true),
```

```

    StructField("company",StringType, true),
    StructField("email",StringType, true),
    StructField("eyeColor",StringType, true),
    StructField("favoriteFruit",StringType, true),
    StructField("gender",StringType, true),
    StructField("name",StringType, true),
    StructField("phone",StringType, true),
    StructField("registered",TimestampType, true),
    StructField("tags",ArrayType(StringType), true)
  )
)

val jsonDfWithSchema=sqlContext.jsonRDD(strRDD, profilesSchema)

jsonDfWithSchema.printSchema() //Has timestamp
jsonDfWithSchema.show()

```



Another advantage of specifying our own schema is that all the columns need not be specified in the `StructType`. We just need to specify the columns that we are interested in, and only those columns will be available in the target `DataFrame`. Also, any column that is declared in the schema but is not available in the dataset will be filled in with null values.

The following is the output.

We can see that the `registered` feature is considered to have a `timestamp` data type and `age` as `integer`:

```

[info] root
[info] |-- id: string (nullable = true)
[info] |-- about: string (nullable = true)
[info] |-- address: string (nullable = true)
[info] |-- age: integer (nullable = true)
[info] |-- company: string (nullable = true)
[info] |-- email: string (nullable = true)
[info] |-- eyeColor: string (nullable = true)
[info] |-- favoriteFruit: string (nullable = true)
[info] |-- gender: string (nullable = true)
[info] |-- name: string (nullable = true)
[info] |-- phone: string (nullable = true)
[info] |-- registered: timestamp (nullable = true)
[info] |-- tags: array (nullable = true)
[info] |   |-- element: string (containsNull = true)

```


Finally, just for kicks, let's fire a filter query based on the timestamp. This involves three steps:

1. Register the schema as a temporary table for querying, as has been done several times in previous recipes. The following line of code registers a table by the name of `profilesTable`:

```
jsonRDDWithSchema.registerTempTable("profilesTable")
```

2. Let's fire away our filter query. The following query returns all profiles that have been registered after August 26, 2014. Since the registered field is a timestamp, we require an additional minor step of casting the parameter into a `TimeStamp`:

```
val filterCount = sqlContext.sql("select * from profilesTable  
where registered > CAST('2014-08-26 00:00:00' AS TIMESTAMP)").count
```

3. Let's print the count:

```
println("Filtered based on timestamp count : " + filterCount)  
//106
```

There's more...

If you aren't comfortable with having the schema in the code and would like to save the schema in a file, it's just a one-liner for you:

```
import scala.reflect.io.File  
import scala.io.Source  
//Writes schema as JSON to file  
File("profileSchema.json").writeAll(profilesSchema.json)
```

Obviously, you would want to reconstruct the schema from JSON, and that's also a one-liner:

```
val loadedSchema = DataType.fromJson(Source.fromFile("profileSchema.  
json").mkString)
```

Let's check whether the `loadedSchema` and the `profileSchema` encapsulate the same schema by doing an equality check on their `json`:

```
println("ProfileSchema == loadedSchema :"+(loadedSchema.  
json==profilesSchema.json))
```

The output is shown as follows:

```
ProfileSchema == loadedSchema :true
```

If we would like to eyeball the `json`, we have a nice method called `prettyJson` that formats the `json`:

```
//Print loaded schema
println(loadedSchema.prettyJson)
```

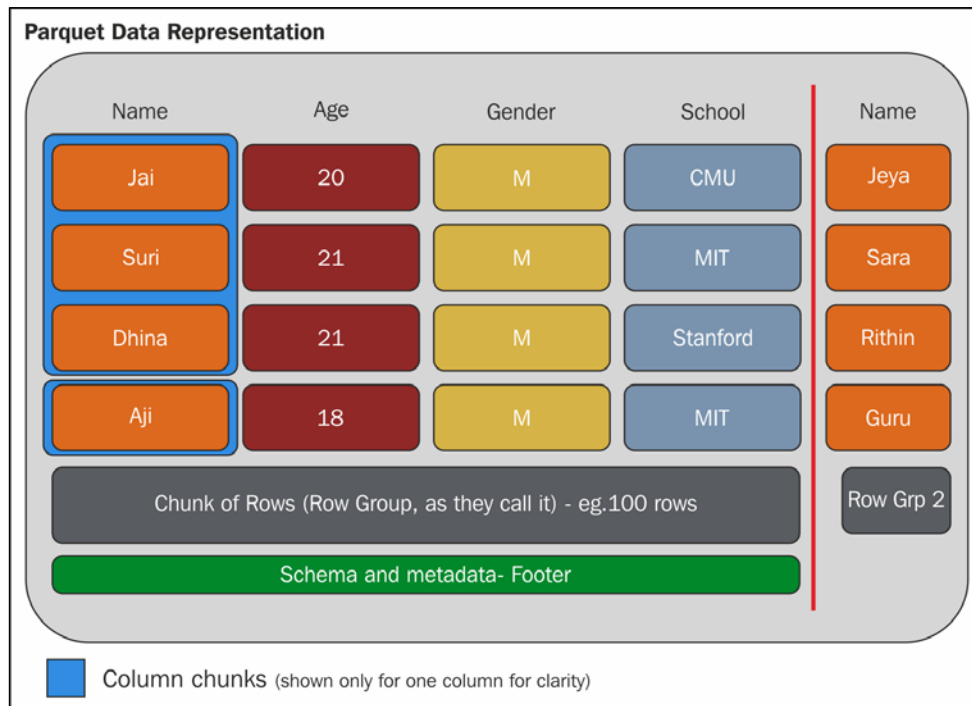
The output is as follows:

```
[info] {
[info]   "type" : "struct",
[info]   "fields" : [ {
[info]     "name" : "id",
[info]     "type" : "string",
[info]     "nullable" : true,
[info]     "metadata" : { }
[info]   }, {
[info]     "name" : "about",
[info]     "type" : "string",
[info]     "nullable" : true,
[info]     "metadata" : { }
[info]   }, {
[info]     "name" : "address",
[info]     "type" : "string",
[info]     "nullable" : true,
[info]     "metadata" : { }
[info]   }, {
[info]     "name" : "age",
[info]     "type" : "integer",
[info]     "nullable" : true,
[info]     "metadata" : { }
[info]   }, {
[info]     "name" : "company",
[info]     "type" : "string",
[info]     "nullable" : true,
[info]     "metadata" : { }
[info]   }, {
[info]     "name" : "email",
[info]     "type" : "string",
[info]     "nullable" : true,
[info]     "metadata" : { }
[info]   }, {
[info]     "name" : "eyeColor",
[info]     "type" : "string",
[info]     "nullable" : true,
[info]     "metadata" : { }
[info]   }, {
[info]     "name" : "favoriteFruit",
```

Storing data as Parquet files

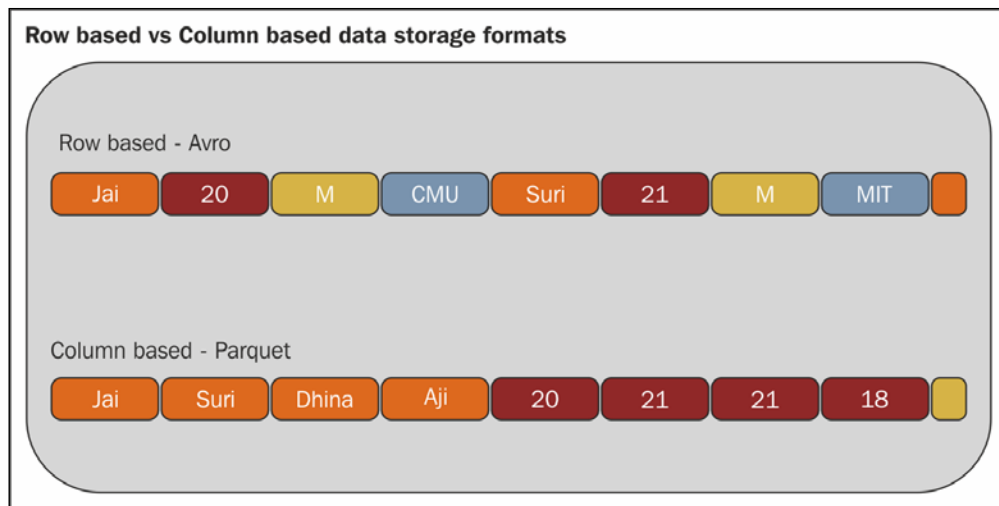
Parquet (<https://parquet.apache.org/>) is rapidly becoming the go-to data storage format in the world of big data because of the distinct advantages it offers:

- ▶ It has a column-based representation of data. This is better represented in a picture, as follows:



As you can see in the preceding screenshot, Parquet stores data in chunks of rows, say 100 rows. In Parquet terms, these are called **RowGroups**. Each of these RowGroups has chunks of columns inside them (or column chunks). Column chunks can hold more than a single unit of data for a particular column (as represented in the blue box in the first column). For example, **Jai**, **Suri**, and **Dhina** form a single chunk even though they are composed of three single units of data for **Name**.

Another unique feature is that these column chunks (groups of a single column's information) can be read independently. Let's consider the following image:



We can see that the items of column data are stored next to each other in a sequence. Since our queries are focused on just a few columns (a projection) most of the time and not on the entire table, this storage mechanism enables us to retrieve data much faster than reading the entire row data that is stored and filtering for columns. Also, with Spark's in-memory computations, the memory requirements are reduced in this way.

- ▶ The second advantage is that there is very little that is needed for our transition from the existing data models that we already use to represent the data. While Parquet has its own native object model, we are pretty much free to choose Avro, ProtoBuf, Thrift, and a variety of existing object models, and use an intermediate converter to serialize our data in Parquet. Most of these converters are readily available at the Parquet-MR project (<https://github.com/Parquet/parquet-mr>).

In this recipe, we'll cover the following steps:

1. Load a simple CSV file and convert it into a DataFrame.
2. Save it as a Parquet file.
3. Install Parquet tools.
4. Use the tools to inspect the Parquet file.
5. Enable compression for the Parquet file.



The entire code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/tree/master/chapter3-data-loading-parquet>.

How to do it...

Before we dive into the steps, let's briefly look at our `build.sbt` file, specifically the library dependencies and Avro settings (which we'll talk about in the following sections):

```
organization := "com.packt"

name := "chapter3-data-loading-parquet"

scalaVersion := "2.10.4"

val sparkVersion="1.4.1"

libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % sparkVersion,
  "org.apache.spark" %% "spark-sql" % sparkVersion,
  "org.apache.spark" %% "spark-mllib" % sparkVersion,
  "org.apache.spark" %% "spark-hive" % sparkVersion,
  "org.apache.avro" % "avro" % "1.7.7",
  "org.apache.parquet" % "parquet-avro" % "1.8.1",
  "com.twitter" %% "chill-avro" % "0.6.0"
)

resolvers += Seq(
  "Apache HBase" at
  "https://repository.apache.org/content/repositories/releases",
  "Typesafe repository" at
  "http://repo.typesafe.com/typesafe/releases/",
  "Twitter" at "http://maven.twttr.com/"
)

fork := true

seq( sbtavro.SbtAvro.avroSettings : _*)

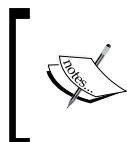
(stringType in avroConfig) := "String"

javaSource in sbtavro.SbtAvro.avroConfig <= (sourceDirectory in
Compile)(_ / "java")
```

Now that we have `build.sbt` out of the way, let's go ahead and look at the code behind each of the listed steps.

Load a simple CSV file, convert it to case classes, and create a DataFrame from it

We can actually create a `DataFrame` directly from CSV using the `com.databricks/spark-csv` file, as we saw in *Chapter 2, Getting Started with Apache Spark DataFrames*, but for this recipe, we'll just tokenize the CSV and create classes from it. The input CSV has a header column. So, the conversion process involves skipping the first row.



The class file that we will discuss in this section is the <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter3-data-loading-parquet/src/main/scala/com/packt/dataload/ParquetCaseClassMain.scala>.

There are just two interesting things that you might notice in the code:

```
sqlContext.setConf("spark.sql.parquet.binaryAsString", "true")
```

Some Parquet producing systems, such as Impala, binary encode the strings. In order to work around this issue, we set the following configuration, which says that if it sees binary data, it should be treated as a string:

Instead of using `sqlContext.createDataFrame`, we just use a `toDF()` on the `RDD[Student]`. The `SQLContext.Implicits` object has a number of implicit conversions that help us convert an `RDD[T]` to a `DataFrame` directly. The only requirement for us, as expected, is to import the implicits:

```
import sqlContext.implicits._
```

The rest of the code is the same as we saw earlier:

```
val conf = new
SparkConf().setAppName("CaseClassToParquet").setMaster("local[2]")
val sc = new SparkContext(conf)
val sqlContext = new SQLContext(sc)

//Treat binary encoded values as Strings
sqlContext.setConf("spark.sql.parquet.binaryAsString", "true")

import sqlContext.implicits._

//Convert each line into Student
val rddOfStudents = convertCSVToStudents("StudentData.csv", sc)

//Convert RDD[Student] to a Dataframe using sqlContext.implicits
val studentDFrame = rddOfStudents.toDF()
```

The `convertCSVToStudents` method, which converts each line into a `Student` object, looks like this:

```
def convertCSVToStudents(filePath: String, sc: SparkContext):
  RDD[Student] = {
    val rddOfStudents: RDD[Student]
  =sc.textFile(filePath).flatMap(line => {
    val data = line.split("\\|")
    if (data(0) == "id") None else Some(Student(data(0),
  data(1), data(2), data(3)))
  })
  rddOfStudents
}
```

Save it as a Parquet file

This is just a one-liner once we have the `DataFrame`. This can be done using either the `saveAsParquetFile` or the `save` method. If you wish to save it in a Hive table (<https://hive.apache.org/>), then there is also a `saveAsTable` method for you:

```
//Save DataFrame as Parquet using saveAsParquetFile
studentDFrame.saveAsParquetFile("studentPq.parquet")
```

```
//OR
```

```
//Save DataFrame as Parquet using the save method
studentDFrame.save("studentPq.parquet", "parquet",
  SaveMode.Overwrite)
```



The `save` method allows the usage of `SaveMode`, which has the following alternatives: `Append`, `ErrorIfExists`, `Ignore`, or `Overwrite`.

The `save` methods create a directory in the location that you specify (here, we simply store it in our project directory). The directory holds the files that represent the serialized data. It is not entirely human readable, but you may notice that the data of a single column is stored together.

Just as we do for the rest of the recipes, let's read the file and sample the data for confirmation:

```
//Read data for confirmation
val pqDFrame=sqlContext.parquetFile("studentPq.parquet")
pqDFrame.show()
```

The following is the output:

id	name	phone	email
151	Baker	1-754-775-9024	lenim@atortorNunc...
152	Xena	1-527-990-8606	in.faucibus.orci...
153	Kasper	1-155-575-9346	velit.eget@pedeCu...
154	Hannah	1-712-794-8145	Phasellus.libero...
155	Reese	1-106-653-2899	aliquet.magna.a@l...
156	Buckminster	1-352-299-2056	cursus.Nunc.mauri...
157	Richard	1-461-925-7084	fringilla.cursus@...
158	Shafira	1-786-210-7819	a@magnamalesuada.ca
159	Frances	1-312-680-5112	lenim.consequat.pu...
160	Ava	1-816-439-4739	ipsum.Phasellus.v...
161	Maxine	1-422-863-3041	aliquet.molestie....
162	Kirk	1-782-749-4287	fringilla@luctusv...
163	Dylan	1-417-943-8961	vehicula.aliquet@...
164	Francesca	1-425-876-2200	nec.euismod.in@co...
165	Tiger	1-316-930-7880	nec@mollisnoncurs...
166	Vance	1-268-680-0857	pellentesque@netu...
167	Hermione	1-673-268-1156	eu.dolor@auctorn...
168	Candice	1-701-263-8889	sit.amet.ornare@...
169	Aiko	1-682-230-7013	turpis.vitae.puru...
170	Quemby	1-380-414-6915	interdum.ligula@e...

Install Parquet tools

Other than using the `printSchema` method of the `DataFrame` to inspect the schema, we can use some interesting parquet tools provided as part of the parquet project to get a variety of other information.



The `parquet-tools` is a subproject of Parquet and is available at <https://github.com/Parquet/parquet-mr/tree/master/parquet-tools>.

Since Spark 1.4.1 uses Parquet 1.6.0rc3, we'll need to download that version of the tools from the Maven repository. The executables and the JARs can be downloaded as one bundle from <https://repo1.maven.org/maven2/com/twitter/parquet-tools/1.6.0rc3/parquet-tools-1.6.0rc3-bin.tar.gz>.

Using the tools to inspect the Parquet file

Let's put the tools into action. Specifically, we'll do three things in this step:

- ▶ Display the schema in Parquet format
- ▶ Display the meta information that is stored in Parquet's footer

- ▶ Sample the data using `head` and `cat`
- ▶ **Displaying the schema:** This can be achieved by calling the `parquet-tools` command with `schema` and the `parquet` file as the parameter. As an example, let's print the schema using one of the part files:

```
bash-3.2$ parquet-tools-1.6.0rc3/parquet-tools meta part-r-00000-20a8b58c-fe1d-43e7-b148-f874b78eb5ec.gz.parquet
```

```
message root {
  optional binary id (UTF8);
  optional binary name (UTF8);
  optional binary phone (UTF8);
  optional binary email (UTF8);
}
```

We see that the schema is indeed available in Parquet format and is derived from our case classes.

- ▶ **Displaying the meta information of a particular Parquet file:** As we saw earlier, meta information is stored in the footer. Let's print it to see it.

We see that the `extra` information has the schema that is specific to the data model we used. This information is used when the data is deserialized. The `meta` parameter of `parquet-tools` will help achieve this:

```
bash-3.2$ parquet-tools-1.6.0rc3/parquet-tools meta part-r-00000-20a8b58c-fe1d-43e7-b148-f874b78eb5ec.gz.parquet
```

```
creator:      parquet-mr version 1.6.0rc3 (build
d4d5a07ec9bd262ca1e93c309f1d7d4a74ebda4c)
extra:        org.apache.spark.sql.parquet.row.metadata = {"type"
:"struct", "fields": [{"name": "id", "type": "string", "nullable": true
, "metadata": {}}, {"name": "name", "type": "string", "nullable": true,
[more]...
```

```
file schema: root
```

```
-----
-----
-----
---
```

```
id:           OPTIONAL BINARY O:UTF8 R:0 D:1
name:         OPTIONAL BINARY O:UTF8 R:0 D:1
phone:        OPTIONAL BINARY O:UTF8 R:0 D:1
```

```
email:          OPTIONAL BINARY O:UTF8 R:0 D:1
```

```
row group 1: RC:50 TS:3516
```

```
-----  
-----  
-----  
---
```

```
id:             BINARY GZIP DO:0 FPO:4 SZ:140/326/2.33 VC:50  
ENC:RLE,BIT_PACKED,PLAIN
```

```
name:          BINARY GZIP DO:0 FPO:144 SZ:313/483/1.54 VC:50  
ENC:RLE,BIT_PACKED,PLAIN
```

```
phone:         BINARY GZIP DO:0 FPO:457 SZ:454/961/2.12 VC:50  
ENC:RLE,BIT_PACKED,PLAIN
```

```
email:         BINARY GZIP DO:0 FPO:911 SZ:929/1746/1.88 VC:50  
ENC:RLE,BIT_PACKED,PLAIN
```

- ▶ **Sampling data using head and cat:** Let's now have a sneak peek at the first few rows of the data. The `head` function will help us do that. It accepts an additional `-n` parameter, where you can specify the number of records to be displayed:

```
bash-3.2$ parquet-tools-1.6.0rc3/parquet-tools head -n 2  
part-r-00001.parquet
```

The preceding command will display only two rows because of the additional `-n 2` parameter.

The following is the output of this command:

```
id = 1  
name = Burke  
phone = 1-300-746-8446  
email = ullaamcorper.velit.in@ametnullaDonec.co.uk
```

```
id = 2  
name = Kamal  
phone = 1-668-571-5046  
email = pede.Suspendisse@interdumenim.edu
```

Optionally, if you wish to display all the records in the file, you can use the `cat` parameter with the `parquet-tools` command:

```
parquet-tools cat part-r-00001.parquet
```

Enable compression for the Parquet file

As you can see from the meta information, the data is gzipped by default. In order to use **Snappy** compression, all that we need to do is set a configuration to our `SQLContext` (actually the `SQLConf` of `SQLContext`). There's just one catch with regard to enabling **Lempel–Ziv–Oberhumer (LZO)** compression—we are required to install `native-lzo` on all the machines where this data is stored. Otherwise, we get a "native-lzo library not available" error message.

Let's enable Snappy (<http://google.github.io/snappy/>) compression by passing the configuration parameter of Parquet compression to Snappy:

```
sqlContext.setConf("spark.sql.parquet.compression.codec", "snappy")
```

After running the program, let's use the `parquet-tools meta` command to verify it:

```
parquet-tools meta part-r-00000-ae54b77-288e-44b2-8f36-53b38a489e8d.snappy.parquet
```

```
creator:  parquet-mr version 1.6.0rc3 (build d4d5a07ec9bd262ca1e93c309f1d7d4a74ebda4c)
extra:    org.apache.spark.sql.parquet.row.metadata = {"type":"struct","fields":[{"name":"id","type":"string","nullable":true,"metadata":{}}, {"name":"name","type":"string","nullable":true, [more]}]}

file schema: root
-----
id:      OPTIONAL BINARY 0:UTF8 R:0 D:1
name:    OPTIONAL BINARY 0:UTF8 R:0 D:1
phone:   OPTIONAL BINARY 0:UTF8 R:0 D:1
email:   OPTIONAL BINARY 0:UTF8 R:0 D:1

row group 1: RC:50 TS:3516
-----
id:      BINARY SNAPPY 0:0 FPO:4 SZ:245/326/1.33 VC:50 ENC:BIT_PACKED,RLE,PLAIN
name:    BINARY SNAPPY 0:0 FPO:249 SZ:423/483/1.14 VC:50 ENC:BIT_PACKED,RLE,PLAIN
phone:   BINARY SNAPPY 0:0 FPO:672 SZ:748/961/1.28 VC:50 ENC:BIT_PACKED,RLE,PLAIN
email:   BINARY SNAPPY 0:0 FPO:1420 SZ:1375/1746/1.27 VC:50 ENC:BIT_PACKED,RLE,PLAIN
```

Using the Avro data model in Parquet

Parquet is a kind of highly efficient columnar storage, but it is also relatively new. Avro (<https://avro.apache.org>) is a widely used row-based storage format. This recipe showcases how we can retain the older and flexible Avro schema in our code but still use the Parquet format during storage.

The Spark MR project (yes, the one that has the Parquet tools we saw in the previous recipe) has converters for almost all the popular data formats. These model converters take your format and convert it into Parquet format before causing it to persist.

How to do it...

In this recipe, we'll use the Avro data model and serialize the data in a Parquet file. The recipe involves the following steps:

1. Create the Avro Model.
2. Generate Avro objects using the `sbt avro` plugin.
3. Construct the RDD of your generated object (`StudentAvro`) from `Students.csv`.
4. Save the `RDD[StudentAvro]` in a Parquet file.
5. Read the file back for verification.
6. Use `Parquet-tools` to verify.

Creation of the Avro model

The Avro schema is defined using JSON. In our case, we'll just use the same `Student.csv` as the input file. So, let's code the four fields—`id`, `name`, `phone`, and `email`—in the schema:

```
{ "namespace": "studentavro.avro",
  "type": "record",
  "name": "StudentAvro",
  "fields": [
    { "name": "id", "type": ["string", "null"] },
    { "name": "name", "type": ["string", "null"] },
    { "name": "phone", "type": ["string", "null"] },
    { "name": "email", "type": ["string", "null"] }
  ]
}
```

Probably, you are already familiar with Avro, or you have already understood the schema just by taking a look at it, but let me bore you with some explanation of the schema anyway.

The `namespace` and `name` attributes in the JSON translate into our package name and class name in our world, respectively. So, our generated class will have a fully qualified name as `studentavro.avro.StudentAvro`. The `"record"` (of the `type` attribute) is one of the complex types in Avro (http://avro.apache.org/docs/1.7.6/spec.html#schema_complex). Let me rephrase this again. A record roughly translates to classes in Java/Scala. It is at the topmost level in the schema hierarchy. A record can have multiple fields encapsulated inside it, and these fields can be primitives (https://avro.apache.org/docs/1.7.7/spec.html#schema_primitive) or other complex types. The last bit about the `type` having an array of types is interesting (`"type": ["string", "null"]`). It just means that the field can be more than one type. In Avro terms, it is called a union.

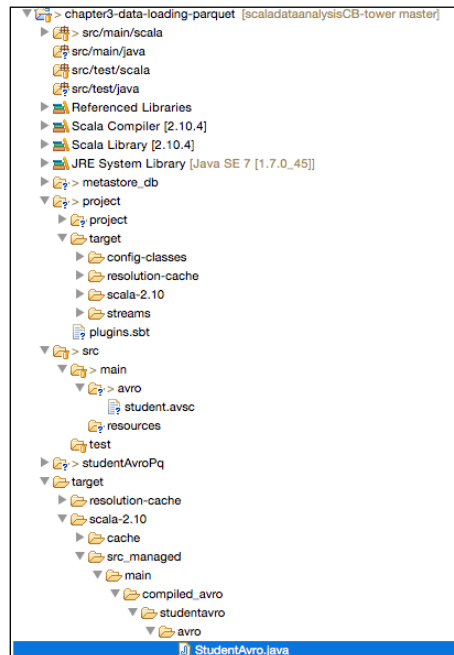
Now that we are done with the schema, let's save this file with an extension of `.avsc`. I have saved it as `student.avsc` in the `src/main/avro` directory.

Generation of Avro objects using the sbt-avro plugin

The next step is to generate a class from the schema. The reason we stored the avro schema file in the `src/main/avro` folder is this: we'll be using an `sbt-avro` plugin (<https://github.com/cavorite/sbt-avro>) to generate a Java class from the schema. Configuring the plugin is as easy as configuring any other plugin for SBT:

- ▶ Let's add the plugin to `project/plugins.sbt`:
`addSbtPlugin("com.cavorite" % "sbt-avro" % "0.3.2")`
- ▶ Add the default settings of the plugin to our `build.sbt`:
`seq(sbtavro.SbtAvro.avroSettings : _*)`
- ▶ Let's generate the Java class now. We can do this by calling `sbt avro:generate`. You can see the generated Java file at `target/scala-2.10/src_managed/main/compiled_avro/studentavro/avro/StudentAvro.java`.

```
Gabriel@Gabriels-MacBook-Pro ~/D/a/S/C/s/chapter3-data-loading-parquet> sbt avro:generate
[info] Loading global plugins from /Users/Gabriel/.sbt/0.13/plugins
[info] Loading project definition from /Users/Gabriel/Dropbox/aron/ScalaDataAnalysis/Code/scaladataanalysisCB-tower/chapter3-dat
a-loading-parquet/project
[warn] Multiple resolvers having different access mechanism configured with same name 'sbt-plugin-releases'. To avoid conflict,
Remove duplicate project resolvers ('resolvers') or rename publishing resolver ('publishTo').
[info] Set current project to chapter3-data-loading-parquet (in build file:/Users/Gabriel/Dropbox/aron/ScalaDataAnalysis/Code/sc
aladataanalysisCB-tower/chapter3-data-loading-parquet/)
[info] Avro compiler using stringType=String
[info] Compiling Avro schema /Users/Gabriel/Dropbox/aron/ScalaDataAnalysis/Code/scaladataanalysisCB-tower/chapter3-data-loading-
parquet/src/main/avro/student.avsc
[Success] Total time: 1 s, completed Sep 20, 2015 9:07:21 AM
```



- ▶ We also need the following library dependencies. Finally, let's perform an SBT compile to compile the class so that the rest of the project picks up the generated Java file:

```
libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % sparkVersion,
  "org.apache.spark" %% "spark-sql" % sparkVersion,
  "org.apache.spark" %% "spark-mllib" % sparkVersion,
  "org.apache.spark" %% "spark-hive" % sparkVersion,
  "org.apache.avro" % "avro" % "1.7.7",
  "org.apache.parquet" % "parquet-avro" % "1.8.1",
  "com.twitter" %% "chill-avro" % "0.6.0"
)
sbt compile
```

Constructing an RDD of our generated object from Students.csv

This step is very similar to the previous recipe in the sense that we use the `convertCSVToStudents` function to generate an RDD of the `StudentAvro` object. Also, since this isn't a Scala class and the generated Java object comes up with a builder inside it, we use the builder to construct the class fluently (http://en.wikipedia.org/wiki/Fluent_interface):

```
val conf = new
SparkConf().setAppName("AvroModelToParquet").setMaster("local[2]")

val sc = new SparkContext(conf)
val sqlContext = new SQLContext(sc)
sqlContext.setConf("spark.sql.parquet.binaryAsString", "true")
val rddOfStudents = convertCSVToStudents("StudentData.csv", sc)

//The CSV has a header row. Zipping with index and skipping the
first row
def convertCSVToStudents(filePath: String, sc: SparkContext):
RDD[StudentAvro] = {
  val rddOfStudents:
RDD[StudentAvro]=sc.textFile(filePath).flatMap(eachLine => {
    val data = eachLine.split("\\|")
    if (data(0) == "id") None
    else Some(StudentAvro.newBuilder()
      .setId(data(0))
      .setName(data(1))
      .setPhone(data(2))
      .setEmail(data(3)).build())
  })
  rddOfStudents
}
```

Saving RDD[StudentAvro] in a Parquet file

This is a tricky step and involves multiple substeps. Let's decipher this step backwards. We fall back to RDD[StudentAvro] in this example instead of a DataFrame because DataFrames can be constructed only from an RDD of case classes (or classes that extend Product, as we saw earlier in this chapter) or from RDD[org.apache.spark.sql.Row]. If you prefer to use DataFrames, you can read the CSV as an array of values, and use RowFactory.create for each array of values. Once an RDD[Row] is available, we can use sqlContext.createDataFrame to convert it to a DataFrame:

- ▶ In order to save the RDD as a Hadoop SequenceFile, we can use saveAsNewAPIHadoopFile. A sequence file is simply a text file that holds key-value pairs. We could have chosen one of the Student attributes as a key, but for the sake of it, let's have it as a Void in this example.

To represent a pair (key-value) in Spark, we use PairRDD (<https://spark.apache.org/docs/1.4.1/api/scala/index.html#org.apache.spark.rdd.PairRDDFunctions>). Not surprisingly, saveAsNewAPIHadoopFile is available only for PairRDDs. To convert the existing RDD[StudentAvro] to a PairRDD[Void, StudentAvro], we use the map function:

```
val pairRddOfStudentsWithNullKey = rddOfStudents.map(each
=> (null, each))
```

- ▶ Spark uses Java serialization by default to serialize the RDD to be distributed across the cluster. However, the Avro model doesn't implement the Serializable interface, and hence it won't be able to leverage Java serialization. That's no reason for worry, however, because Spark provides another 10x performant serialization mechanism called **Kryo**. The only downside is that we need to explicitly register our serialization candidates:

```
val conf = new
SparkConf().setAppName("AvroModelToParquet").setMaster("local[2]")
conf.set("spark.kryo.registrator",
classOf[StudentAvroRegistrator].getName)
conf.set("spark.serializer",
"org.apache.spark.serializer.KryoSerializer")
```

So, we say using the "spark.serializer" configuration that we intend to use KryoSerializer, and that our registrator is StudentAvroRegistrator. As you may expect, what the Registrator does is register our StudentAvro class as a candidate for Kryo serialization. The twitter-chill project (<https://github.com/twitter/chill>) provides a nice extension to delegate the Kryo serializer to use the Avro serialization:

```
class StudentAvroRegistrator extends KryoRegistrator {
  override def registerClasses(kryo: Kryo) {
```

```

    kryo.register(classOf[StudentAvro],
    AvroSerializer.SpecificRecordBinarySerializer[StudentAvro])
  }
}

```

- ▶ The intent of this recipe is to write a Parquet file, but the data model (schema) is Avro. Since we are going to write this down as a sequence file, we'll be using a bunch of Hadoop APIs. The `org.apache.hadoop.mapreduce.OutputFormat` specifies the output format of the file that we are going to write, and as expected, we use `ParquetOutputFormat` (this is available in the `parquet-hadoop` subproject in the `parquet-mr` project). There are two things that an `OutputFormat` requires:

- The `WriteSupport` class, which knows how to convert the Avro data model to the actual format. This is achieved with the following line:

```

    ParquetOutputFormat.setWriteSupportClass(job,
    classOf[AvroWriteSupport])

```

- The schema needs to be written to the footer of the Parquet file too. The schema of `StudentAvro` is accessible by using the `getClassSchema` function. This line of code achieves that:

```

    AvroParquetOutputFormat.setSchema(job, StudentAvro.
    getClassSchema)

```

Now, what's that `job` parameter doing here in these two lines of code? The `job` object is just an instance of `org.apache.hadoop.mapreduce.Job`:

```

    val job = new Job()

```

When we call the `setWriteSupportClass` and `setSchema` methods of `ParquetOutputFormat` and `AvroParquetOutputFormat`, the resulting configuration is captured inside the `JobConf` encapsulated inside the `Job` object. We'll be using this `job` configuration while saving the data in a sequence file.

- ▶ Finally, we save the file by calling `saveAsNewAPIHadoopFile`. The `save` method requires a bunch of parameters, each of which we have already discussed. The first parameter is the filename, followed by the key and the value classes. The fourth is the `OutputFormat` of the file, and finally comes the `job` configuration itself:

```

pairRddOfStudentsWithNullKey.saveAsNewAPIHadoopFile("studentAvro
Pq",
    classOf[Void],
    classOf[StudentAvro],
    classOf[AvroParquetOutputFormat],
    job.getConfiguration())

```


We saw the entire program in bits and pieces, so for the sake of completion, let's see it completely:

```
object ParquetAvroSchemaMain extends App {

  val conf = new
SparkConf().setAppName("AvroModelToParquet").setMaster("local[2]")
  conf.set("spark.kryo.registrator",
classOf[StudentAvroRegistrator].getName)
  conf.set("spark.serializer",
"org.apache.spark.serializer.KryoSerializer")

  val job = new Job()

  val sc = new SparkContext(conf)
  val sqlContext = new SQLContext(sc)
  sqlContext.setConf("spark.sql.parquet.binaryAsString",
"true")
  val rddOfStudents =
convertCSVToStudents("StudentData.csv", sc)

  ParquetOutputFormat.setWriteSupportClass(job,
classOf[AvroWriteSupport])
  AvroParquetOutputFormat.setSchema(job,
StudentAvro.getClassSchema)

  val pairRddOfStudentsWithNullKey = rddOfStudents.map(each
=>
(null, each))

pairRddOfStudentsWithNullKey.saveAsNewAPIHadoopFile("studentAvro
Pq",
  classOf[Void],
  classOf[StudentAvro],
  classOf[AvroParquetOutputFormat],
  job.getConfiguration())

  //The CSV has a header row. Zipping with index and
skipping the first row
  def convertCSVToStudents(filePath: String, sc:
SparkContext):
RDD[StudentAvro] = {
    val rddOfStudents:
RDD[StudentAvro]=sc.textFile(filePath).flatMap(eachLine =>
{
      val data = eachLine.split("\\|")
```

```

        if (data(0) == "id") None
        else Some(StudentAvro.newBuilder()
            .setId(data(0))
            .setName(data(1))
            .setPhone(data(2))
            .setEmail(data(3)).build())
    })
    rddOfStudents
}

}

class StudentAvroRegistrar extends KryoRegistrar {
  override def registerClasses(kryo: Kryo) {
    kryo.register(classOf[StudentAvro],
        AvroSerializer.SpecificRecordBinarySerializer[StudentAvro])
  }
}

```

Reading the file back for verification

As always, let's read the file back for confirmation. The function to be called for this is `newAPIHadoopFile`, which accepts a similar set of parameters as `saveAsNewAPIHadoopFile`: the name of the file, `InputFormat`, the key class, the value class, and finally the job configuration. Note that we are using `newAPIHadoopFile` instead of the previously used `parquetFile` method. This is because we are reading from a Hadoop sequence file:

```

//Reading the file back for confirmation.
ParquetInputFormat.setReadSupportClass(job, classOf[AvroWriteSupport])
val readStudentsPair = sc.newAPIHadoopFile("studentAvroPq", classOf[AvroParquetInputFormat[StudentAvro]], classOf[Void], classOf[StudentAvro], job.getConfiguration())
val justStudentRDD: RDD[StudentAvro] = readStudentsPair.map(_._2)
val studentsAsString = justStudentRDD.collect().take(5).mkString("\n")
println(studentsAsString)

```

This is the output:

```

[info] {"id": "1", "name": "Burke", "phone": "1-300-746-8446", "email": "ullamcorper.velit.in@ametnullaDonec.co.uk"}
[info] {"id": "2", "name": "Kamal", "phone": "1-668-571-5046", "email": "pede.Suspendisse@interdumenim.edu"}
[info] {"id": "3", "name": "Olga", "phone": "1-956-311-1686", "email": "Aenean.eget.metus@dictumcursusNunc.edu"}
[info] {"id": "4", "name": "Belle", "phone": "1-246-894-6340", "email": "vitae.aliquet.nec@neque.co.uk"}
[info] {"id": "5", "name": "Trevor", "phone": "1-300-527-4967", "email": "dapibus.id@acturpisegestas.net"}

```

Using Parquet tools for verification

We'll also use Parquet tools to confirm that the schema that is stored in the Parquet file is indeed an `avro` schema:

```
/Users/Gabriel/Dropbox/arun/ScalaDataAnalysis/git/parquet-mr/parquet-  
tools/target/parquet-tools-1.6.0rc3/parquet-tools meta /Users/Gabriel/  
Dropbox/arun/ScalaDataAnalysis/Code/scaladataanalysisCB-tower/chapter3-  
data-loading-parquet/studentAvroPq
```

Yup! Looks like it is! The `extra` section in `meta` does confirm that the `avro` schema is stored:

```
creator:    parquet-mr  
extra:     parquet.avro.schema = {"type": "record", "name": "StudentAvro",  
"namespace": "studentavro.avro", "fields": [{"name": "id", "type": [{"type": "st  
ring", "avro.java.string": "Stri [more]...
```

```
creator:    parquet-mr  
extra:     parquet.avro.schema = {"type": "record", "name": "StudentAvro", "namespace": "studentavro.avro", "fields": [{"name": "id", "type": [{"type": "string", "avro.java.string": "String"}]}]  
file schema: studentavro.avro.StudentAvro  
-----  
id:        OPTIONAL BINARY 0:UTF8 R:0 D:1  
name:     OPTIONAL BINARY 0:UTF8 R:0 D:1  
phone:    OPTIONAL BINARY 0:UTF8 R:0 D:1  
email:    OPTIONAL BINARY 0:UTF8 R:0 D:1  
-----  
row group 1: RC:50 TS:3382  
-----  
id:        BINARY UNCOMPRESSED D0:0 FPO:4 SZ:316/316/1.00 VC:50 ENC:PLAIN,RLE,BIT_PACKED  
name:     BINARY UNCOMPRESSED D0:0 FPO:320 SZ:470/470/1.00 VC:50 ENC:PLAIN,RLE,BIT_PACKED  
phone:    BINARY UNCOMPRESSED D0:0 FPO:790 SZ:925/925/1.00 VC:50 ENC:PLAIN,RLE,BIT_PACKED  
email:    BINARY UNCOMPRESSED D0:0 FPO:1715 SZ:1671/1671/1.00 VC:50 ENC:PLAIN,RLE,BIT_PACKED
```

Loading from RDBMS

As the final recipe on loading, let's try to load data from an RDBMS data source, which is MySQL in our case. This recipe assumes that you have already installed MySQL in your machine.

How to do it...

Let's go through the prerequisite steps first. If you already have a MySQL table to play with, you can safely ignore this step. We are just going to create a new database and a table and load some sample data into it.

The prerequisite step (optional):

1. Creating a database and a table: This is achieved in MySQL by using the `create database` and the `create table DDL`:

```
create database scalada;  
  
use scalada
```

```
CREATE TABLE student (
  id varchar(20),
  `name` varchar(200),
  phone varchar(50),
  email varchar(200),
  PRIMARY KEY (id));
```

2. Loading data into the table: Let's dump some data into the table. I wrote a very simple app to do this. Alternatively, you can use the `load data infile` command if you have `"local-infile=1"` enabled on your server and the client. Refer to <https://dev.mysql.com/doc/refman/5.1/en/load-data.html> for details about this command.

As you can see, the program loads the `Student.csv` that we saw in *Chapter 2, Getting Started with Apache Spark DataFrames*, when we saw how to use DataFrames with Spark using the `databricks.csv` connector. Then, for each line, the data is inserted into the table using the plain old JDBC insert. As you might have already figured out, we need to add the MySQL connector `java` dependency to our `build.sbt` too:

```
"mysql" % "mysql-connector-java" % "5.1.34"

object LoadDataIntoMySQL extends App {

  val conf = new
SparkConf().setAppName("LoadDataIntoMySQL").setMaster("local[2]")
  val config=ConfigFactory.load()
  val sc = new SparkContext(conf)
  val sqlContext = new SQLContext(sc)

  val students = sqlContext.csvFile(filePath =
"StudentData.csv", useHeader = true, delimiter = '|')

  students.foreachPartition { iter=>
    val conn =
DriverManager.getConnection(config.getString("mysql.connection.
url"))
    val statement = conn.prepareStatement("insert into
scalada.student (id, name, phone, email) values (?, ?, ?, ?)
")

    for (eachRow <- iter) {
      statement.setString(1, eachRow.getString(0))
      statement.setString(2, eachRow.getString(1))
      statement.setString(3, eachRow.getString(2))
      statement.setString(4, eachRow.getString(3))
    }
  }
}
```

```
        statement.addBatch()
    }

    statement.executeBatch()
    conn.close()
    println ("All rows inserted successfully")
}

}
```

A "select * from scalada.student" on the MySQL client should confirm this, as shown here:

id	name	phone	email
10	Maya	1-271-683-2698	accumsan.convallis@ornarelectusjusto.edu
100	Mannix	1-804-635-5645	rutrum@per.org
11	Emi	1-467-270-1337	est@nunc.com
12	Caleb	1-683-212-0896	Suspendisse@Quisque.edu
13	Florence	1-603-575-2444	sit.amet.dapibus@lacusAliquamrutrum.ca
14	Anika	1-856-828-7883	euismod@ligulaelit.co.uk
15	Tarik	1-398-171-2268	turpis@felisorci.com

Steps for loading RDBMS data into DataFrame:

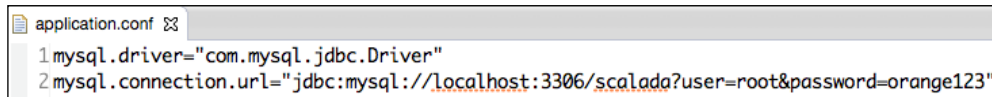
The recommended approach to loading data from RDBMS databases is using the SQLContext's load method:

1. Creating the Spark and SQLContext: You may have already become familiar with this step by looking at the previous recipes:

```
val conf = new
SparkConf().setAppName("DataFromRDBMS").setMaster("local[2]")
val sc = new SparkContext(conf)
val sqlContext = new SQLContext(sc)
```

2. Constructing a map of options: This map is expected to have not only the driver and the connection URL, but also the query to be invoked in order to load the data. In this example, we'll store the parameter values in an external Typesafe config file and load the values into our program.

The Typesafe application.conf is located at src/main/resources as per standard SBT/Maven conventions. Here is a screenshot that shows the contents of application.conf:



```
application.conf
1 mysql.driver="com.mysql.jdbc.Driver"
2 mysql.connection.url="jdbc:mysql://localhost:3306/scalada?user=root&password=orange123"
```

Now let's look at the code that constructs the map:

```
val config = ConfigFactory.load()

val options = Map(
  "driver" -> config.getString("mysql.driver"),
  "url" -> config.getString("mysql.connection.url"),
  "dbtable" -> "(select * from student) as student",
  "partitionColumn" -> "id",
  "lowerBound" -> "1",
  "upperBound" -> "100",
  "numPartitions"-> "2")
```

The first three parameters are straightforward. The `numPartitions` specifies the number of partitions for this job, and `partitionColumn` specifies the column in the table based on which the job has to be partitioned. The `lowerBound` and `upperBound` are values of the "id" field. The amount of data to be handled by a single partition is calculated using the number of partitions and the lower and upper bounds.

3. Loading data from the table: The `load` function of `SQLContext` expects two parameters. The first one specifies that the source of the data is through "jdbc", and the second parameter is the options that we constructed in step 2. Let's now print the schema and show the first 20 rows, as we always do:

```
val dFrame=sqlContext.load("jdbc", options)
dFrame.printSchema()
dFrame.show()
```

This is the output:

```
root
|-- id: string (nullable = false)
|-- name: string (nullable = true)
|-- phone: string (nullable = true)
|-- email: string (nullable = true)
|-- gender: string (nullable = true)
```

We see that the schema of the `DataFrame` is derived from the MySQL table definition by examining the `not nullable` constraint of the `id` field.

The output is as follows:

```
[info] id name phone email
[info] 10 Maya 1-271-683-2698 accumsan.convalli...
[info] 100 Mannix 1-804-635-5645 rutrum@per.org
[info] 11 Emi 1-467-270-1337 est@nunc.com
[info] 12 Caleb 1-683-212-0896 Suspendisse@Quisq...
[info] 13 Florence 1-603-575-2444 sit.amet.dapibus@...
[info] 14 Anika 1-856-828-7883 euismod@ligulaeli...
[info] 15 Tarik 1-398-171-2268 turpis@felisorci.com
[info] 16 Amena 1-878-250-3129 lorem.luctus.ut@s...
[info] 17 Blossom 1-154-406-9596 Nunc.commodo.auct...
[info] 18 Guy 1-869-521-3230 senectus.et.netus...
[info] 19 Malachi 1-608-637-2772 Proin.mi.Aliquam@...
[info] 2 Kamal 1-668-571-5046 pede.Suspendisse@...
[info] 20 Edward 1-711-710-6552 lectus@aliquetlib...
[info] 21 1-598-439-7549 consectetuer.adip...
[info] 22 Talon 1-880-986-1269 nec.malesuada.ut@...
[info] 23 Julie 1-430-807-5430 turpis.Nulla.aliq...
[info] 24 Marsden 1-477-629-7528 Donec.dignissim.m...
[info] 25 Igor 1-903-815-5364 conubia@tellus.co.uk
[info] 26 Amela 1-526-909-2605 in@vitaesodales.edu
[info] 27 Bianca 1-842-558-2906 posuere.cubilia@s...
```

Preparing data in Dataframes

Other than filtering, conversions, and transformations (with DataFrames which we saw in *Chapter 2, Getting Started with Apache Spark DataFrames*), let's see a few more data preparation tricks in this recipe. We'll also be looking at specific data preparation in *Chapter 5, Learning from Data*, where we will focus on using various machine learning algorithms.

How to do it...

While preprocessing data, we may be required to:

- ▶ Merge two different datasets
- ▶ Perform set operations on two datasets
- ▶ Sort the DataFrame by casting an attribute value
- ▶ Choose a member from one dataset over another based on the predicate
- ▶ Parse arbitrary date/time inputs

We'll use the `StudentPrep1.csv` and `StudentPrep2.csv` datasets for the first four tasks, and for the last one, we'll use `StrangeDate.json`, a JSON-based dataset. The CSV and the JSON dataset are chosen primarily for convenience—the input data could be anything.

The StudentPrep1.csv dataset is shown in this screenshot:

```
1|Burke|1-300-746-8446|ullamcorper.velit.in@ametnullaDonec.co.uk
2|Kamal|1-668-571-5046|pede.Suspendisse@interdumenim.edu
3|Olga|1-956-311-1686|Aenean.eget.metus@dictumcursusNunc.edu
4|Belle|1-246-894-6340|vitae.aliquet.nec@neque.co.uk
5|Trevor|1-300-527-4967|dapibus.id@acturpisegestas.net
6|Laurel|1-691-379-9921|adipiscing@consectetueripsum.edu
7|Sara|1-608-140-1995|Donec.nibh@enimEtiamimperdiet.edu
8|Kaseem|1-881-586-2689|cursus.et.magna@euismod.org
9|Lev|1-916-367-5608|Vivamus.nisi@ipsumdolor.com
10|Maya|1-271-683-2698|accumsan.convallis@ornarelectusjusto.edu
```

The StudentPrep2.csv dataset is shown in the following screenshot:

```
id|studentName|phone|email
1|Burke|DifferentName|1-300-746-8446|ullamcorper.velit.in@ametnullaDonec.co.uk
2|Kamal|DifferentName|1-668-571-5046|pede.Suspendisse@interdumenim.edu
3|Olga|1-956-311-1686|Aenean.eget.metus@dictumcursusNunc|DifferentEmail.edu
4|Belle|DifferentName|1-246-894-6340|vitae.aliquet.nec@neque.co.uk
5|Trevor|1-300-527-4967|dapibus|DifferentEmail.id@acturpisegestas.net
6|Laurel|InvalidPhone|00000000|adipiscing@consectetueripsum.edu
7|Sara|1-608-140-1995|Donec.nibh@enimEtiamimperdiet.edu
8|Kaseem|1-881-586-2689|cursus.et.magna@euismod.org
9|Lev|1-916-367-5608|Vivamus.nisi@ipsumdolor.com
10|Maya|1-271-683-2698|accumsan.convallis@ornarelectusjusto.edu
999|Lev|UniqueToSecondRDD|1-916-367-5608|Vivamus.nisi@ipsumdolor.com
```



The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/tree/master/chapter3-data-loading>.

Let's convert them into a DataFrame using the `databricks/spark-csv` library, which we used in *Chapter 2, Getting Started with Apache Spark DataFrames*, when we talked about loading DataFrames from CSV:

```
import com.databricks.spark.csv.CsvContext

val students1=sqlContext.csvFile(filePath="StudentPrep1.csv",
useHeader=true, delimiter='|')
val students2=sqlContext.csvFile(filePath="StudentPrep2.csv",
useHeader=true, delimiter='|')
```


1. **Merging datasets:** The DataFrame provides a convenient way to merge another DataFrame—`unionAll`. The `unionAll` accepts another DataFrame as an argument. Not surprisingly, the merged DataFrame maintains duplicates inside it:

```
val allStudents=students1.unionAll(students2)
allStudents.show(allStudents.count().toInt)
```

The output is shown as follows:

id	studentName	phone	email
1	Burke	1-300-746-8446	lullamcorper.velit...
2	Kamal	1-668-571-5046	pede.Suspendisse@...
3	Olga	1-956-311-1686	Aenean.eget.metus...
4	Belle	1-246-894-6340	vitae.aliquet.nec...
5	Trevor	1-300-527-4967	dapibus.id@acturp...
6	Laurel	1-691-379-9921	adipiscing@consec...
7	Sara	1-608-140-1995	Donec.nibh@enimEt...
8	Kaseem	1-881-586-2689	cursus.et.magna@e...
9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...
10	Maya	1-271-683-2698	accumsan.convalli...
1	BurkeDifferentName	1-300-746-8446	lullamcorper.velit...
2	KamalDifferentName	1-668-571-5046	pede.Suspendisse@...
3	Olga	1-956-311-1686	Aenean.eget.metus...
4	BelleDifferentName	1-246-894-6340	vitae.aliquet.nec...
5	Trevor	1-300-527-4967	dapibusDifferentE...
6	LaurelInvalidPhone	000000000	adipiscing@consec...
7	Sara	1-608-140-1995	Donec.nibh@enimEt...
8	Kaseem	1-881-586-2689	cursus.et.magna@e...
9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...
10	Maya	1-271-683-2698	accumsan.convalli...
999	LevUniqueToSecondRDD	1-916-367-5608	Vivamus.nisi@ipsu...

2. **Performing set operations:** Just like `unionAll`, the DataFrame has functions for various set operations.

The intersection of two DataFrames would just entail calling the `intersect` function:

```
val intersection=students1.intersect(students2)
intersection.foreach(println)
```

```
[7,Sara,1-608-140-1995,Donec.nibh@enimEtiamimperdiet.edu]
[8,Kaseem,1-881-586-2689,cursus.et.magna@euismod.org]
[10,Maya,1-271-683-2698,accumsan.convallis@ornarelectusjusto.edu]
[9,Lev,1-916-367-5608,Vivamus.nisi@ipsumdolor.com]
```

Deriving the difference of one DataFrame from another is done by calling the `except ()` function with another DataFrame as the parameter:

```
val subtraction=students1.except(students2)
subtraction.foreach(println)
```

Here is the output:

```
[6,Laurel,1-691-379-9921,adipiscing@consectetueripsum.edu]
[4,Belle,1-246-894-6340,vitae.aliquet.nec@neque.co.uk]
[2,Kamal,1-668-571-5046,pede.Suspendisse@interdumenim.edu]
[5,Trevor,1-300-527-4967,dapibus.id@acturpisegestas.net]
[3,Olga,1-956-311-1686,Aenean.eget.metus@dictumcursusNunc.edu]
[1,Burke,1-300-746-8446,ullamcorper.velit.in@ametnullaDonec.co.uk]
```

If there are duplicates in the data, the `distinct` function will ignore them and return a DataFrame with only unique data:

```
val distinctStudents=allStudents.distinct
distinctStudents.foreach(println)
println(distinctStudents.count())
```

The following is the output:

```
[4,BelleDifferentName,1-246-894-6340,vitae.aliquet.nec@neque.co.uk]
[1,Burke,1-300-746-8446,ullamcorper.velit.in@ametnullaDonec.co.uk]
[2,KamalDifferentName,1-668-571-5046,pede.Suspendisse@interdumenim.edu]
[999,LevUniqueToSecondRDD,1-916-367-5608,Vivamus.nisi@ipsumdolor.com]
[1,BurkeDifferentName,1-300-746-8446,ullamcorper.velit.in@ametnullaDonec.co.uk]
[2,Kamal,1-668-571-5046,pede.Suspendisse@interdumenim.edu]
[3,Olga,1-956-311-1686,Aenean.eget.metus@dictumcursusNunc.edu]
[7,Sara,1-608-140-1995,Donec.nibh@enimEtiamimperdiet.edu]
[8,Kaseem,1-881-586-2689,cursus.et.magna@euismod.org]
[5,Trevor,1-300-527-4967,dapibus.id@acturpisegestas.net]
[4,Belle,1-246-894-6340,vitae.aliquet.nec@neque.co.uk]
[6,Laurel,1-691-379-9921,adipiscing@consectetueripsum.edu]
[6,LaurelInvalidPhone,000000000,adipiscing@consectetueripsum.edu]
[9,Lev,1-916-367-5608,Vivamus.nisi@ipsumdolor.com]
```

```
[3,Olga,1-956-311-1686,Aenean.eget.metus@
dictumcursusNuncDifferentEmail.edu]
[5,Trevor,1-300-527-4967,dapibusDifferentEmail.id@acturpisegestas.
net]
[10,Maya,1-271-683-2698,accumsan.convallis@ornarelectusjusto.edu]
```

Count output:

17

3. **Sorting the DataFrame by casting an attribute value:** Sometimes, our DataFrame inferences an integer attribute as a string. Since, DataFrames are immutable, the correct way of converting an attribute from one type to another is by creating another DataFrame. In this recipe, we'll not only cast one attribute type to another, but also sort the DataFrame based on that attribute. The simplest way to achieve this is by using the Spark SQL expression:

```
val sortedCols=allStudents.selectExpr("cast(id as int) as id",
"studentName", "phone", "email").sort("id")
println ("sorting")
sortedCols.show(sortedCols.count.toInt)
```

The output is shown here:

id	studentName	phone	email
1	Burke	1-300-746-8446	lullamcorper.velit...
1	BurkeDifferentName	1-300-746-8446	lullamcorper.velit...
2	Kamal	1-668-571-5046	pede.Suspendisse@...
2	KamalDifferentName	1-668-571-5046	pede.Suspendisse@...
3	Olga	1-956-311-1686	Aenean.eget.metus...
3	Olga	1-956-311-1686	Aenean.eget.metus...
4	Belle	1-246-894-6340	vitae.aliquet.nec...
4	BelleDifferentName	1-246-894-6340	vitae.aliquet.nec...
5	Trevor	1-300-527-4967	dapibusDifferentE...
5	Trevor	1-300-527-4967	dapibus.id@acturp...
6	Laurel	1-691-379-9921	adipiscing@consec...
6	LaurelInvalidPhone	00000000	adipiscing@consec...
7	Sara	1-608-140-1995	Donec.nibh@animEt...
7	Sara	1-608-140-1995	Donec.nibh@animEt...
8	Kaseem	1-881-586-2689	cursus.et.magna@e...
8	Kaseem	1-881-586-2689	cursus.et.magna@e...
9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...
9	Lev	1-916-367-5608	Vivamus.nisi@ipsu...
10	Maya	1-271-683-2698	accumsan.convalli...
10	Maya	1-271-683-2698	accumsan.convalli...
1999	LevUniqueToSecondRDD	1-916-367-5608	Vivamus.nisi@ipsu...

4. **Choosing a member from one dataset over another based on predicate:** Let's assume that for a given student ID across two different datasets, you would like to pick only the one that has a longer name (or matches some predicate). The result would be just one row per ID.

This involves three mini-steps:

1. Map the merged DataFrame (using `unionAll`) and spit out an RDD of pairs with the key as the ID (or any other field based on which you would like to merge):

```
val
idStudentPairs=allStudents.rdd.map(eachRow=>(eachRow.
getString(0),eachRow))
```

2. The next step is to use a function called `reduceByKey`. It accepts a function that takes two rows and returns a single row. In our case, we simply write the logic to choose the row with the longer name:

```
//Removes duplicates by id and holds on to the row with
the longest name

val idStudentPairs=allStudents.rdd.map(eachRow=>(eachRow.
getString(0),eachRow))

val longestNameRdd=idStudentPairs.reduceByKey((row1, row2)
=>
    if (row1.getString(1).length()>row2.getString(1).
length()) row1 else row2
)
```

3. Let's print the output:

```
longestNameRdd.values.foreach(println)
```

The output is as follows:

```
[4,BelleDifferentName,1-246-894-6340,vitae.aliquet.nec@neque.
co.uk]
[8,Kaseem,1-881-586-2689,cursus.et.magna@euismod.org]
[6,LaurelInvalidPhone,000000000,adipiscing@consecteturipsum.edu]
[2,KamalDifferentName,1-668-571-5046,pede.Suspendisse@
interdumenim.edu]
[7,Sara,1-608-140-1995,Donec.nibh@enimEtiamimperdiet.edu]
[5,Trevor,1-300-527-4967,dapibusDifferentEmail.id@acturpisegestas.
net]
[9,Lev,1-916-367-5608,Vivamus.nisi@ipsumdolor.com]
[3,Olga,1-956-311-1686,Aenean.eget.metus@
dictumcursusNuncDifferentEmail.edu]
```

```
[999, LevUniqueToSecondRDD, 1-916-367-5608, Vivamus.nisi@ipsumdolor.com]
```

```
[1, BurkeDifferentName, 1-300-746-8446, ullahcorper.velit.in@ametnullaDonec.co.uk]
```

```
[10, Maya, 1-271-683-2698, accumsan.convallis@ornarelectusjusto.edu]
```

5. **Parsing arbitrary date/time inputs and convert an array into a comma-separated string:** While preparing the data, we see that, particularly, the date and time appear in some crazy formats. As always, our aim is to standardize them. For this subrecipe, we'll be using a JSON that looks like this:

```
{ "name": "Cecelia Duke", "dob": "09/06/2014 05:25:39", "tags": ["reprehenderit", "cupidatat", "elit", "esse", "exercitation", "enim", "sunt"] },  
{ "name": "Conrad Lucas", "dob": "04/08/2014 05:54:02", "tags": ["occaecat", "amet", "adipiscing", "in", "est", "reprehenderit", "reprehenderit"] },  
{ "name": "Tasha Duran", "dob": "02/10/2014 00:29:27", "tags": ["voluptate", "consectetur", "esse", "ad", "et", "dolor", "ea"] },  
{ "name": "Faulkner Jackson", "dob": "07/03/2014 15:13:08", "tags": ["anim", "eiusmod", "commodo", "consequat", "aliqua", "ad", "non"] },  
{ "name": "Reed Joseph", "dob": "03/07/2014 00:19:31", "tags": ["voluptate", "enim", "ullamco", "incididunt", "cillum", "consectetur", "velit"] }
```

As we saw in previous recipes, we could bring in this JSON as a DataFrame, but the date format isn't ISO 8601, which means that it won't be considered as a timestamp and would be treated as plain string. In this subrecipe, let's see how to convert a string into a date format. This subrecipe involves four steps:



Performing arbitrary transformations is a work in progress
(<https://issues.apache.org/jira/browse/SPARK-4190>).

1. Import JSON as a text file:

```
val stringRDD = sc.textFile("StrangeDate.json")
```

2. Create a new `org.joda.time.format.DateTimeFormat` for the specific pattern that our input is in:

```
val formatter = DateTimeFormat.forPattern("MM/dd/yyyy  
HH:mm:ss")
```

3. We add `json4s` as our dependency in `build.sbt`:

```
"org.json4s" % "json4s-core_2.10" % "3.2.11",  
"org.json4s" % "json4s-jackson_2.10" % "3.2.11"
```

4. For each line of the JSON string, parse, and convert the string to `org.json4s.JsonValue`. The advantage of `JsonValue` is that we can traverse the JSON object with XPath-like expressions.

Chaining the compact and render function will help us convert `JsonValue` to `String`. In the following code, we extract the `name` field as is, convert an array of tags into a comma-separated string using the `extract` function, parse the date string using the `DateTimeFormat` that we created earlier, and construct a `Timestamp` object. Finally, we yield a case class called `JsonDateModel` out of the `for` comprehension that wraps around the `name`, `date`, and `tags`:

```
case class JsonDateModel (name:String, dob:Timestamp, tags:String)
  import org.json4s._
  import org.json4s.jackson.JsonMethods._
  implicit val formats = DefaultFormats

  val dateModelRDD = for {
    json <- stringRDD
    jsonValue = parse(json)
    name = compact(render(jsonValue \ "name"))
    dateAsString=compact(render(jsonValue \ "dob")).replace("\\", "")
    date = new Timestamp(formatter.parseDateTime(dateAsString).
getMillis())
    tags = render(jsonValue \ "tags").extract[List[String]].
mkString(",")
  } yield JsonDateModel(name, date, tags)
```

After that, we construct a `DataFrame` out of this case class `RDD` and print the schema to confirm:

```
import sqlContext.implicits._
val df=dateModelRDD.toDF()
df.printSchema()
df.show(df.count.toInt)
```

The output is as follows:

- Schema:

```
[info] root
[info] |-- name: string (nullable = true)
[info] |-- dob: timestamp (nullable = true)
[info] |-- tags: string (nullable = true)
```

- Data:

```
[info] name      dob      tags
[info] "Cecelia Duke"  2014-09-06 05:25:... ["reprehenderit",...
[info] "Conrad Lucas"  2014-04-08 05:54:... ["occaecat", "amet...
[info] "Tasha Duran"   2014-02-10 00:29:... ["voluptate", "con...
[info] "Faulkner Jackson" 2014-07-03 15:13:... ["anim", "eiusmod"...
[info] "Reed Joseph"   2014-03-07 00:19:... ["voluptate", "eni...
```


4

Data Visualization

In this chapter, we will cover the following recipes:

- ▶ Visualizing using Zeppelin
- ▶ Creating scatter plots with Bokeh-Scala
- ▶ Creating a time series MultiPlot with Bokeh-Scala

Introduction

In all honesty, free / open source data visualization tools in Scala aren't that rich compared to those in other mature data analysis languages, such as R or Python. We might partly attribute this to the lack of rich charting frameworks in Java, and visualization has never been a strong point for big data analytics.

That said, Scala (or more specifically the Hadoop world, including Spark) is catching up with the presence of the Apache incubator project Zeppelin and the highly active Scala bindings (<https://github.com/bokeh/bokeh-scala>) for the Bokeh project (<http://bokeh.pydata.org/en/latest/>). With R becoming the first-class citizen in Spark—with the availability of SparkR DataFrames from 1.4 onwards—Spark gets additional visualization from R other than the already existing Python APIs.

As a side note, all existing Java libraries are accessible from Scala. Hence, we are free to borrow any visualization library from Java.

Visualizing using Zeppelin

Apache Zeppelin is a nifty web-based tool that helps us visualize and explore large datasets. From a technical standpoint, Apache Zeppelin is a web application on steroids. We aim to use this application to render some neat, interactive, and shareable graphs and charts.

The interesting part of Zeppelin is that it has a bunch of built-in interpreters—ones that can interpret and invoke all API functions in Spark (with a `SparkContext`) and Spark SQL (with a `SQLContext`). The other interpreters that are built in are for Hive, Flink, Markdown, and Scala. It also has the ability to run remote interpreters (outside of Zeppelin's own JVM) via Thrift. To look at the list of built-in interpreters, you can go through `conf/interpreter.json` in the `zeppelin` installation directory. Alternatively, you can view and customize the interpreters from `http://localhost:8080/#/interpreter` once you start the `zeppelin` daemon.

How to do it...

In this recipe, we'll be using the built-in `SparkContext` and `SQLContext` inside Zeppelin and transform data using Spark. At the end, we'll register the transformed data as a table and use Spark SQL to query the data and visualize it.

The list of subrecipes in this section is as follows:

- ▶ Installing Zeppelin
- ▶ Customizing Zeppelin's server and websocket port
- ▶ Visualizing data on HDFS – parameterizing inputs
- ▶ Using custom functions during visualization
- ▶ Adding external dependencies to Zeppelin
- ▶ Pointing to an external Spark cluster

Installing Zeppelin

Zeppelin (<http://zeppelin-project.org/>) doesn't have a binary bundle yet. However, just as its project site claims, it is pretty easy to build from source. We just ought to run one command to install it on our local machine. At the end of this recipe, we'll take a look at how to point our Zeppelin to an external Spark master:

```
git clone https://github.com/apache/incubator-zeppelin.git
cd incubator-zeppelin
mvn clean package -Pspark-1.4 -Dhadoop.version=2.2.0 -Phadoop-2.2
-DskipTests
```

```

[INFO] Reactor Summary:
[INFO]
[INFO] Zeppelin ..... SUCCESS [3.364s]
[INFO] Zeppelin: Interpreter ..... SUCCESS [15.299s]
[INFO] Zeppelin: Zengine ..... SUCCESS [6.053s]
[INFO] Zeppelin: Spark ..... SUCCESS [36.770s]
[INFO] Zeppelin: Markdown interpreter ..... SUCCESS [2.342s]
[INFO] Zeppelin: Angular interpreter ..... SUCCESS [2.430s]
[INFO] Zeppelin: Shell interpreter ..... SUCCESS [2.055s]
[INFO] Zeppelin: Hive interpreter ..... SUCCESS [3.454s]
[INFO] Zeppelin: Tajo interpreter ..... SUCCESS [2.624s]
[INFO] Zeppelin: web Application ..... SUCCESS [31.395s]
[INFO] Zeppelin: Server ..... SUCCESS [16.905s]
[INFO] Zeppelin: Packaging distribution ..... SUCCESS [0.546s]
[INFO] -----
[INFO] BUILD SUCCESS
[INFO] -----
[INFO] Total time: 2:03.650s
[INFO] Finished at: Fri May 29 23:10:52 SGT 2015
[INFO] Final Memory: 97M/1323M
[INFO] -----

```

Once built, we can start the Zeppelin daemon using the following command:

```
bin/zeppelin-daemon.sh start
```

```

Gabriel@Gabriels-MacBook-Pro ~/A/incubator-zeppelin> bin/zeppelin-daemon.sh start
Log dir doesn't exist, create /Users/Gabriel/Apps/incubator-zeppelin/logs
Pid dir doesn't exist, create /Users/Gabriel/Apps/incubator-zeppelin/run
Zeppelin start [ OK ]

```

To stop the daemon, we can use this command:

```
bin/zeppelin-daemon.sh stop
```



If you come across the following error, you can check with `rat.txt`, only to find that it complains about your data file:

Failed to execute goal org.apache.rat:apache-rat-plugin:0.11:check (verify.rat) on project zeppelin: Too many files with unapproved license: 3

Simply move your data file to a different location and initiate the build again.

Customizing Zeppelin's server and websocket port

Zeppelin runs on port 8080 by default, and it has a websocket port enabled at the +1 port (8081) by default. We can customize the port by copying `conf/zeppelin-site.xml.template` to `conf/zeppelin-site.xml` and changing the ports and various other properties, if necessary. Since the Spark standalone cluster master web UI also runs on 8080, when we are running Zeppelin on the same machine as the Spark master, we have to change the ports to avoid conflicts.



```
1 |<?xml version="1.0"?>
2 |<?xml-stylesheet type="text/xsl" href="configuration.xsl"?>
3 |<!--
4 | Licensed to the Apache Software Foundation (ASF) under one or more
5 | contributor license agreements. See the NOTICE file distributed with
6 | this work for additional information regarding copyright ownership.
7 | The ASF licenses this file to You under the Apache License, Version 2.0
8 | (the "License"); you may not use this file except in compliance with
9 | the License. You may obtain a copy of the License at
10 |
11 | http://www.apache.org/licenses/LICENSE-2.0
12 |
13 | Unless required by applicable law or agreed to in writing, software
14 | distributed under the license is distributed on an "AS IS" BASIS,
15 | WITHOUT WARRANTIES OR CONDITIONS OF ANY KIND, either express or implied.
16 | See the License for the specific language governing permissions and
17 | limitations under the License.
18 | -->
19 |
20 | <configuration>
21 |
22 | <property>
23 |   <name>zeppelin.server.addr</name>
24 |   <value>0.0.0.0</value>
25 |   <description>Server address</description>
26 | </property>
27 |
28 | <property>
29 |   <name>zeppelin.server.port</name>
30 |   <value>8180</value>
31 |   <description>Server port. port+1 is used for web socket.</description>
32 | </property>
33 |
34 | <property>
35 |   <name>zeppelin.websocket.addr</name>
36 |   <value>0.0.0.0</value>
37 |   <description>Testing websocket address</description>
38 | </property>
39 |
40 | <!-- If the port value is negative, then it'll default to the server
41 | port + 1.
42 | -->
43 | <property>
44 |   <name>zeppelin.websocket.port</name>
45 |   <value>-1</value>
46 |   <description>Testing websocket port</description>
47 | </property>
48 |
```

1. For now, let's change the port to 8180. In order for this to take effect, let's restart Zeppelin using `bin/zeppelin-daemon restart`

Visualizing data on HDFS – parameterizing inputs

Once we start the daemon, we can point our browser to `http://localhost:8080` (change the port as per your modified port configuration) to view the Zeppelin UI. Zeppelin organizes its contents as notes and paragraphs. A note is simply a list of all the paragraphs on a single web page.

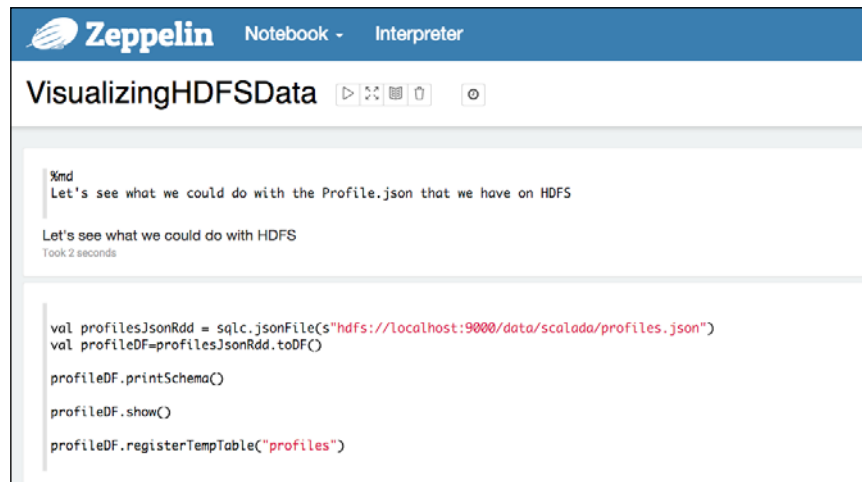
Using data from HDFS simply means that we point to the HDFS location instead of the local filesystem location.

Before we consume the file from HDFS, let's quickly check the Spark version that Zeppelin uses. This can be achieved by issuing `sc.version` on a paragraph. The `sc` is an implicit variable representing the `SparkContext` inside Zeppelin, which simply means that we need not programmatically create a `SparkContext` within Zeppelin.

```
sc.version
res0: String = 1.4.0
Took 1 seconds
```

Next, let's load the `profiles.json` sample data file, convert it into a `DataFrame`, and print the schema and the first 20 rows (`show`) for verification. Let's also finally register the `DataFrame` as a table. Just like the implicit variable for `SparkContext`, `SQLContext` is represented by the `sqlc` implicit variable inside Zeppelin:

```
val profilesJsonRdd = sqlc.jsonFile("hdfs://localhost:9000/data/scalada/
profiles.json")
val profileDF=profilesJsonRdd.toDF()
profileDF.printSchema()
profileDF.show()
profileDF.registerTempTable("profiles")
```



The output looks like this:

```

val profilesJsonRdd = sqlc.jsonFile(s"hdfs://localhost:9000/data/scalada/profiles.json")
val profileDF=profilesJsonRdd.toDF()

profileDF.printSchema()

profileDF.show()

profileDF.registerTempTable("profiles")

profilesJsonRdd: org.apache.spark.sql.DataFrame = [_id: string, about: string, address: string, age: bigint, c
ing, phone: string, registered: string, tags: array<string>]
profileDF: org.apache.spark.sql.DataFrame = [_id: string, about: string, address: string, age: bigint, company
hone: string, registered: string, tags: array<string>]
root
 |-- _id: string (nullable = true)
 |-- about: string (nullable = true)
 |-- address: string (nullable = true)
 |-- age: long (nullable = true)
 |-- company: string (nullable = true)
 |-- email: string (nullable = true)
 |-- eyeColor: string (nullable = true)
 |-- favoriteFruit: string (nullable = true)
 |-- gender: string (nullable = true)
 |-- name: string (nullable = true)
 |-- phone: string (nullable = true)
 |-- registered: string (nullable = true)
 |-- tags: array (nullable = true)
 |   |-- element: string (containsNull = true)

 _id          about          address          age  company  email          eyeColor fav
55578ccb0cc5b350d... Eu excepteur esse... 694 Oriental Cour... 30  ENDIPIN  tracynguyen@endip... brown  app
55578ccb6975c4e2a... Proident exercita... 267 Amber Street,... 23  WARETEL  leannagarrett@war... brown  str
55578ccb33399a615... Aute proident Lor... 243 Bridgewater S... 24  IMPERIUM  blairwhite@imperi... brown  ban
55578ccb0f1d5ab09... Officia cillum nu... 647 Loring Avenue... 24  BEADZZA  andrearay@beadzza... blue  app
55578ccb591a45d4e... Sit fugiat mollit... 721 Bijou Avenue,... 27  AUSTECH  penningtongilbert... green  app
55578ccb9f0cd20c4... Minim do eiusmod ... 694 Llama Court, ... 21  PYRAMIA  shelleburns@pyra... green  ban
55578ccb8d0accc28... Qui proident ulla... 498 Perry Terrace... 40  EDECINE  nicolefigueroa@ed... green  app
55578ccb682cca21... Labore exercitati... 243 Stillwell Ave... 32  SINGAVERA  galealvarado@sing... blue  ban
55578ccb0d9025ddd... Velit cillum Lore... 649 Beard Street,... 36  FURNITECH  melindaparker@fur... blue  str
55578ccb5be70de0d... Laborum tempor mi... 972 Marconi Place... 36  DIGIAL  byerscarson@digia... blue  app
55578ccbc5a1050a5... Duis fugiat Lorem... 483 Hanson Place,... 31  ASSURITY  kristiemckinney@... green  ban
55578ccb07fa02369... Consequat fugiat ... 540 Woodpoint Roa... 40  MICROLUXE  salazarburks@micr... brown  str
55578ccb809e55bf0... Lorem culpa Lorem... 442 Ainslie Stree... 32  VIOCLULAR  hopkinspatterson@... green  app
55578ccb204ff8ee6... Qui ad cillum mag... 444 Argyle Road, ... 23  IMKAN  maysrosario@imkan... green  app
55578ccb4b062fc61... Duis ex velit du... 571 Sunnyside Ave... 38  HELIXO  atkinshancock@hel... blue  str
55578ccb5ff361a9... Et magna laboris ... 385 Meeker Avenue... 40  SLOFAST  edwinarobertson@... blue  str
55578ccb386940ac3... Labore sit mollit... 936 Cheever Place... 37  FLEETMIX  elsienoe@fleetmi... blue  app
55578ccbf41ff7fe... Consequat eiusmod... 406 Lake Place, M... 36  EVENTAGE  mirandamarsh@even... green  app
55578ccbfa6b6c300... Duis fugiat conse... 364 Metropolitan ... 31  BALOOBA  sharronmcconnell@... brown  app
55578ccbdd6650d81... Consequat et magn... 113 Applegate Cou... 29  EURON  mcdowellwelch@eur... blue  str

Took 1 seconds

```



Be careful not to explicitly create `SQLContext` or `SparkContext`. If we create a `SQLContext` explicitly and register our temporary tables to it, it won't be accessible from the SQL queries that we execute. We'll get this error:

no such table List ([YOUR TEMP TABLE NAME])

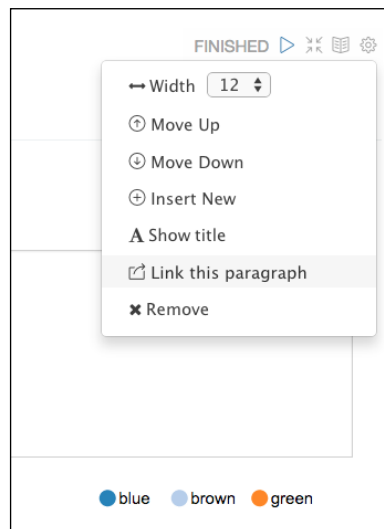
Let's now run a simple query to understand eye colors and their counts for men in the dataset:

```
%sql select eyeColor, count(eyeColor) as count from profiles where gender='male' group by eyeColor
```

The `%sql` at the beginning of the paragraph indicates to Zeppelin that we are about to execute a Spark SQL query in this paragraph.



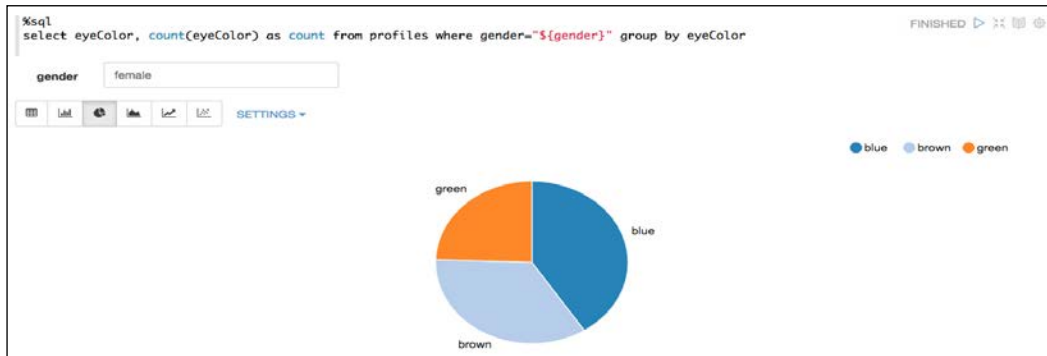
Now, if we wish to share this chart with someone or link it to an external website, we can do so by clicking on the gear icon in this paragraph and then clicking on **Link this paragraph**, as shown in the following screenshot:



Data Visualization

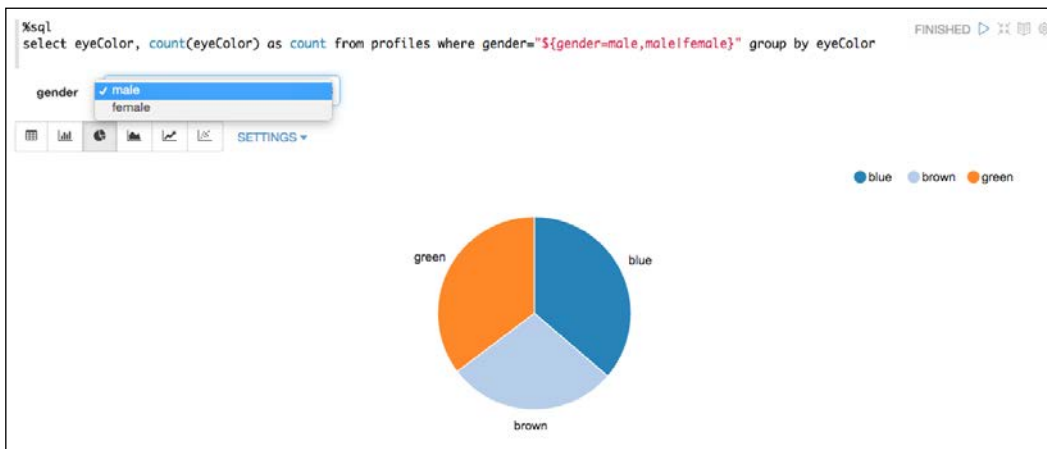
We can actually parameterize the input for gender instead of altering our query every time. This is achieved by the use of `${PARAMETER PLACEHOLDER}`:

```
%sql select eyeColor, count(eyeColor) as count from profiles where gender="${gender}" group by eyeColor
```



Finally, if parameterizing using free-form text isn't enough, we can use a dropdown instead:

```
%sql select eyeColor, count(eyeColor) as count from profiles where gender="${gender=male,male|female}" group by eyeColor
```



Running custom functions

While Spark SQL doesn't support a range of functions as wide as ANSI SQL does, it has an easy and powerful mechanism for registering a normal Scala function and using it inside the SQL context.

Let's say we would like to find out how many profiles fall under each age group. We have a simple function called `ageGroup`. Given an age, it returns a string representing the age group:

```
def ageGroup(age: Long) = {
  val buckets = Array("0-10", "11-20", "20-30", "31-40", "41-50", "51-60", "61-70", "71-80", "81-90", "91-100", ">100")
  buckets(math.min((age.toInt - 1) / 10, buckets.length - 1))
}
```

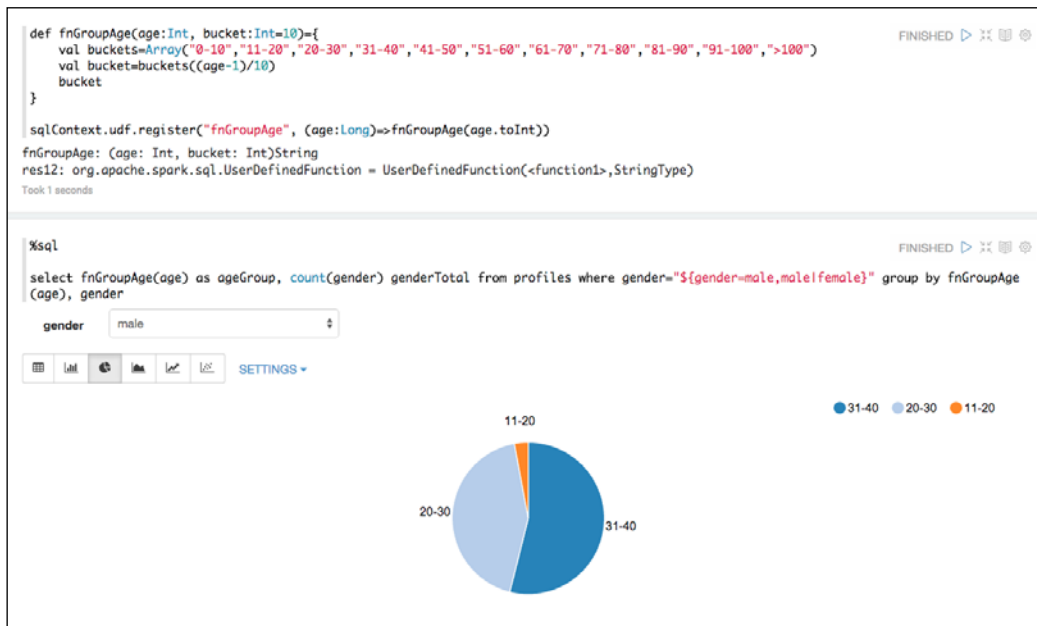
Now, in order to register this function to be used inside Spark SQL, all that we need to do is give it a name and call the `register` method of the `SQLContext`'s user-defined function object:

```
sqlContext.udf.register("ageGroup", (age:Long)=>ageGroup(age.toInt))
```

Let's fire our query and see the use of the function in action:

```
%sql select ageGroup(age) as group,
      count(1) as total
from profiles
where gender='${gender=male,male|female}' group by ageGroup(age)
order by group
```

Here is the output:



Adding external dependencies to Zeppelin

Sooner or later, we would be depending on external libraries than that come bundled with Zeppelin, say for an efficient CSV import or RDBMS data import. Let's see how to load a MySQL database driver and visualize data from a table.

In order to load a `mysql` connector `java` driver, we just need to specify the group ID, artifact ID, and version number, and the JAR gets downloaded from the `maven` repository. `%dep` indicates that the paragraph adds a dependency, and the `z` implicit variable represents the Zeppelin context:

```
%dep
z.load("mysql:mysql-connector-java:5.1.35")
```

If we would like to point to our enterprise Maven repository or some other custom repository, we can add them by calling the `addRepo` method of the Zeppelin context available via the same `z` implicit variable:

```
%dep
z.addRepo("RepoName").url("RepoURL")
```

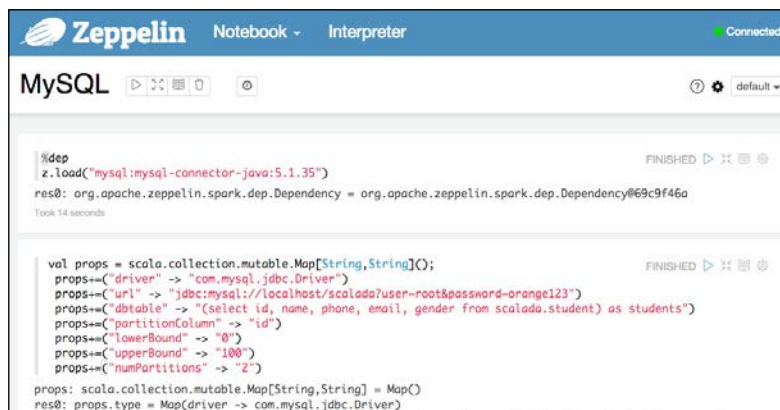
Alternatively, we can load the `jar` from the local filesystem using the overloaded `load` method:

```
%dep
z.load("/path/to.jar")
```

The only thing that we need to watch out for while using `%dep` is that the dependency paragraph should be used before using the libraries that are being loaded. So, it is generally advised to load the dependencies at the top of the Notebook.

Let's see the use in action:

- ▶ Loading the dependency:



The screenshot shows a Zeppelin Notebook interface with the title 'MySQL'. The top bar indicates 'Connected'. The notebook content is divided into two paragraphs. The first paragraph is a dependency paragraph starting with `%dep` and `z.load("mysql:mysql-connector-java:5.1.35")`. The output shows a successful dependency resolution: `res0: org.apache.zeppelin.spark.dep.Dependency = org.apache.zeppelin.spark.dep.Dependency@69c9f46a`. The second paragraph is a Scala code paragraph defining a `props` map with various properties for a MySQL query. The output shows the `props` map and its type: `res0: props.type = Map(driver -> com.mysql.jdbc.Driver)`.

```

%dep
z.load("mysql:mysql-connector-java:5.1.35")
res0: org.apache.zeppelin.spark.dep.Dependency = org.apache.zeppelin.spark.dep.Dependency@69c9f46a
Took 14 seconds

val props = scala.collection.mutable.Map[String,String]();
props+=("driver" -> "com.mysql.jdbc.Driver")
props+=("url" -> "jdbc:mysql://localhost/scalada?user=root&password=orange123")
props+=("dbtable" -> "(select id, name, phone, email, gender from scalada.student) as students")
props+=("partitionColumn" -> "id")
props+=("lowerBound" -> "0")
props+=("upperBound" -> "100")
props+=("numPartitions" -> "2")
props: scala.collection.mutable.Map[String,String] = Map()
res0: props.type = Map(driver -> com.mysql.jdbc.Driver)

```

Once we have loaded the dependencies, we need to construct the options required to connect to the MySQL database:

```
val props = scala.collection.mutable.Map[String,String] () ;
  props+=("driver" -> "com.mysql.jdbc.Driver")
  props+=("url" -> "jdbc:mysql://localhost/scalada?user=root&password=orange123")
  props+=("dbtable" -> "(select id, name, phone, email, gender
from scalada.student) as students")
  props+=("partitionColumn" -> "id")
  props+=("lowerBound" -> "0")
  props+=("upperBound" -> "100")
  props+=("numPartitions" -> "2")
```

- ▶ Using the connection to create a DataFrame:

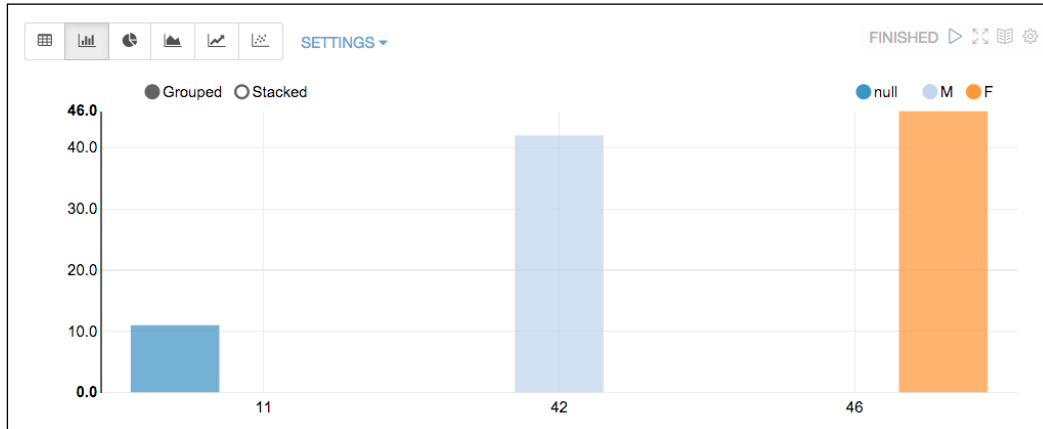
```
import scala.collection.JavaConverters._
val studentDf = sqlContext.load("jdbc", props.asJava)
studentDf.printSchema()
studentDf.show()
studentDf.registerTempTable("students")

import scala.collection.JavaConverters._
warning: there were 1 deprecation warning(s); re-run with -deprecation for details
studentDf: org.apache.spark.sql.DataFrame = [id: string, name: string, phone: string, email: string, gender: string]
root
 |-- id: string (nullable = false)
 |-- name: string (nullable = true)
 |-- phone: string (nullable = true)
 |-- email: string (nullable = true)
 |-- gender: string (nullable = true)

+----+-----+-----+-----+-----+
|id|  name|  phone|  email|gender|
+----+-----+-----+-----+-----+
|10| Maya|1-271-683-2698|accumsan.convalli...| F|
|11| Emil|1-467-270-1337|est@nunc.com| F|
|12| Caleb|1-683-212-0896|Suspendisse@Quisq...| M|
|13| Florence|1-603-575-2444|sit.amet.dapibus@...| F|
```

```
import scala.collection.JavaConverters._
val studentDf = sqlContext.load("jdbc", props.asJava)
studentDf.printSchema()
studentDf.show()
studentDf.registerTempTable("students")
```

- ▶ Visualizing the data:



Pointing to an external Spark cluster

Running Zeppelin with built-in Spark is all good, but in most of our cases, we'll be executing the Spark jobs initiated by Zeppelin on a cluster of workers. Achieving this is pretty simple; we need to configure Zeppelin to point its Spark `master` property to an external Spark master URL. We'll be looking at how to install and run a Spark cluster on AWS, or a truly distributed cluster, in a later chapter (*Chapter 6, Scaling Up*), but for this example, I have a simple and standalone external Spark cluster running on my local machine. Please note that we will have to run Zeppelin on a different port because of the Zeppelin UI port's conflict with the Spark standalone cluster master web UI over 8080:

For this example, let's download the Spark source for 1.4.1 and build it for Hadoop version 2.2:

```
build/mvn -Pyarn -Phadoop-2.2 -Dhadoop.version=2.2.0 -DskipTests clean package
```

Similarly, let's download the `zeppelin` incubator and build it, specifying the Hadoop version to be 2.2:

```
mvn clean install -Pspark-1.4 -Dhadoop.version=2.2.0 -Phadoop-2.2 -DskipTests -Pyarn
```

Let's bring up the Spark cluster. From inside your Spark source, execute this:

```
sbin/start-all.sh
```

Finally, let's modify `conf/interpreter.json` and `conf/zeppelin-env.sh` to point the `master` property to the host on which the Spark VM is running. In this case, it will be my `localhost`, with the port being `7077`, which is the default master port.

1. The `conf/interpreter.json` file:

```
"ZARAAA1GU": {
  "id": "ZARAAA1GU",
  "name": "spark",
  "group": "spark",
  "properties": {
    "spark.cores.max": "",
    "spark.yarn.jar": "",
    "master": "spark://Gabriels-MacBook-Pro.local:7077",
    "zeppelin.spark.maxResult": "1000",
    "zeppelin.dep.localrepo": "local-repo",
    "spark.app.name": "Zeppelin",
    "spark.executor.memory": "512m",
    "zeppelin.spark.useHiveContext": "true",
    "zeppelin.spark.concurrentSQL": "false",
    "spark.home": "",
    "args": ""
  }
}
```

2. The `conf/zeppelin-env.sh` file:

```
# export JAVA_HOME=
export MASTER=spark://Gabriels-MacBook-Pro.local:7077
```

Now, when we rerun Spark SQL from Zeppelin, we can see that the job runs on the external Spark instance, as shown here:

The screenshot displays the Spark Master web interface for the instance at `spark://Gabriels-MacBook-Pro.local:7077`. The interface includes the following information:

- Spark Master at spark://Gabriels-MacBook-Pro.local:7077**
- URL: `spark://Gabriels-MacBook-Pro.local:7077`
- REST URL: `spark://Gabriels-MacBook-Pro.local:6066 (cluster mode)`
- Workers: 1
- Cores: 8 Total, 8 Used
- Memory: 15.0 GB Total, 512.0 MB Used
- Applications: 1 Running, 0 Completed
- Drivers: 0 Running, 0 Completed
- Status: ALIVE

Workers

Worker Id	Address	State	Cores	Memory
worker-20150614200314-192.168.2.117-61797	192.168.2.117:61797	ALIVE	8 (8 Used)	15.0 GB (512.0 MB Used)

Running Applications

Application ID	Name	Cores	Memory per Node	Submitted Time	User	State	Duration
app-20150614205658-0000	Zeppelin	8	512.0 MB	2015/06/14 20:56:58	Gabriel	RUNNING	25 s

Completed Applications

Application ID	Name	Cores	Memory per Node	Submitted Time	User	State	Duration
----------------	------	-------	-----------------	----------------	------	-------	----------

Creating scatter plots with Bokeh-Scala

While Zeppelin is powerful enough to quickly execute our Spark SQLs and visualize data, it is still an evolving platform. In this section, we'll take a brief look at the most popular visualizing framework in Python, called Bokeh, and use its (also fast evolving) Scala bindings to the framework. Breeze also has a visualization API called **breeze-viz**, which is built on JFreeChart. Unfortunately, at the time of writing this book, the API is not actively maintained, and therefore we won't be discussing it here.

The power of Zeppelin lies in the ability to share and view graphics on the browser. This is brought forth by the backing of the D3.js JavaScript visualization library. Bokeh is also backed by another JavaScript visualization library, called BokehJS. The Scala bindings library (`bokeh-scala`) not only gives an easier way to construct glyphs (lines, circles, and so on) out of Scala objects, but also translates glyphs into a format that is understandable by the BokehJS JavaScript components.

There is a warning here: the Bokeh-Scala bindings are still evolving and act at a lower level. Sometimes, this is more cumbersome than its Python counterpart. That said, I am still sure that we all would be able to appreciate the amazing graphs that we can create right out of Scala.

How to do it...

In this recipe, we will be creating a scatter plot using iris data (<https://archive.ics.uci.edu/ml/datasets/Iris>), which has the length and width attributes of flowers belonging to three different species of the same plant. Drawing a scatter plot on this dataset involves a series of interesting substeps.

For the purpose of representing the iris data in a Breeze matrix, I have naïvely transformed the species categories into numbers:

- ▶ *Iris setosa*: 0
- ▶ *Iris versicolor*: 1
- ▶ *Iris virginica*: 2

This is available in `irisNumeric.csv`. Later, we'll see how we can load the original iris data (`iris.data`) into a Spark DataFrame and use that as a source for plotting.

For the sake of clarity, let's define what the various terms in Bokeh actually mean:

- ▶ **Glyph**: All geometric shapes that we can think of—circles, squares, lines, and so on—are glyphs. This is just the UI representation and doesn't hold any data. All the properties related to this object just help us modify the UI properties: `color`, `x`, `y`, `width`, and so on.

- ▶ **Plot:** A plot is like a canvas on which we arrange various objects relevant to the visualization, such as the legend, x and y axes, grid, tools, and obviously, the core of the graph—the data itself. We construct various accessory objects and finally add them to the list of renderers in the plot object.
- ▶ **Document:** The document is the component that does the actual rendering. It accepts the plot as an argument, and when we call the `save` method in the document, it uses all the child renderers in the plot object and constructs a JSON from the wrapped elements. This JSON is eventually read by the BokehJS widgets to render the data in a visually pleasing manner. More than one plot can be rendered in the document by adding it to a grid plot (we'll look at how this is done in the next recipe, *Creating a time series MultiPlot with Bokeh-Scala*).

A plot is a composition of multiple widgets/glyphs.

This consists of a series of steps:

1. Preparing our data.
2. Creating the Plot and Document objects.
3. Creating a point (marker object) and a renderer for it.
4. Setting the x and y axes' data range for the plot.
5. Drawing the x and the y axes.
6. Viewing the marker objects with varying colors.
7. Adding Grid lines.
8. Adding a legend to the plot.

Preparing our data

Bokeh plots require our data to be in a format that it understands, but it's really easy to do it. All that we need to do is create a new source object that inherits from `ColumnDataSource`. The other options are `AjaxDataSource` and `RemoteDataSource`.

So, let's overlay our Breeze data source on `ColumnDataSource`:

```
import breeze.linalg._

object IrisSource extends ColumnDataSource {

  private val colormap = Map[Int, Color](0 -> Color.Red, 1 ->
Color.Green, 2 -> Color.Blue)

  private val iris = csvread(file = new File("irisNumeric.csv"),
separator = ',')
```

```
    val sepalLength = column(iris(:, 0))
    val sepalWidth = column(iris(:, 1))
    val petalLength = column(iris(:, 2))
    val petalWidth = column(iris(:, 3))
    val species = column(iris(:, 4))
}
```

The first line just reads `irisNumeric.csv` using the `csvread` function of the Breeze library. The color map is something that we'll be using later while plotting. The purpose of this map is to translate each species of flower into a different color. The final piece is where we convert the Breeze matrix into `ColumnDataSource`. As required by `ColumnDataSource`, we select and map specific columns in the Breeze matrix to corresponding columns.

Creating Plot and Document objects

Let's have our image's title as `Iris Petal Length vs Width` and create a document object so that we can save the final HTML by the name `IrisBokehBreeze.html`. Since we haven't specified the full path of the target file in the `save` method, the file will be saved in the same directory as the project itself:

```
val plot = new Plot().title("Iris Petal Length vs Width")

val document = new Document(plot)
val file = document.save("IrisBokehBreeze.html")

println(s"Saved the chart as ${file.url}")
```

Creating a marker object

Our plot has neither data nor any glyphs. Let's first create a marker object that marks the data point. There are a variety of marker objects to choose from: `Asterisk`, `Circle`, `CircleCross`, `CircleX`, `Cross`, `Diamond`, `DiamondCross`, `InvertedTriangle`, `PlainX`, `Square`, `SquareCross`, `SquareX`, and `Triangle`.

Let's choose `Diamond` for our purpose:

```
val diamond = new Diamond()
    .x(petalLength)
    .y(petalWidth)
    .fill_color(Color.Blue)
    .fill_alpha(0.5)
    .size(5)

val dataPointRenderer = new GlyphRenderer().data_source(IrisSource).
glyph(diamond)
```

While constructing the marker object, other than the UI attributes, we also say what the x and the y coordinates for it are. Note that we have also mentioned that the color of this marker is blue. We'll change that in a while using the color map.

Setting the X and Y axes' data range for the plot

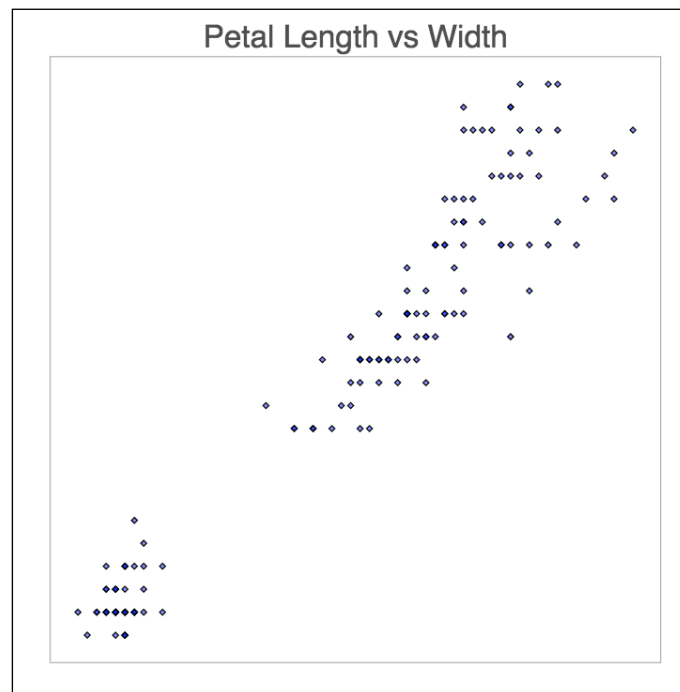
The plot needs to know what the x and y data ranges of the plot are before rendering. Let's do that by creating two `DataRange` objects and setting them to the plot:

```
val xRange = new DataRangeId().sources(petal_length :: Nil)
val yRange = new DataRangeId().sources(petal_width :: Nil)
```

```
plot.x_range(xRange).y_range(yRange)
```

Let's try and run the first cut of this program.

The following is the output:



We see that this needs a lot of work to be done. Let's do it bit by bit.

Drawing the x and the y axes

Let's now draw the axes, set their bounds, and add them to the plot's renderers. We also need to let the plot know which location each axis belongs to:

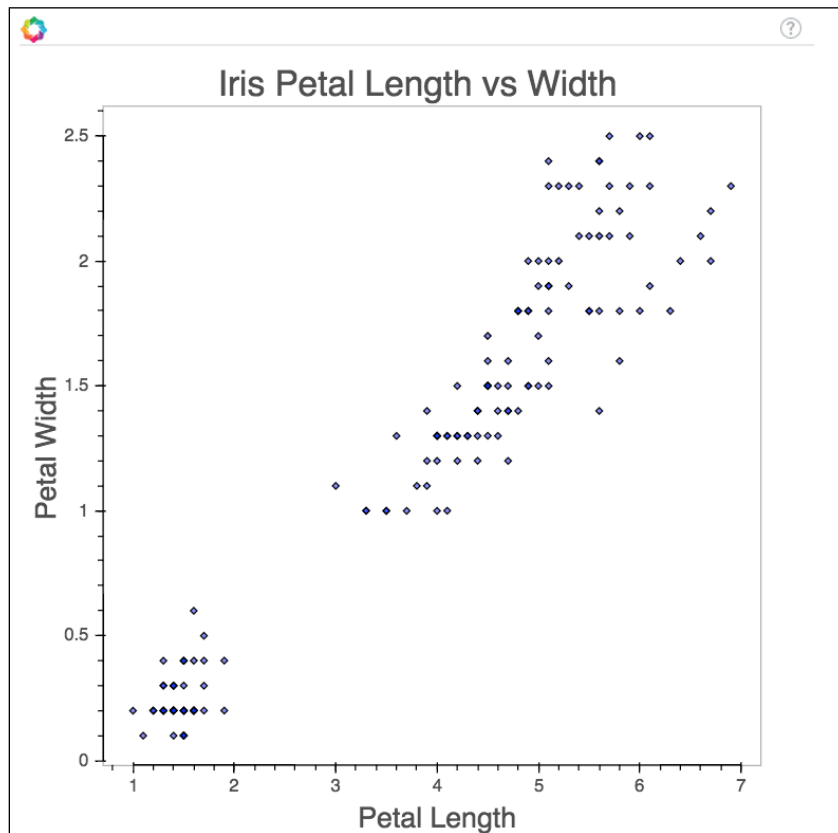
```
//X and Y Axis
val xAxis = new LinearAxis().plot(plot).axis_label("Petal Length").
bounds((1.0, 7.0))

val yAxis = new LinearAxis().plot(plot).axis_label("Petal Width").
bounds((0.0, 2.5))

plot.below <<= (listRenderer => (xAxis :: listRenderer))
plot.left <<= (listRenderer => (yAxis :: listRenderer))

//Add the renderer to the plot
plot.renderers := List(xAxis, yAxis, dataPointRenderer)
```

Here is the output:



Viewing flower species with varying colors

All the data points are marked with blue as of now, but we would really like to differentiate the species visually. This is a simple two-step process:

1. Add new derived data (`speciesColor`) into our `ColumnDataSource` to hold colors that represent the species:

```
object IrisSource extends ColumnDataSource {

  private val colormap = Map[Int, Color](0 -> Color.Red, 1
-> Color.Green, 2 -> Color.Blue)

  private val iris = csvread(file = new
File("irisNumeric.csv"), separator = ',')

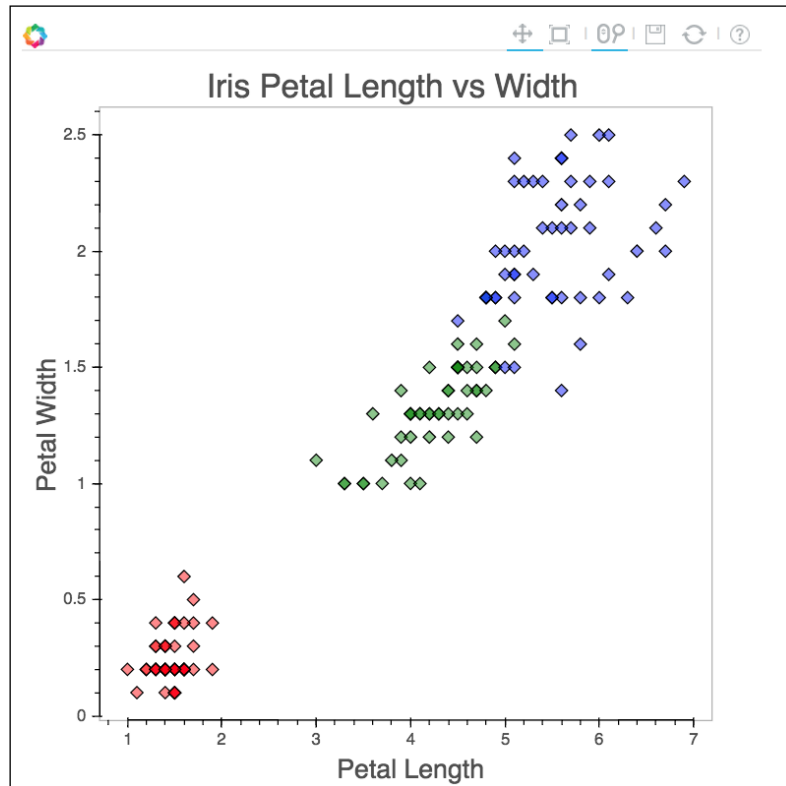
  val sepalLength = column(iris(:, 0))
  val sepalWidth = column(iris(:, 1))
  val petalLength = column(iris(:, 2))
  val petalWidth = column(iris(:, 3))
  val speciesColor = column(species.value.map(v =>
colormap(v.round.toInt)))
}
```

So, we assign red to *Iris setosa*, green to *Iris versicolor* and blue to *Iris virginica*.

2. Modify the `diamond` marker to take this as input instead of accepting a static blue:

```
val diamond = new Diamond()
  .x(petalLength)
  .y(petalWidth)
  .fill_color(speciesColor)
  .fill_alpha(0.5)
  .size(10)
```

The output is as follows:

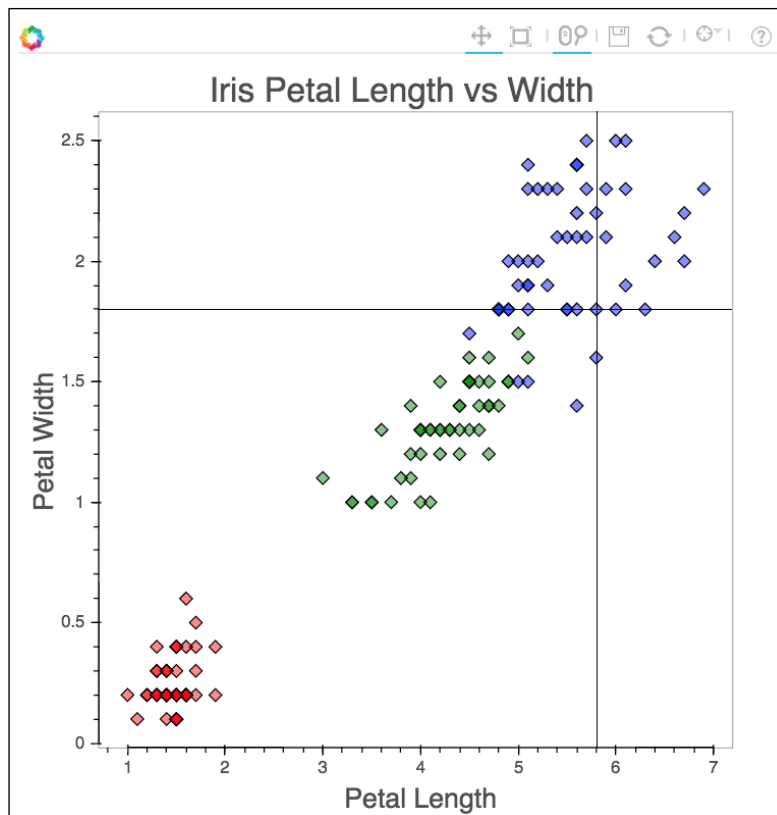


It looks fairly okay now. Let's add some tools to the image. Bokeh has some nice tools that can be attached to the image: `BoxSelectTool`, `BoxZoomTool`, `CrosshairTool`, `HoverTool`, `LassoSelectTool`, `PanTool`, `PolySelectTool`, `PreviewSaveTool`, `ResetTool`, `ResizeTool`, `SelectTool`, `TapTool`, `TransientSelectTool`, and `WheelZoomTool`.

Let's add a few of them to see them for fun:

```
val panTool = new PanTool().plot(plot)
    val wheelZoomTool = new WheelZoomTool().plot(plot)
    val previewSaveTool = new PreviewSaveTool().plot(plot)
    val resetTool = new ResetTool().plot(plot)
    val resizeTool = new ResizeTool().plot(plot)
    val crosshairTool = new CrosshairTool().plot(plot)

plot.tools := List(panTool, wheelZoomTool, previewSaveTool, resetTool,
    resizeTool, crosshairTool)
```



Adding grid lines

While we have the crosshair tool, which helps us locate the exact x and y values of a particular data point, it would be nice to have a data grid too. Let's add two data grids, one for the x axis and one for the y axis:

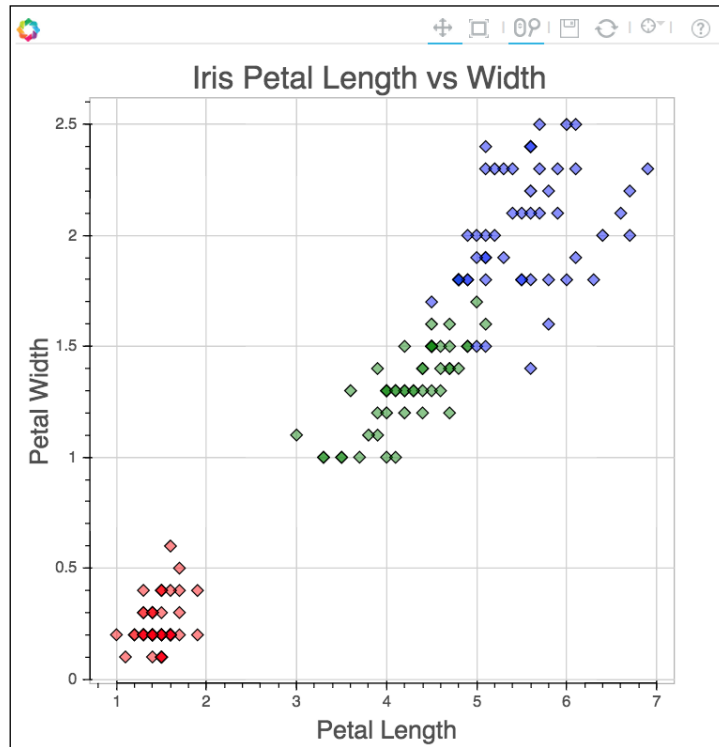
```
val xAxis = new LinearAxis().plot(plot).axis_label("Petal Length").
bounds((1.0, 7.0))

val yAxis = new LinearAxis().plot(plot).axis_label("Petal Width").
bounds((0.0, 2.5))

val xgrid = new Grid().plot(plot).axis(xAxis).dimension(0)
val ygrid = new Grid().plot(plot).axis(yAxis).dimension(1)
```

Next, let's add the grids to the plot renderer list too:

```
plot.renderers := List(xAxis, yAxis, dataPointRenderer, xgrid, ygrid)
```



Adding a legend to the plot

This step is a bit tricky in the Scala binding of Bokeh due to the lack of high-level graphing objects, such as `scatter`. For now, let's cook up our own legend. The `legends` property of the `Legend` object accepts a list of tuples - a label and a `GlyphRenderer` pair. Let's explicitly create three `GlyphRenderer` wrapping diamonds of three colors, which represent the species. We then add them to the plot:

```
val setosa = new Diamond().fill_color(Color.Red).size(10).fill_alpha(0.5)
  val setosaGlyphRnd=new GlyphRenderer().glyph(setosa)
  val versicolor = new Diamond().fill_color(Color.Green).size(10).fill_alpha(0.5)
  val versicolorGlyphRnd=new GlyphRenderer().glyph(versicolor)
  val virginica = new Diamond().fill_color(Color.Blue).size(10).fill_alpha(0.5)
  val virginicaGlyphRnd=new GlyphRenderer().glyph(virginica)
```

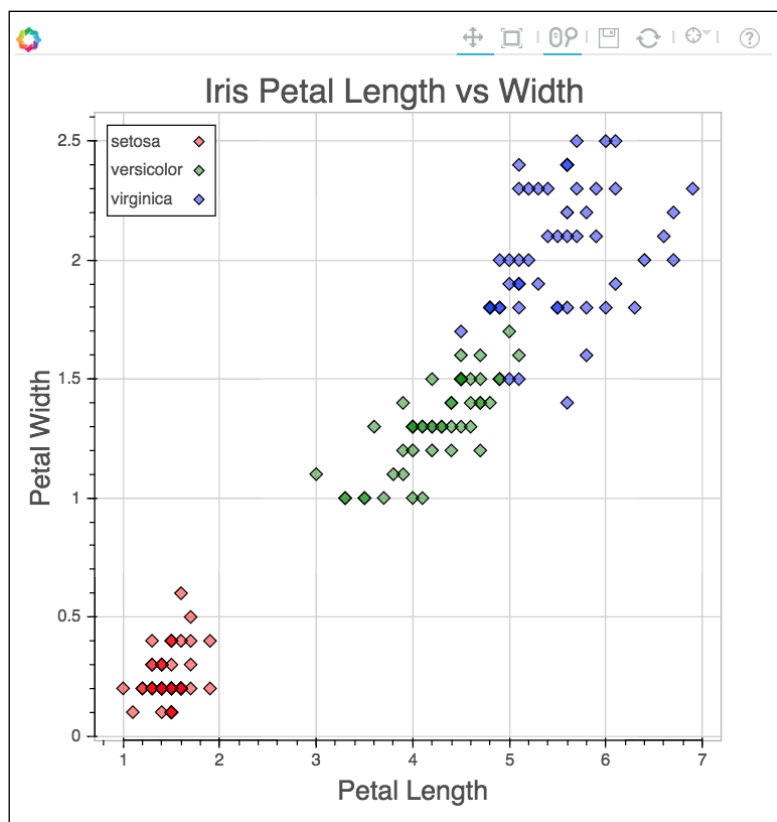
```

val legends = List("setosa" -> List(setosaGlyphRnd),
                  "versicolor" -> List(versicolorGlyphRnd),
                  "virginica" -> List(virginicaGlyphRnd))

val legend = new Legend().orientation(LegendOrientation.TopLeft).
plot(plot).legends(legends)

plot.renderers := List(xAxis, yAxis, dataPointRenderer, xgrid, ygrid,
legend, setosaGlyphRnd, virginicaGlyphRnd, versicolorGlyphRnd)

```



The code for this recipe can be found at <https://github.com/aronuma/ScalaDataAnalysisCookbook/blob/master/chapter4-visualization/src/main/scala/com/packt/scalada/viz/breeze>.

Creating a time series MultiPlot with Bokeh-Scala

In this second recipe on plotting using Bokeh, we'll see how to plot a time series graph with a dataset borrowed from <https://archive.ics.uci.edu/ml/datasets/Dow+Jones+Index>. We will also see how to plot multiple charts in a single document.

How to do it...

We'll be using only two fields from the dataset: the closing price of the stock at the end of the week, and the last business day of the week. Our dataset is comma separated. Let's take a look at some samples, as shown here:

```
quarter,stock,date,open,high,low,close,volume,percent_change_price,percent_change_volume_over_last_wk,previous_weeks_vol
1,AA,1/7/2011,$15.82,$16.72,$15.78,$16.42,239655616,3.79267,,,$16.71,$15.97,-4.42849,26,0.182704
1,AA,1/14/2011,$16.71,$16.71,$15.64,$15.97,242963398,-4.42849,1.380223028,239655616,$16.19,$15.79,-2.47066,19,0.187852
1,AA,1/21/2011,$16.19,$16.38,$15.60,$15.79,138428495,-2.47066,-43.02495926,242963398,$15.87,$16.13,1.63831,12,0.189994
1,AA,1/28/2011,$15.87,$16.63,$15.82,$16.13,151379173,1.63831,9.355500109,138428495,$16.18,$17.14,5.93325,5,0.185989
1,AA,2/4/2011,$16.18,$17.39,$16.18,$17.14,154387761,5.93325,1.987451735,151379173,$17.33,$17.37,0.230814,97,0.175029
1,AA,2/11/2011,$17.33,$17.48,$16.97,$17.37,114691279,0.230814,-25.71219489,154387761,$17.39,$17.28,-0.632547,90,0.172712
1,AA,2/18/2011,$17.39,$17.68,$17.28,$17.28,80023895,-0.632547,-30.22669579,114691279,$16.98,$16.68,-1.76678,83,0.173611
1,AA,2/25/2011,$16.98,$17.15,$15.96,$16.68,132981863,-1.76678,66.17769355,80023895,$16.81,$16.58,-1.36823,76,0.179856
1,AA,3/4/2011,$16.81,$16.94,$16.13,$16.58,109493077,-1.36823,-17.66315005,132981863,$16.58,$16.03,-3.31725,69,0.180941
1,AA,3/11/2011,$16.58,$16.75,$15.42,$16.03,114332562,-3.31725,4.419900447,109493077,$15.95,$16.11,1.00313,62,0.187149
1,AA,3/18/2011,$15.95,$16.33,$15.43,$16.11,130374108,1.00313,14.03060136,114332562,$16.38,$17.09,4.33455,55,0.18622
1,AA,3/25/2011,$16.38,$17.24,$16.26,$17.09,95550392,4.33455,-26.71060729,130374108,$17.13,$17.47,1.98482,48,0.175541
```

Preparing our data

In contrast to the previous recipe, where we used the Breeze matrix to construct the Bokeh ColumnDataSource, we'll use the Spark DataFrame to construct the source this time. The `getSource` method accepts a ticker (MSFT-Microsoft and CAT-Caterpillar) and a `SQLContext`. It runs a Spark SQL, fetches the data from the table, and constructs a `ColumnDataSource` from it:

```
import org.joda.time.format.DateTimeFormat

object StockSource {

  val formatter = DateTimeFormat.forPattern("MM/dd/yyyy");

  def getSource(ticker: String, sqlContext: SQLContext) = {
    val stockDf = sqlContext.sql(s"select stock, date, close from
stocks where stock= '$ticker'")
    stockDf.cache()
  }
}
```

```

    val dateData: Array[Double] =
stockDf.select("date").collect.map(eachRow =>
formatter.parseDateTime(eachRow.getString(0)).getMillis().toDouble)
    val closeData: Array[Double] =
stockDf.select("close").collect.map(eachRow =>
eachRow.getString(0).drop(1).toDouble)

    object source extends ColumnDataSource {
      val date = column(dateData)
      val close = column(closeData)
    }
    source
  }
}

```

Earlier, we constructed `SQLContext` and registered the dataset as a table, like this:

```

val conf = new SparkConf().setAppName("csvDataFrame").
setMaster("local[2]")
val sc = new SparkContext(conf)
val sqlContext = new SQLContext(sc)
val stocks = sqlContext.csvFile(filePath = "dow_jones_index.data",
useHeader = true, delimiter = ',')
stocks.registerTempTable("stocks")

```

The only tricky thing that we do here is convert the date value into milliseconds. This is because the `Plot` point requires a double. We use the **Joda-Time** API to achieve this.

Creating a plot

Let's go ahead and create the `Plot` object from the source:

```

//Create Plot
val plot = new Plot().title(ticker).x_range(xdr).y_range(ydr).width(800).
height(400)

```

Let's have our image's title as the ticker name of the stock and create a `Document` object so that we can save the final HTML by the name `ClosingPrices.html`:

```

val msDocument = new Document(microsoftPlot)
val msHtml = msDocument.save("ClosingPrices.html")

```


Creating a line that joins all the data points

As we saw earlier with the `Diamond` marker, we'll have to pass the `x` and the `y` positions of the data points. Also, we will need to wrap the `Line` glyph into a renderer so that we can add it to `Plot`:

```
val line = new Line().x(date).y(close).line_color(color).line_width(2)
val lineGlyph = new GlyphRenderer().data_source(source).glyph(line)
```

Setting the x and y axes' data range for the plot

The plot needs to know what the `x` and `y` data ranges of the plot are before rendering. Let's do that by creating two `DataRange` objects and setting them to the plot:

```
val xdr = new DataRangeId().sources(List(date))
val ydr = new DataRangeId().sources(List(close))
```

```
plot.x_range(xdr).y_range(ydr)
```

Drawing the axes and the grids

Drawing the axes and the grids is the same as before. We added some labels to the axis, formatted the display of the `x` axis, and then added them to the `Plot`:

```
val xformatter = new DatetimeTickFormatter().formats(Map(DatetimeUnits.
Months -> List("%b %Y")))
val xaxis = new DatetimeAxis().plot(plot).formatter(xformatter).axis_
label("Month")
val yaxis = new LinearAxis().plot(plot).axis_label("Price")
plot.below <<= (xaxis :: _)
plot.left <<= (yaxis :: _)
val xgrid = new Grid().plot(plot).dimension(0).axis(xaxis)
val ygrid = new Grid().plot(plot).dimension(1).axis(yaxis)
```

Adding tools

As before, let's add some tools to the image—and to the plot:

```
//Tools
val panTool = new PanTool().plot(plot)
val wheelZoomTool = new WheelZoomTool().plot(plot)
val previewSaveTool = new PreviewSaveTool().plot(plot)
val resetTool = new ResetTool().plot(plot)
val resizeTool = new ResizeTool().plot(plot)
```

```

val crosshairTool = new CrosshairTool().plot(plot)

plot.tools := List(panTool, wheelZoomTool, previewSaveTool,
resetTool, resizeTool, crosshairTool)

```

Adding a legend to the plot

Since we already have the `Glyph` renderer for the `line`, all we need to do is add it to the legend. The properties of the line automatically propagate to the legend:

```

//Legend
val legends = List(ticker -> List(lineGlyph))
val legend = new Legend().plot(plot).legends(legends)

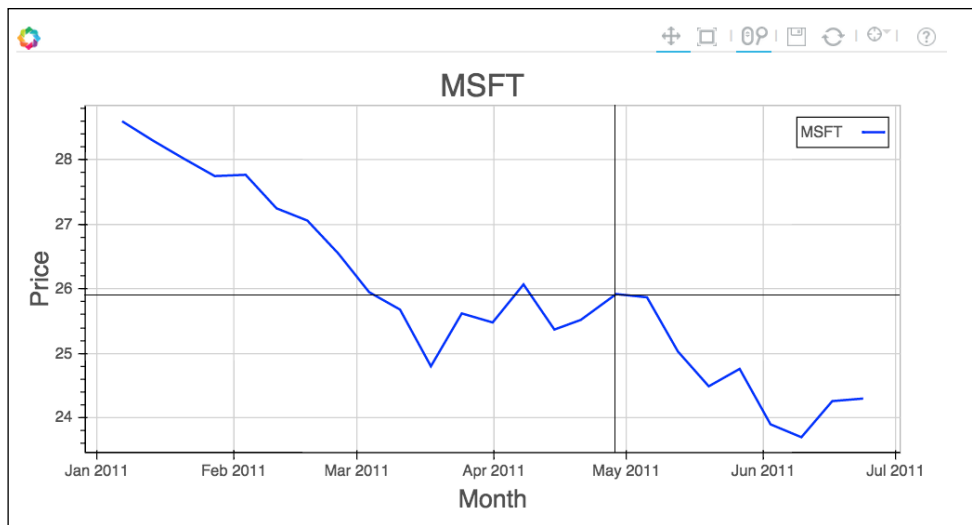
```

Next, let's add all the renderers that we created before to the plot:

```

plot.renderers <=<= (xaxis :: yaxis :: xgrid :: ygrid :: lineGlyph ::
legend :: _)

```



As the final step, let's try plotting multiple plots in the same document.

Multiple plots in the document

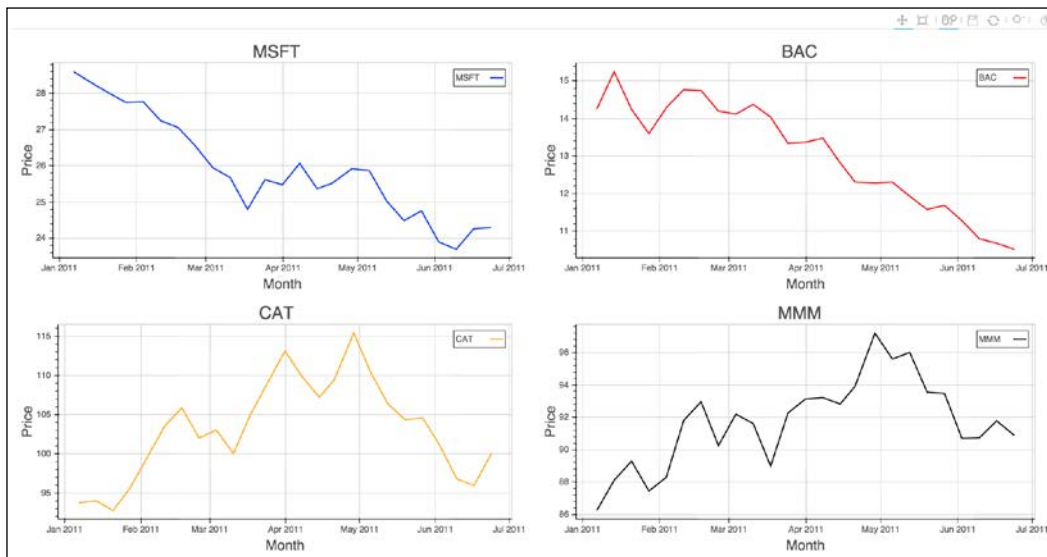
Creating multiple plots in the same document is child's play. All that we need to do is create all our plots and then add them into a grid. Finally, instead of passing our individual plot object into the document, we pass in `GridPlot`:


```
val children = List(List(microsoftPlot, bofaPlot), List(caterPillarPlot,
mmmPlot))

val grid = new GridPlot().children(children)

val document = new Document(grid)

val html = document.save("DJClosingPrices.html")
```



 The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter4-visualization/src/main/scala/com/packt/scalada/viz/breeze>.

In this chapter, we explored two methods of visualization and built some basic graphs and charts using Scala. As I mentioned earlier, the visualization libraries in Scala are actively being developed and cannot be compared to advanced visualizations that can be generated using R or, for that sake, Tableau.

5

Learning from Data

In this chapter, we will cover the following recipes:

- ▶ Predicting continuous values using linear regression
- ▶ Binary classification using LogisticRegression and SVM
- ▶ Binary classification using LogisticRegression with the Pipeline API
- ▶ Clustering using K-means
- ▶ Feature reduction using principal component analysis

Introduction

In previous chapters, we saw how to load, prepare, and visualize data. Now, let's start doing some interesting stuff with it. In this chapter, we'll be looking into applying various machine learning techniques on top of it. We'll look at a few examples for the two broad classifications of machine learning techniques: supervised and unsupervised learning. Before that, however, let's briefly see what these terms mean.

Supervised and unsupervised learning

If you are reading this book, you probably already know what supervised and unsupervised learning are, but for the sake of completion, let's briefly summarize what they mean. In supervised learning, we train the algorithms with labeled data. Labeled data is nothing but input data along with the outcome variable. For example, if our intention is to predict whether a website is about news, we would be preparing a sample dataset of website content with "news" and "not news" as labels. This dataset is called the training dataset.

With supervised learning, our end goal is to use the training dataset and come up with a function that maps our input variables to an output variable with least margin of error. We call input variables (or x variables) features or explanatory variables, and the output variable (also known as the y variable or label) the target or dependent variable. In the news website example, the text content in the website would be the input variable and "news" or "not news" would be the target variable. The function, along with its parameters (or weights or θ), is our hypothesis, or model.

In the case of unsupervised learning, we aim to find a structure within the data— groups and relationships among these groups or the participants of a group. Unlike supervised learning, we don't know any information about the data or even its subset. An example would be to see whether there are similar buying patterns among a group of people (which helps cross-selling) or to see which group of people is more likely to buy pizza from our newly opened store.

Gradient descent

With supervised learning, in order for the algorithm to learn the relationship between the input and the output features, we provide a set of manually curated values for the target variable (y) against a set of input variables (x). We call it the training set. The learning algorithm then has to go over our training set, perform some optimization, and come up with a model that has the least cost—deviation from the true values. So technically, we have two algorithms for every learning problem: an algorithm that comes up with the function and (an initial set of) weights for each of the x features, and a supporting algorithm (also called cost minimization or optimization algorithm) that looks at our function parameters (feature weights) and tries to minimize the cost as much as possible.

There are a variety of cost minimization algorithms, but one of the most popular is gradient descent. Imagine gradient descent as climbing down a mountain. The height of the mountain represents the cost, and the plain represents the feature weights. The highest point is your function with the maximum cost, and the lowest point has the least cost. Therefore, our intention is to walk down the mountain. What gradient descent does is as follows: for every single step down the slope that it takes of a particular size (the step size), it goes through the entire dataset (!) and updates all the values of the weights for x features. This goes on until it reaches a state where the cost is the minimum. This flavor of gradient descent, in which it sees all of the data per iteration and updates all the parameters during every iteration, is called batch gradient descent. The trouble with using this algorithm against the size of the data that Spark aims to handle is that going through millions of rows per iteration is definitely not optimal. So, Spark uses a variant of gradient descent, called **Stochastic Gradient Descent (SGD)**, wherein the parameters are updated for each training example as it looks at it one by one. In this way, it starts making progress almost immediately, and therefore the computational effort is considerably reduced. The SGD settings can be customized using the `optimizer` attribute inside each of the ML algorithm. We'll look at this in detail in the recipes.

In the following recipes, we'll be looking at linear regression, logistic regression, and support vector machines as examples of supervised learning and K-means clustering, as well as dimensionality reduction using **Principal Component Analysis (PCA)** as an example of unsupervised learning. We'll also briefly look at the Stanford NLP toolkit and Scala NLP's Epic, popular natural language processing libraries, as examples of fitting a third-party library into Spark jobs.

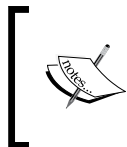
Predicting continuous values using linear regression

At the risk of stating the obvious, linear regression aims to find the relationship between an output (y) based on an input (x) using a mathematical model that is linear to the input variables. The output variable, y , is a continuous numerical value. If we have more than one input/explanatory variable (x), as in the example that we are going to see, we call it multiple linear regression. The dataset that we'll use for this recipe, for lack of creativity, is lifted from the UCI website at <http://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/>. This dataset has 1599 instances of various red wines, their chemical composition, and their quality. We'll use it to predict the quality of a red wine.

How to do it...

Let's summarize the steps:

1. Importing the data.
2. Converting each instance into a `LabeledPoint`.
3. Preparing the training and test data.
4. Scaling the features.
5. Training the model.
6. Predicting against the test data.
7. Evaluating the model.
8. Regularizing the parameters.
9. Mini batching.



The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/tree/master/chapter5-learning/src/main/scala/com/packt/scalada/learning/LinearRegressionWine.scala>.

"Step zero" of this process is the creation of `SparkConf` and the `SparkContext`. There is nothing fancy here:

```
val conf = new SparkConf().setAppName("linearRegressionWine").
setMaster("local[2]")
val sc = new SparkContext(conf)
```

Importing the data

We then import the semicolon-separated text file. We map each line into an `Array[String]` by splitting each of them using semicolons. We end up with `RDD[Array[String]]`:

```
val rdd = sc.textFile("winequality-red.csv").map(line => line.split(";"))
```

Converting each instance into a LabeledPoint

As we discussed earlier, supervised learning requires training data to be provided. We are also required to test the model that we create for its accuracy against another set of data—the test data. If we have two different datasets for this, we can import them separately and mark them as a training set and a test set. In our example, we'll use a single dataset and split it into training and test sets.

```
7.4;0.7;0;1.9;0.076;11;34;0.9978;3.51;0.56;9.4;5
7.8;0.88;0;2.6;0.098;25;67;0.9968;3.2;0.68;9.8;5
7.8;0.76;0.04;2.3;0.092;15;54;0.997;3.26;0.65;9.8;5
11.2;0.28;0.56;1.9;0.075;17;60;0.998;3.16;0.58;9.8;6
7.4;0.7;0;1.9;0.076;11;34;0.9978;3.51;0.56;9.4;5
7.4;0.66;0;1.8;0.075;13;40;0.9978;3.51;0.56;9.4;5
7.9;0.6;0.06;1.6;0.069;15;59;0.9964;3.3;0.46;9.4;5
7.3;0.65;0;1.2;0.065;15;21;0.9946;3.39;0.47;10;7
7.8;0.58;0.02;2;0.073;9;18;0.9968;3.36;0.57;9.5;7
7.5;0.5;0.36;6.1;0.071;17;102;0.9978;3.35;0.8;10.5;5
6.7;0.58;0.08;1.8;0.097;15;65;0.9959;3.28;0.54;9.2;5
7.5;0.5;0.36;6.1;0.071;17;102;0.9978;3.35;0.8;10.5;5
```

Each of our training samples has the following format: the last field is the quality of the wine, a rating from 1 to 10, and the first 11 fields are the properties of the wine. So, from our perspective, the quality of the wine is the *y* variable (the output) and the rest of them are *x* variables (input). Now, let's represent this in a format that Spark understands—a `LabeledPoint`. A `LabeledPoint` is a simple wrapper around the input features (our *x* variables) and our pre-predicted value (*y* variable) for these *x* input values:

```
val dataPoints=rdd.map(row=>new LabeledPoint(row.last.toDouble, Vectors.
dense(row.take(row.length-1).map(str=>str.toDouble))))
```

The first parameter to the constructor of the `LabeledPoint` is the label (*y* variable), and the second parameter is a vector of input variables.

Preparing the training and test data

As we discussed earlier, we can have two different independent datasets for training and testing. However, it is a common practice to split the dataset into training and test datasets. In this recipe, we will be splitting the dataset into training and test sets in the ratio of 80:20, with each of the elements being selected randomly. This random shuffling of data is one of the prerequisites for better performance of the SGD too:

```
val dataSplit = dataPoints.randomSplit(Array(0.8, 0.2))
val trainingSet = dataSplit(0)
val testSet = dataSplit(1)
```

Scaling the features

Running a quick summary statistics reveals that our features aren't in the same range:

```
val featureVector = rdd.map(row => Vectors.dense(row.take(row.length-1).
map(str => str.toDouble)))
print(s"Max : ${stats.max}, Min : ${stats.min}, and Mean : ${stats.mean}
and Variance : ${stats.variance}")
println ("Min "+ stats.min)
println ("Max "+ stats.max)
```

Here is the output:

```
Min [4.6,0.12,0.0,0.9,0.012,1.0,6.0,0.99007,2.74,0.33,8.4]
Max [15.9,1.58,1.0,15.5,0.611,72.0,289.0,1.00369,4.01,2.0,14.9]
Variance : [3.031416388997815,0.0320623776515516,0.0379
4748313440582,1.987897132985963,0.002215142653300991,10
9.41488383305895,1082.1023725325845,3.56202945332629E-
6,0.02383518054541292,0.02873261612976197,1.135647395000472]
```

It is always recommended that the input variables have a mean of 0. This is easily achieved with the help of the `StandardScaler` built into the Spark ML library itself. The one thing that we have to watch out for here is that we have to scale the training and the test sets uniformly. The way we do it is by creating a scaler for trainingSplit and using the same scaler to scale the test set. Another side note is that feature scaling helps with faster convergence in SGD:

```
val scaler = new StandardScaler(withMean = true, withStd = true).
fit(trainingSet.map(dp => dp.features))

val scaledTrainingSet = trainingSet.map(dp => new LabeledPoint(dp.label,
scaler.transform(dp.features))).cache()

val scaledTestSet = testSet.map(dp => new LabeledPoint(dp.label, scaler.
transform(dp.features))).cache()
```


Training the model

The next step is to use our training data to create a model. This just involves creating an instance of `LinearRegressionWithSGD` and passing in a few parameters: one for the `LinearRegression` algorithm and two for the SGD. The SGD parameters can be accessed through the use of the `optimizer` attribute inside `LinearRegressionWithSGD`:

- ▶ `setIntercept`: While predicting, we are more interested in the slope. This setting will force the algorithm to find the intercept too.
- ▶ `optimizer.setNumIterations`: This determines the number of iterations that our algorithm needs to go through on the training set before finalizing the hypothesis. An optimal number would be 10^6 divided by the number of instances in your dataset. In our case, we'll set it to 1000.
- ▶ `setStepSize`: This tells the gradient descent algorithm while it tries to reduce the parameters how big a step it needs to take during every iteration. Setting this parameter is really tricky because we would like the SGD to take bigger steps in the beginning and smaller steps towards the convergence. Setting a fixed small number would slow down the algorithm, and setting a fixed bigger number would not give us a function that is a reasonable minimum. The way Spark handles our `setStepSize` input parameter is as follows: it divides the input parameter by a root of the iteration number. So initially, our step size is huge, and as we go further down, it becomes smaller and smaller. The default step size parameter is 1.

```
val regression=new LinearRegressionWithSGD().setIntercept(true)
regression.optimizer.setNumIterations(1000).setStepSize(0.1)
```

```
//Let's create a model out of our training examples.
val model=regression.run(scaledTrainingSet)
```

Predicting against test data

This step is just a one-liner. We use the resulting model to predict the output (y) based on the features of the test set:

```
val predictions:RDD[Double]=model.predict(scaledTestSet.map(point=>point.features))
```

Evaluating the model

Let's evaluate our model against one of the most popular regression evaluation metrics—**mean squared error**. Let's get the actual values that our test data has (the y variable prepared manually) and then compare it with the predictions from our model:

```
val actuals:RDD[Double]=scaledTestSet.map(_.label)
```

Mean squared error

The mean squared error is given by this formula:

$$\text{MSE} = \frac{1}{n} \sum_{i=1}^n (y_i - \tilde{y}_i)^2$$

So, we take the difference between the actual and the predicted values (errors), square them, and calculate the sum of them all. We then divide this sum by the number of values, thereby calculating the mean:

```
val predictsAndActuals: RDD[(Double, Double)] = predictions.zip(actuals)

val sumSquaredErrors=predictsAndActuals.map{case (pred,act)=>
  println (s"act, pred and difference $act, $pred ${act-pred}")
  math.pow(act-pred,2)
}.sum()

val meanSquaredError = sumSquaredErrors / scaledTestSet.count

println(s"SSE is $sumSquaredErrors")
println(s"MSE is $meanSquaredError")
```

Here is the output:

```
SSE is 162.21647197365706
MSE is 0.49607483783992984
```

In our example, we selected all the features that are present in our dataset. Later, we'll take a look at dimensionality reduction, which helps us reduce the number of features while still maintaining the variance of the dataset at a reasonably higher level.

Regularizing the parameters

Before we see what regularization is, let's briefly see what overfitting is. A model is said to be overfit (or having high variance) when it memorizes the training set. The result of this is that the algorithm fails to generalize and therefore performs badly with unseen datasets. One way to solve the problem of overfitting is to manually select the important features that will be used to create the model, but for a large-dimensional dataset, it is hard to decide which ones to keep and which ones to throw away.

The other popular option is to retain all the features but reduce the magnitudes of the feature weights. Thus, even with a model that is complex (with higher degree polynomials), if the feature weights are really small, the resulting model would be simple. In other words, given two equally (or almost equally) performing models, with one model being complex (with higher degree polynomial) and the other model being simple, regularization chooses the simple model. The reasoning behind this is that models with simple parameters have a higher probability of predicting unseen data (also known as generalization).

The Spark MLlib comes with implementations for the most common L1 and L2 regularizations. As a side note, `LinearRegressionWithSGD`, by default, uses a `SimpleUpdater`, which does not regularize the parameters. Interestingly, Spark has implementations of regression algorithms that are based on top of the L1 and L2 updaters; they are called the Lasso (that uses the L1 updater) and Ridge (that uses the L2 updater by default).

While the L1 regularizer offers some feature selection when the dataset that we have is sparse (or if the dataset's rows are smaller than the feature itself), most of the time, it is recommended is to use the L2 regularizer. The new Pipeline API also has out-of-the-box support for ElasticNet regularization, which uses both the L1 and L2 regularizations internally. Now, let's go over the code:

```
def algorithm(algo: String, iterations: Int, stepSize: Int) = algo
match {
  case "linear" => {
    val algo = new LinearRegressionWithSGD()
    algo.setIntercept(true).optimizer.setNumIterations(iterations).
    setStepSize(stepSize)
    algo
  }
  case "lasso" => {
    val algo = new LassoWithSGD()
    algo.setIntercept(true).optimizer.setNumIterations(iterations).
    setStepSize(stepSize)
    algo
  }
  case "ridge" => {
    val algo = new RidgeRegressionWithSGD()
    algo.setIntercept(true).optimizer.setNumIterations(iterations).
    setStepSize(stepSize)
    algo
  }
}
```

As discussed earlier, `LassoWithSGD` wraps an L1 updater and `RidgeRegressionWithSGD` wraps an L2 updater. From a code perspective, all that we need to do is change the name of the class. The optimizer (gradient descent) now accepts a regularization parameter that penalizes larger parameters for the features. The default value of the regularization parameter is 0.01 in Spark. A smaller regularization parameter would result in underfitting, and a large parameter would result in overfitting.

The following output shows that regularizing the parameters has reduced our error values:

```
***** Printing metrics for Linear Regression with SGD
*****

SSE is 132.39124792957116
MSE is 0.4124337941731189

***** Printing metrics for Lasso Regression with SGD
*****

SSE is 132.3943810653321
MSE is 0.4124435547206608

***** Printing metrics for Ridge Regression with SGD
*****

SSE is 132.44011034123344
MSE is 0.4125860135240917
```

Mini batching

Instead of going through our dataset one by one in the case of SGD, or seeing the entire dataset for every iteration (in the case of batch gradient descent) while updating the parameter vector, we can settle for something in the middle. With the mini batch fraction parameter, for every single iteration, the SGD considers that fraction of the dataset to process for the parameter update. Let's set the batch size to 5 percent:

```
algo.setIntercept(true).optimizer.setNumIterations(iterations).
setStepSize(stepSize).setRegParam(0.001).setMiniBatchFraction(0.05)
```

The results are as follows:

```
***** Printing metrics for Linear Regression with SGD
*****

SSE is 112.96958667767147
MSE is 0.3574986920179477
SST is 183.05305027649794
Residual sum of squares is 0.38285875866568087

***** Printing metrics for Lasso Regression with SGD
*****
```

```
SSE is 112.95392101963424
MSE is 0.35744911715074124
SST is 183.05305027649794
Residual sum of squares is 0.3829443385454675
***** Printing metrics for Ridge Regression with SGD
*****
SSE is 112.9218089913291
MSE is 0.3573474968080035
SST is 183.05305027649794
Residual sum of squares is 0.3831197632557175
```

The advantage that we get from using mini batches is that this obviously gives better performance than plain SGD without batches. This is because with plain SGD, for every iteration, only one example is considered to update the parameters. However, with mini batches, we consider a batch of examples. That said, the improvement in the mean squared error from the previous run is not the result of using batches, but just a feature of SGD—roaming around the minima and not converging at a fixed point.

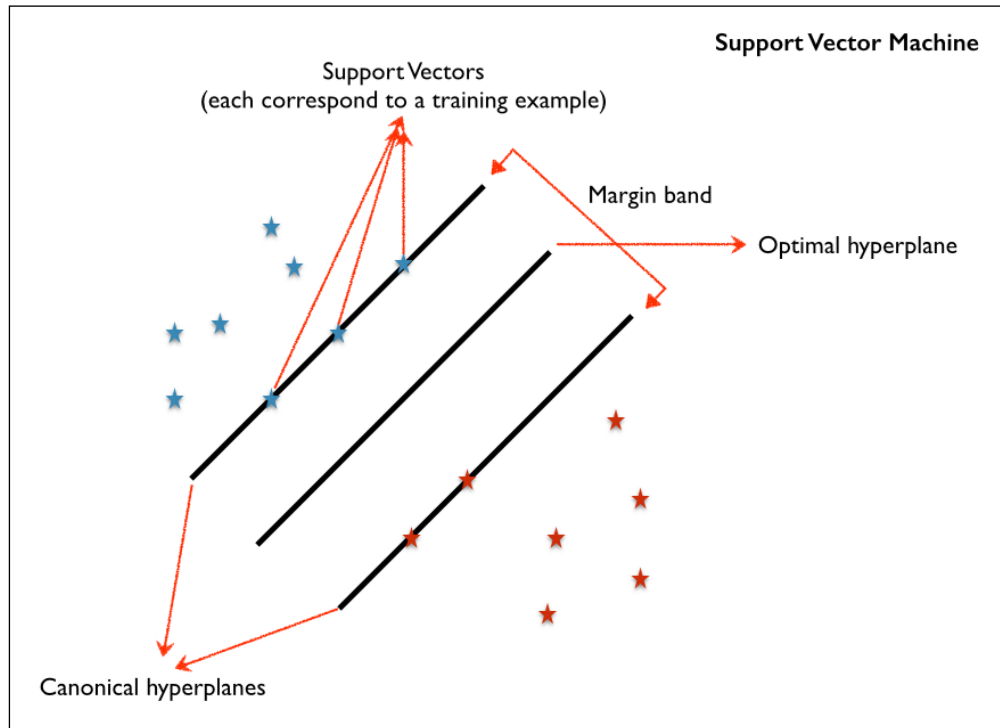
Binary classification using LogisticRegression and SVM

Unlike linear regression, wherein we predicted continuous values for the outcome (the y variable), logistic regression and the **Support Vector Machine (SVM)** are used to predict just one out of the n possibilities for the outcome (the y variable). If the outcome is one of two possibilities, then the classification is called a binary classification.

Logistic regression, when used for binary classification, looks at each data point and estimates the probability of that data point falling under the positive case. If the probability is less than a threshold, then the outcome is negative (or 0); otherwise, the outcome is positive (or 1).

As with any other supervised learning techniques, we will be providing training examples for logistic regression. We then add a bit of code for feature extraction and let the algorithm create a model that encapsulates the probability of each of the features belonging to one of the binary outcomes.

What SVM tries to do is map all of the training data as points in the feature space. The algorithm comes up with a hyperplane that separates the positive and negative training examples in such a way that the distance (margin band) between them is maximum. This is better illustrated with a diagram:



When a new and unseen data point comes up for prediction, the algorithm looks at that point and tries to find the closest point to the input data point. The label corresponding to that point will be predicted as the label for the input point as well.

How to do it...

Both the implementations of LogisticRegression and SVM in Spark use L2 regularization by default, but we are free to switch to L1 by setting the updater explicitly.


In this recipe, we'll classify a spam/ham dataset (<https://archive.ics.uci.edu/ml/datasets/SMS+Spam+Collection>) against three variants of classification algorithms:

- ▶ Logistic regression with SGD as the optimization algorithm
- ▶ Logistic regression with BFGS as the optimization algorithm
- ▶ Support vector machine with SGD as the optimization algorithm

The BFGS optimization algorithm provides the benefits of converging to the minimum faster than SGD. Also, for BFGS, we need not break our heads coming up with an optimal learning rate.

Let's summarize the steps:

1. Importing the data.
2. Tokenizing the data and converting it into LabeledPoints.
3. Factoring the Inverse Document Frequency (IDF).
4. Preparing the training and test data.
5. Constructing the algorithm.
6. Training the model and predicting the test data.
7. Evaluating the model.

 The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter5-learning/src/main/scala/com/packt/scalada/learning/BinaryClassificationSpam.scala>.

Importing the data

As usual, our input data is in the form of a text file—SMSSpamCollection. The data file looks like this:

```
1ham Go until jurong point, crazy.. Available only in bugis n great world la e buffet... Cine there got amore wat...
2ham Ok lar... Joking wif u oni...
3spam Free entry in 2 a wkly comp to win FA Cup final tkts 21st May 2005. Text FA to 87121 to receive entry question(std txt rate)T&C's apply 08452810075over18's
4ham U dun say so early hor... U c already then say...
5ham Nah I don't think he goes to usf, he lives around here though
6spam FreeMsg Hey there darling it's been 3 week's now and no word back! I'd like some fun you up for it still? Td ok! XxX std chgs to send, £1.50 to rcv
7ham Even my brother is not like to speak with me. They treat me like aids patient.
8ham As per your request 'Melle Melle (Oru Minnaminunginte Nurrungu Vettam)' has been set as your callertune for all Callers. Press *9 to copy your friends Callertune
9spam WINNER!! As a valued network customer you have been selected to receivea £900 prize reward! To claim call 09061701461. Claim code KL341. Valid 12 hours only.
10spam Had your mobile 11 months or more? U R entitled to Update to the latest colour mobiles with camera for Free! Call The Mobile Update Co FREE on 08002986030
11ham I'm gonna be home soon and i don't want to talk about this stuff anymore tonight, k? I've cried enough today.
12spam SIX chances to win CASH! From 100 to 20,000 pounds txt> CSH11 and send to 87575. Cost 150p/day, 6days, 16+ TsandCs apply Reply HL 4 info
13spam URGENT! You have won a 1 week FREE membership in our £100,000 Prize Jackpot! Txt the word: CLAIM to No: 81010 T&C www.dbuk.net LCCLTD POBOX 4403LDNW1A7RW18
14ham I've been searching for the right words to thank you for this breather. I promise i wont take your help for granted and will fulfil my promise. You have been wonder
15ham I HAVE A DATE ON SUNDAY WITH WILL!!
```

As we can see, the label and the data are separated by a tab. So, while reading each line, we split the label and the content, and then populate a simple case class named Document. This Document class is just a temporary placeholder. In the next step, we'll convert these documents into LabeledPoints:

```
//Frankly, we could make this a tuple but this looks neat
case class Document(label: String, content: String)

val docs = sc.textFile("SMSSpamCollection").map(line => {
  val words = line.split("\t")
  Document(words.head.trim(), words.tail.mkString(" "))
})
```

Tokenizing the data and converting it into LabeledPoints

For the tokenization, instead of relying on the tokenizer provided inside Spark, we'll see how to plug in two external NLP libraries—the Stanford CoreNLP and Scala NLP's Epic libraries. These are the two most popular NLP libraries: one from the Java world and the other from Scala. However, one thing that we ought to watch out for while using external libraries is that the instantiation of these APIs, and therefore the creation of heavyweight objects required for the use of these APIs (such as a tokenizer), should be done at the partition level. If we do it at the level of a closure, such as a map over RDD, we'll end up creating new instance of the API object for every single instance of the data.

In the case of Epic, we just split the documents into sentences and then tokenize them into words. We also add two more restrictions. Only those tokens that contain letters or digits will be considered, and the tokens should be of at least two characters:

```
import epic.preprocess.TreebankTokenizer
import epic.preprocess.MLSentenceSegmenter
//Use Scala NLP - Epic
    val labeledPointsUsingEpicRdd: RDD[LabeledPoint] =
docs.mapPartitions { docIter =>

    val segmenter = MLSentenceSegmenter.bundled().get
    val tokenizer = new TreebankTokenizer()
    val hashingTf = new HashingTF(5000)

    docIter.map { doc =>
        val sentences = segmenter(doc.content)
        val tokens = sentences.flatMap(sentence =>
tokenizer(sentence))

        //consider only features that are letters or digits and
cut off all words that are less than 2 characters
        val filteredTokens=tokens.toList.filter(token =>
token.forall(_.isLetterOrDigit)).filter(_.length() > 1)

        new LabeledPoint(if (doc.label=="ham") 0 else 1,
hashingTf.transform(filteredTokens))
    }
}.cache()
```

`MLSentenceSegmenter` splits the paragraph into sentences. The sentences are then split into terms (or words) using the tokenizer. `HashingTF` creates a map of terms with their frequency of occurrence. Finally, to construct a `LabeledPoint` for each document, we convert these terms into a term frequency vector for that document using the `transform` function of `HashingTF`. Also, we restrict the maximum number of interested terms to 5,000 by way of setting the `numFeatures` in `HashingTF`.

With Stanford CoreNLP, the process is a little more involved, in the sense that we reduce the tokens to lemmas (<https://en.wikipedia.org/wiki/Lemmatisation>). In order to do this, we create an NLP pipeline that splits sentences, tokenizes, and finally reduces the tokens to lemmas:

```
def corePipeline(): StanfordCoreNLP = {
    val props = new Properties()
    props.put("annotators", "tokenize, ssplit, pos, lemma")
    new StanfordCoreNLP(props)
}

def lemmatize(nlp: StanfordCoreNLP, content: String):
List[String] = {
    //We are required to prepare the text as 'annotatable'
before we annotate :-)
    val document = new Annotation(content)
    //Annotate
    nlp.annotate(document)
    //Extract all sentences
    val sentences =
document.get(classOf[SentencesAnnotation]).asScala

    //Extract lemmas from sentences
    val lemmas = sentences.flatMap { sentence =>
        val tokens =
sentence.get(classOf[TokensAnnotation]).asScala
        tokens.map(token =>
token.getString(classOf[LemmaAnnotation]))
    }
    //Only lemmas with letters or digits will be considered.
Also consider only those words which has a length of at least 2
    lemmas.toList.filter(lemma =>
lemma.forall(_.isLetterOrDigit)).filter(_.length() > 1)
}

val labeledPointsUsingStanfordNLPRdd: RDD[LabeledPoint] =
docs.mapPartitions { docIter =>
    val corenlp = corePipeline()
    val stopwords = Source.fromFile("stopwords.txt").getLines()
    val hashingTf = new HashingTF(5000)

    docIter.map { doc =>
        val lemmas = lemmatize(corenlp, doc.content)
        //remove all the stopwords from the lemma list
        lemmas.filterNot(lemma => stopwords.contains(lemma))
    }
}
```

```

//Generates a term frequency vector from the features
val features = hashingTf.transform(lemmas)

//example : List(until, jurong, point, crazy, available,
only, in, bugi, great, world, la, buffet, Cine, there, get, amore,
wat)
new LabeledPoint(
  if (doc.label.equals("ham")) 0 else 1,
  features)
}
}.cache()

```

Factoring the inverse document frequency

With `HashingTF`, we have a map of terms along with their frequency of occurrence in the documents. Now, the problem with taking this metric is that common words such as "the" and "a" get higher rankings compared to rare words. The **inverse document frequency (IDF)** calculates the occurrences of a word in all the documents and gives higher weight to a term that is uncommon. We'll now factor in the inverse document frequency so that we have the TF-IDF score (<https://en.wikipedia.org/wiki/Tf-idf>) for each term. This is easily achievable in Spark with the availability of `org.apache.spark.mllib.feature.IDFModel`. We extract all term frequencies from `LabeledPoints` and pass them to the transform function `IDFModel` to generate the TF-IDF:

```

val labeledPointsUsingStanfordNLPRdd=getLabeledPoints(docs,
"STANFORD")
val lpTfIdf=withIdf(labeledPointsUsingStanfordNLPRdd).cache()

def withIdf(lpPoints: RDD[LabeledPoint]): RDD[LabeledPoint] = {
  val hashedFeatures = labeledPointsWithTf.map(lp =>
lp.features)
  val idf: IDF = new IDF()
  val idfModel: IDFModel = idf.fit(hashedFeatures)

  val tfIdf: RDD[Vector] = idfModel.transform(hashedFeatures)

  val lpTfIdf= labeledPointsWithTf.zip(tfIdf).map {
    case (originalLPoint, tfIdfVector) => {
      new LabeledPoint(originalLPoint.label, tfIdfVector)
    }
  }

  lpTfIdf
}

val lpTfIdf=withIdf(labeledPointsWithTf).cache()

```

Prepare the training and test data

Our test data has a skewed distribution of spam and ham data. We just have to make sure that when we split the data into training and test data into 80% and 20%, we first split the training and test data into two subsets and then split it into the 80:20 ratio. At the end of this, the training data and test data will have a ratio of 4:1 spam and ham samples.

The spam and ham counts in our dataset are 747 and 4827, respectively:

```
//Split dataset
val spamPoints = lpTfIdf.filter(point => point.label ==
1).randomSplit(Array(0.8, 0.2))
val hamPoints = lpTfIdf.filter(point => point.label ==
0).randomSplit(Array(0.8, 0.2))

println ("Spam
count:"+(spamPoints(0).count)+"::"+(spamPoints(1).count))
println ("Ham count:"+(hamPoints(0).count)+"::"+(hamPoints(1).
count))

val trainingSpamSplit = spamPoints(0)
val testSpamSplit = spamPoints(1)

val trainingHamSplit = hamPoints(0)
val testHamSplit = hamPoints(1)

val trainingSplit = trainingSpamSplit ++ trainingHamSplit
val testSplit = testSpamSplit ++ testHamSplit
```

Constructing the algorithm

Now that we have our training and test sets, the next obvious step is to train a model out of these examples. Let's create instances of the three variants of the algorithms that we would like to experiment with:

```
val logisticWithSGD = getAlgorithm("logsgd", 100, 1, 0.001)
val logisticWithBfgs = getAlgorithm("logbfgs", 100, Double.NaN,
0.001)
val svmWithSGD = getAlgorithm("svm", 100, 1, 0.001)

def getAlgorithm(algo: String, iterations: Int, stepSize:
Double, regParam: Double) = algo match {
  case "logsgd" => {
    val algo = new LogisticRegressionWithSGD()
```

```

algo.setIntercept(true).optimizer.setNumIterations(iterations).
setStepSize(stepSize).setRegParam(regParam)
  algo
}
case "logbfgs" => {
  val algo = new LogisticRegressionWithLBFGS()
algo.setIntercept(true).optimizer.setNumIterations(iterations).
setRegParam(regParam)
  algo
}
case "svm" => {
  val algo = new SVMWithSGD()
algo.setIntercept(true).optimizer.setNumIterations(iterations).
setStepSize(stepSize).setRegParam(regParam)
  algo
}
}

```

We can notice that the `stepSize` parameter isn't set for logistic regression with BFGS.

Training the model and predicting the test data

Like linear regression, training and predicting the labels for the test set is just a matter of calling the `run` and `predict` methods of the classification algorithm.

Soon after the prediction is done, the next logical step is to evaluate the model. In order to generate metrics for this, we extract the predicted and the actual labels. Our `runClassification` function trains the model using the training data and makes predictions against the test data. It then zips the predicted and the actual outcomes into a value called `predictsAndActuals`. This value is returned from the function.

The `runClassification` accepts a `GeneralizedLinearAlgorithm` as the parameter, which is the parent of `LinearRegressionWithSGD`, `LogisticRegressionWithSGD`, and `SVMWithSGD`:

```

val
logisticWithSGDPredictsActuals=runClassification(logisticWithSGD,
trainingSplit, testSplit)
val
logisticWithBfgsPredictsActuals=runClassification(logisticWithBfgs,
trainingSplit, testSplit)
val svmWithSGDPredictsActuals=runClassification(svmWithSGD,
trainingSplit, testSplit)

```

```
def runClassification(algorithm: GeneralizedLinearAlgorithm[_ <:
  GeneralizedLinearModel], trainingData: RDD[LabeledPoint],
  testData: RDD[LabeledPoint]): RDD[(Double, Double)] = {
  val model = algorithm.run(trainingData)
  val predicted = model.predict(testData.map(point =>
point.features))
  val actuals = testData.map(point => point.label)
  val predictsAndActuals: RDD[(Double, Double)] =
predicted.zip(actuals)
  predictsAndActuals
}
```

Evaluating the model

For generating the metrics, Spark has some inbuilt APIs. The two most common metrics used to evaluate a classification model are the area under curve and the confusion matrix. The `org.apache.spark.mllib.evaluation.BinaryClassificationMetrics` gives us the area under the curve, and `org.apache.spark.mllib.evaluation.MulticlassMetrics` gives us the confusion matrix. We also calculate the simple accuracy measure manually using the values of `predicted` and `actuals`. The accuracy is simply the result of dividing the correctly classified count of the test dataset by the total count of the test dataset. Refer to https://en.wikipedia.org/wiki/Accuracy_and_precision#In_binary_classification for more details:

```
def calculateMetrics(predictsAndActuals: RDD[(Double, Double)],
algorithm: String) {

  val accuracy = 1.0*predictsAndActuals.filter(predActs => predActs._1
== predActs._2).count() / predictsAndActuals.count()
  val binMetrics = new BinaryClassificationMetrics(predictsAndActuals)
  println(s"***** Printing metrics for $algorithm
*****")
  println(s"Area under ROC ${binMetrics.areaUnderROC}")
  //println(s"Accuracy $accuracy")

  val metrics = new MulticlassMetrics(predictsAndActuals)
  val f1=metrics.fMeasure
  println(s"F1 $f1")
  println(s"Precision : ${metrics.precision}")
  println(s"Confusion Matrix \n${metrics.confusionMatrix}")
  println(s"***** ending metrics for $algorithm
*****")

}
```

As we can see from the output, `LogisticRegressionWithSGD` and `SVMWithSGD` have a slightly bigger area under curve than `LogisticRegressionWithBFGS`, which means that the two models perform a tad bit better.

This is a sample output (your output could vary):

```
***** Printing metrics for Logistic Regression with SGD
*****
Area under ROC 0.9208860759493671
Accuracy 0.9769585253456221
Confusion Matrix
927.0  0.0
25.0   133.0
***** ending metrics for Logistic Regression with SGD
*****

***** Printing metrics for SVM with SGD *****
Area under ROC 0.9318656156156157
Precision : 0.9784845650140318
Confusion Matrix
921.0  4.0
19.0   125.0
***** ending metrics for SVM with SGD *****

***** Printing metrics for Logistic Regression with BFGS
*****
Area under ROC 0.8790559620074445
Accuracy 0.9596136962247586
Confusion Matrix
971.0  9.0
37.0   122.0
***** ending metrics for Logistic Regression with BFGS *****
*****
```

Binary classification using LogisticRegression with Pipeline API

Earlier, with the spam example on binary classification, we saw how we prepared the data, separated it into training and test data, trained the model, and evaluated it against test data before we finally arrived at the metrics. This series of steps can be abstracted in a simplified manner using Spark's Pipeline API.

In this recipe, we'll take a look at how to use the Pipeline API to solve the same classification problem. Imagine the pipeline to be a factory assembly line where things happen one after another. In our case, we'll pass our raw unprocessed data through various processors before we finally feed the data into the classifier.

How to do it...

In this recipe, we'll classify the same spam/ham dataset (<https://archive.ics.uci.edu/ml/datasets/SMS+Spam+Collection>) first using the plain Pipeline, and then using a cross-validator to select the best model for us given a grid of parameters.

Let's summarize the steps:

1. Importing and splitting data as test and training sets.
2. Constructing the participants of the Pipeline.
3. Preparing a pipeline and training a model.
4. Predicting against test data.
5. Evaluating the model without cross-validation.
6. Constructing parameters for cross-validation.
7. Constructing a cross-validator and fitting the best model.
8. Evaluating a model with cross-validation.



The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter5-learning/src/main/scala/com/packt/scalada/learning/BinaryClassificationSpamPipeline.scala>.

Importing and splitting data as test and training sets

This process is a little different from the previous recipe, in the sense that we don't construct `LabeledPoint` now. Instead of an RDD of `LabeledPoint`, the pipeline requires a `DataFrame`. So, we convert each line of text into a `Document` object (with the label and the content) and then convert `RDD[Document]` into a `DataFrame` by calling the `toDF()` function on the RDD:

```
case class Document(label: Double, content: String)

val docs = sc.textFile("SMSSpamCollection").map(line => {
  val words = line.split("\t")
  val label = if (words.head.trim() == "spam") 1.0 else 0.0
  Document(label, words.tail.mkString(" "))
})

//Split dataset
val spamPoints = docs.filter(doc => doc.label == 1.0).
randomSplit(Array(0.8, 0.2))
val hamPoints = docs.filter(doc => doc.label == 0.0).
randomSplit(Array(0.8, 0.2))

println("Spam count:" + (spamPoints(0).count) + " :: " + (spamPoints(1).
count))
println("Ham count:" + (hamPoints(0).count) + " :: " + (hamPoints(1).
count))

val trainingSpamSplit = spamPoints(0)
val testSpamSplit = spamPoints(1)

val trainingHamSplit = hamPoints(0)
val testHamSplit = hamPoints(1)

val trainingSplit = trainingSpamSplit ++ trainingHamSplit
val testSplit = testSpamSplit ++ testHamSplit

import sqlContext.implicits._
val trainingDataFrame = trainingSplit.toDF()
val testDataFrame = testSplit.toDF()
```


Construct the participants of the Pipeline

In order to arrange the pipeline, we need to construct its participants. There are three unique participants (or pipeline stages) of this pipeline, and we have to line them up in the right order:

- ▶ **Tokenizer:** This disintegrates the sentence into tokens
- ▶ **HashingTF:** This creates a term frequency vector from the terms
- ▶ **IDF:** This creates an inverse document frequency vector from the terms
- ▶ **VectorAssembler:** This combines the TF-IDF vector and the label vector to form a single vector, which will form the input features for the classification algorithm
- ▶ **LogisticRegression:** This is the classification algorithm itself

Let's construct these first:

```
val tokenizer=new Tokenizer().setInputCol("content").
setOutputCol("tokens")
    val hashingTf=new HashingTF().setInputCol(tokenizer.getOutputCol).
setOutputCol("tf")
    val idf = new IDF().setInputCol(hashingTf.getOutputCol).
setOutputCol("tfidf")
    val assembler = new VectorAssembler().setInputCols(Array("tfidf",
"label")).setOutputCol("features")

val logisticRegression=new LogisticRegression().
setFeaturesCol("features").setLabelCol("label").setMaxIter(10)
```

When `RDD[Document]` is run against the first pipeline stage, that is, `Tokenizer`, the `"content"` field of the `Document` is taken as the input column, and the output of the tokenizer is a bag of words that is captured in the `"tokens"` output column. `HashingTF` takes the `"tokens"` and converts them into a TF vector. Notice that the input column of `HashingTF` is the same as the output column from the previous stage. `IDF` takes the `tf` vector and returns a `tf-idf` vector. `VectorAssembler` merges the `tf-idf` vector and the label to form a single vector. This will be used as an input to the classification algorithm. Finally, for the `LogisticRegression` stage, we specify the features column and the label column. However, if the input `DataFrame` has a column named `"label"` with a `Double` type and `"features"` of type `Vector`, there is no need to explicitly mention that. So, in our case, since we have `"label"` as an attribute of the `Document` case class and the output column of the `HashingTF` is named `"features"`, there is no need for us to specify them explicitly. The following code would work just fine:

```
val logisticRegression=new LogisticRegression().setMaxIter(10)
```

Internally, this implementation of `LogisticRegression` constructs `LabeledPoints` for each instance of the data, and uses some advanced optimization algorithms to derive a model from the training data.

At every stage, each of these transformations occurs against the input `DataFrame` of that particular stage, and the transformed `DataFrame` gets passed along until the final stage.

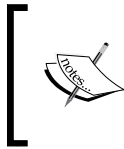
Preparing a pipeline and training a model

As the next step, we just need to form a pipeline out of the various pipeline stages that we constructed in the previous step. We then train a model by calling the `pipeline.fit` function:

```
val pipeline=new Pipeline()

pipeline.setStages(Array(tokenizer, hashingTf, logisticRegression))

val model=pipeline.fit(trainingDFrame)
```



If you are getting `java.lang.IllegalArgumentException: requirement failed: Column label must be of type DoubleType but was actually StringType`, it just means that your label isn't of the `Double` type.

Predicting against test data

Using the newly constructed model to predict the data is just a matter of calling the `transform` method of the model. Then, we also extract the actual label and the predicted value to calculate the metrics:

```
val predictsAndActualsNoCV:RDD[(Double,Double)]=model.
transform(testDFrame).map(r => (r.getAs[Double]("label"), r.getAs[Double]
("prediction"))).cache
```

Evaluating a model without cross-validation

Cross-validation is a multiple-iteration model validation technique in which our training and test sets are split into different partitions. The entire dataset is split into subsets, and for each iteration, analysis is done on one subset and validation on a different subset. For this recipe, we'll run the algorithm first without cross-validation, and then with cross-validation.

Firstly, we'll use the same validation metric and method that we used in the previous recipe. We will simply calculate the area under the ROC curve, the precision, and the confusion matrix:

```
def calculateMetrics(predictsAndActuals: RDD[(Double, Double)],
algorithm: String) {

    val accuracy = 1.0 * predictsAndActuals.filter(predActs =>
predActs._1 == predActs._2).count() / predictsAndActuals.count()
    val binMetrics = new BinaryClassificationMetrics(predictsAndActuals)
    println(s"***** Printing metrics for $algorithm
*****")
    println(s"Area under ROC ${binMetrics.areaUnderROC}")
    println(s"Accuracy $accuracy")

    val metrics = new MulticlassMetrics(predictsAndActuals)
    println(s"Precision : ${metrics.precision}")
    println(s"Confusion Matrix \n${metrics.confusionMatrix}")
    println(s"***** ending metrics for $algorithm
*****")
}
```

A sample output of this pipeline without cross-validation is as follows:

```
***** Printing metrics for Without Cross validation
*****
Area under ROC 0.9676924738149228
Accuracy 0.9656357388316151
Confusion Matrix
993.0  36.0
4.0    131.0
***** ending metrics for Without Cross validation
*****
```

Constructing parameters for cross-validation

Before we use the cross-validator to choose the best model that fits the data, we would want to provide each of the parameters a set of alternate values that the validator can choose from.

The way we provide alternate values is in the form of a parameter grid:

```
val paramGrid=new ParamGridBuilder()
    .addGrid(hashingTf.numFeatures, Array(1000, 5000, 10000))
```

```
.addGrid(logisticRegression.regParam, Array(1, 0.1, 0.03, 0.01))
.build()
```

So, we say that the number of term frequency vectors that we want HashingTF to generate could be one of 1,000, 5,000, and 10,000, and the regularization parameter for logistic regression could be one of 1, 0.1, 0.03, and 0.01. Thus, in essence, we are passing a 3 x 4 matrix as the parameter grid.

Constructing cross-validator and fit the best model

Next, we construct a cross-validator and pass in the following parameters:

- ▶ The parameter grid that we constructed in the previous step.
- ▶ The pipeline that we constructed in step 3.
- ▶ An evaluator for the cross-validator to decide which model is better.
- ▶ The number of folds. Say, if we set the number of folds to 10, the training data would be split into 10 blocks. For each iteration (10 iterations), the first block would be selected as the cross-validation set, and the other nine would be the training sets:

```
val crossValidator=new CrossValidator()
  .setEstimator(pipeline)
  .setEvaluator(new BinaryClassificationEvaluator())
  .setEstimatorParamMaps(paramGrid)
  .setNumFolds(10)
```

We finally let the cross-validator run against the training dataset and derive the best model out of it. Contrast the following line with `pipeline.fit`, where we skipped cross-validation:

```
val bestModel=crossValidator.fit(trainingDFrame)
```

Evaluating the model with cross-validation

Now, let's evaluate the model that is generated against the actual test data set (rather than the test dataset that the cross-validator uses internally):

```
val predictsAndActualsWithCV:RDD[(Double,Double)]=bestModel.
transform(testDFrame).map(r => (r.getAs[Double]("label"), r.getAs[Double]
("prediction"))).cache
```

```
calculateMetrics(predictsAndActualsWithCV, "Cross validation")
```

A sample output of this pipeline with cross-validation is as follows:

```
***** Printing metrics for Cross validation *****
Area under ROC 0.9968220338983051
```

Accuracy 0.994579945799458

Confusion Matrix

938.0 6.0

0.0 163.0

***** ending metrics for Cross validation *****

As we can see, the area under ROC is far better for this model than for any of our previously generated models.

Clustering using K-means

Clustering is a class of unsupervised learning algorithms wherein the dataset is partitioned into a finite number of clusters in such a way that the points within a cluster are similar to each other in some way. This, intuitively, also means that the points of two different clusters should be dissimilar.

K-means is one of the popular clustering algorithms, and in this recipe, we'll be looking at how Spark implements K-means and how to use the algorithm to cluster a sample dataset. Since the number of clusters is a crucial input for the K-means algorithm, we'll also see the most common method of arriving at the optimal number of clusters for the data.

How to do it...

Spark provides two initialization modes for cluster center (centroid) initialization: the original Lloyd's method (https://en.wikipedia.org/wiki/K-means_clustering), and a parallelizable and scalable variant of K-means++ (<https://en.wikipedia.org/wiki/K-means%2B%2B>). K-means++ itself is a variant of the original K-means and differs in the way in which the initial centroids of the clusters are picked up. We can switch between the original and the parallelized K-means++ versions by passing `KMeans.RANDOM` or `KMeans.PARALLEL` as the initialization mode. Let's first look at the details of the implementation.

KMeans.RANDOM

In the regular K-means (the `KMeans.RANDOM` initialization mode in the case of Spark), the algorithm randomly selects k points (equal to the number of clusters that we expect to see) and marks them as cluster centers (centroids). Then it iteratively does the following:

- ▶ It marks all the points as belonging to a cluster based on the distance between a point and its nearest centroid.
- ▶ The mean of all the points in a cluster is calculated. This mean is now set as the new centroid of that cluster.
- ▶ The rest of the data points are reassigned their clusters based on this new centroid.

Since we generally deal with more than one feature in a dataset, each instance of the data and the centroids are vectors. In Spark, we represent them as `org.apache.spark.mllib.linalg.Vector`.

KMeans.PARALLEL

Scalable K-means or K-means|| is a variant of K-means++. Let's look at what these variants of K-means actually do.

K-means++

Instead of choosing all the centroids randomly, the K-means++ algorithm does the following:

1. It chooses the first centroid randomly (uniform)
2. It calculates the distance squared of each of the rest of the points from the current centroid
3. A probability is attached to each of these points based on how far they are. The farther the centroid candidate is, the higher is its probability.
4. We choose the second centroid from the distribution that we have in step 3.
5. On the i th iteration, we have $1+i$ clusters. Find the new centroid by going over the entire dataset and forming a distribution out of these points based on how far they are from all the precomputed centroids.

These steps are repeated over $k-1$ iterations until k centroids are selected. K-means++ is known for considerably increasing the quality of centroids. However, as we see, in order to select the initial set of centroids, the algorithm goes through the entire dataset k times. Unfortunately, with a large dataset, this becomes a problem.

K-means||

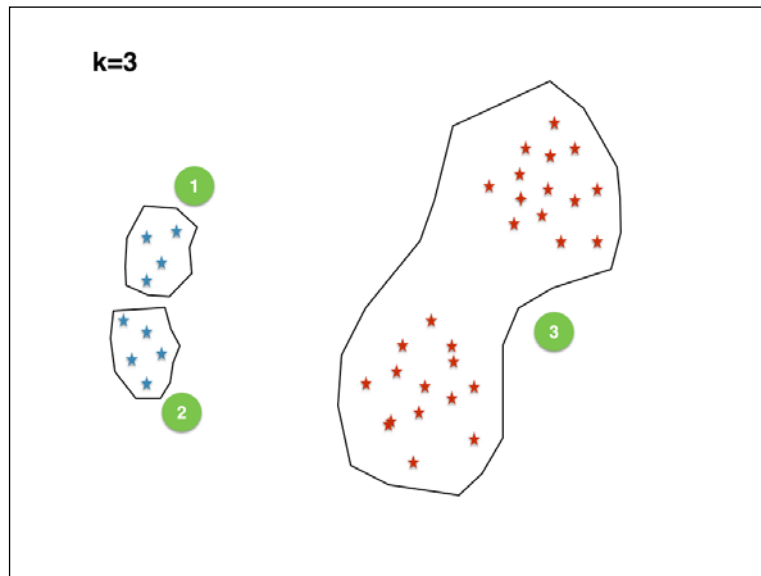
With K-means parallel (K-means||), for each iteration, instead of choosing a single point after calculating the probability distribution of each of the points in the dataset, a lot more points are chosen. In the case of Spark, the number of samples that are chosen per step is $2 * k$. Once these initial centroid candidates are selected, a K-means++ is run against these data points (instead of going through the entire dataset).

Let's now look at the most important parameters that are passed to the algorithm.

Max iterations

There are worst-case scenarios for both random and parallel. In the case of random, since the points in K-means are chosen at random, there is a distinct possibility that the model identifies two centroids from the same cluster. Say with $k=3$, there is a possibility of two clusters becoming a part of a single cluster and a single cluster being separated into two. A similar case applies to K-means++ with a bad choice of the initial set of centroids.

The following figure proves that though we can see three clusters, a bad choice of centroids separates a single cluster into two and makes two clusters one:



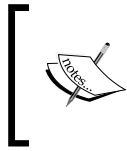
To solve this problem, we run the same algorithm with a different set of randomly initialized centroids. This is determined by the `maxIterations` parameter. The distance between the centroid and the points in the cluster is calculated (a mean squared difference in distances). This will be the cost of the model. The iteration with the least cost is chosen and returned. The metric that Spark uses to calculate the distance is the Euclidean distance.

Epsilon

How does the K-means algorithm know when to stop? There will always be a small distance that the centroid can move if the clusters aren't separated by a huge margin. If all the centroids have moved by a distance less than the epsilon parameter, it's the cue to the algorithm that it has converged. In other words, the epsilon is nothing but a **convergence threshold**.

Now that we have the parameters that need to be passed to the K-means cluster out of the way, let's look at the steps needed to run this algorithm to find the clusters:

1. Importing the data and converting it into a vector.
2. Feature scaling the data.
3. Deriving the number of clusters.
4. Constructing the model.
5. Evaluating the model.



The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter5-learning/src/main/scala/com/packt/scalada/learning/KMeansClusteringIris.scala>.

Importing the data and converting it into a vector

As usual, our input data is in the form of a text file—`iris.data`. Since we are clustering, we can ignore the label (species) in the data. The data file looks like this:

```
5.1,3.5,1.4,0.2,Iris-setosa
4.9,3.0,1.4,0.2,Iris-setosa
4.7,3.2,1.3,0.2,Iris-setosa
4.6,3.1,1.5,0.2,Iris-setosa
5.0,3.6,1.4,0.2,Iris-setosa
5.4,3.9,1.7,0.4,Iris-setosa
4.6,3.4,1.4,0.3,Iris-setosa
5.0,3.4,1.5,0.2,Iris-setosa
4.4,2.9,1.4,0.2,Iris-setosa
4.9,3.1,1.5,0.1,Iris-setosa
5.4,3.7,1.5,0.2,Iris-setosa
4.8,3.4,1.6,0.2,Iris-setosa
4.8,3.0,1.4,0.1,Iris-setosa
```

```
val data = sc.textFile("iris.data").map(line => {
  val dataArray = line.split(",").take(4)
  Vectors.dense(dataArray.map(_.toDouble))
})
```

Feature scaling the data

When we look at the summary statistics of the data, the data looks alright, but it is always advisable perform do feature scaling before running a K-means:

```
val stats = Statistics.colStats(data)
println("Statistics before scaling")
print(s"Max : ${stats.max}, Min : ${stats.min}, and Mean : ${stats.mean}
and Variance : ${stats.variance}")
```

Here is the statistics before scaling:

```
Max : [7.9,4.4,6.9,2.5]
Min : [4.3,2.0,1.0,0.1]
```



```
Mean : [5.843333333333332,3.0540000000000003,3.758666666666666,1.1986666666666668]
```

```
Variance : [0.685693512304251,0.18800402684563744,3.113179418344516,0.5824143176733783]
```

We run the data using `StandardScaler` and cache the resulting RDD. Since K-means goes through the dataset multiple times, caching the data is strongly recommended to avoid recomputation:

```
//Scale data
val scaler = new StandardScaler(withMean = true, withStd = true).
fit(data)
val scaledData = scaler.transform(data).cache()
```

The following is the statistics after scaling:

```
Max : [2.483698580557868,3.1042842692548858,1.7803768862629268,1.7051890410833728]
```

```
Min : [-1.8637802962695154,-2.4308436996988485,-1.5634973589465175,-1.4396268133736672], and Mean : [1.6653345369377348E-15,-7.216449660063518E-16,-1.1102230246251565E-16,-3.3306690738754696E-16]
```

```
Variance : [0.9999999999999997,1.0000000000000007,1.000000000000013,0.9999999999999997]
```

Deriving the number of clusters

Many times, we already know the number of clusters that are there in the dataset. But at times, if we aren't sure, the general method is to plot the number of clusters against the cost and watch out for the point from which the cost stops falling drastically. If the data is large, running the entire set of data just to obtain the number of clusters is computationally expensive. Instead, we can take a random sample and come up with the k value. In this example, we have taken a random 20% sample, but the sample percentage depends entirely on your dataset:

```
//Take a sample to come up with the number of clusters
val sampleData = scaledData.sample(false, 0.2).cache()
//Decide number of clusters
val clusterCost = (1 to 7).map { noOfClusters =>

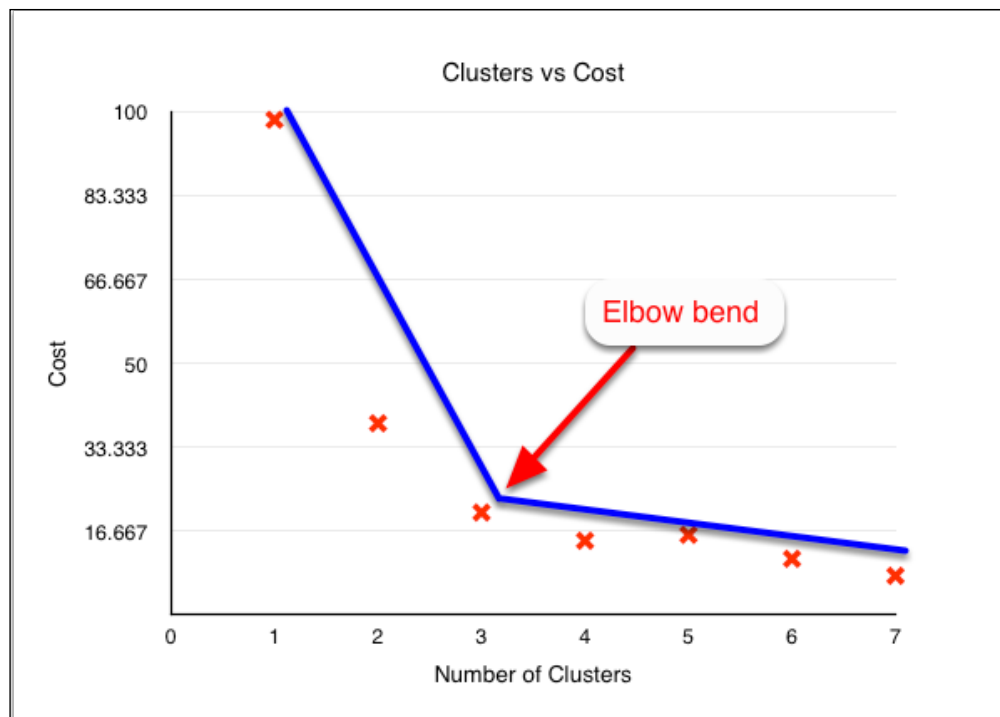
    val kmeans = new KMeans()
    .setK(noOfClusters)
    .setMaxIterations(5)
    .setInitializationMode(KMeans.K_MEANS_PARALLEL) //KMeans | |

    val model = kmeans.run(sampleData)
```

```
(noOfClusters, model.computeCost(sampleData))  
}  
  
println ("Cluster cost on sample data")  
clusterCost.foreach(println)
```

Cluster	Cost
1	98.34739863322832
2	38.07068957755217
3	20.357460464958457
4	14.755544266868153
5	15.923133807959202
6	11.165034661812456
7	7.794137577588026

When we plot this, we can see that after cluster **3**, the cost does not reduce drastically. This point is called an **Elbow bend**, as shown here:



Constructing the model

Now that we have figured out the number of clusters, let's run the algorithm against the entire dataset:

```
//Let's do the real run for 3 clusters
val kmeans = new KMeans()
    .setK(3)
    .setMaxIterations(5)
    .setInitializationMode(KMeans.K_MEANS_PARALLEL) //KMeans | |

val model = kmeans.run(scaledData)
```

Evaluating the model

The last step is to evaluate the model by printing the cost of this model. The cost is nothing but the square of the distance between all points in a cluster to its centroid. Therefore, a good model must have the least cost:

```
//Cost
println("Total cost " + model.computeCost(scaledData))
printClusterCenters(model)

def printClusterCenters(model:KMeansModel) {
    //Cluster centers
    val clusterCenters: Array[Vector] = model.clusterCenters
    println("Cluster centers")
    clusterCenters.foreach(println)
}
}
```

Here is the output:

```
Total cost 34.98320617204239
Cluster centers
[-0.011357501034038157, -
0.8699705596441868, 0.3756258413625911, 0.3106129627676019]
[1.1635361185919766, 0.1532643388373168, 0.999796072473665, 1.02619470887105
72]
[-1.0111913832028123, 0.839494408624649, -1.3005214861029282, -
1.250937862106244]
```

Feature reduction using principal component analysis

Quoting the curse of dimensionality (https://en.wikipedia.org/wiki/Curse_of_dimensionality), large number of features are computationally expensive. One way of reducing the number of features is by manually choosing and ignoring certain features. However, identification of the same features (represented differently) or highly correlated features is laborious when we have a huge number of features. Dimensionality reduction is aimed at reducing the number of features in the data while still retaining its variability.

Say, we have a dataset of housing prices and there are two features that represent the area of the house in feet and meters; we can always drop one of these two. Dimensionality reduction is very useful when dealing with text where the number of features easily runs into a few thousands.

In this recipe, we'll be looking into **Principal Component Analysis (PCA)** as a means to reduce the dimensions of data that is meant for both supervised and unsupervised learning.

How to do it...

As we have seen earlier, the only difference between the data for supervised and unsupervised learning is that the training and the test data for supervised learning have labels attached to them. This brings in a little complication, considering that we are interested only in reducing the dimensions of the feature vector and would like to retain the labels as they are.

Dimensionality reduction of data for supervised learning

The only thing that we have to watch out for while reducing the dimensions of data to be used as training data for supervised learning is that PCA must be applied on training data only. The test set must not be used to extract the components. Using test data for PCA would bleed the information in the test data into the components. This may result in higher accuracy numbers while testing, but it could perform poorly on unseen production data.

The least number of components that can be chosen while maintaining a sufficiently high variance is facilitated by the singular value vector available in the `SingularValueDecomposition` object. The singular values, available by calling the `svd.s`, show the amount of variance captured by the components. The first component will be the most important (by contributing the highest variance), and the importance will slowly diminish.

In order to come up with the probable number of dimensions, we can watch out for the difference and the extent to which the singular values diminish. Alternatively, we can just use simple heuristics and come up with a reasonable number if the features extend to a few thousand:

```
val dimensionDecidingSample=new RowMatrix((trainingSplit.
randomSplit(Array(0.8,0.2))(1)).map(lp=>lp.features))


    val svd = dimensionDecidingSample.computeSVD(500, computeU = false)
    val sum = svd.s.toArray.sum

    //Calculate the number of principal components which retains a variance
of 95%
    val featureRange=(0 to 500)

    val placeholder=svd.s.toArray.zip(featureRange).foldLeft(0.0) {
        case (cum, (curr, component)) =>
            val percent = (cum + curr) / sum
            println(s"Component and percent ${component + 1} :: $percent :::
Singular value is : $curr")
            cum + curr
    }
}
```

The steps that are involved are as follows:

1. Mean-normalizing the training data.
2. Extracting the principal components.
3. Preparing the labeled data.
4. Preparing the test data.
5. Classify and evaluate the metrics.

 The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter5-learning/src/main/scala/com/packt/scalada/learning/PCASpam.scala>.

Mean-normalizing the training data

It is highly recommended that the data be centered before running it by PCA. We achieve this using the `fit` and `transform` functions of `StandardScaler`. However, since the scaler in Spark accepts a `DenseVector` as the argument, we'll use the `Vectors.dense` factory method to convert the features in the labeled point into a `DenseVector`:

```
val docs = sc.textFile("SMSSpamCollection").map(line => {
  val words = line.split("\t")
  Document(words.head.trim(), words.tail.mkString(" "))
}).cache()

val labeledPointsWithTf = getLabeledPoints(docs)
val lpTfIdf = withIdf(labeledPointsWithTf).cache()

//Split dataset
val spamPoints = lpTfIdf.filter(point => point.label ==
1).randomSplit(Array(0.8, 0.2))
val hamPoints = lpTfIdf.filter(point => point.label ==
0).randomSplit(Array(0.8, 0.2))

val trainingSpamSplit = spamPoints(0)
val trainingHamSplit = hamPoints(0)

val trainingData = trainingSpamSplit ++ trainingHamSplit

val unlabeledTrainData = trainingData.map(lp => Vectors.dense(lp.
features.toArray)).cache()

//Scale data - Does not support scaling of SparseVector.
val scaler = new StandardScaler(withMean = true, withStd = false).
fit(unlabeledTrainData)
val scaledTrainingData = scaler.transform(unlabeledTrainData).cache()
```

Extracting the principal components

The `computePrincipalComponents` function is available in `RowMatrix`. So, we wrap our scaled training data into a `RowMatrix` and then extract 100 principal components out of it (as shown earlier, the number 100 is based on a run against a sample set of data and on investigating the singular value vector of the SVD). Our training data is currently a 4419 x 5000 matrix—4419 instances of data * 5000 features restricted by us while generating the term frequency using `HashingTF`. We then multiply this training matrix (4419 x 5000) by the principal component matrix (5000 x 100) to arrive at a 4419 * 100 matrix—4419 instances of data by 100 features (principal components). We can extract the feature vectors from this matrix by calling the `rows()` function:

```
val trainMatrix = new RowMatrix(scaledTrainingData)
val pcomp: Matrix = trainMatrix.computePrincipalComponents(100)

val reducedTrainingData = trainMatrix.multiply(pcomp).rows.cache()
```

Preparing the labeled data

Now that we have reduced the data fifty-fold, the next step that we have to take is to use this reduced data in our algorithm to see how it fares. The classification algorithm (in this case, `LogisticRegressionWithBFGS`) requires an RDD of `LabeledPoints`. To construct the `LabeledPoint`, we extract the label from the original `trainingData` and the feature vector from the dimension-reduced dataset:

```
val reducedTrainingSplit = trainingData.zip(reducedTrainingData).map {
  case (labeled, reduced) => new LabeledPoint(labeled.label, reduced) }
```

Preparing the test data

Before predicting our test data against the algorithm, we need to bring the test data to the same dimension as the training data. This is achieved by multiplying the principal components with the test matrix. As discussed earlier, we just need to make sure that we don't compute the principal components fresh here:

```
val unlabeledTestData=testSplit.map(lpoint=>lpoint.features)
val testMatrix = new RowMatrix(unlabeledTestData)
val reducedTestData=testMatrix.multiply(pcomp).rows.cache()
val reducedTestSplit=testSplit.zip(reducedTestData).map{case
(labeled,reduced) => new LabeledPoint (labeled.label, reduced)}
```

Classify and evaluate the metrics

The final step is to classify and evaluate the results of the algorithm. This step is the same as the classification recipe that we saw earlier. From the output, we can see that we not only reduced the number of features from 5,000 to 100, but also managed to maintain the accuracy of the algorithm at the same levels:

```
val logisticWithBFGS = getAlgorithm(10, 1, 0.001)
  val logisticWithBFGSPredictsActuals = runClassification(logisticWithBFGS,
    reducedTrainingSplit, reducedTestSplit)
  calculateMetrics(logisticWithBFGSPredictsActuals, "Logistic with BFGS")

def getAlgorithm(iterations: Int, stepSize: Double, regParam: Double) =
{
  val algo = new LogisticRegressionWithLBFGS()
  algo.setIntercept(true).optimizer.setNumIterations(iterations).
  setRegParam(regParam)
  algo
}

def runClassification(algorithm: GeneralizedLinearAlgorithm[_ <:
  GeneralizedLinearModel], trainingData: RDD[LabeledPoint],
  testData: RDD[LabeledPoint]): RDD[(Double, Double)] = {
  val model = algorithm.run(trainingData)
  println("predicting")
  val predicted = model.predict(testData.map(point => point.features))
  val actuals = testData.map(point => point.label)
  val predictsAndActuals: RDD[(Double, Double)] = predicted.
  zip(actuals)
  println(predictsAndActuals.collect)
  predictsAndActuals
}

def calculateMetrics(predictsAndActuals: RDD[(Double, Double)],
  algorithm: String) {

  val accuracy = 1.0 * predictsAndActuals.filter(predActs =>
    predActs._1 == predActs._2).count() / predictsAndActuals.count()
  val binMetrics = new BinaryClassificationMetrics(predictsAndActuals)
  println(s"***** Printing metrics for $algorithm
  *****")
  println(s"Area under ROC ${binMetrics.areaUnderROC}")
}
```




```
println(s"Accuracy $accuracy")

val metrics = new MulticlassMetrics(predictsAndActuals)
println(s"Precision : ${metrics.precision}")
println(s"Confusion Matrix \n${metrics.confusionMatrix}")
println(s"***** ending metrics for $algorithm
*****")
}
```

This is the output:

Compared to the area under the ROC at around the same levels (95%), we have considerably reduced the time of the run by reducing the dimensions of the features ten-fold:

```
***** Printing metrics for Logistic with BFGS *****
Area under ROC 0.9428948576675849
Accuracy 0.9829136690647482
Confusion Matrix
965.0  3.0
16.0   128.0
***** ending metrics for Logistic with BFGS *****
```

 Note that the entire code for this recipe can be found at <https://github.com/arunma/ScalaDataAnalysisCookbook/blob/master/chapter5-learning/src/main/scala/com/packt/scalada/learning/PCASpam.scala>.

Dimensionality reduction of data for unsupervised learning

Unlike reducing the dimensions of data with labels, reducing the dimensionality of data for unsupervised learning is very simple. We just apply the PCA to the entire dataset. This helps a lot in improving the performance of algorithms such as K-means, where the entire set of features has to be plotted on a higher dimension and the entire data must be visited multiple times. A lesser number of features means a lesser number of dimensions and less data to be held in the memory.

For this recipe, we use the `Iris.data` that we used for clustering earlier. The dataset already has four features, and this isn't a great candidate for dimensionality reduction as such. However, the process around reducing dimensions for unlabeled data is the same as for any other dataset.

The steps that are involved are as follows:

1. Mean-normalizing the training data.
2. Extracting the principal components.
3. Arriving at the number of components.
4. Evaluating the metrics.



The code for this recipe can be found at <https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter5-learning/src/main/scala/com/packt/scalada/learning/PCAIris.scala>.

Mean-normalizing the training data

As we saw earlier, scaling is a must before reducing dimensions:

```
val scaler = new StandardScaler(withMean = true, withStd = false).
fit(data)

val scaledData = scaler.transform(data).cache()
```

Extracting the principal components

As we saw earlier, to compute the principal components, we need to wrap our scaled training data into a `RowMatrix`. We then multiply the matrix by the principal component matrix to arrive at the reduced matrix. We can extract the feature vector from this matrix by calling the `rows()` function:

```
val pcomp: Matrix = matrix.computePrincipalComponents(3)
val reducedData = matrix.multiply(pcomp).rows
```

Arriving at the number of components

While we would like to have the least number for the components, the other goal is to retain the highest variance in the data. In this case, a run against three components was made, and we could see that holding on to just two components out of the four, we retained 90% of the variance. However, since we wanted at least 95%, 3 was chosen:

```
val svd = matrix.computeSVD(3)

val sum = svd.s.toArray.sum

svd.s.toArray.zipWithIndex.foldLeft(0.0) {
```

```
case (cum, (curr, component)) =>
  val percent = (cum + curr) / sum
  println(s"Component and percent ${component + 1} :: $percent ::::
Singular value is : $curr")
  cum + curr
}
```

The output is as follows:

```
Component and percent 1 :: 0.6893434455825798 :::: Singular value is :
25.089863978899867
Component and percent 2 :: 0.8544090583609627 :::: Singular value is :
6.0078525425063365
Component and percent 3 :: 0.9483881906752903 :::: Singular value is :
3.4205353829523646
Component and percent 4 :: 1.0 :::: Singular value
is : 1.878502340103494
```

Evaluating the metrics

After we have reduced the dimensions of the data from four to three (!?), for fun, we run the data against a range of one to seven clusters to see the elbow bend. When we compare the results of this with the K-means clustering without dimensionality reduction, the results looks practically the same:

```
val clusterCost = (1 to 7).map { noOfClusters =>
  val kmeans = new KMeans()
  .setK(noOfClusters)
  .setMaxIterations(5)
  .setInitializationMode(KMeans.K_MEANS_PARALLEL) //KMeans | |

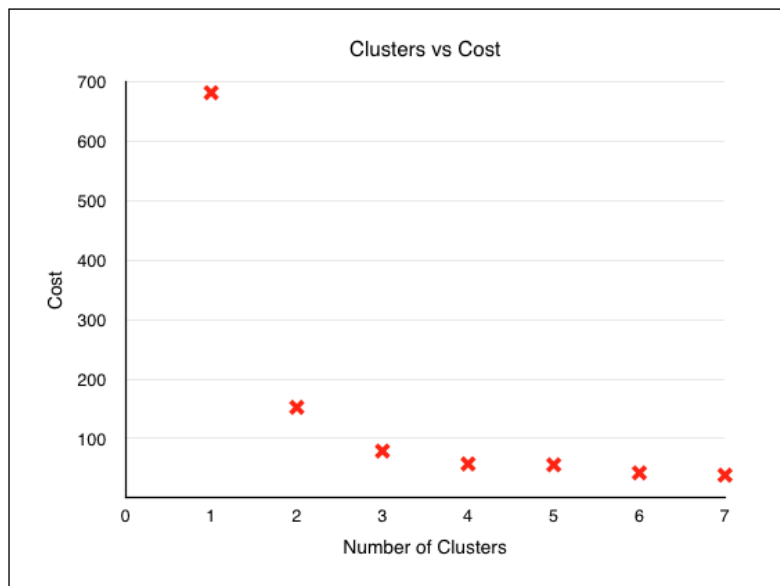
  val model = kmeans.run(reducedData)
  (noOfClusters, model.computeCost(reducedData))
}
```

Here is the output:

The following screenshot shows the cost across various numbers of clusters:

Cluster	Cost
1	680.824
2	152.369
3	78.941
4	57.345
5	55.821
6	42.327
7	38.466

Here is a screenshot that shows strikingly similar results for the elbow bend:



In this chapter, we first saw the difference between supervised and unsupervised learning. Then we explored a sample of machine learning algorithms in Spark: LinearRegression for predicting continuous values, LogisticRegression and SVM for classification, K-means for clustering, and finally PCA for dimensionality reduction. There are a plenty of other algorithms in Spark, and more algorithms are being added to Spark with every version, both batch and streaming.

6

Scaling Up

In this chapter, we will cover the following recipes:

- ▶ Building the Uber JAR
- ▶ Submitting jobs to the Spark cluster (local)
- ▶ Running the Spark standalone cluster on EC2
- ▶ Running the Spark job on Mesos (local)
- ▶ Running the Spark job on YARN (local)

Introduction

In this chapter, we'll be looking at how to bundle our Spark application and deploy it on various distributed environments.

As we discussed earlier in *Chapter 3, Loading and Preparing Data – DataFrame* the foundation of Spark is the RDD. From a programmer's perspective, the composability of RDDs such as a regular Scala collection is a huge advantage. RDD wraps three vital (and two subsidiary) pieces of information that help in reconstruction of data. This enables fault tolerance. The other major advantage is that while the processing of RDDs could be composed into hugely complex graphs using RDD operations, the entire flow of data itself is not very difficult to reason with.

Other than optional optimization attributes, such as data location, an RDD at its core wraps only three vital pieces of information:

- ▶ The dependent/parent RDD (empty if not available)
- ▶ The number of partitions
- ▶ The function that needs to be applied to each element of the RDD

Spark spawns one task per partition. So, a partition is the basic unit of parallelism in Spark.

The number of partitions could be any of these:

- ▶ Dictated by the number of blocks in the case of reading files
- ▶ A number set by the `spark.default.parallelism` parameter (set while starting the cluster)
- ▶ A number set by calling `repartition` or `coalesce` on the RDD

So far, we have just run our Spark application in the self-contained single JVM mode. While the programs work just fine, we have not yet exploited the distributed nature of the RDDs.



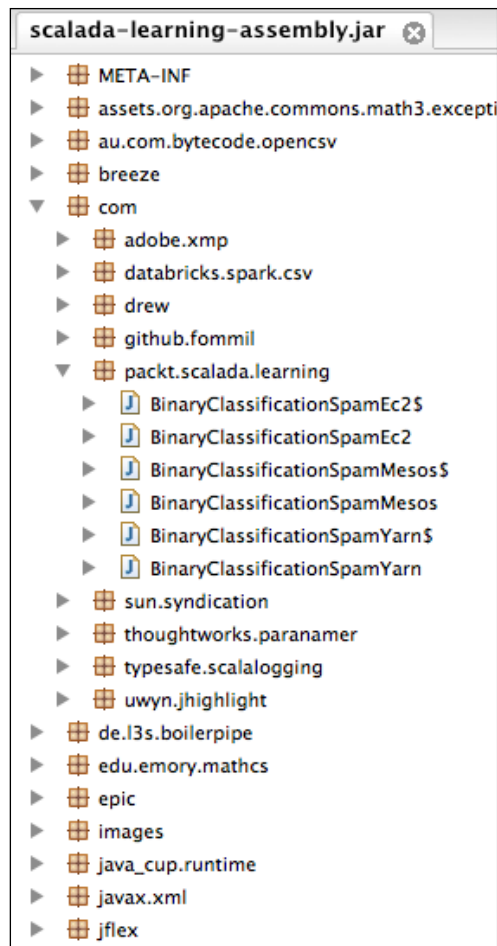
As always, all the code snippets for this chapter can be downloaded from <https://github.com/aronma/ScalaDataAnalysisCookbook/tree/master/chapter6-scalingup>.

Building the Uber JAR

The first step for deploying our Spark application on a cluster is to bundle it into a single Uber JAR, also known as the `assembly` JAR. In this recipe, we'll be looking at how to use the SBT `assembly` plugin to generate the `assembly` JAR. We'll be using this `assembly` JAR in subsequent recipes when we run Spark in distributed mode. We could alternatively set dependent JARs using the `spark.driver.extraClassPath` property (<https://spark.apache.org/docs/1.3.1/configuration.html#runtime-environment>). However, for a large number of dependent JARs, this is inconvenient.

How to do it...

The goal of building the `assembly` JAR is to build a single, Fat JAR that contains all dependencies and our Spark application. Refer to the following screenshot, which shows the innards of an `assembly` JAR. You can see not only the application's files in the JAR, but also all the packages and files of the dependent libraries:



The assembly JAR can easily be built in SBT using the SBT assembly plugin (<https://github.com/sbt/sbt-assembly>).

In order to install the `sbt-assembly` plugin, let's add the following line to our `project/assembly.sbt`:

```
addSbtPlugin("com.eed3si9n" % "sbt-assembly" % "0.13.0")
```

Next, the most common issue that we face while trying to build the assembly JAR (or Uber JAR) is the problem of duplicates—duplicate transitive dependency JARs, or simply duplicate files located at the same location (such as `MANIFEST.MF`) in different bundled JARs. The easiest way to figure out is to install the `sbt-dependency-graph` plugin (<https://github.com/jrudolph/sbt-dependency-graph>) and check which two trees bring in the conflicting JAR.

In order to add the `sbt-dependency-graph` plugin, let's add the following line to our `project/plugins.sbt`:

```
addSbtPlugin("net.virtual-void" % "sbt-dependency-graph" %  
"0.7.5")
```

Let's try to build the Uber JAR using `sbt assembly`. When we issue this command from the root of the project, we get an error that tells us that we have duplicate files in our JAR.

Let's see an example of a duplicate error message that we might face:

```
deduplicate: different file contents found in the following:  
/Users/Gabriel/.ivy2/cache/org.apache.xmlbeans/xmlbeans/jars/xmlbeans-  
2.3.0.jar:org/w3c/dom/DOMStringList.class  
/Users/Gabriel/.ivy2/cache/xml-apis/xml-apis/jars/xml-apis-1.4.01.  
jar:org/w3c/dom/DOMStringList.class  
deduplicate: different file contents found in the following:  
/Users/Gabriel/.ivy2/cache/org.apache.xmlbeans/xmlbeans/jars/xmlbeans-  
2.3.0.jar:org/w3c/dom/TypeInfo.class  
/Users/Gabriel/.ivy2/cache/xml-apis/xml-apis/jars/xml-apis-1.4.01.  
jar:org/w3c/dom/TypeInfo.class  
deduplicate: different file contents found in the following:  
/Users/Gabriel/.ivy2/cache/org.apache.xmlbeans/xmlbeans/jars/xmlbeans-  
2.3.0.jar:org/w3c/dom/UserDataHandler.class  
/Users/Gabriel/.ivy2/cache/xml-apis/xml-apis/jars/xml-apis-1.4.01.  
jar:org/w3c/dom/UserDataHandler.class
```

This happens most commonly if:

- ▶ Two different libraries in our `sbt` dependencies depend on the same external library (or libraries that have bundled the classes with the same package)
- ▶ We have explicitly stated the transitive dependency as a separate dependency in `sbt`

Whatever the case, it is always recommended to go through the entire dependency tree to trim it down.

Transitive dependency stated explicitly in the SBT dependency

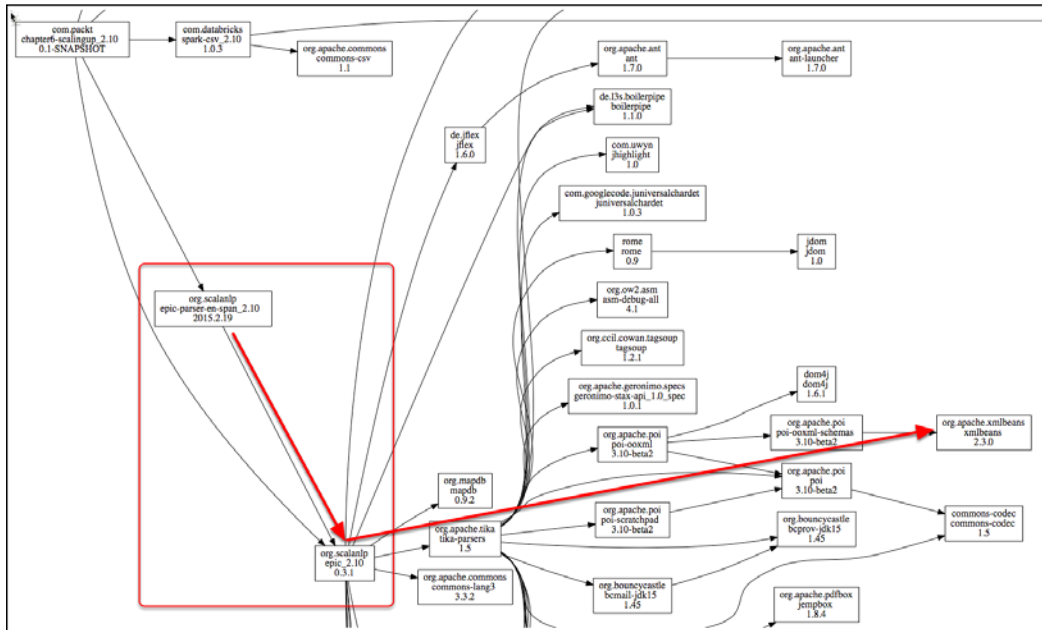
A simpler way is to export the dependency tree in an ASCII tree format and eyeball it to find the two instances where the `xmlbeans` JAR is referred to. The `sbt-dependency-graph` plugin lets us do that. Once we have installed the plugin as per the instructions, we can export and inspect the dependency tree:

```
sbt dependency-tree > deptree.txt
```

The graph can also be visualized using a real graph (however, this lacks the text search capabilities). The `sbt` dependency graph helps us analyze that too. We can export the same tree as a `.dot` file using this code:

```
sbt dependency-dot > depdot.dot
```

It outputs a `depdot.dot` file in our target directory, which can be opened using Graphviz (<http://www.graphviz.org/>). Refer to the following screenshot to see what the visualization of a `.dot` file in Graphviz looks like:



As we can see in lines 96 and 573 of the dependency tree (refer to https://github.com/aronma/ScalaDataAnalysisCookbook/blob/master/chapter6-scalingup/depgraph_xmlbeans_duplicate.txt; its screenshot is given), there are two instances of the import of `xmlbeans`: once in the tree that leads to `org.scalanlp.epic-parser-en-span_2.10:2015.2.19`, and once in the tree that leads to `org.scalanlp.epic_2.10:0.3.1`. If you notice the second level of the `epic-parser` library, you will realize that it is the `epic` library itself.

So, we can resolve this error by removing `scalanlp:epic_2.10:0.3.1` from the list of dependencies in our `build.sbt` file.

Two different libraries depend on the same external library

Even after we have removed the `epic` library, we still see some issues with the `xercesImpl` and `xmlapi` JARs. When we analyze the dependency tree, we see that two dependent libraries of `epic` depend on `xerces`, the `xml` API and the `scala` library itself!

```

+-org.mapdb:mapdb:0.9.2
+-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
+-org.scalanlp:breeze-config_2.10:0.9.1 [S]
  +-com.thoughtworks.paranamer:paranamer:2.2
  +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.4 [S]
    +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
+-org.scalanlp:breeze_2.10:0.11-M0 [S]
  +-com.github.fommil.netlib:core:1.1.2
  | +-net.sourceforge.f2j:arpack_combined_all:0.1
  |
  +-com.github.rwl:jtransforms:2.4.0
  | +-junit:junit:4.8.2
  |
  +-net.sf.opencsv:opencsv:2.3
  +-net.sourceforge.f2j:arpack_combined_all:0.1
  +-org.apache.commons:commons-math3:3.2
  +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
  +-org.scalanlp:breeze-macros_2.10:0.11-M0 [S]
    +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
    +-org.scala-lang:scala-reflect:2.10.3 (evicted by: 2.10.4)
    +-org.scala-lang:scala-reflect:2.10.4 [S]
      +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
+-org.scalamacros:quasiquotes_2.10:2.0.0 [S]
  +-org.scala-lang:scala-library:2.10.2 (evicted by: 2.10.4)
  +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.2 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.4 [S]
    +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
+-org.scalamacros:quasiquotes_2.10:2.0.0-M8 [S] (evicted by: 2.0.0)
  +-org.scala-lang:scala-library:2.10.2 (evicted by: 2.10.4)
  +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.2 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.4 [S]
    +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
+-org.slf4j:slf4j-api:1.7.5 (evicted by: 1.7.7)
+-org.slf4j:slf4j-api:1.7.6 (evicted by: 1.7.7)
+-org.slf4j:slf4j-api:1.7.7
+-org.spire-math:spire_2.10:0.7.4 [S]
  +-org.scala-lang:scala-library:2.10.2 (evicted by: 2.10.4)
  +-org.scala-lang:scala-library:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.2 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.3 (evicted by: 2.10.4)
  +-org.scala-lang:scala-reflect:2.10.4 [S]

```

We notice that the Epic library has a dependency on the Scala library, but we also know that the Scala library should already be available on the master and the worker nodes. We can exclude the Scala library altogether from getting bundled using the `assemblyOption` key:

```
assemblyOption in assembly := (assemblyOption in
assembly).value.copy(includeScala = false)
```

Next, in order to exclude the `xml-apis` library from the `epic` library, we use the `exclude` function:

```
libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % sparkVersion % "provided",
  "org.apache.spark" %% "spark-sql" % sparkVersion % "provided",
  "org.apache.spark" %% "spark-mllib" % sparkVersion % "provided",
  "com.databricks" %% "spark-csv" % "1.0.3",
  ("org.scalanlp" % "epic-parser-en-span_2.10" % "2015.2.19").
  exclude("xml-apis", "xml-apis")
)
```

As for the rest of the conflicting files, we can use the assembly plugin's merge strategy to resolve the conflict. Since we are merging contents of multiple JARs, there is a distinct possibility of a similarly named file being available on the same path, for example, `MANIFEST.MF`. The `sbt-assembly` plugin provides various strategies to resolve conflicts if the contents of the file in the same location don't match. The default strategy is to throw an error, but we can customize the strategy to suit our needs.

In the merge strategy, we append the contents of `application.conf` if there are multiple `conf` files in the JARs, use the first matching class/file in the order of the class path for the `org.cyberneko.html` package, and discard all the `manifest` files. For all others, we apply the default strategy:

```
assemblyMergeStrategy in assembly := {
  case "application.conf" =>
MergeStrategy.concat
  case PathList("org", "cyberneko", "html", xs @ _*) =>
MergeStrategy.first
  case m if m.toLowerCase.endsWith("manifest.mf") =>
MergeStrategy.discard
  case f =>
(assemblyMergeStrategy in assembly).value(f)
}
```

The entire `build.sbt` looks like this:

```
organization := "com.packt"

name := "chapter6-scalingup"

scalaVersion := "2.10.4"
val sparkVersion="1.4.1"

libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % sparkVersion % "provided",
  "org.apache.spark" %% "spark-sql" % sparkVersion % "provided",
  "org.apache.spark" %% "spark-mllib" % sparkVersion % "provided",
  "com.databricks" %% "spark-csv" % "1.0.3",
  ("org.scalanlp" % "epic-parser-en-span_2.10" % "2015.2.19").
    exclude("xml-apis", "xml-apis")
)

assemblyJarName in assembly := "scalada-learning-assembly.jar"

assemblyOption in assembly := (assemblyOption in
assembly).value.copy(includeScala = false)

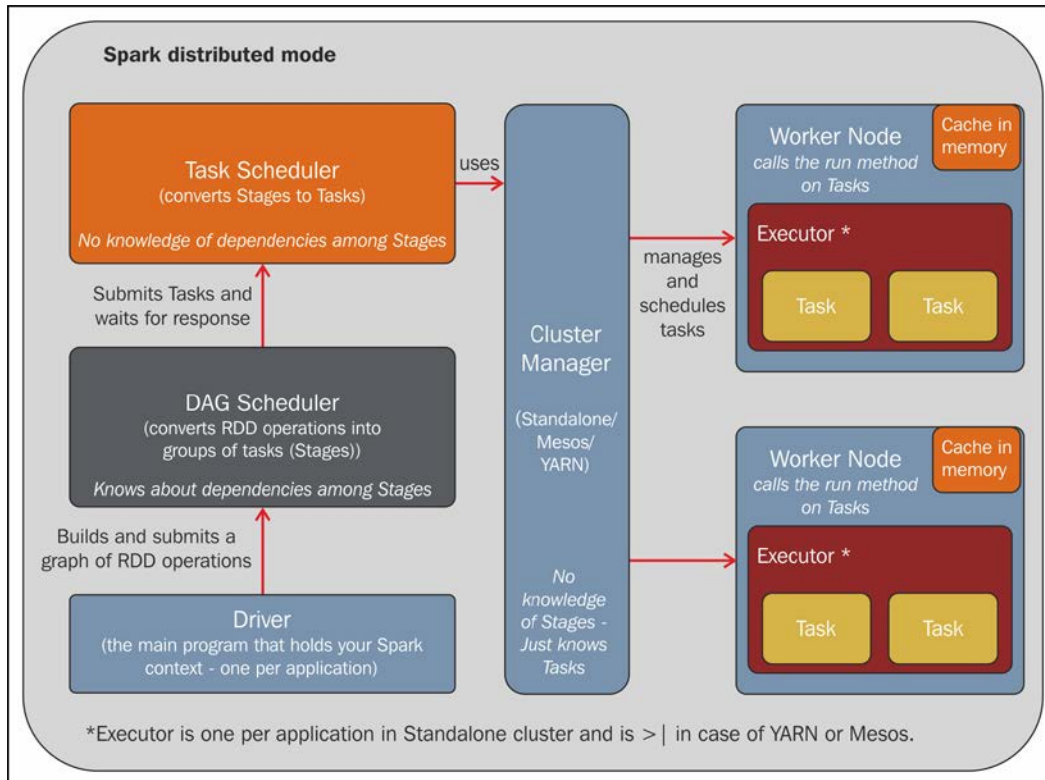
assemblyMergeStrategy in assembly := {
  case "application.conf" =>
MergeStrategy.concat
  case PathList("org", "cyberneko", "html", xs @ _*) =>
MergeStrategy.first
  case m if m.toLowerCase.endsWith("manifest.mf") =>
MergeStrategy.discard
  case f =>
(assembleMergeStrategy in assembly).value(f)
}
```

So finally, when we do an `sbt assembly`, `scalada-learning-assembly.jar` is created. If you would like the JAR name to be picked up from the `build.sbt` file's name and version, just delete the `assemblyJarName` key from `build.sbt`:

```
> sbt clean assembly
```

Submitting jobs to the Spark cluster (local)

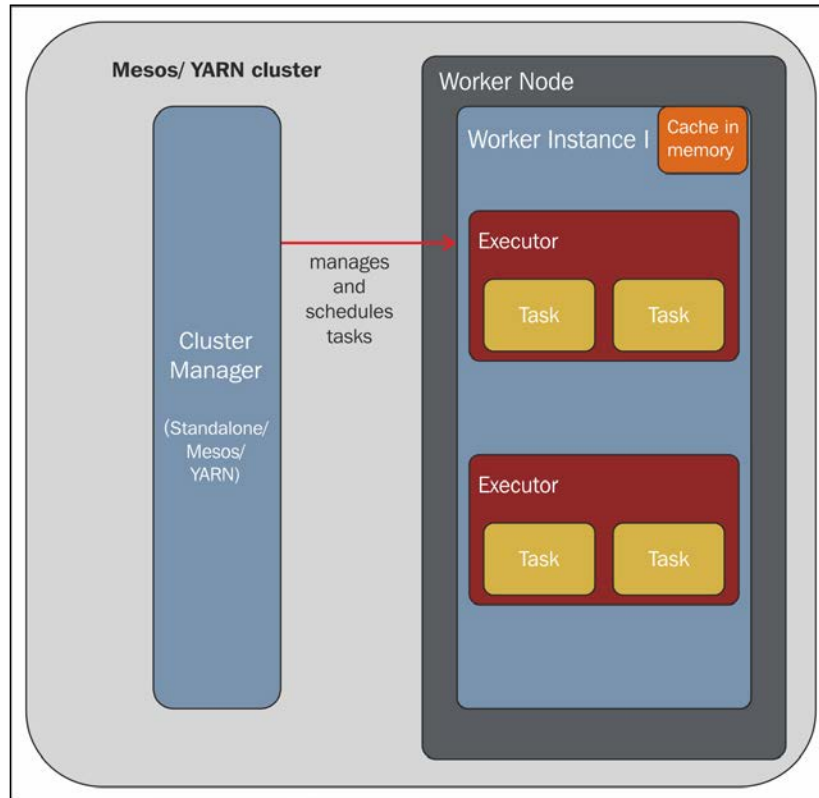
There are multiple components involved in running Spark in distributed mode. In the self-contained application mode (the main program that we have run throughout this book so far), all of these components run on a single JVM. The following diagram elaborates the various components and their functions in running the Scala program in distributed mode:




As a first step, the RDD graph that we construct using the various operations on our RDD (map, filter, join, and so on) is passed to the **Directed Acyclic Graph (DAG)** scheduler. The DAG scheduler optimizes the flow and converts all RDD operations into groups of tasks called stages. Generally, all tasks before a shuffle are wrapped into a stage. Consider operations in which there is a one-to-one mapping between tasks; for example, a map or filter operator yields one output for every input. If there is a map on an element on RDD followed by a filter, they are generally pipelined (the map and the filter) to form a single task that can be executed by a single worker, not to mention the benefits of data locality. Relating this to our traditional Hadoop MapReduce, where data is written to the disk at every stage, would help us really appreciate the Spark lineage graph.

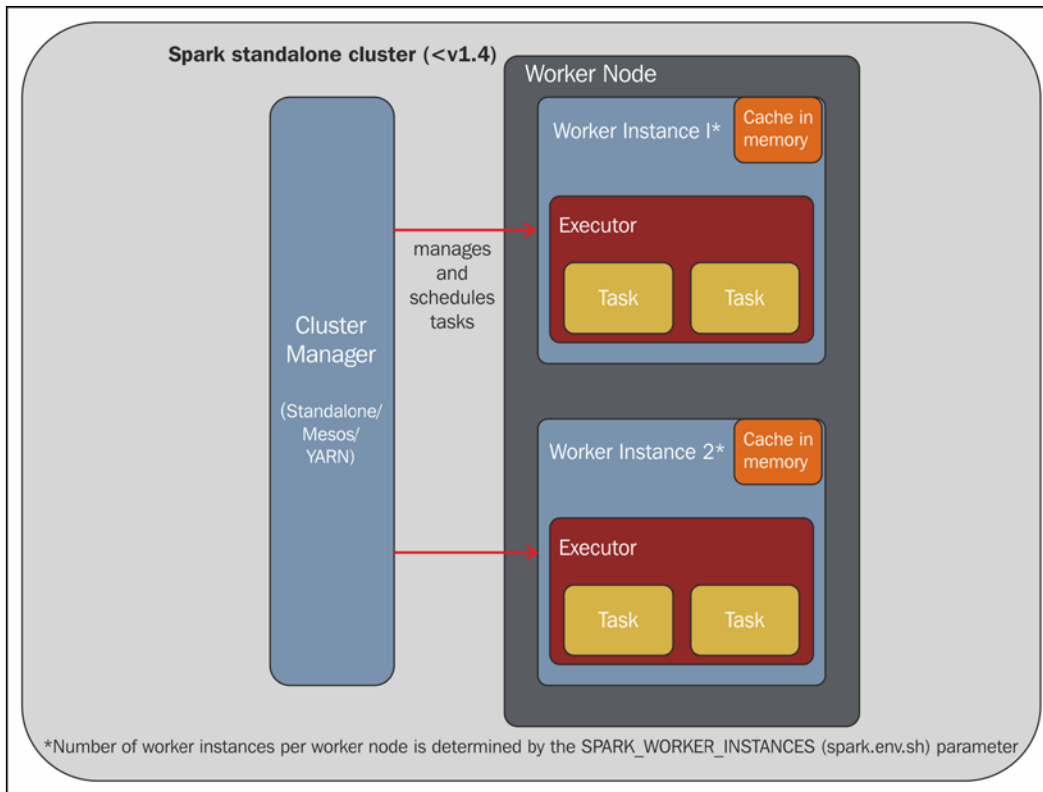
These shuffle-separated stages are then passed to the task scheduler, which splits them into tasks and submits them to the cluster manager. Spark comes bundled with a simple cluster manager that can receive the tasks and run it against a set of worker nodes. However, Spark applications can also be run on popular cluster managers, such as Mesos and YARN.

With YARN/Mesos, we can run multiple executors on the same worker node. Besides, YARN and Mesos can host non-Spark jobs in their cluster along with Spark jobs.



In the Spark standalone cluster, prior to Spark 1.4, the number of executors per worker node per application was limited to 1. However, we could increase the number of worker instances per worker node using the `SPARK_WORKER_INSTANCES` parameter. With Spark 1.4 (<https://issues.apache.org/jira/browse/SPARK-1706>), we are able to run multiple executors on the same node, just as in Mesos/YARN.

 If we intend to run multiple worker instances within a single machine, we must ensure that we configure the `SPARK_WORKER_CORES` property to limit the number of cores that can be used by each worker. The default is *all*!



In this recipe, we will be deploying the Spark application on a standalone cluster running on a single machine. For all the recipes in this chapter, we'll be using the binary classification app that we built in the previous chapter as a deployment candidate. This recipe assumes that you have some knowledge of the concepts of HDFS and basic operations on them.

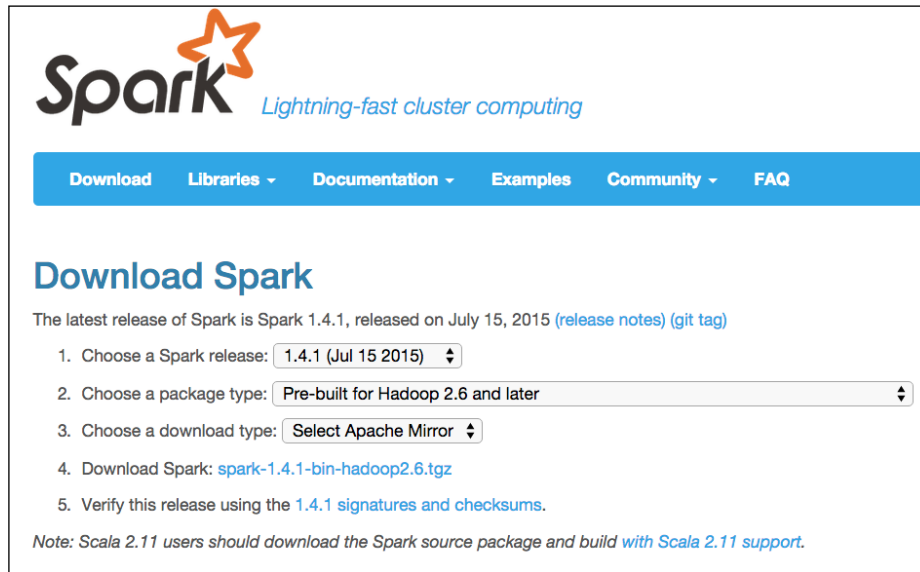
How to do it...

Submitting a Spark job to the local cluster involves the following steps:

1. Downloading Spark.
2. Running HDFS on pseudo-clustered mode.
3. Running the Spark master and slave locally.
4. Pushing data into HDFS.
5. Submitting the Spark application on the cluster.

Downloading Spark

Throughout this book, we have been using Spark version 1.4.1, as we can see in our `build.sbt`. Now, let's head over to the download page (<https://spark.apache.org/downloads.html>) and download the `spark-1.4.1-bin-hadoop2.6.tgz` bundle, as shown here:



Running HDFS on Pseudo-clustered mode

Instead of loading the file from the local filesystem for our Spark application, let's have the file stored away in HDFS. In order to do this, let's have a locally running Pseudo-distributed cluster (https://hadoop.apache.org/docs/stable/hadoop-project-dist/hadoop-common/SingleCluster.html#Pseudo-Distributed_Operation) of Hadoop 2.6.0.

After formatting our name node using `bin/hdfs namenode -format` and bringing up our data node and name node using `sbin/start-dfs.sh`, let's confirm that all the processes that we need are running properly. We do this using `Jps`. The following screenshot shows what you are expected to see once you start the `dfs` daemon:

```
3747 DataNode
3627 NameNode
3953 SecondaryNameNode
4057 Jps
```

Running the Spark master and slave locally

In order to submit our `assembly JAR` to a Spark cluster, we have to first bring up the Spark master and worker nodes.

All that we need to do to run Spark on the local machine is go to the downloaded (and extracted) `spark` folder and run `sbin/start-all.sh` from the `spark` home directory. This will bring up the Master and a Worker node of Spark. The Master's web UI is accessible from port 8080. We use this port to check the status of the job. The default service port of the Master is 7077. We'll be using this port to submit our `assembly JAR` as a job to the Spark cluster.

```
bash-3.2$ pwd
/Users/Gabriel/Apps/spark-1.4.1-bin-hadoop2.6
bash-3.2$ sbin/start-all.sh
```

Let's confirm the running of the Master and the Worker nodes using `Jps`:

```
4144 Master
3747 DataNode
3627 NameNode
4435 Jps
4326 Worker
3953 SecondaryNameNode
```

Pushing data into HDFS

This just involves running the `mkdir` and `put` commands on HDFS:

```
bash-3.2$ hadoop fs -mkdir /scalada
```

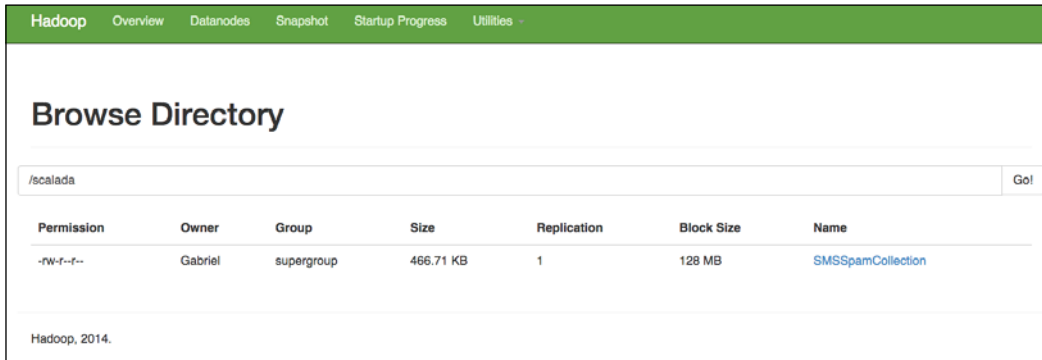
```
bash-3.2$ hadoop fs -put /Users/Gabriel/Apps/SMSSpamCollection /scalada/
```

```
bash-3.2$ hadoop fs -ls /scalada
```

```
Found 1 items
```

```
-rw-r--r--  1 Gabriel supergroup    477907 2015-07-18 16:59 /scalada/
SMSSpamCollection
```

We can also confirm this via the HDFS web interface at 50070 and by going to **Utilities** | **Browse the file system**, as shown here:



Permission	Owner	Group	Size	Replication	Block Size	Name
-rw-r--r--	Gabriel	supergroup	466.71 KB	1	128 MB	SMSSpamCollection

Submitting the Spark application on the cluster

Before we submit the Spark application to be run against the local cluster, let's change the classification program (BinaryClassificationSpam) to point to the HDFS location:

```
val docs =
  sc.textFile("hdfs://localhost:9000/scalada/SMSSpamCollection").
  map(line => {
    val words = line.split("\t")
    Document(words.head.trim(), words.tail.mkString(" "))
  })
```

By default, Spark 1.4.1 uses Hadoop 2.2.0. Now that we are trying to run the job on Hadoop 2.6.0, and are using the Spark binary prebuilt for Hadoop 2.6 and later, let's change `build.sbt` to reflect that:

```
libraryDependencies += Seq(
  "org.apache.spark" %% "spark-core" % sparkVersion % "provided",
  "org.apache.spark" %% "spark-sql" % sparkVersion % "provided",
  "org.apache.spark" %% "spark-mllib" % sparkVersion % "provided",
  "com.databricks" %% "spark-csv" % "1.0.3",
  "org.apache.hadoop" % "hadoop-client" % "2.6.0",
  ("org.scalanlp" % "epic-parser-en-span_2.10" % "2015.2.19").
  exclude("xml-apis", "xml-apis")
)
```

Run `sbt clean assembly` to build the Uber JAR, like this:

```
Gabriel@Gabriels-MacBook-Pro ~/D/a/S/C/s/chapter6-scalingup> sbt clean assembly
[info] Loading global plugins from /Users/Gabriel/.sbt/0.13/plugins
[warn] Multiple resolvers having different access mechanism configured with same name 'sbt-plugin-
lver ('publishTo').
```

```
./bin/spark-submit \
  --class com.packt.scalada.learning.BinaryClassificationSpam \
  --master spark://localhost:7077 \
  --executor-memory 2G \
  --total-executor-cores 2 \
  <project root>/target/scala-2.10/scalada-learning-assembly.jar
```

Here is the output:

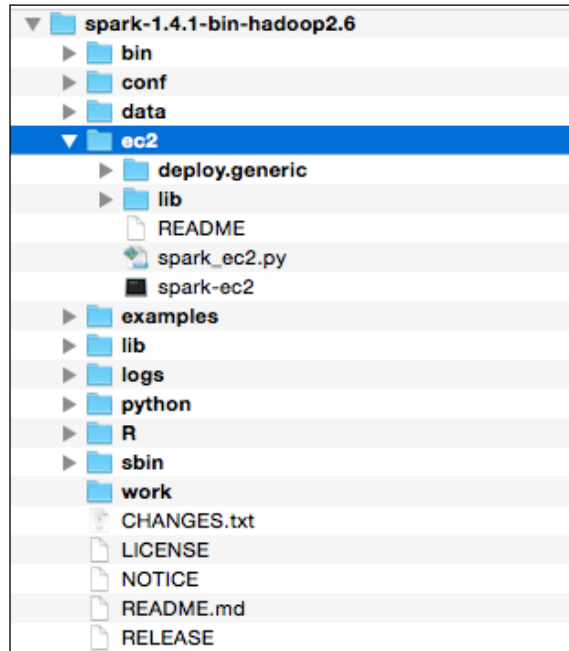
The following screenshot shows that we have successfully run our classification job on a Spark cluster as against the standalone app that we used in the previous chapter:

```
15/07/18 18:49:05 INFO DAGScheduler: Job 45 finished: collectASMap at MulticlassMetrics.scala:52, took 0.061985 s
Confusion Matrix
887.0  7.0
23.0  129.0
***** ending metrics for Logistic Regression with BFGS *****
```

Running the Spark Standalone cluster on EC2

The easiest way to create a Spark cluster and run our Spark jobs in a truly distributed mode is Amazon EC2 instances. The `ec2` folder inside the Spark installation directory wraps all the scripts and libraries that we need to create a cluster. Let's quickly go through the steps that entail the creation of our first distributed cluster.

This recipe assumes that you have a basic understanding of the Amazon EC2 ecosystem, specifically how to spawn a new EC2 instance.



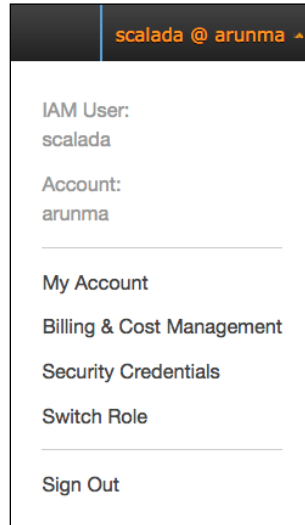
How to do it...

We'll have to ensure that we have the access key and the **Privacy Enhanced Mail (PEM)** files for AWS before proceeding with the steps. In fact, we are required to have these before launching any EC2 instance if we intend to log in to the machines.

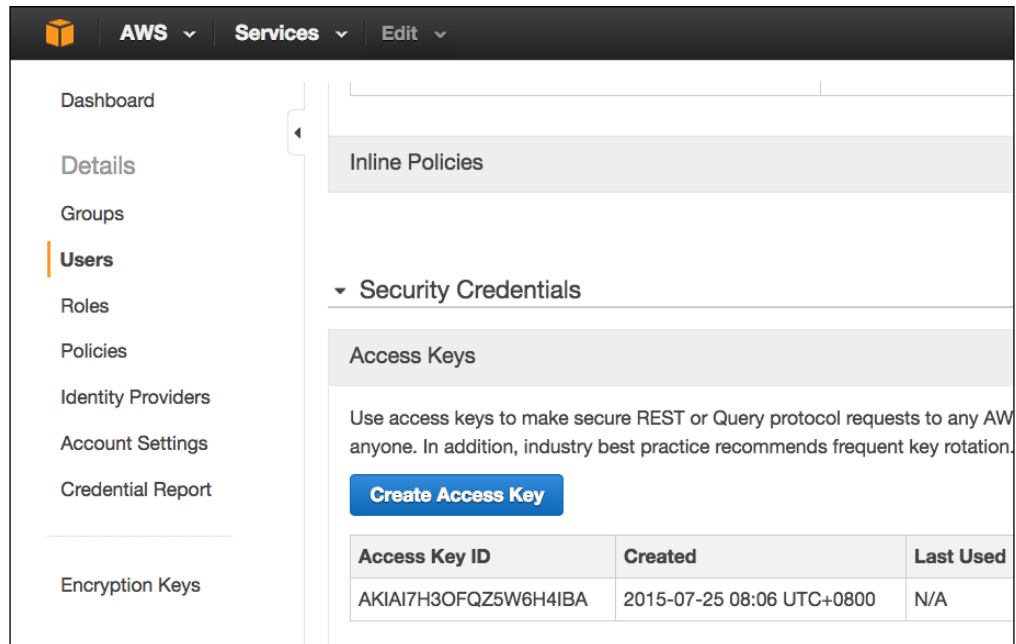
Creating the AccessKey and pem file

Instructions for creating a key pair and the pem key are available at <http://docs.aws.amazon.com/AWSEC2/latest/UserGuide/ec2-key-pairs.html>. Anyway, the following are the relevant screenshots.

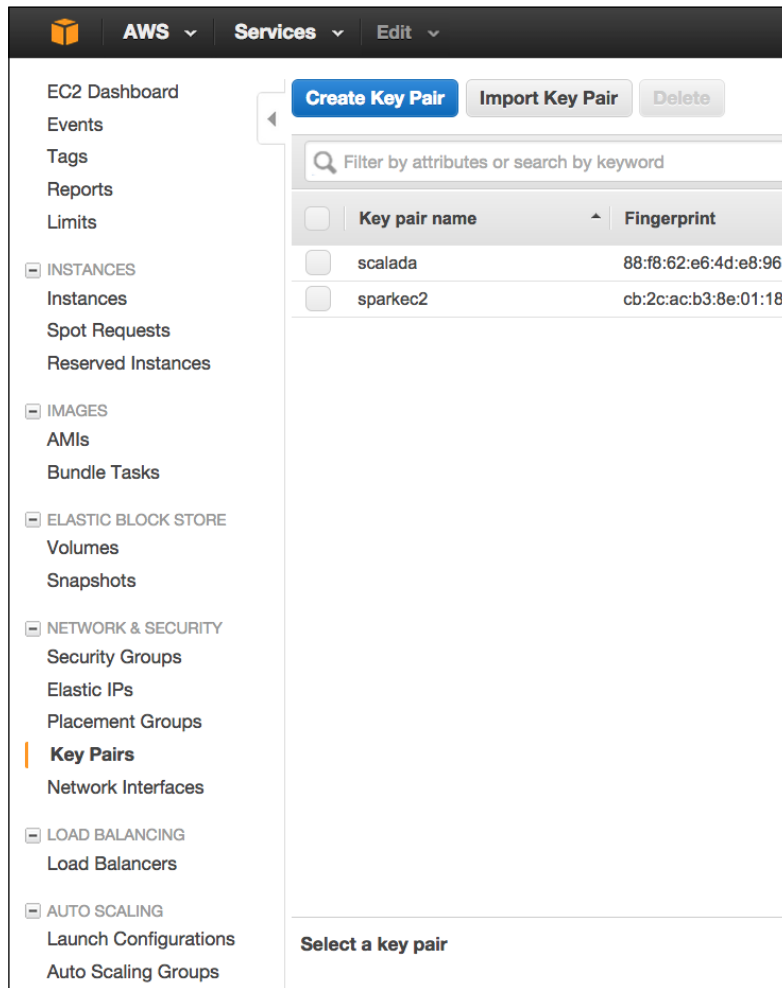
Select **Security Credentials** from the user menu, like this:



Click on the **Users** menu and create an access key, as shown in the following screenshot. Download the credentials. We'll be using this to create the EC2 instances for the Spark master and the worker nodes:



The key pair can be created from inside the EC2 instances page using the **Key Pairs** menu, as shown in the next screenshot. Your browser will automatically download the `pem` file once you create a pair:



Once you have the `pem` file, ensure that the file permission for the `pem` file is `400`. Otherwise, an error message stating that your `pem` file's permissions are too open will be shown:

```
chmod 400 spark.pem
```

Launching and running our Spark application involves the following steps:

1. Setting the environment variables.
2. Running the launch script.

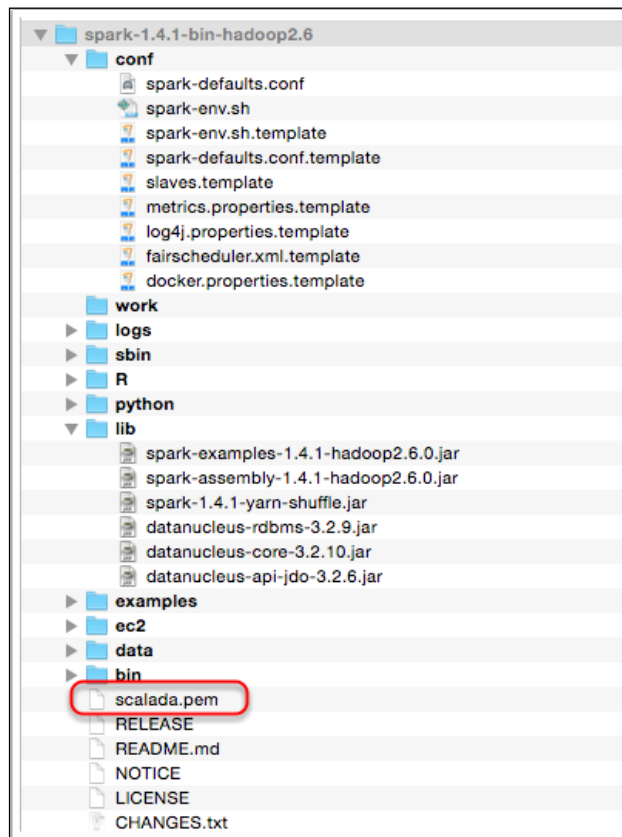
3. Verifying installation.
4. Making changes to the code.
5. Transferring the data and job files.
6. Loading the dataset into HDFS.
7. Running the job.
8. Destroying the cluster.

Setting the environment variables

As the first step, let's export the access and the secret access keys as environment variables. The `ec2` script for launching our instances will use these commands:

```
export AWS_ACCESS_KEY_ID=AKIAI7H3OFQZ5W6H4IBA
export AWS_SECRET_ACCESS_KEY=[YOUR SECRET ACCESS KEY]
```

I have also copied the `pem` file to the spark installation root directory, just to make the launch command shorter (by not specifying the entire path of the `pem` file), as marked here:



Running the launch script

Now that we have the access key (and the secret key) exported and the pem file in the root folder, let's spawn a new cluster:

```
cd spark-1.4.1-bin-hadoop2.6
```

```
./ec2/spark-ec2 --key-pair=scalada --identity-file=scalada.pem --slaves=2  
--instance-type=m3.medium --hadoop-major-version=2 launch scalada-cluster
```

The parameters, as is clearly evident, represent the following:

- ▶ `key-pair`: This is the name of the user to whom the access key and the secret access key you exported as environment variables belong.
- ▶ `identity-file`: This is the location of the pem file.
- ▶ `slaves`: This is the number of worker nodes.
- ▶ `instance-type`: This is one of the AWS instance types (<http://aws.amazon.com/ec2/instance-types/>). M3 medium has one core and 3.75 GB in memory.
- ▶ `hadoop-major-version`: This is the version of Hadoop that we want Spark to be bundled with. The spark version itself is derived from our local installation (which is 1.4.1).

We can also confirm this from the EC2 console, as shown in the following screenshot:



Name	Instance Type	Instance St.	Status Checks	Public DNS	Key Na	Launch Time	Security Groups
scalada-cluster-master-i-34dc259f	m3.medium	running	2/2 checks ...	ec2-54-161-176-58.compute-1.amazonaws.com	scalada	August 8, 2015...	scalada-cluster-master
scalada-cluster-slave-i-31dc259a	m3.medium	running	2/2 checks ...	ec2-54-147-209-103.compute-1.amazonaws.com	scalada	August 8, 2015...	scalada-cluster-slaves
scalada-cluster-slave-i-30dc259b	m3.medium	running	2/2 checks ...	ec2-54-161-198-238.compute-1.amazonaws.com	scalada	August 8, 2015...	scalada-cluster-slaves

Verifying installation

Let's log in to the Master to see the services that are running on each node:

```
ssh -i scalada.pem root@ec2-54-161-176-58.compute-1.amazonaws.com
```

Doing a `jps` on the master node shows that the Spark Master, the HDFS name node, and the Secondary name node are running on the Spark master node, as depicted in this screenshot:

```
bash-3.2$ ssh -i scalada.pem root@ec2-54-161-176-58.compute-1.amazonaws.com
Last login: Sat Aug  8 05:00:06 2015 from 132.147.72.227

  __|  __|_ )
  _| (    /  Amazon Linux AMI
  ___|\___|___|

https://aws.amazon.com/amazon-linux-ami/2013.03-release-notes/
Amazon Linux version 2015.03 is available.
root@ip-10-150-76-158 ~]$ jps
3436 NameNode
4556 Jps
4332 TachyonMaster
4006 Master
3620 SecondaryNameNode
```

Similarly, on the worker nodes, we see that the Spark Worker and the HDFS data nodes are running, as follows:

```
bash-3.2$ ssh -i scalada.pem root@ec2-54-147-209-103.compute-1.amazonaws.com
Last login: Sat Aug  8 05:01:58 2015 from 132.147.72.227

  __|  __|_ )
  _| (    /  Amazon Linux AMI
  ___|\___|___|

https://aws.amazon.com/amazon-linux-ami/2013.03-release-notes/
Amazon Linux version 2015.03 is available.
root@ip-10-63-156-126 ~]$ jps
3149 DataNode
3593 TachyonWorker
3373 Worker
3785 Jps
```

Making changes to the code

There is a small change that is required in our code in order to make it run on this cluster—the location of the dataset in HDFS. This, however, is not the recommended way of doing it, and the URL should be sourced from an external configuration file:

```
val conf = new
SparkConf().setAppName("BinaryClassificationSpamEc2")
  val sc = new SparkContext(conf)
  val sqlContext = new SQLContext(sc)

  val docs = sc.textFile("hdfs://ec2-54-159-166-156.compute-1.
amazonaws.com:9000/scalada/SMSSpamCollection").map(line => {
  val words = line.split("\t")
  Document(words.head.trim(), words.tail.mkString(" "))
})
```

Transferring the data and job files

As the next step, let's copy the dataset and the assembly JAR to the master node for execution from the directory where you have the pem file:

```
scp -i scalada.pem <REPO_DIR>/chapter5-learning/SMSSpamCollection root@
ec2-54-161-176-58.compute-1.amazonaws.com:~/.
```

```
scp -i scalada.pem <REPO_DIR>/chapter6-scalingup/target/scala-2.10/
scalada-learning-assembly.jar root@ec2-54-161-176-58.compute-1.amazonaws.
com:~/.
```

An `ls` on the home folder of the master confirms this, as shown in the following screenshot:

```
root@ip-10-150-76-158 ~]$ ls
ephemeral-hdfs  mapreduce      scala          SMSSpamCollection  spark-ec2
hadoop-native  persistent-hdfs scalada-learning-assembly.jar  spark          tachyon
```

Loading the dataset into HDFS

Now that we have uploaded our dataset to the master's local folder, let's push it to HDFS. As we saw earlier when we verified the installation, the Spark EC2 script creates and runs an HDFS cluster for us. Let's go to the `ephemeral-hdfs` folder in the root and format the filesystem. Note that the files in this HDFS, as the name indicates, will be wiped off upon restarting the cluster. Ideally, we should be installing a separate HDFS cluster on these nodes instead of depending on the ephemeral installation that was created by the Spark EC2 script.

Just as in our previous recipe, let's push the `SMSSpamCollection` dataset into the `/scalada` folder in HDFS:

```
root@ip-10-150-76-158 ephemeral-hdfs] $ ./bin/hdfs namenode -format
root@ip-10-150-76-158 ephemeral-hdfs] $ ./bin/hadoop fs -mkdir /scalada
root@ip-10-150-76-158 ephemeral-hdfs] $ ./bin/hadoop fs -put ../
SMSSpamCollection /scalada/
```

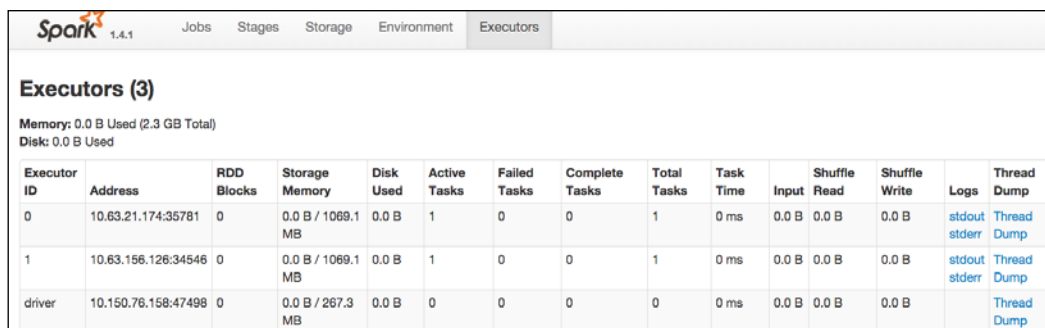
```
root@ip-10-150-76-158 ephemeral-hdfs]$ ./bin/hadoop fs -ls /scalada
Found 1 items
-rw-r--r--   3 root supergroup      477907 2015-08-08 05:24 /scalada/
SMSSpamCollection
```

Running the job

As with the previous recipe, we'll use the `spark-submit` script to submit the job to the cluster. Let's enter the spark home directory (`/root/spark`) and execute the following lines:

```
./bin/spark-submit \
  --class com.packt.scalada.learning.BinaryClassificationSpamEc2 \
  --master spark://ec2-54-161-176-58.compute-1.amazonaws.com:7077 \
  --executor-memory 2G \
  --total-executor-cores 2 \
  ../scalada-learning-assembly.jar
```

We can see that the job runs on both worker nodes of the cluster, as shown in this screenshot:



Executor ID	Address	RDD Blocks	Storage Memory	Disk Used	Active Tasks	Failed Tasks	Complete Tasks	Total Tasks	Task Time	Input	Shuffle Read	Shuffle Write	Logs	Thread Dump
0	10.63.21.174:35781	0	0.0 B / 1069.1 MB	0.0 B	1	0	0	1	0 ms	0.0 B	0.0 B	0.0 B	stdout stderr	Thread Dump
1	10.63.156.126:34546	0	0.0 B / 1069.1 MB	0.0 B	1	0	0	1	0 ms	0.0 B	0.0 B	0.0 B	stdout stderr	Thread Dump
driver	10.150.76.158:47498	0	0.0 B / 267.3 MB	0.0 B	0	0	0	0	0 ms	0.0 B	0.0 B	0.0 B	Thread Dump	

Scaling Up

We can also see the various stages of this Job from the **Stages** tab, as shown in the following screenshot:

Stage Id	Description	Submitted	Duration	Tasks: Succeeded/Total	Input	Output	Shuffle Read	Shuffle Write
8	count at LBFSGS.scala:170	2015/08/08 05:27:45	2 s	2/4	234.5 KB			

Stage Id	Description	Submitted	Duration	Tasks: Succeeded/Total	Input	Output	Shuffle Read	Shuffle Write
7	treeAggregate at StandardScaler.scala:52	2015/08/08 05:27:44	0.4 s	4/4	1218.8 KB			
6	count at DataValidators.scala:38	2015/08/08 05:27:44	0.3 s	4/4	2.3 MB			
5	first at GeneralizedLinearAlgorithm.scala:182	2015/08/08 05:27:43	0.1 s	1/1	728.4 KB			
4	count at BinaryClassificationSpamEc2.scala:53	2015/08/08	0.1 s	2/2	1456.1			

Not surprisingly, the accuracy measure is approximately the same, except that now we can use this cluster to handle much bigger data.

```
15/08/08 05:28:01 INFO BlockManagerInfo: Removed broadcast_77_piece0 on 10.63.21.174:58477 in memory (size: 1363.0 B, free: 1066.9 MB)
15/08/08 05:28:01 INFO BlockManagerInfo: Removed broadcast_77_piece0 on 10.63.156.126:58790 in memory (size: 1363.0 B, free: 1066.9 MB)
15/08/08 05:28:01 INFO ContextCleaner: Cleaned shuffle 3
Confusion Matrix
960.0  4.0
30.0  116.0
***** ending metrics for Logistic Regression with BFGS *****
```

Destroying the cluster

Finally, if you would like to destroy the cluster, you can use the same `ec2` script with the `destroy` action. From your local Spark installation directory, execute this line:

```
./ec2/spark-ec2 destroy scalada-cluster
```

```
bash-3.2$ ./ec2/spark-ec2 destroy scalada-cluster
Searching for existing cluster scalada-cluster in region us-east-1...
Found 1 master, 2 slaves.
The following instances will be terminated:
> ec2-54-161-176-58.compute-1.amazonaws.com
> ec2-54-147-209-103.compute-1.amazonaws.com
> ec2-54-161-198-238.compute-1.amazonaws.com
ALL DATA ON ALL NODES WILL BE LOST!!
Are you sure you want to destroy the cluster scalada-cluster? (y/N) y
Terminating master...
Terminating slaves...
```

Running the Spark Job on Mesos (local)

Unlike the Spark standalone cluster manager, which can run only Spark apps, Mesos is a cluster manager that can run a wide variety of applications, including Python, Ruby, or Java EE applications. It can also run Spark jobs. In fact, it is one of the popular go-to cluster managers for Spark. In this recipe, we'll see how to deploy our Spark application on the Mesos cluster. The prerequisite for this recipe is a running HDFS cluster.

How to do it...

Running a Spark job on Mesos is very similar to running it against the standalone cluster. It involves the following steps:

1. Installing Mesos.
2. Starting the Mesos master and slave.
3. Uploading the Spark binary package and the dataset to HDFS.
4. Running the job.

Installing Mesos

Download Mesos on the local machine by following the instructions at <http://mesos.apache.org/gettingstarted/>.

After you have installed the OS-specific tools needed to build Mesos, you have to run the configure and make commands (with root privileges) to build Mesos (this will take a long time) unless you pass `-j <number of cores> V=0` to your make command, as shown here:

```
bash-3.2$ pwd
/Users/Gabriel/Apps/mesos-0.22.1/build
bash-3.2$ sudo make -j 2 V=0
Making all in .
make[1]: Nothing to be done for `all-am'.
Making all in 3rdparty
```

As a side note, just like Spark, the `ec2` folder inside the `mesos` installation directory provides scripts to spawn a new EC2 `mesos` cluster.

Starting the Mesos master and slave

Now that we have Mesos installed, the next step is to start the Mesos master and slave:

```
bash-3.2$ pwd
/Users/Gabriel/Apps/mesos-0.22.1/build
bash-3.2$ sudo ./bin/mesos-master.sh --ip=127.0.0.1 --work_dir=/var/lib/mesos
```

```
bash-3.2$ pwd
/Users/Gabriel/Apps/mesos-0.22.1/build
bash-3.2$ sudo ./bin/mesos-master.sh --ip=127.0.0.1 --work_dir=/var/lib/mesos
Password:
I0725 17:29:27.133007 2005725952 main.cpp:181] Build: 2015-07-25 17:17:47 by Gabriel
I0725 17:29:27.133209 2005725952 main.cpp:183] Version: 0.22.1
I0725 17:29:27.136255 2005725952 leveldb.cpp:176] Opened db in 2558us
I0725 17:29:27.136720 2005725952 leveldb.cpp:183] Compacted db in 440us
I0725 17:29:27.136772 2005725952 leveldb.cpp:198] Created db iterator in 23us
I0725 17:29:27.136806 2005725952 leveldb.cpp:204] Searched to beginning of db in 11us
I0725 17:29:27.136821 2005725952 leveldb.cpp:273] Iterated through 0 keys in the db in 11us
I0725 17:29:27.136898 2005725952 replica.cpp:744] Replica recovered with log positions 0 -> 0 with 1 holes and 0 unlearned
I0725 17:29:27.138012 204685312 recover.cpp:449] Starting replica recovery
I0725 17:29:27.138303 204685312 recover.cpp:475] Replica is in EMPTY status
I0725 17:29:27.138816 2005725952 main.cpp:306] Starting Mesos master
I0725 17:29:27.139452 204148736 replica.cpp:641] Replica in EMPTY status received a broadcasted recover request
I0725 17:29:27.139735 203612160 recover.cpp:195] Received a recover response from a replica in EMPTY status
I0725 17:29:27.140017 205221888 recover.cpp:566] Updating replica status to STARTING
I0725 17:29:27.140393 206295040 master.cpp:349] Master 20150725-172927-16777343-5050-86707 (localhost) started on 127.0.0.1:5050
```

In another terminal window, let's bring up a worker node:

```
Gabriel@Gabriels-MacBook-Pro ~/A/m/build> pwd
/Users/Gabriel/Apps/mesos-0.22.1/build
Gabriel@Gabriels-MacBook-Pro ~/A/m/build> ./bin/mesos-slave.sh
--master=127.0.0.1:5050
```

```
Gabriel@Gabriels-MacBook-Pro ~/A/m/build> pwd
/Users/Gabriel/Apps/mesos-0.22.1/build
Gabriel@Gabriels-MacBook-Pro ~/A/m/build> ./bin/mesos-slave.sh --master=127.0.0.1:5050
I0725 17:29:47.496588 2005725952 main.cpp:156] Build: 2015-07-25 17:17:47 by Gabriel
I0725 17:29:47.496911 2005725952 main.cpp:158] Version: 0.22.1
I0725 17:29:47.497195 2005725952 containerizer.cpp:110] Using isolation: posix/cpu,posix/mem
I0725 17:29:47.504981 2005725952 main.cpp:200] Starting Mesos slave
I0725 17:29:47.506161 256000000 slave.cpp:174] Slave started on 1)@192.168.2.117:5051
I0725 17:29:47.506695 256000000 slave.cpp:322] Slave resources: cpus(*):8; mem(*):15360; disk(*):470808; ports(*):[31000-32000]
I0725 17:29:47.507113 256000000 slave.cpp:351] Slave hostname: 192.168.2.117
I0725 17:29:47.507129 256000000 slave.cpp:352] Slave checkpoint: true
I0725 17:29:47.511113 255463424 state.cpp:35] Recovering state from '/tmp/mesos/meta'
I0725 17:29:47.511363 253317120 status_update_manager.cpp:197] Recovering status update manager
I0725 17:29:47.511500 255463424 containerizer.cpp:307] Recovering containerizer
I0725 17:29:47.511998 256000000 slave.cpp:3808] Finished recovery
I0725 17:29:47.512924 254926848 status_update_manager.cpp:171] Pausing sending status updates
I0725 17:29:47.512960 254390272 slave.cpp:647] New master detected at master@127.0.0.1:5050
I0725 17:29:47.513219 254390272 slave.cpp:672] No credentials provided. Attempting to register without authentication
I0725 17:29:47.513274 254390272 slave.cpp:683] Detecting new master
I0725 17:29:48.369973 253317120 slave.cpp:815] Registered with master master@127.0.0.1:5050; given slave ID 20150725-172927-16777343-5050-86707-50
I0725 17:29:48.370090 252780544 status_update_manager.cpp:178] Resuming sending status updates
I0725 17:30:47.507956 253317120 slave.cpp:3648] Current disk usage 94.85%. Max allowed age: 0ms
```

We can now look at the Mesos status page at <http://127.0.0.1:5050>, and this is what we will see:

The screenshot shows the Mesos status page for a master node. The page has a navigation bar with 'Mesos', 'Frameworks', 'Slaves', and 'Offers'. The main content area shows the master ID '20150725-172927-16777343-5050-86707'. On the left, there is a sidebar with 'Cluster: (Unnamed)', 'Server: 127.0.0.1:5050', 'Version: 0.22.1', 'Built: 15 minutes ago by Gabriel', 'Started: 3 minutes ago', and 'Elected: 3 minutes ago'. Below this is a 'LOG' section and a 'Slaves' table with columns 'Activated' (1) and 'Deactivated' (0). On the right, there are two sections: 'Active Tasks' and 'Completed Tasks'. Both sections have a table with columns 'ID', 'Name', 'State', and 'Started'. The 'Active Tasks' table shows 'No active tasks.' and the 'Completed Tasks' table shows 'No completed tasks.'

Uploading the Spark binary package and the dataset to HDFS

Mesos requires that all worker nodes have Spark installed on the machines. We can achieve this either by configuring the `spark.mesos.executor.home` property in the spark configuration, or by simply uploading the entire Spark tar bundle to HDFS and making it available to the Mesos workers:

```
./bin/hadoop fs -mkdir /scalada
```

```
./bin/hadoop fs -put /Users/Gabriel/Apps/spark-1.4.1-bin-hadoop2.6.tgz /scalada/spark-1.4.1-bin-hadoop2.6.tgz
```


Let's set the spark binary as the executor URI

```
export SPARK_EXECUTOR_URI=hdfs://localhost:9000/scalada/spark-1.4.1-bin-hadoop2.6.tgz
```

Also, let's upload the dataset to HDFS:

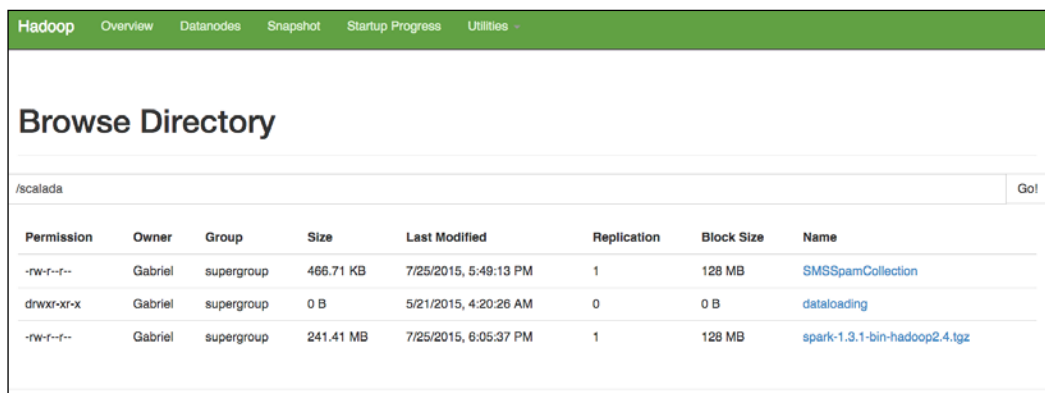
```
./bin/hadoop fs -mkdir /scalada
```

```
./bin/hadoop fs -put /Users/Gabriel/Apps/SMSSpamCollection /scalada/
```

Running the job

There is one thing that we need to do before running the program itself— configure the location of the `libmesos` native library. This file can be found in the `/usr/local/lib` folder as `libmesos.so` or `libmesos.dylib`, depending on your operating system:

```
export MESOS_NATIVE_JAVA_LIBRARY=/usr/local/lib/libmesos-0.22.1.dylib
```



The screenshot shows the Hadoop web interface with a green header bar containing navigation links: Hadoop, Overview, Datanodes, Snapshot, Startup Progress, and Utilities. The main content area is titled "Browse Directory" and shows the contents of the `/scalada` directory. A "Go!" button is visible in the top right corner of the directory view. Below the header, there is a table with columns for Permission, Owner, Group, Size, Last Modified, Replication, Block Size, and Name. The table lists three files: `SMSSpamCollection` (466.71 KB, modified 7/25/2015, 5:49:13 PM), `dataloading` (0 B, modified 5/21/2015, 4:20:26 AM), and `spark-1.3.1-bin-hadoop2.4.tgz` (241.41 MB, modified 7/25/2015, 6:05:37 PM).

Permission	Owner	Group	Size	Last Modified	Replication	Block Size	Name
-rw-r--r--	Gabriel	supergroup	466.71 KB	7/25/2015, 5:49:13 PM	1	128 MB	SMSSpamCollection
drwxr-xr-x	Gabriel	supergroup	0 B	5/21/2015, 4:20:26 AM	0	0 B	dataloading
-rw-r--r--	Gabriel	supergroup	241.41 MB	7/25/2015, 6:05:37 PM	1	128 MB	spark-1.3.1-bin-hadoop2.4.tgz

Now, let's use `cd` to enter the Spark installation directory, and then run the job:

```
cd /Users/Gabriel/Apps/spark-1.4.1-bin-hadoop2.6
```

```
export MESOS_NATIVE_JAVA_LIBRARY=/usr/local/lib/libmesos-0.22.1.dylib
```

```
./bin/spark-submit \  
  --class com.packt.scalada.learning.BinaryClassificationSpamMesos \  
  --master mesos://localhost:5050 \  
  --executor-memory 2G \  
  --total-executor-cores 2 \  
  <REPO_FOLDER>/chapter6-scalingup/target/scala-2.10/scalada-learning-assembly.jar
```

As you can see in the following screenshot, the tasks run fine on this single-worker-node cluster:

The screenshot shows the Mesos UI for a cluster with ID 20150725-174711-16777343-5050-89118. The cluster is unnamed and the server is 127.0.0.1:5050. It was built 1 hour ago by Gabriel and started 48 minutes ago. The cluster has 1 activated slave and 0 deactivated slaves. There are 389 staged tasks, 0 started tasks, and 380 finished tasks. The active tasks table shows two tasks running on host 192.168.2.117 in a sandbox.

ID	Name	State	Started	Host
0	task 0.0 in stage 0.0	RUNNING	just now	192.168.2.117
1	task 1.0 in stage 0.0	RUNNING	just now	192.168.2.117

The next screenshot shows the list of tasks that are already completed:

The screenshot shows the Mesos UI for a cluster with ID 20150808-122009-16777343-5050-50466. The cluster is unnamed and the server is 127.0.0.1:5050. It was built 2 weeks ago by Gabriel and started 36 minutes ago. The cluster has 1 activated slave and 0 deactivated slaves. There are 388 staged tasks, 0 started tasks, 360 finished tasks, 0 killed tasks, 0 failed tasks, and 24 lost tasks. The resources section shows 8 CPUs and 15.0 GB of memory. The active tasks table shows four tasks: three in a STAGING state and one in a RUNNING state on localhost. The completed tasks table shows a list of 24 finished tasks on localhost in a sandbox.

ID	Name	State	Started	Stopped	Host
180	task 2.0 in stage 53.0	STAGING			localhost
181	task 3.0 in stage 53.0	STAGING			localhost
179	task 1.0 in stage 53.0	STAGING			localhost
178	task 0.0 in stage 53.0	RUNNING	just now		localhost

ID	Name	State	Started	Stopped	Host
177	task 3.0 in stage 52.0	FINISHED	just now	just now	localhost
176	task 2.0 in stage 52.0	FINISHED	just now	just now	localhost
175	task 1.0 in stage 52.0	FINISHED	just now	just now	localhost
174	task 0.0 in stage 52.0	FINISHED	just now	just now	localhost
173	task 3.0 in stage 51.0	FINISHED	just now	just now	localhost
172	task 2.0 in stage 51.0	FINISHED	just now	just now	localhost
171	task 1.0 in stage 51.0	FINISHED	just now	just now	localhost
170	task 0.0 in stage 51.0	FINISHED	just now	just now	localhost
169	task 3.0 in stage 50.0	FINISHED	just now	just now	localhost
168	task 2.0 in stage 50.0	FINISHED	just now	just now	localhost
167	task 1.0 in stage 50.0	FINISHED	just now	just now	localhost
166	task 0.0 in stage 50.0	FINISHED	just now	just now	localhost
165	task 0.0 in stage 49.0	FINISHED	just now	just now	localhost
164	task 3.0 in stage 49.0	FINISHED	just now	just now	localhost
163	task 2.0 in stage 49.0	FINISHED	just now	just now	localhost
162	task 1.0 in stage 49.0	FINISHED	just now	just now	localhost

Running the Spark Job on YARN (local)

Hadoop has a long history, and in most cases, organizations have already invested in the Hadoop infrastructure before they move their MR jobs to Spark. Unlike the Spark standalone cluster manager, which can run only Spark jobs, and Mesos, which can run a variety of applications, YARN runs Hadoop jobs as first-class. At the same time, it can run Spark jobs as well. This means that when a team decides to replace some of their MR jobs with Spark jobs, they can use the same cluster manager to run Spark jobs. In this recipe, we'll see how to deploy our Spark application on the YARN cluster manager.

How to do it...

Running a Spark job on YARN is very similar to running it against a Spark standalone cluster. It involves the following steps:

1. Installing the Hadoop cluster.
2. Starting HDFS and YARN.
3. Pushing the Spark assembly and dataset to HDFS.
4. Running the Spark Job in the `yarn-client` mode.
5. Running the Spark Job in the `yarn-cluster` mode.

Installing the Hadoop cluster

While the setup of the cluster itself is beyond the scope of this recipe, for the sake of completeness, let's quickly look at the relevant site XML configurations that were made while setting up a single-node pseudo-distributed cluster on a local machine. Refer to http://www.bogotobogo.com/Hadoop/BigData_hadoop_install_on_ubuntu_single_node_cluster.php for the complete details on how to set up a local YARN/HDFS cluster:

The `core-site.xml` file:

```
<configuration>
  <property>
    <name>fs.default.name</name>
    <value>hdfs://localhost:54310</value>
  </property>
</configuration>
```

The `mapred-site.xml` file:

```
<configuration>
  <property>
    <name>mapred.job.tracker</name>
    <value>localhost:54311</value>
  </property>
</configuration>
```

The `hdfs-site.xml` file:

```
<configuration>
  <property>
    <name>dfs.replication</name>
    <value>1</value>
  </property>
</configuration>
```

Starting HDFS and YARN

Once the setup of the cluster is done, let's format HDFS and start the cluster (`dfs` and `yarn`):

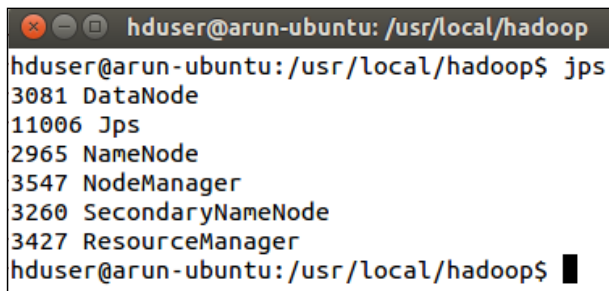
Format namenode:

```
hdfs namenode -format
```

Start both HDFS and YARN:

```
sbin/start-all.sh
```

Let's confirm that the services are running through `jps`, and this is what we should see:



```
hduser@arun-ubuntu: /usr/local/hadoop
hduser@arun-ubuntu: /usr/local/hadoop$ jps
3081 DataNode
11006 Jps
2965 NameNode
3547 NodeManager
3260 SecondaryNameNode
3427 ResourceManager
hduser@arun-ubuntu: /usr/local/hadoop$ █
```

Pushing Spark assembly and dataset to HDFS

Ideally, when we do a `spark-submit`, YARN should be able to pick our `spark-assembly` JAR (or Uber JAR) and upload it to HDFS. However, this doesn't happen correctly and results in the following error:

```
Error: Could not find or load main class org.apache.spark.deploy.yarn.  
ExecutorLauncher
```

In order to work around this issue, let's upload our `spark-assembly` JAR manually to HDFS and change our `conf/spark-env.sh` to reflect the location. The Hadoop config directory should also be specified in `spark-env.sh`:

Uploading the spark assembly to HDFS.

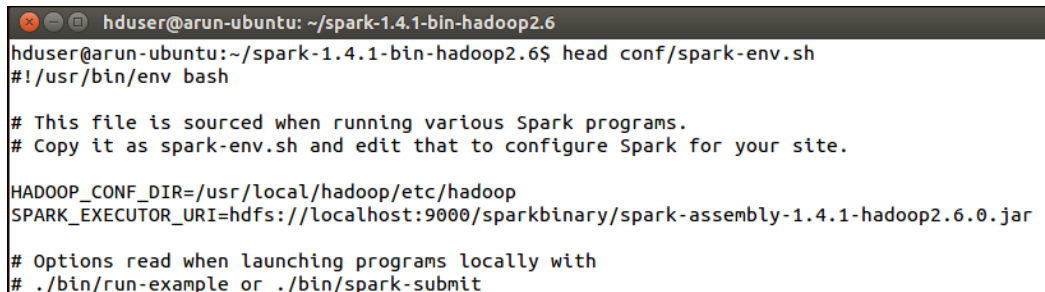
```
hadoop fs -mkdir /sparkbinary  
hadoop fs -put /Users/Gabriel/Apps/spark-1.4.1-bin-hadoop2.6/lib/spark-  
assembly-1.4.1-hadoop2.6.0.jar /sparkbinary/  
hadoop fs -ls /sparkbinary
```

Uploading the Spam dataset to HDFS:

```
hadoop fs -mkdir /scalada  
hadoop fs -put ~/SMSSpamCollection /scalada/  
hadoop fs -ls /scalada
```

Entries in `spark-env.sh`:

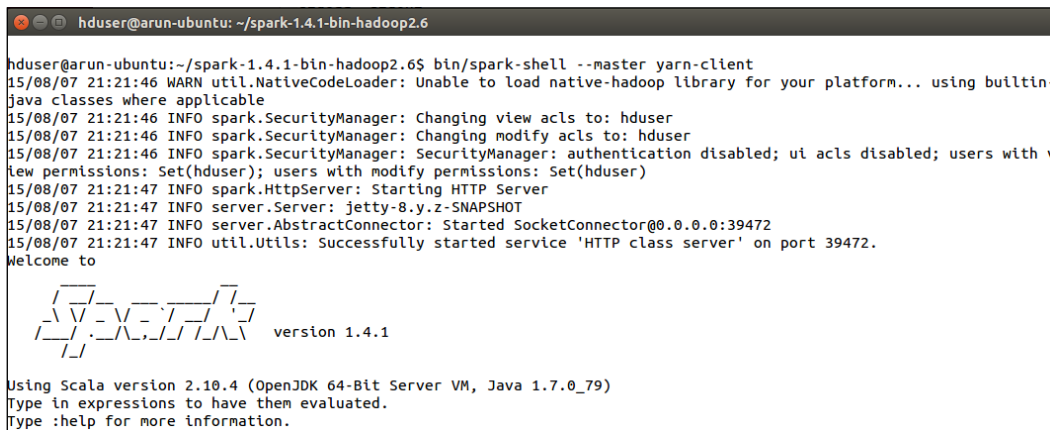
```
HADOOP_CONF_DIR=/usr/local/hadoop/etc/hadoop  
SPARK_EXECUTOR_URI=hdfs://localhost:9000/sparkbinary/spark-assembly-  
1.4.1-hadoop2.6.0.jar
```



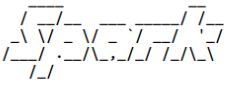
```
hduser@arun-ubuntu: ~/spark-1.4.1-bin-hadoop2.6  
hduser@arun-ubuntu:~/spark-1.4.1-bin-hadoop2.6$ head conf/spark-env.sh  
#!/usr/bin/env bash  
  
# This file is sourced when running various Spark programs.  
# Copy it as spark-env.sh and edit that to configure Spark for your site.  
  
HADOOP_CONF_DIR=/usr/local/hadoop/etc/hadoop  
SPARK_EXECUTOR_URI=hdfs://localhost:9000/sparkbinary/spark-assembly-1.4.1-hadoop2.6.0.jar  
  
# Options read when launching programs locally with  
# ./bin/run-example or ./bin/spark-submit
```

Before we submit our Spark job to the YARN cluster, let's confirm that our setup is fine using the Spark shell. The Spark shell is a wrapper around the Scala REPL, with Spark libraries set in the classpath. Configuring `HADOOP_CONF_DIR` to point to the Hadoop `config` directory ensures that Spark will now use YARN to run its jobs. However, there are two modes in which we can run the Spark job in YARN, namely `yarn-client` and `yarn-cluster`. Let's explore both of them in this subrecipe. But before we do that, to validate our configuration, we'll launch the Spark shell pointing the master to the `yarn-client`. After a rain of logs, we should be able to see a Scala prompt. This confirms that our configuration is good:

```
bin/spark-shell --master yarn-client
```



```
hduser@arun-ubuntu: ~/spark-1.4.1-bin-hadoop2.6
hduser@arun-ubuntu:~/spark-1.4.1-bin-hadoop2.6$ bin/spark-shell --master yarn-client
15/08/07 21:21:46 WARN util.NativeCodeLoader: Unable to load native-hadoop library for your platform... using builtin-
java classes where applicable
15/08/07 21:21:46 INFO spark.SecurityManager: Changing view acls to: hduser
15/08/07 21:21:46 INFO spark.SecurityManager: Changing modify acls to: hduser
15/08/07 21:21:46 INFO spark.SecurityManager: SecurityManager: authentication disabled; ut acls disabled; users with v
iew permissions: Set(hduser); users with modify permissions: Set(hduser)
15/08/07 21:21:47 INFO spark.HttpServer: Starting HTTP Server
15/08/07 21:21:47 INFO server.Server: jetty-8.y.z-SNAPSHOT
15/08/07 21:21:47 INFO server.AbstractConnector: Started SocketConnector@0.0.0.0:39472
15/08/07 21:21:47 INFO util.Utils: Successfully started service 'HTTP class server' on port 39472.
Welcome to

 version 1.4.1

Using Scala version 2.10.4 (OpenJDK 64-Bit Server VM, Java 1.7.0_79)
Type in expressions to have them evaluated.
Type :help for more information.
```

Running a Spark job in yarn-client mode

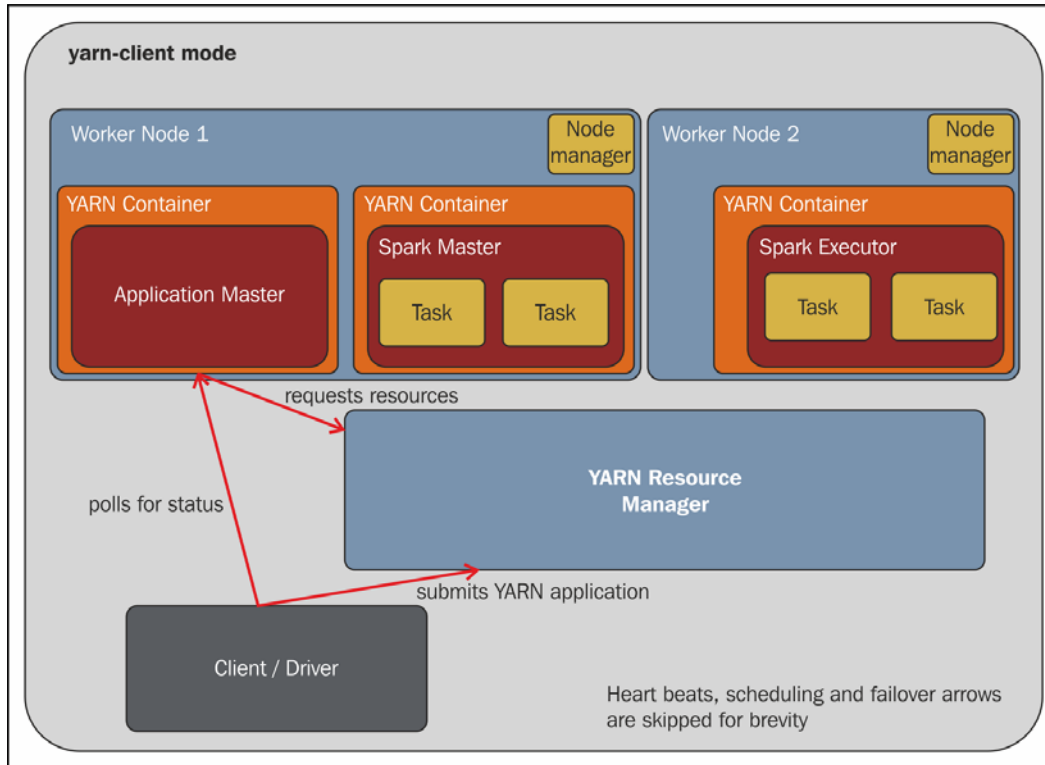
Now that we have confirmed that the shell loads up fine against the YARN master, let's head over to deploying our Spark job on YARN.

As we discussed earlier, there are two modes in which we can run a Spark application on YARN: the `yarn-client` mode and the `yarn-cluster` mode. In the `yarn-client` mode, the driver program resides on the client side and the YARN worker nodes are used only to execute the job. All of the brain of the application resides in the client JVM that polls the application master for the status. The application master does nothing except watching out for failure of the executor nodes and reporting and requesting for resources accordingly to the resource manager. This also means that the client (our driver JVM) needs to run as long as the application executes:

```
./bin/spark-submit \
  --class com.packt.scalada.learning.BinaryClassificationSpamYarn \
  --master yarn-client \
```

Scaling Up

```
--executor-memory 1G \  
~/scalada-learning-assembly.jar
```



As we see from the YARN console, our job is running fine. Here is a screenshot that shows this:

The screenshot shows the Hadoop YARN console interface. The main heading is **RUNNING Applications**. A table displays cluster metrics and application details.

Cluster Metrics															
Apps Submitted	Apps Pending	Apps Running	Apps Completed	Containers Running	Memory Used	Memory Total	Memory Reserved	VCores Used	VCores Total	VCores Reserved	Active Nodes	Decommissioned Nodes	Lost Nodes	Unhealthy Nodes	Rebooted Nodes
8	0	1	7	3	5 GB	8 GB	0 B	3	8	0	1	0	0	0	0

ID	User	Name	Application Type	Queue	StartTime	FinishTime	State	FinalStatus	Progress	Tracking UI
application_1438940079068_0008	hduser	BinaryClassificationSpamYarn	SPARK	default	Sat, 08 Aug 2015 01:43:22 GMT	N/A	RUNNING	UNDEFINED		ApplicationMaster

Showing 1 to 1 of 1 entries

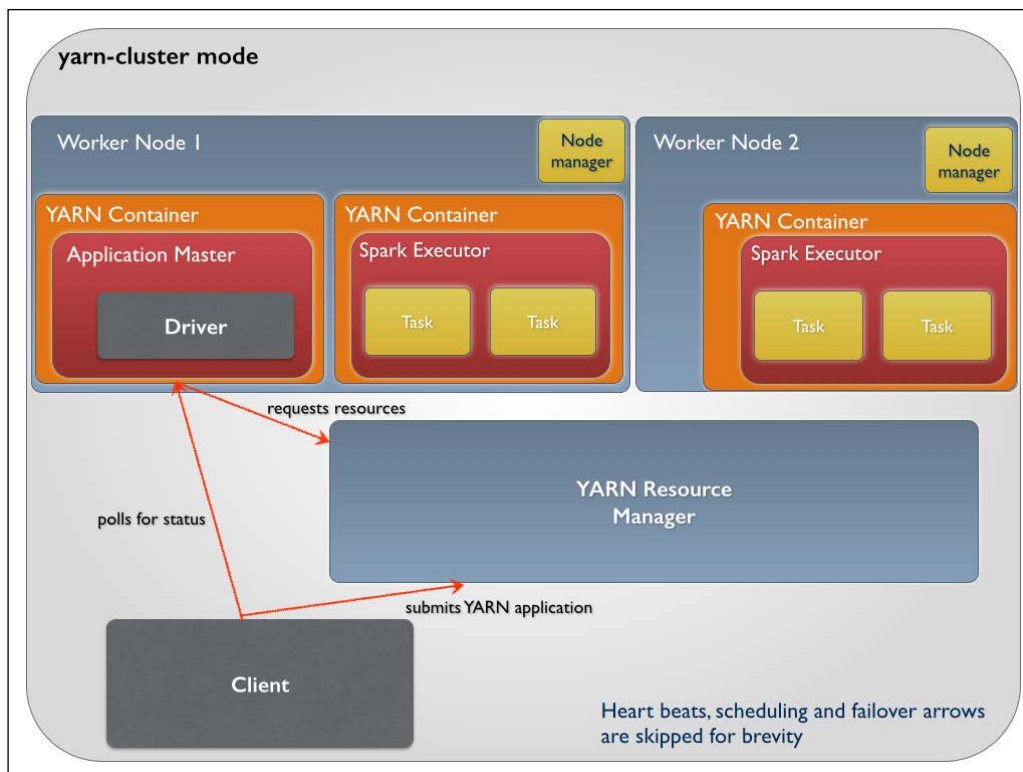
Finally, we can see the output on the client JVM (the driver) itself:

```
Confusion Matrix
913.0  7.0
35.0   127.0
***** ending metrics for Logistic Regression with BFGS *****
```

Running Spark job in yarn-cluster mode

In the `yarn-cluster` mode, the client JVM doesn't do anything at all. In fact, it just submits and polls the Application master for status. The driver program itself runs on the Application master, which now has all the brains of the program. Unlike the `yarn-client` mode, the user logs won't be displayed on the client JVM because the driver, which consolidates the results, is executing inside the YARN cluster:

```
./bin/spark-submit \
  --class com.packt.scalada.learning.BinaryClassificationSpamYarn \
  --master yarn-cluster \
  --executor-memory 1g \
  ~/scalada-learning-assembly.jar
```

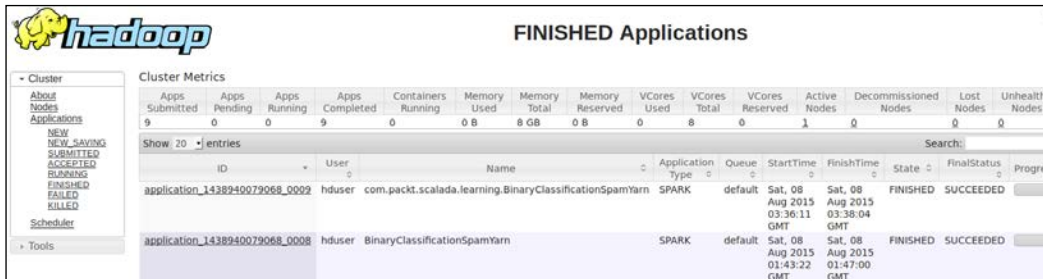


Scaling Up

As expected, the client JVM indicates that the job has run successfully. It doesn't, however, show the user logs.

```
15/08/07 23:38:01 INFO yarn.Client: Application report for application_1438940079068_0009 (state: RUNNING)
15/08/07 23:38:02 INFO yarn.Client: Application report for application_1438940079068_0009 (state: RUNNING)
15/08/07 23:38:03 INFO yarn.Client: Application report for application_1438940079068_0009 (state: RUNNING)
15/08/07 23:38:04 INFO yarn.Client: Application report for application_1438940079068_0009 (state: FINISHED)
15/08/07 23:38:04 INFO yarn.Client:
client token: N/A
diagnostics: N/A
ApplicationMaster host: 10.0.2.15
ApplicationMaster RPC port: 0
queue: default
start time: 1439004971922
final status: SUCCEEDED
tracking URL: http://arun-ubuntu:8088/proxy/application_1438940079068_0009/A
user: hduser
15/08/07 23:38:04 INFO util.Utils: Shutdown hook called
15/08/07 23:38:04 INFO util.Utils: Deleting directory /tmp/spark-08e26d88-e459-4c55-8813-5d00f35f6ad7
```

The following screenshot shows the final status of our client and the cluster mode runs:



FINISHED Applications														
Cluster Metrics														
Apps Submitted	Apps Pending	Apps Running	Apps Completed	Containers Running	Memory Used	Memory Total	Memory Reserved	VCores Used	VCores Total	VCores Reserved	Active Nodes	Decommissioned Nodes	Lost Nodes	Unhealthy Nodes
9	0	0	9	0	0 B	8 GB	0 B	0	0	0	1	0	0	0
Show 20 entries														
ID	User	Name	Application Type	Queue	StartTime	FinishTime	State	FinalStatus	Progress					
application_1438940079068_0002	hduser	com.packt.scalada.learning.BinaryClassificationSpamYarn	SPARK	default	Sat, 08 Aug 2015 03:36:11 GMT	Sat, 08 Aug 2015 03:38:04 GMT	FINISHED	SUCCEEDED						
application_1438940079068_0008	hduser	BinaryClassificationSpamYarn	SPARK	default	Sat, 08 Aug 2015 01:43:22 GMT	Sat, 08 Aug 2015 01:47:00 GMT	FINISHED	SUCCEEDED						

The actual output of this program is inside the Hadoop user logs. We can either go to the logs directory of Hadoop, or check it out from the Hadoop console itself, when we click on the application link and then on the logs link in the console.

As you can see in the following screenshot, the `stdout` file shows our embarrassing `println` commands:



```
Logs for container_1438940079068_0009_01_000001 - Mozilla Firefox
Logs for container_143... x | Namenode information | Spark Master at spark/... x
http://arun-ubuntu:8042/node/containerlogs/container_1438940079068_0009_01_000001/hduser/stdout/?start=-4096
hadoop
Logs for container_1438940079068_0009_01_000001
ResourceManager
RM Home
NodeManager
Tools
Spam count:615::133
Ham count:3844::983
***** Printing metrics for Logistic Regression with BFGS *****
Area under ROC 0.9894646585946045
F1 0.9722222222222222
Precision : 0.9722222222222222
Confusion Matrix
975.0 8.0
23.0 110.0
***** ending metrics for Logistic Regression with BFGS *****
```

In this chapter, we took an example Spark application and deployed it on a Spark standalone cluster manager, YARN, and Mesos. Along the way, we touched upon the internals of these cluster managers.

7

Going Further

In this chapter, we will cover the following recipes:

- ▶ Using Spark Streaming to subscribe to a Twitter stream
- ▶ Using Spark as an ETL tool (pulling data from ElasticSearch and publishing it to Kafka)
- ▶ Using StreamingLogisticRegression to classify a Twitter stream using Kafka as a training stream
- ▶ Using GraphX to analyze Twitter data
- ▶ Watching other Scala libraries of interest

Introduction

So far, the entire book has concentrated a little around Breeze and a lot around Spark, specifically DataFrames and machine learning. However, there are a whole lot of other libraries, both in Java and Scala that could be leveraged while analyzing data from Scala. This chapter goes a little more into Spark's other components, streaming and GraphX. Note that each recipe in this chapter feeds into the next recipe.



All the code related to this chapter can be downloaded from
[https://github.com/aronma/ScalaDataAnalysisCookbook/
tree/master/chapter7-goingfurther](https://github.com/aronma/ScalaDataAnalysisCookbook/tree/master/chapter7-goingfurther).

Using Spark Streaming to subscribe to a Twitter stream

Just like all the other components of Spark, Spark Streaming is also scalable and fault-tolerant, it's just that it manages a stream of data instead of a large amount of data that Spark generally does. The way that Spark Streaming approaches streaming is unique in the sense that it accumulates streams into small batches called DStreams and then processes them as mini-batches, an approach usually called **micro-batching**. The component that receives the stream of data and splits it into time-bound windows of batches is called the receiver.

Once these batches are received, Spark takes these batches up, converts them into RDDs, and processes the RDDs in the same way as static datasets. The regular framework components such as the driver and executor stay the same. However, in terms of Spark Streaming, a DStream or Discretized stream is just a continuous stream of RDDs. Also, just like `SQLContext` served as an entry point to use SQL in Spark, there's `StreamingContext` that serves as an entry point for Spark Streaming.

In this recipe, we will subscribe to a Twitter stream and index (store) the tweets into ElasticSearch (<https://www.elastic.co/>).

How to do it...

The prerequisite to run this recipe is to have a running ElasticSearch instance on your machine.

1. **Running ElasticSearch:** Running an instance of ElasticSearch is as simple as it gets. Just download the installable from <https://www.elastic.co/downloads/elasticsearch> and run `bin/elasticsearch`. This recipe uses the latest version 1.7.1.

```
bash-3.2$ pwd
/Users/Gabriel/apps/elasticsearch-1.7.1
bash-3.2$ bin/elasticsearch
[2015-08-15 13:47:33,047][INFO ][node                ] [Harry Leland] version[1.7.1], pid[65232], build[b88f43f/2015-07-29T09:54:16Z]
[2015-08-15 13:47:33,047][INFO ][node                ] [Harry Leland] initializing ...
[2015-08-15 13:47:33,156][INFO ][plugins              ] [Harry Leland] loaded [], sites []
[2015-08-15 13:47:33,207][INFO ][env                  ] [Harry Leland] using [1] data paths, mounts [ [/dev/disk1]], net usable_spac
e [15.3gb], net total_space [464.7gb], types [hfs]
[2015-08-15 13:47:35,860][INFO ][node                ] [Harry Leland] initialized
[2015-08-15 13:47:35,860][INFO ][node                ] [Harry Leland] starting ...
[2015-08-15 13:47:35,964][INFO ][transport            ] [Harry Leland] bound_address {inet[/0:0:0:0:0:0:9300]}, publish_address {in
et[/192.168.2.117:9300]}
```

2. **Creating a Twitter app:** In order to subscribe to tweets, Twitter requires us to create a Twitter app. Let's quickly set up a Twitter app in order to get the consumer key and the secret key. Visit <https://apps.twitter.com/> using your login and click **Create New App**.

Create an application

Application Details

Name *

Your application name. This is used to attribute the source of a tweet and in user-facing

Description *

Your application description, which will be shown in user-facing authorization screens. E

Website *

We will be using the consumer key, consumer secret key, the access token, and the access secret in our application.

scalada

Details Settings **Keys and Access Tokens** Permissions

Application Settings

Keep the "Consumer Secret" a secret. This key should never be human-readable in your application.

Consumer Key (API Key)	pwb1BHKR99eEk24DC74iF94Pg
Consumer Secret (API Secret)	3uCYAxYVmWJjcuMp9PI6Hg9vUYFm8xFuw0x0RxBpHT3h7r1Gm
Access Level	Read and write (modify app permissions)

- Adding Spark Streaming and the Twitter dependency:** There are two dependencies that need to be added here, the `spark-streaming` and the `spark-streaming-twitter` libraries:

```
"org.apache.spark" %% "spark-streaming" % sparkVersion %
"provided",
"org.apache.spark" %% "spark-streaming-twitter" %
sparkVersion
```

4. **Creating a Twitter stream:** Creating a Twitter stream is super easy in Spark. We just need to use `TwitterUtils.createStream` for this. `TwitterUtils` wraps around the `twitter4j` library (<http://twitter4j.org/en/index.html>) to provide first-class support in Spark.

`TwitterUtils.createStream` expects a few parameters. Let's construct them one by one.

- **StreamingContext:** `StreamingContext` could be constructed by passing in `SparkContext` and the time window of the batch:

```
val streamingContext=new StreamingContext(sc, Seconds(5))
```

- **OAuthAuthorization:** The access and the consumer keys that comprise the OAuth credentials need to be passed in order to subscribe to the Twitter stream:

```
val builder = new ConfigurationBuilder()
    .setOAuthConsumerKey(consumerKey)
    .setOAuthConsumerSecret(consumerSecret)
    .setOAuthAccessToken(accessToken)
    .setOAuthAccessTokenSecret(accessTokenSecret)
    .setUseSSL(true)
```

```
val twitterAuth = Some(new
OAuthAuthorization(builder.build()))
```

- **Filter criteria:** You are free to skip this parameter if your intention is to subscribe to (a sample of) the universe of the tweets. For this recipe, we'll add some filter criteria to it:

```
val filter=List("fashion", "tech", "startup", "spark")
```

- **StorageLevel:** This is where our received objects that come in batches need to be stored. The default is memory with a capability to overflow to disk. Once this is constructed, let's construct the Twitter stream itself:

```
val stream=TwitterUtils.createStream(streamingContext,
twitterAuth, filter, StorageLevel.MEMORY_AND_DISK)
```

5. **Saving the stream to ElasticSearch:** Writing the Tweets to ElasticSearch involves three steps:

1. Adding the `ElasticSearch-Spark` dependency: Let's add the appropriate version of `ElasticSearch Spark` to our `build.sbt`:

```
"org.elasticsearch" %% "elasticsearch-spark" % "2.1.0"
```

2. Configuring the Elasticsearch server location in the Spark configuration: Elasticsearch has a subproject called `elasticsearch-spark` that makes Elasticsearch a first-class citizen in the Spark world. The `org.elasticsearch.spark` package exposes some convenient functions that convert a case class to JSON (deriving types) and indexes to Elasticsearch. The package also provides some really cool implicits that provide functions to save RDD into Elasticsearch and load data from Elasticsearch as an RDD. We'll be looking at those functions shortly.

The Elasticsearch target node URL could be specified in the Spark configuration. By default, it points to localhost and port 9200. If required, we could customize it:

```
//Default is localhost. Point to ES node when required

val conf = new SparkConf()
  .setAppName("TwitterStreaming")
  .setMaster("local[2]")
  .set(ConfigurationOptions.ES_NODES, "localhost")
  .set(ConfigurationOptions.ES_PORT, "9200")
```

3. Converting the stream into a case class: If we are not interested in pushing the data to Elasticsearch and are interested only in printing some values in `twitter4j.Status`, `stream.foreach` will help us iterate through the `RDD[Status]`. However, in this recipe, we will be extracting some data from `twitter4j.Status` and pushing it to Elasticsearch. For this purpose, a case class `SimpleStatus` is created. The reason why we are extracting data out as a case class is that `twitter4j.Status` has way too much information that we don't want to index:

```
case class SimpleStatus(id:String, content:String,
  date:Date, hashTags:Array[String]=Array[String](),
  urls:Array[String]=Array[String](),
  user:String, userName:String,
  userFollowerCount:Long)
```

The `twitter4j.Status` is converted to `SimpleStatus` using a `convertToSimple` function that extracts only the required information:

```
def convertToSimple(status: twitter4j.Status): SimpleStatus = {
  val hashTags: Array[String] =
    status.getHashtagEntities().map(eachHT => eachHT.getText())
  val urlArray = if (status.getURLEntities != null)
    status.getURLEntities().foldLeft((Array[String]()))((r, c) => (r
    :+ c.getExpandedURL())) else Array[String]()
  val user = status.getUser()
```


Going Further

```
val utcDate = new
Date(dateTimeZone.convertLocalToUTC(status.getCreatedAt.getTime,
false))

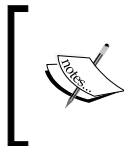
SimpleStatus(id = status.getId.toString, content =
status.getText(), utcDate,
hashTags = hashTags, urls = urlArray,
user = user.getScreenName(), userName = user.getName,
userFollowerCount = user.getFollowersCount)
}
```

Once we map the `twitter4j.Status` to `SimpleStatus`, we now have a `RDD[SimpleStatus]`. We can now iterate over the `RDD[SimpleStatus]` and push every RDD to ElasticSearch's "spark" index. "twstatus" is the index type. In RDBMS terms, an index is like a database schema and the index type is like a table:

```
stream.map(convertToSimple).foreachRDD { statusRdd =>
println(statusRdd)
statusRdd.saveToEs("spark/twstatus")
}
```

We could confirm the indexing by pointing to ElasticSearch's spark index using Sense, a must-have Chrome plugin for ElasticSearch, or simply by performing a curl request:

```
curl -XGET "http://localhost:9200/spark/_search" -d'
{
  "query": {
    "match_all": {}
  }
}'
```



The Sense plugin for Chrome can be downloaded from the Chrome store at: <https://chrome.google.com/webstore/detail/sense-beta/lhjgkml1caadmopgmanpapmpjgmfcfig?hl=en>.

```

Server localhost:9200/
59 GET _search
60 {
61   "query": {
62     "match_all": {}
63   }
64 }
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
1 {
2   "took": 3,
3   "timed_out": false,
4   "_shards": {
5     "total": 5,
6     "successful": 5,
7     "failed": 0
8   },
9   "hits": {
10    "total": 24849,
11    "max_score": 1,
12    "hits": [
13      {
14        "_index": "spark",
15        "_type": "twstatus",
16        "_id": "AU8rx-n1vKjZvIITcMgA",
17        "_score": 1,
18        "_source": {
19          "urls": [
20            "http://www.mensshirts.org.uk/stores/visit.php?store=austin-need"
21          ]
22        }
23      }
24    ]
25  }
26 }

```

Using Spark as an ETL tool

In the previous recipe, we subscribed to a Twitter stream and stored it in Elasticsearch. Another common source of streaming is Kafka, a distributed message broker. In fact, it's a distributed log of messages, which in simple terms means that there can be multiple brokers that has the messages partitioned among them.

In this recipe, we'll be subscribing the data that we ingested into Elasticsearch in the previous recipe and publishing the messages into Kafka. Soon after we publish the data to Kafka, we'll be subscribing to Kafka using the Spark Stream API. While this is a recipe that demonstrates treating Elasticsearch data as an RDD and publishing to Kafka using a **KryoSerializer**, the true intent of this recipe is to run a streaming classification algorithm against Twitter, which is our next recipe.

How to do it...

Let's look at the various steps involved in doing this.

1. **Setting up Kafka:** This recipe uses Kafka version 0.8.2.1 for Spark 2.10, which can be downloaded from https://www.apache.org/dyn/closer.cgi?path=/kafka/0.8.2.1/kafka_2.10-0.8.2.1.tgz.

Once downloaded, let's extract, start the Kafka server, and create a Kafka topic through three commands from inside our Kafka home directory:

1. **Starting Zookeeper:** Kafka uses Zookeeper (<https://zookeeper.apache.org/>) to hold coordination information between Kafka servers. It also holds the commit offset information of the data so that if a Kafka node fails, it knows where to resume from. The Zookeeper data directory and the client port (default 2181) is present in `zookeeper.properties`. The `zookeeper-server-start.sh` expects this to be passed as a parameter for it to start:

```
bin/zookeeper-server-start.sh config/zookeeper.properties
```

2. **Starting the Kafka server:** Again, in order to start Kafka, the configuration file to be passed to it is `server.properties`. The `server.properties`, among many things specifies the port on which the Kafka server listens (9092) and the Zookeeper port it needs to connect to (2181). This is passed to the `kafka-server-start.sh` startup script:

```
bin/kafka-server-start.sh config/server.properties
```

3. **Creating a Kafka topic:** In really simple terms, a topic can be compared to a JMS topic with the difference that there could be multiple publishers as well as a single subscriber in Kafka. Since we are running the Kafka in a non-replicated and non-partitioned mode using just one Kafka server, the topic named `twtopic` (Twitter topic) is created with a replication factor of 1 and the number of partitions is 1 as well:

```
bin/kafka-topics.sh --create --zookeeper localhost:2181
--replication-factor 1 --partitions 1 --topic twtopic
```

2. **Pulling data from ElasticSearch:** The next step is to pull the data from ElasticSearch and treat it as a Spark DataFrame other than the optional setting in Spark configuration to point to the correct host and port. This is just a one-liner.

The configuration change (if needed) is:

```
//Default is localhost. Point to ES node when required
val conf = new SparkConf()
  .setAppName("KafkaStreamProducerFromES")
  .setMaster("local[2]")
  .set(ConfigurationOptions.ES_NODES, "localhost")
  .set(ConfigurationOptions.ES_PORT, "9200")
```

The following line queries the `"spark/twstatus"` index (that we published to in the last recipe) for all documents and extracts the data into a DataFrame. Optionally, you can pass in a query as a second argument (for example, `"?q=fashion"`):

```
val twStatusDf=sqlContext.esDF("spark/twstatus")
```

Let's try to sample the DataFrame using `show()`:

```
twStatusDf.show()
```

The output is:

l	content	date	hashTags	id	url	user	userFollowerCount	userName
l	HEY GUYS there's ...	2015-08-14 10:36:...	Buffer(Fashion, M...	632138605465612289	Buffer(http://www...	lowpricesuk	4491	LowPrices.co.uk
l	Harbok Import Kor...	2015-08-14 10:36:...	Buffer()	632138602667905028	Buffer(https://w...	happykoreamart	3721	Happy Korea Mart
l	Fashion brands an...	2015-08-14 10:33:...	Buffer()	632137887492866048	Buffer(http://www...	thehansindia	13871	The Hans India
l	@ParkaLondonUK we...	2015-08-14 10:36:...	Buffer(menswear, ...	632138612847546368	Buffer()	riddlemagazine	14771	Riddle Magazine
l	I Forget Retro. The...	2015-08-14 10:36:...	Buffer(fashion)	632138616379211776	Buffer(http://wor...	WordLinkFASHION	2071	WordLink #FASHION
l	IRT @MarketingUK: ...	2015-08-14 10:33:...	Buffer()	632137891435651072	Buffer(http://bit...	GrimwoodAssoci	3201	Jane Grimwood
l	Summer Fashion Sa...	2015-08-14 10:36:...	Buffer()	632138611232653312	Buffer(http://bit...	Iam_Flamenkant	4981	Lee kuam yew
l	Summer Fashion Sa...	2015-08-14 10:36:...	Buffer()	632138619394744320	Buffer(http://bit...	ismelhai	5431	Still mel
l	Fashion For Women...	2015-08-14 10:36:...	Buffer()	632138612688166912	Buffer(http://fb...	ibothman	5591	Ibrahim Othman
l	IRT @SadHappyAnazi...	2015-08-14 10:36:...	Buffer()	632138604240850944	Buffer()	ItsCristalBro	6361	Ceel
l	#6: Champion Men'...	2015-08-14 10:36:...	Buffer(fashion, a...	632138634078982144	Buffer(http://am...	InstantTimeDeal	8541	Instant Time Deals
l	Boots by #NancySi...	2015-08-14 10:36:...	Buffer(NancySinat...	632138625275158528	Buffer(http://dlv...	DealsMalls	1551	Deals Malls
l	#6: Champion Men'...	2015-08-14 10:36:...	Buffer(fashion, a...	632138629662400512	Buffer(http://am...	RSSDealFeeds	5271	RSS Deal Feeds
l	Summer Fashion Sa...	2015-08-14 10:36:...	Buffer()	632138621135417344	Buffer(http://bit...	bajulus	1321	Bajulu Olaitan
l	Summer Fashion Sa...	2015-08-14 10:36:...	Buffer()	632138648767459328	Buffer(http://bit...	its_3lvyz	9071	@eLVis
l	Ijam Tangan Wanita...	2015-08-14 10:36:...	Buffer()	632138657453838336	Buffer(https://w...	DUNIANETdotCOM	5871	DUNIANET.com
l	http://t.co/42Zx8...	2015-08-14 10:36:...	Buffer(Deals, Fas...	632138659811172352	Buffer(http://ft...	Xu_D3_004	511	FASHION DEALS CHECK
l	Summer Fashion Sa...	2015-08-14 10:36:...	Buffer()	632138668690403329	Buffer(http://bit...	HottestQ	6921	IG:hottestq
l	#LatestNews: Summ...	2015-08-14 10:36:...	Buffer(LatestNews)	632138691637575680	Buffer()	diamondnewsgr	1871	Diamond Report
l	Women's Retro fas...	2015-08-14 10:36:...	Buffer()	63213877650176000	Buffer(http://rov...	Dounhi_Siopki	13561	Dounhi Siopki

3. **Preparing data to be published to Kafka:** Before we do this step, let's go over what we aim to achieve from this step. Like we discussed at the beginning of the recipe, we will be running a classification algorithm against streaming data in the next recipe. As you know, any supervised learning algorithm requires a training dataset. Instead of us manually curating the dataset, we will be doing that in a very primitive fashion by marking all the tweets that have the word `fashion` in them as belonging to the `fashion` class and the rest of the tweets as not belonging to the `fashion` class.

We will just take the content of the tweet and convert it into a case class called `LabeledContent` (similar to `LabeledPoint` in Spark MLlib):

```
case class LabeledContent(label: Double, content:
Array[String])
```

`LabeledContent` only has two fields:

- ❑ `label`: This indicates whether the tweet is about `fashion` or not (1.0 if the tweet is on `fashion` and 0.0 if it is not)
- ❑ `content`: This holds a space-tokenized version of the tweet itself

```
def convertToLabeledContentRdd(twStatusDf: DataFrame) = {
  //Convert the content alone to a (label, content) pair
  val labeledPointRdd = twStatusDf.map{row =>
    val content =
      row.getAs[String]("content").toLowerCase()
    val tokens = content.split(" ") //A very primitive
    space based tokenizer
```

```
        val labeledContent = if (content.contains("fashion"))
            LabeledContent(1, tokens)
        else LabeledContent(0, tokens)
        println (labeledContent.label, content)
        labeledContent
    }
    labeledPointRdd
}
```

4. **Publishing data to Kafka using KryoSerializer:** Now that we have the publish candidate (`LabeledContent`) ready, let's publish it to the Kafka topic. This involves just three lines.

- **Constructing the connection and transport properties:** In `properties`, we configure the Kafka server port location and register the serializer that we use to serialize `LabeledContent`:

```
val properties = Map[String,
Object] (ProducerConfig.BOOTSTRAP_SERVERS_CONFIG ->
"localhost:9092").asJava
```

- **Constructing the Kafka producer using the connection properties and the key and value serializer:** The next step is to construct a Kafka producer using the `properties` we constructed earlier. The producer also needs a key and a value serializer. Since we don't have a key for our message, we fall back to Kafka's default, which fills in the hashcode by default, which we aren't interested on receipt.

```
val producer = new KafkaProducer[String,
Array[Byte]](properties, new StringSerializer, new
ByteArraySerializer)
```

- **Sending data to the Kafka topic using the send method:** We then serialize `LabeledContent` using `KryoSerializer` and send it to the Kafka topic `"twtopic"` (the one that we created earlier) using the `producer.send` method. The only purpose of using a `KryoSerializer` here is to speed up the serialization process:

```
val serializedPoint = KryoSerializer.serialize(lContent)
    producer.send(new ProducerRecord[String,
Array[Byte]]("twtopic", serializedPoint))
```

For the `KryoSerializer`, we use Twitter's `chill` library (<https://github.com/twitter/chill>), which provides an easier abstraction over the serialization for Scala.

The actual `KryoSerializer` is just five lines of code:

```
object KryoSerializer {
  private val kryoPool = ScalaKryoInstantiator.defaultPool

  def serialize[T](anObject: T): Array[Byte] =
    kryoPool.toBytesWithClass(anObject)
  def deserialize[T](bytes: Array[Byte]): T =
    kryoPool.fromBytes(bytes).asInstanceOf[T]
}
```

The dependency for Twitter `chill` that needs to be added to our `build.sbt` is:

```
"com.twitter" %% "chill" % "0.7.0"
```

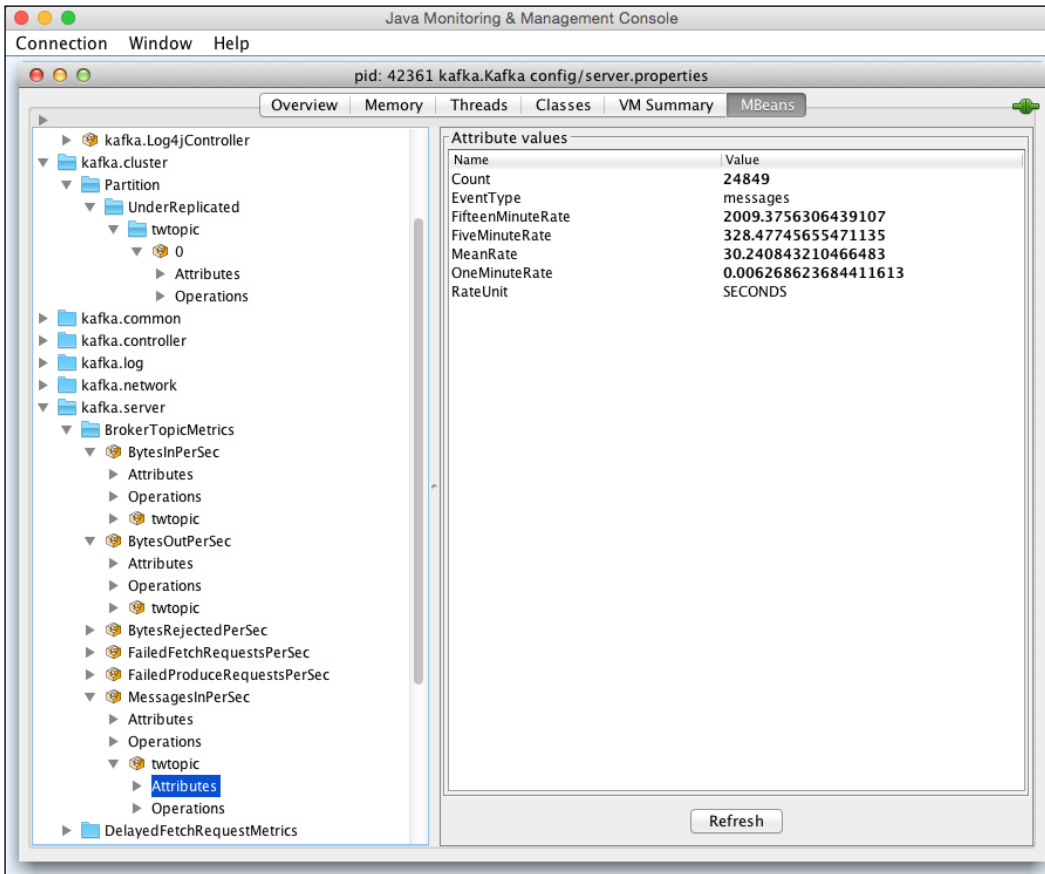
The entire publishing method looks like this:

```
def publishToKafka(labeledPointRdd: RDD[LabeledContent])
{
  labeledPointRdd.foreachPartition { iterator =>

    val properties = Map[String, Object](ProducerConfig.
    BOOTSTRAP_SERVERS_CONFIG ->
    "localhost:9092", "serializer.class" ->
    "kafka.serializer.DefaultEncoder").asJava
    val producer = new KafkaProducer[String,
    Array[Byte]](properties, new StringSerializer, new
    ByteArraySerializer)

    iterator.foreach { lContent =>
      val serializedPoint =
        KryoSerializer.serialize(lContent)
      producer.send(new ProducerRecord[String,
        Array[Byte]]("twtopic", serializedPoint))
    }
  }
}
```

5. **Confirming receipt in Kafka:** We could confirm whether the data is in Kafka using the JMX MBeans exposed by it. We'll use JConsole UI to explore MBeans. As you can see, the count of the messages is **24849**, which matches the ElasticSearch document count (that was published in the previous recipe).



Using Streaming Logistic Regression to classify a Twitter stream using Kafka as a training stream

In the previous recipe, we published all the tweets that were stored in ElasticSearch to a Kafka topic. In this recipe, we'll subscribe to the Kafka stream and train a classification model out of it. We will later use this trained model to classify a live Twitter stream.

How to do it...

This is a really small recipe that is composed of 3 steps:

1. **Subscribing to a Kafka stream:** There are two ways to subscribe to a Kafka stream and we'll be using the `DirectStream` method, which is faster. Just like Twitter streaming, Spark has first-class support for subscribing to a Kafka stream. This is achieved by adding the `spark-streaming-kafka` dependency. Let's add it to our `build.sbt` file:

```
"org.apache.spark" %% "spark-streaming-kafka" %
sparkVersion
```

The subscription process is more or less the reverse of the publishing process even in terms of the properties that we pass to Kafka:

```
val topics = Set("twtopic")
val kafkaParams = Map[String,
String] ("metadata.broker.list" -> "localhost:9092")
```

Once the properties are constructed, we subscribe to `twtopic` using `KafkaUtils.createDirectStream`:

```
val kafkaStream = KafkaUtils.createDirectStream[String,
Array[Byte], StringDecoder,
DefaultDecoder](streamingContext, kafkaParams,
topics).repartition(2)
```

With the stream at hand, let's reconstruct `LabeledContent` out of it. We can do that through `KryoSerializer`'s `deserialize` function:

```
val trainingStream = kafkaStream.map {
  case (key, value) =>
    val labeledContent =
KryoSerializer.deserialize(value).asInstanceOf[LabeledContent]
```

2. **Training the classification model:** Now that we are receiving the `LabeledContent` objects from the Kafka stream, let's train our classification model out of them. We will use `StreamingLogisticRegressionWithSGD` for this, which as the name indicates, is a streaming version of the `LogisticRegressionWithSGD` algorithm we saw in *Chapter 5, Learning from Data*. In order to train the model, we have to construct a `LabeledPoint`, which is a pair of labels (represented as a double) and a feature vector. Since this is a text, we'll use the `HashingTF`'s `transform` function to generate the feature vector for us:

```
val hashingTf = new HashingTF(5000)
```

```
val kafkaStream = KafkaUtils.createDirectStream[String,
Array[Byte], StringDecoder,
DefaultDecoder](streamingContext, kafkaParams,
topics).repartition(2)
```



```
val trainingStream = kafkaStream.map {
  case (key, value) =>
    val labeledContent =
      KryoSerializer.deserialize(value).asInstanceOf[LabeledContent]
    val vector =
      hashingTf.transform(labeledContent.content)
    LabeledPoint(labeledContent.label, vector)
}
```

trainingStream now is a stream of LabeledPoint, which we will be using to train our model:

```
val model = new StreamingLogisticRegressionWithSGD()
  .setInitialWeights(Vectors.zeros(5000))
  .setNumIterations(25).setStepSize(0.1).setRegParam(0.001)

model.trainOn(trainingStream)
```

Since we specified the maximum number of features in our `HashingTF` to be 5000, we set the initial weights to be 0 for all 5,000 features. The rest of the parameters are the same as the regular `LogisticRegressionWithSGD` algorithm that trains on a static dataset.

3. **Classifying a live Twitter stream:** Now that we have the model in hand, let's use it to predict whether the incoming stream of tweets is about *fashion* or not. The Twitter setup in this section is the same as the first recipe where we subscribed to a Twitter stream:

```
val filter = List("fashion", "tech", "startup", "spark")
val twitterStream =
  TwitterUtils.createStream(streamingContext, twitterAuth,
    filter, StorageLevel.MEMORY_AND_DISK)
```

The crucial part is the invocation of `model.predictOnValues`, which gives us the predicted label. Once the prediction is made, we save them as text files in our local directory. It's not the best way to do it and we will probably want to push this data to some *appendable* data source instead.

```
val contentAndFeatureVector=twitterStream.map { status =>
  val tokens=status.getText().toLowerCase().split(" ")
  val vector=hashingTf.transform(tokens)
  (status.getText(), vector)
}
```

```
val contentAndPrediction=model.predictOnValues(contentAndFeatureVector)
```

```
//Not the best way to store the results. Creates a whole lot of files
```

```
contentAndPrediction.saveAsTextFiles("predictions", "txt")
```

In order to consolidate the predictions that are spread over multiple files, a really simple aggregation command was used:

```
find predictions* -name "part*" |xargs cat >> output.txt
```

```
Gabriel@Gabriels-MacBook-Pro ~/D/a/S/C/s/chapter7-goingfurther> pwd
/Users/Gabriel/Dropbox/aron/ScalaDataAnalysis/Code/scaladataanalysisCB-tower/chapter7-goingfurther
Gabriel@Gabriels-MacBook-Pro ~/D/a/S/C/s/chapter7-goingfurther>
find predictions-1439587* -name "part*" |xargs cat >> output.txt
```

Here is a sample of the prediction. The results are fairly okay considering the training dataset itself was not classified in a very scientific way. Also, the tokenization is just space-based, the data isn't scaled nor was the IDF used.

```
(RT vee_vetrano: its always the ppl that talk about fashion all the time that actually have no idea what it is theyre talking about. #stfu,1.0)
(RT @fieldsofvintage: Etsy #voguet #vintage #jewelry #fashion #silverware #homedecor #accessories http://t.co/mqrCC9xCnC #etsyretwt #etsy ht...,1.0)
(New York City is getting a fleet of eco-friendly food carts http://t.co/2B1Ydryxqk #tech,0.0)
(RT ZubizuBags: RT lefrenchgem: Summer Fashion Earrings, Sun Earrings, Long Dangle Earrings, Summer Jewelry for the ... ,1.0)
(Which are the communal benefits in relation with stream of fashion lanyards: pUD,1.0)
(RT @darylelockhart: Red Planet Fashion: Mars Colony Project Inspires Sportswear Line http://t.co/BET12Jekb8,0.0)
(Tianjin explosion destroys over 8,000 new cars in China http://t.co/TVFFK6CIA6 #tech | https://t.co/xWWL9JpwM http://t.co/Nato2evHlUJ,0.0)
(Read The Best Fashion,Travel, and Cuisine Coverage, at http://t.co/72e8y16AKr https://t.co/OtpVbYqRe2,0.0)
(RT eclippings: Fashion Womens Envelope Clutch Purse Lady Handbag Tote Shoulder Evening on http://t.co/DbEErSei4p http://t.co/QFS1oVwSun,1.0)
(1961 Schlitz Beer Ski Theme Blonde Man Sweater Skiing Vintage 60's Fashion Ad http://t.co/0cg2VLGK7o #Deals_US http://t.co/XMqUQHtDZL,1.0)
(Free Shipping !10PCS Original monster high dolls fashion clothing accessories b90 - Only ... http://t.co/iy7171CaNV http://t.co/z7IatL27my,1.0)
(Free Shipping !10PCS Original monster high dolls fashion clothing accessories b90 - Only ... http://t.co/Kx9juvZVYp http://t.co/5G048dGqJI,1.0)
(RT GetHiggWit_it: Now this is fashion https://t.co/o1ZNNdnpCf,1.0)
(#KCA #VoteJKT48ID BusEconYMO_HGS: Documents confirm #Apple is building #self-driving #CARvsBUF #automotive #tech #business #economics,0.0)
(RT FlasherNight: #fashion "orbib cek Villarreal telah mencapai kesepakatan untuk merekrut penyerang Totten... http://t.co/4caquAH8J Foll...,1.0)
(The ticket read "broke adapter while trying to move computer" via /r/techsupportgore http://t.co/hEoLAV550G #tech_ http://t.co/nwhdgjF6SW,0.0)
(RT Nina_LaChapelle: From bananas to phones: How cheaper #yuan could reverberate http://t.co/ee96Nm84FA)
#china #finance #fashion #lifestyle...,1.0)
(RT @BBGMedia: Fashion meets function in Montblanc's e-strap @montblanc_world http://t.co/L92aN8ylzc http://t.co/sRGHCWzMH,1.0)
(RT FlasherNight: #fashion "orbib cek Bayern Muenchen mengalahkan Hamburg dengan skor telak 5-0 pada laga p... http://t.co/UCFBGUZT8T Foll...,1.0)
(Gostei de um video @YouTube de @davyjonesrj http://t.co/ArYISJTaLn GTA V - QUEM É MAIS RIDÍCULO? PIRATAS FASHION WEEK,1.0)
(Dow tumbles on weak United Tech, IBM earnings,0.0)
(@Got_Six @TourneySport That one is over https://t.co/MRptEhcG2,0.0)
(RT @blingThings2011: A Mermaid's Tale by Lilli Carter http://t.co/qa3a2k0cXY via @GrowthhackRt #growthhacking #entrepreneurship #startup,0.0)
```

Using GraphX to analyze Twitter data

GraphX is Spark's approach to graphs and computation against graphs. In this recipe, we will see a preview of what is possible with the GraphX component in Spark.

How to do it...

Now that we have the Twitter data stored in the ElasticSearch index, we will perform the following tasks on this data using a graph:

1. Convert the ElasticSearch data into a Spark Graph.
2. Sample vertices, edges, and triplets in the graph.
3. Find the top group of connected hashtags (connected component).
4. List all the hashtags in that component.

1. **Converting the ElasticSearch data into a graph:** This involves two steps:

1. **Converting ElasticSearch data into a DataFrame:** This step, like we saw in an earlier recipe, is just a one-liner:

```
def convertElasticSearchDataToDataFrame (sqlContext :
SQLContext) = {
    val twStatusDf = sqlContext.esDF("spark/twstatus")
    twStatusDf
}
```

2. **Converting DataFrame to a graph:** Spark Graph construction requires an RDD for a vertex and an RDD of edges. Let's construct them one by one.

Vertex RDD requires an RDD of a tuple representing a `vertexId` and a `vertex property`. In our case, we'll just do a primitive hash code on the `hashTag` as the vertex ID and `hashTag` itself as the property:

```
val verticesRdd:RDD[(Long,String)] = df.flatMap { tweet =>
    val hashTags =
    tweet.getAs[Buffer[String]]("hashTags")
    hashTags.map { tag =>
        val lowercaseTag = tag.toLowerCase()
        val tagHashCode=lowercaseTag.hashCode().toLong
        (tagHashCode, lowercaseTag)
    }
}
```

For the edges, we construct an `RDD[Edge]`, which wraps a pair of vertex IDs and a property. In our case, we use the first URL (if present) as a property to the edge (we aren't using it for this recipe so an empty string should also be fine). Since there is a possibility of multiple hashtags for a tweet, we use the `combinations` function to choose pairs and then connect them together as an edge:

```
val edgesRdd:RDD[Edge[String]] =df.flatMap { row =>
    val hashTags = row.getAs[Buffer[String]]("hashTags")

    val urls = row.getAs[Buffer[String]]("urls")
    val topUrl=if (urls.length>0) urls(0) else ""

    val combinations=hashTags.combinations(2)

    combinations.map{ combs=>
        val firstHash=combs(0).toLowerCase().hashCode.toLong
        val
        secondHash=combs(1).toLowerCase().hashCode.toLong
        Edge(firstHash, secondHash, topUrl)
    }
}
```

Finally, we construct the graph using both RDDs:

```
val graph=Graph(verticesRdd, edgesRdd)
```

2. **Sampling vertices, edges, and triplets in the graph:** Now that we have our graph constructed, let's sample and see what the vertices, edges, and triplets of the Graph look like. A triple is a representation of an edge and two vertices connected by that edge:

```
graph.vertices.take(20).foreach(println)
```

The output is:

```
(-980086641,rtくれたeighterさんで気になった人お迎え)
(114820,thx)
(1280862560,statementneckpiece)
(789040,恋愛)
(-706379056,shoppershour)
(165548515,silversurfers)
(-1221262756,health)
(3155,bu)
(110132375,taste)
(231197415,ridnola15)
(109801725,supra)
(106006350,order)
(-121429366,shoebkidsnaaldwijk)
(3046020,cams)
(1444965940,sneakpreview)
(47780855,2488y)
(100270,edm)
(98371450,gizmo)
(249051115,blogmonetization)
(-1638853121,citycenterdc)
```

```
graph.edges.take(20).foreach(println)
```

The output is:

```
Edge(-2137707097,-1266394726,https://instagram.com/p/6aGvaIqDv3/)
Edge(-2132286556,-1109908296,https://instagram.com/p/6XNiG2rrhy/)
Edge(-2132286556,-1077469768,https://instagram.com/p/6XNiG2rrhy/)
Edge(-2132286556,108486107,https://instagram.com/p/6XNiG2rrhy/)
Edge(-2132286556,109201981,https://instagram.com/p/6XNiG2rrhy/)
Edge(-2132286556,109780401,https://instagram.com/p/6XNiG2rrhy/)
Edge(-2132286556,1728911401,https://instagram.com/p/6XNiG2rrhy/)
Edge(-2128842253,-2128633716,)
Edge(-2128842253,844562933,)
Edge(-2128633716,844562933,)
Edge(-2128468089,1316818326,http://bit.ly/10UEvIz)
Edge(-2121085849,-1077469768,http://ldig.it/1LyY3nH)
Edge(-2121085849,729501500,http://ldig.it/1LyY3nH)
Edge(-2120890375,3267670,http://neuvoo.com/job.php?id=dstcj5hvsb&source=twitter&lang
Edge(-2120890375,1075463261,http://neuvoo.com/job.php?id=dstcj5hvsb&source=twitter&l
Edge(-2120156555,3555990,http://trkt.co/1LbQ1NR)
Edge(-2118473344,109270,http://ift.tt/1UHhQ6h)
Edge(-2118473344,3555990,http://ift.tt/1UHhQ6h)
Edge(-2116411129,-1392531550,https://instagram.com/p/6N-c0zFVnt/)
Edge(-2116411129,-1077469768,https://instagram.com/p/6N-c0zFVnt/)
```

```
graph.triplets.take(20).foreach(println)
```

The output is:

```
((-2137707097,traditional),(-1266394726,french),https://instagram.com/p/6aGvaIqDv3/)
((-2132286556,instamakeup),(-1109908296,lashes),https://instagram.com/p/6XNiG2rrhy/)
((-2132286556,instamakeup),(-1077469768,fashion),https://instagram.com/p/6XNiG2rrhy/)
((-2132286556,instamakeup),(108486107,glamour),https://instagram.com/p/6XNiG2rrhy/)
((-2132286556,instamakeup),(109201981,saLon),https://instagram.com/p/6XNiG2rrhy/)
((-2132286556,instamakeup),(109780401,style),https://instagram.com/p/6XNiG2rrhy/)
((-2132286556,instamakeup),(1728911401,natural),https://instagram.com/p/6XNiG2rrhy/)
((-2128842253,startcoin),(-2128633716,startjoin),)
((-2128842253,startcoin),(844562933,maxcoin),)
((-2128633716,startjoin),(844562933,maxcoin),)
((-2128468089,startpath),(1316818326,startups),http://bit.ly/10UEvIz)
((-2121085849,earthtweet),(-1077469768,fashion),http://ldig.it/1LyY3nH)
((-2121085849,earthtweet),(729501500,ecofriendly),http://ldig.it/1LyY3nH)
((-2120890375,cardiovascular),(3267670,jobs),http://neuvoo.com/job.php?id=dstcj5hvsb&source=twitter&
((-2120890375,cardiovascular),(1075463261,technologist),http://neuvoo.com/job.php?id=dstcj5hvsb&source=twitter&
((-2120156555,mobilenews),(3555990,tech),http://trkt.co/1LbQ1NR)
((-2118473344,happening),(109270,now),http://ift.tt/1UHhQ6h)
((-2118473344,happening),(3555990,tech),http://ift.tt/1UHhQ6h)
((-2116411129,ecofashion),(-1392531550,berlin),https://instagram.com/p/6N-c0zFVnt/)
((-2116411129,ecofashion),(-1077469768,fashion),https://instagram.com/p/6N-c0zFVnt/)
```

3. **Finding the top group of connected hashtags (connected component):** As you know, a graph is made of vertices and edges. A connected component of a graph is just a part of the graph (a subgraph) whose vertices are connected to each other by some edge. If there is a vertex that is not connected to another vertex directly or indirectly through another vertex, then they are not connected and therefore don't belong to the same connected component.

GraphX's `graph.connectedComponents` provides a graph of all the vertices along with their component IDs:

```
val connectedComponents=graph.connectedComponents.cache()
```

Let's take the component ID with the maximum number of vertices and then extract the vertices (and eventually the hashtags) that belong to that component:

```
val ccCounts:Map[VertexId,
Long]=connectedComponents.vertices.map{case (_, vertexId)
=> vertexId}.countByValue

//Get the top component Id and count
val topComponent:(VertexId,
Long)=ccCounts.toSeq.sortBy{case (componentId, count) =>
count}.reverse.head
```

Since `topComponent` just has the component ID, in order to fetch the `hashTags` of the top component, we need to have a representation that maps `hashTag` to a component ID. This is achieved by joining the graph's vertices to the `connectedComponent` vertices:

```
//RDD of HashTag-Component Id pair. Joins using vertexId
val
hashtagComponentRdd:VertexRDD[(String,VertexId)]=graph.vertices.
innerJoin(connectedComponents.vertices){ case
(vertexId, hashTag, componentId)=>
    (hashTag, componentId)
}
```

Now that we have `componentId` and `hashTag`, let's filter only the `hashTags` for the top component ID:

```
val topComponentHashTags=hashtagComponentRdd
    .filter{ case (vertexId, (hashTag,
componentId)) => (componentId==topComponent._1)}
    .map{case (vertexId, (hashTag,componentId)) =>
hashTag
}

topComponentHashTags
```

The entire method looks like this:

```
def getHashTagsOfTopConnectedComponent (graph:Graph[String,String])
:RDD[String]={
    //Get all the connected components
    val connectedComponents=graph.connectedComponents.cache()

    import scala.collection._

    val ccCounts:Map[VertexId,
Long]=connectedComponents.vertices.map{case (_, vertexId) =>
vertexId}.countByValue

    //Get the top component Id and count
    val topComponent:(VertexId,
Long)=ccCounts.toSeq.sortBy{case (componentId, count) =>
count}.reverse.head
```

```

//RDD of HashTag-Component Id pair. Joins using
vertexId
  val
hashtagComponentRdd:VertexRDD[(String,VertexId)]=graph.vertices.
innerJoin(connectedComponents.vertices){ case
(vertexId, hashtag, componentId)=>
  (hashtag, componentId)
}

//Filter the vertices that belong to the top component alone
val topComponentHashTags=hashtagComponentRdd
  .filter{ case (vertexId, (hashtag,
componentId)) => (componentId==topComponent._1)}
  .map{case (vertexId, (hashtag,componentId)) =>
hashtag
}

topComponentHashTags

}

```

4. **List all the hashtags in that component:** Saving the hashTags to a file is as simple as calling `saveAsTextFile`. The `repartition(1)` is done just so that we have a single output file. Alternatively, you could use `collect()` to bring all the data to the driver and inspect it:

```

def saveTopTags(topTags:RDD[String]){
  topTags.repartition(1).saveAsTextFile("topTags.txt")
}

```


The number of hashtags in the top connected component for our run was 7,320. This shows that in our sample stream there are about 7,320 tags related to fashion that are interrelated. They could be synonyms, closely related, or remotely related to fashion. A snapshot of the file looks like this:

```
plussize
empowerment
la
tagstagram
fredericksburg
macaraibo
fez
topnotchscolars
芸能
paca
tshirt
homes
investment
indiegamelover
pregnancy
florence
mayoristas
가지마
uae
nba
search
forver
fifthfashionue
traceitchi
flagship
shrewsbury
garden
bloggerstyle
olshopmedan
property
americasnexttopmodel
newyork
j2tlaunchparty
winter
frrole
lookoftheday
pittsburgh
snow
```

In this chapter, we briefly touched upon Spark streaming, Streaming ML, and GraphX. Please note that this is by no means an exhaustive recipe list for both topics and aims to just provide a taste of what Streaming and GraphX in Spark could do.

Module 3

Scala for Machine Learning

*Leverage Scala and Machine Learning to construct and study systems
that can learn from data*

1

Getting Started

It is critical for any computer scientist to understand the different classes of machine learning algorithms and be able to select the ones that are relevant to the domain of their expertise and dataset. However, the application of these algorithms represents a small fraction of the overall effort needed to extract an accurate and performing model from input data. A common data mining workflow consists of the following sequential steps:


1. Loading the data.
2. Preprocessing, analyzing, and filtering the input data.
3. Discovering patterns, affinities, clusters, and classes.
4. Selecting the model features and the appropriate machine learning algorithm(s).
5. Refining and validating the model.
6. Improving the computational performance of the implementation.

As we will emphasize throughout this book, each stage of the process is critical to build the *right* model.

This first chapter introduces you to the taxonomy of machine learning algorithms, the tools and frameworks used in the book, and a simple application of logistic regression to get your feet wet.

Mathematical notation for the curious

Each chapter contains a small section dedicated to the formulation of the algorithms for those interested in the mathematical concepts behind the science and art of machine learning. These sections are optional and defined within a tip box. For example, the mathematical expression of the mean and the variance of a variable X mentioned in a tip box will be as follows:

	<p>Mean value of a variable $X = \{x\}$ is defined as:</p> $E(X) = \frac{1}{n} \sum x_j$ <p>The variance of a variable $X = \{x\}$ is defined as:</p> $Var(X) = \frac{\sum (E(X) - x_j)^2}{n - 1}$
---	--

Why machine learning?

The explosion in the number of digital devices generates an ever-increasing amount of data. The best analogy I can find to describe the need, desire, and urgency to extract knowledge from large datasets is the process of extracting a precious metal from a mine, and in some cases, extracting blood from a stone.

Knowledge is quite often defined as a model that can be constantly updated or tweaked as new data comes into play. Models are obviously domain-specific ranging from credit risk assessment, face recognition, maximization of quality of service, classification of pathological symptoms of disease, optimization of computer networks, and security intrusion detection, to customers' online behavior and purchase history.

Machine learning problems are categorized as classification, prediction, optimization, and regression.

Classification

The purpose of classification is to extract knowledge from historical data. For instance, a classifier can be built to identify a disease from a set of symptoms. The scientist collects information regarding the body temperature (continuous variable), congestion (discrete variables HIGH, MEDIUM, and LOW), and the actual diagnostic (flu). This dataset is used to create a model such as `IF temperature > 102 AND congestion = HIGH THEN patient has the flu (probability 0.72)`, which doctors can use in their diagnostic.

Prediction

Once the model is extracted and validated against the past data, it can be used to draw inference from the future data. A doctor collects symptoms from a patient, such as body temperature and nasal congestion, and anticipates the state of his/her health.

Optimization

Some global optimization problems are intractable using traditional linear and non-linear optimization methods. Machine learning techniques improve the chances that the optimization method converges toward a solution (intelligent search). You can imagine that fighting the spread of a new virus requires optimizing a process that may evolve over time as more symptoms and cases are uncovered.

Regression

Regression is a classification technique that is particularly suitable for a continuous model. Linear (least square), polynomial, and logistic regressions are among the most commonly used techniques to *fit* a parametric model, or function, $y = f(x_j)$, to a dataset. Regression is sometimes regarded as a specialized case of classification for which the output variables are continuous instead of categorical.

Why Scala?

Like most functional languages, Scala provides developers and scientists with a toolbox to implement iterative computations that can be easily woven dynamically into a coherent dataflow. To some extent, Scala can be regarded as an extension of the popular MapReduce model for distributed computation of large amounts of data. Among the capabilities of the language, the following features are deemed essential to machine learning and statistical analysis.

Abstraction

Monoids and monads are important concepts in functional programming.

Monads are derived from the category and group theory allowing developers to create a high-level abstraction as illustrated in **Twitter's Algebird** (<https://github.com/twitter/algebird>) or **Google's Breeze Scala** (<https://github.com/dlwh/breeze>) libraries.

A **monoid** defines a binary operation op on a dataset \mathbb{T} with the property of closure, identity operation, and associativity.

Let's consider the `+` operation is defined for a set `T` using the following monoidal representation:

```
trait Monoid[T] {  
  def zero: T  
  def op(a: T, b: T): T  
}
```

Monoids are associative operations. For instance, if `ts1`, `ts2`, and `ts3` are three time series, then the property `ts1 + (ts2 + ts3) = (ts1 + ts2) + ts3` is true. The associativity of a monoid operator is critical in regards to parallelization of computational workflows.

Monads are structures that can be seen either as containers by programmers or as a generalization of Monoids. The collections bundled with the Scala standard library (`list`, `map`, and so on) are constructed as monads [1:1]. Monads provide the ability for those collections to perform the following functions:

1. Create the collection.
2. Transform the elements of the collection.
3. Flatten nested collections.

A common categorical representation of a monad in Scala is a trait, `Monad`, parameterized with a container type `M`:

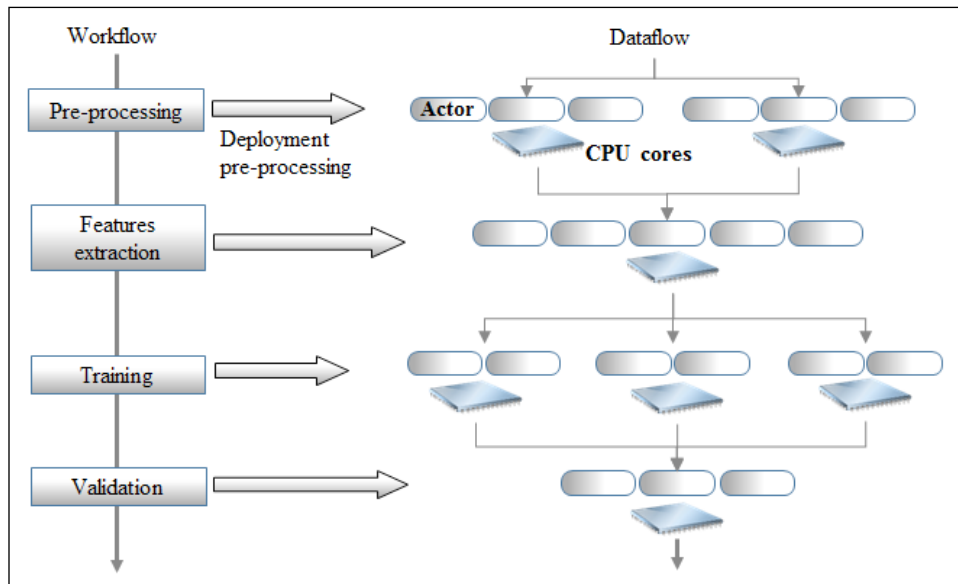
```
trait Monad[M[_]] {  
  def apply[T](a: T): M[T]  
  def flatMap[T, U](m: M[T])(f: T=>M[U]): M[U]  
}
```

Monads allow those collections or containers to be chained to generate a workflow. This property is applicable to any scientific computation [1:2].

Scalability

As seen previously, monoids and monads enable parallelization and chaining of data processing functions by leveraging the Scala higher-order methods. In terms of implementation, **Actors** are the core elements that make Scala scalable. Actors act as coroutines, managing the underlying threads pool. Actors communicate through passing asynchronous messages. A distributed computing Scala framework such as Akka and Spark extends the capabilities of the Scala standard library to support computation on very large datasets. Akka and Spark are described in detail in the last chapter of this book [1:3].

In a nutshell, a workflow is implemented as a sequence of activities or computational tasks. Those tasks consist of high-order Scala methods such as `flatMap`, `map`, `fold`, `reduce`, `collect`, `join`, or `filter` applied to a large collection of observations. Scala allows these observations to be partitioned by executing those tasks through a cluster of actors. Scala also supports message dispatching and routing of messages between local and remote actors. The engineers can decide to execute a workflow either locally or distributed across CPU cores and servers with no code or very little code changes.



Deployment of a workflow as a distributed computation

In this diagram, a controller, that is, the master node, manages the sequence of tasks 1 to 4 similar to a scheduler. These tasks are actually executed over multiple worker nodes that are implemented by the Scala actors. The master node exchanges messages with the workers to manage the state of the execution of the workflow as well as its reliability. High availability of these tasks is implemented through a hierarchy of supervising actors.

Configurability

Scala supports **dependency injection** using a combination of abstract variables, self-referenced composition, and stackable traits. One of the most commonly used dependency injection patterns, the **cake pattern**, is used throughout this book to create dynamic computation workflows and plots.

Maintainability

Scala embeds **Domain Specific Languages (DSL)** natively. DSLs are syntactic layers built on top of Scala native libraries. DSLs allow software developers to abstract computation in terms that are easily understood by scientists. The most notorious application of DSLs is the definition of the emulation of the syntax used in the MATLAB program, which data scientists are familiar with.

Computation on demand

Lazy methods and values allow developers to execute functions and allocate computing resources on demand. The Spark framework relies on lazy variables and methods to chain **Resilient Distributed Datasets (RDD)**.

Model categorization

A model can be predictive, descriptive, or adaptive.

Predictive models discover patterns in historical data and extract fundamental trends and relationships between factors. They are used to predict and classify future events or observations. Predictive analytics is used in a variety of fields such as marketing, insurance, and pharmaceuticals. Predictive models are created through supervised learning using a preselected training set.

Descriptive models attempt to find unusual patterns or affinities in data by grouping observations into clusters with similar properties. These models define the first level in knowledge discovery. They are generated through unsupervised learning.

A third category of models, known as **adaptive modeling**, is generated through reinforcement learning. **Reinforcement learning** consists of one or several decision-making agents that recommend and possibly execute actions in the attempt of solving a problem, optimizing an objective function, or resolving constraints.

Taxonomy of machine learning algorithms

The purpose of machine learning is to teach computers to execute tasks without human intervention. An increasing number of applications such as genomics, social networking, advertising, or risk analysis generate a very large amount of data that can be analyzed or mined to extract knowledge or provide insight into a process, a customer, or an organization. Ultimately, machine learning algorithms consist of identifying and validating models to optimize a performance criterion using historical, present, and future data [1:4].

Data mining is the process of extracting or identifying patterns in a dataset.

Unsupervised learning

The goal of **unsupervised learning** is to discover patterns of regularities and irregularities in a set of observations. The process known as density estimation in statistics is broken down into two categories: discovery of data clusters and discovery of latent factors. The methodology consists of processing input data to understand patterns similar to the natural learning process in infants or animals. Unsupervised learning does not require labeled data, and therefore, is easy to implement and execute because no expertise is needed to validate an output. However, it is possible to label the output of a clustering algorithm and use it for future classification.

Clustering

The purpose of data clustering is to partition a collection of data into a number of clusters or data segments. Practically, a clustering algorithm is used to organize observations into clusters by minimizing the observations within a cluster and maximizing the observations between clusters. A clustering algorithm consists of the following steps:

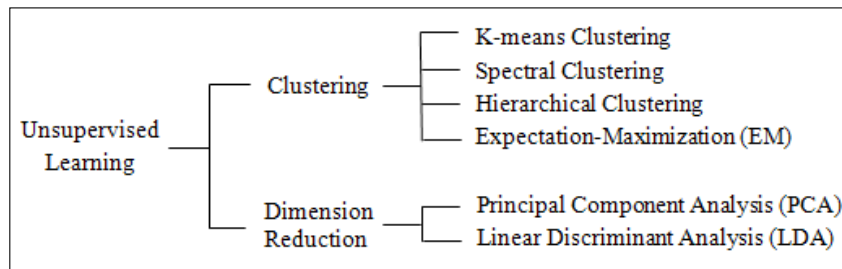
1. Creating a model by making an assumption on the input data.
2. Selecting the objective function or goal of the clustering.
3. Evaluating one or more algorithms to optimize the objective function.

Data clustering is also known as data segmentation or data partitioning.

Dimension reduction

Dimension reduction techniques aim at finding the smallest but most relevant set of features that models dataset reliability. There are many reasons for reducing the number of features or parameters in a model, from avoiding overfitting to reducing computation costs.

There are many ways to classify the different techniques used to extract knowledge from data using unsupervised learning. The following taxonomy breaks down these techniques according to their purpose, although the list is far from being exhaustive, as shown in the following diagram:



Supervised learning

The best analogy for supervised learning is function approximation or curve fitting. In its simplest form, supervised learning attempts to extract a relation or function f $x \rightarrow y$ from a training set $\{x, y\}$. Supervised learning is far more accurate and reliable than any other learning strategy. However, a domain expert may be required to label (tag) data as a training set for certain types of problems.

Supervised machine learning algorithms can be broken into two categories:

- Generative models
- Discriminative models

Generative models


In order to simplify the description of statistics formulas, we adopt the following simplification: the probability of an event X is the same as the probability of the discrete random variable X to have a value x , $p(X) = p(X=x)$. The notation of joint probability (resp. conditional probability) becomes $p(X, Y) = p(X=x, Y=y)$ (resp. $p(X|Y)=p(X=x | Y=y)$).

Generative models attempt to fit a joint probability distribution, $p(X, Y)$, of two events (or random variables), X and Y , representing two sets of observed and hidden (latent) variables x and y . Discriminative models learn the conditional probability $p(Y|X)$ of an event or random variable Y of hidden variables y , given an event or random variable X of observed variables x . Generative models are commonly introduced through the Bayes' rule. The conditional probability of an event Y , given an event X , is computed as the product of the conditional probability of the event X , given the event Y , and the probability of the event X normalized by the probability of event Y [1:5].

Join probability (if X and Y are independent):

$$p(X, Y) = p(X \cap Y) = p(X) \cdot p(Y)$$

Conditional probability:



$$p(Y|X) = P(Y, X)/P(X)$$

The Bayes' rule:

$$P(Y|X) = P(X|Y) \cdot P(X)/P(Y)$$

The Bayes' rule is the foundation of the Naïve Bayes classifier, which is the topic of *Chapter 5, Naïve Bayes Classifiers*.

Discriminative models

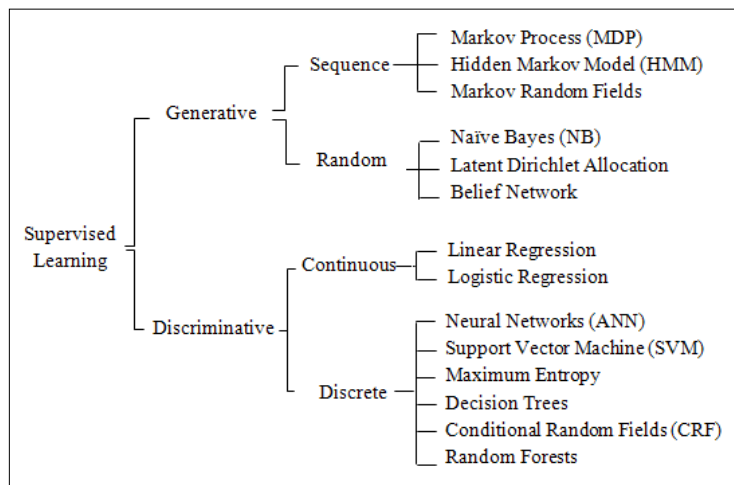
Contrary to generative models, discriminative models compute the conditional probability $p(Y|X)$ directly, using the same algorithm for training and classification.

Generative and discriminative models have their respective advantages and drawbacks. Novice data scientists learn to match the appropriate algorithm to each problem through experimentation. Here is a brief guideline describing which type of models makes sense according to the objective or criteria of the project:

Objective	Generative models	Discriminative models
Accuracy	Highly dependent on the training set.	Probability estimates tend to be more accurate.
Modeling requirements	There is a need to model both observed and hidden variables, which requires a significant amount of training.	The quality of the training set does not have to be as rigorous as for generative models.

Objective	Generative models	Discriminative models
Computation cost	This is usually low. For example, any graphical method derived from the Bayes' rule has low overhead.	Most algorithms rely on optimization of a convex that introduces significant performance overhead.
Constraints	These models assume some degree of independence among the model features.	Most discriminative algorithms accommodate dependencies between features.

We can further refine the taxonomy of supervised learning algorithms by segregating between sequential and random variables for generative models and breaking down discriminative methods as applied to continuous processes (regression) and discrete processes (classification):

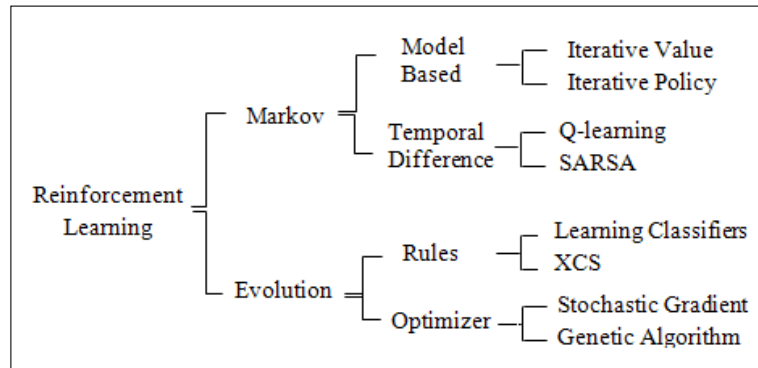


Reinforcement learning

Reinforcement learning is not as well understood as supervised and unsupervised learning outside the realms of robotics or game strategy. However, since the 90s, genetic-algorithms-based classifiers have become increasingly popular to solve problems that require collaboration with a domain expert. For some types of applications, reinforcement learning algorithms output a set of recommended actions for the *adaptive* system to execute. In its simplest form, these algorithms compute or estimate the best course of action. Most complex systems based on reinforcement learning establish and update policies that can be vetoed by an expert. The foremost challenge developers of reinforcement learning systems face is that the recommended action or policy may depend on partially observable states and how to deal with uncertainty.

Genetic algorithms are not usually considered part of the reinforcement learning toolbox. However, advanced models such as learning classifier systems use genetic algorithms to classify and reward the rules and policies.

As with the two previous learning strategies, reinforcement learning models can be categorized as Markovian or evolutionary:



This is a brief overview of machine learning algorithms with a suggested taxonomy. There are almost as many ways to introduce machine learning as there are data and computer scientists. We encourage you to browse through the list of references at the end of the book and find the documentation appropriate to your level of interest and understanding.

Tools and frameworks

Before getting your hands dirty, you need to download and deploy a minimum set of tools and libraries so as not to reinvent the wheel. A few key components have to be installed in order to compile and run the source code described throughout the book. We focus on open source and commonly available libraries, although you are invited to experiment with equivalent tools of your choice. The learning curve for the frameworks described here is minimal.

Java

The code described in the book has been tested with **JDK 1.7.0_45** and **JDK 1.8.0_25** on **Windows x64** and **MacOS X x64**. You need to install the Java Development Kit if you have not already done so. Finally, the environment variables `JAVA_HOME`, `PATH`, and `CLASSPATH` have to be updated accordingly.

Scala

The code has been tested with Scala 2.10.4. We recommend using Scala version 2.10.3 or higher and SBT 0.13 or higher. Let's assume that Scala runtime (REPL) and libraries have been properly installed and environment variables `SCALA_HOME` and `PATH` have been updated. The description and installation instructions of the Scala plugin for Eclipse are available at <http://scala-ide.org/docs/user/gettingstarted.html>.

You can also download the Scala plugin for IntelliJ IDEA from the JetBrains website at <http://confluence.jetbrains.com/display/SCA/>.

The ubiquitous **simple build tool** (`sbt`) will be our primary building engine. The syntax of the build file `sbt/build.sbt` conforms to version 0.13, and is used to compile and assemble the source code presented throughout this book.

Apache Commons Math

Apache Commons Math is a Java library for numerical processing, algebra, statistics, and optimization [1:6].

Description

This is a lightweight library that provides developers with a foundation of small, ready-to-use Java classes that can be easily weaved into a machine learning problem. The examples used throughout the book require version 3.3 or higher.

The main components of Apache Commons Math are:

- Functions, differentiation, and integral and ordinary differential equations
- Statistics distribution
- Linear and nonlinear optimization
- Dense and Sparse vectors and matrices
- Curve fitting, correlation, and regression

For more information, visit <http://commons.apache.org/proper/commons-math>.

Licensing

We need Apache Public License 2.0; the terms are available at <http://www.apache.org/licenses/LICENSE-2.0>.

Installation

The installation and deployment of the Commons Math library are quite simple:

1. Go to the download page, http://commons.apache.org/proper/commons-math/download_math.cgi.
2. Download the latest `.jar` files in the **Binaries** section, `commons-math3-3.3-bin.zip` (for version 3.3, for instance).
3. Unzip and install the `.jar` files.
4. Add `commons-math3-3.3.jar` to classpath as follows:
 - For Mac OS X, use the command `export CLASSPATH=$CLASSPATH:/Commons_Math_path/commons-math3-3.3.jar`
 - For Windows, navigate to **System property | Advanced system settings | Advanced | Environment variables...**, then edit the entry of the `CLASSPATH` variable
5. Add the `commons-math3-3.3.jar` file to your IDE environment if needed (that is, for Eclipse, navigate to **Project | Properties | Java Build Path | Libraries | Add External JARs**).

You can also download `commons-math3-3.3-src.zip` from the **Source** section.

JFreeChart

JFreeChart is an open source chart and plotting Java library, widely used in the Java programmer community. It was originally created by David Gilbert [1:7].

Description

The library supports a variety of configurable plots and charts (scatter, dial, pie, area, bar, box and whisker, stacked, and 3D). We use JFreeChart to display the output of data processing and algorithms throughout the book, but you are encouraged to explore this great library on your own, as time permits.

Licensing

It is distributed under the terms of the **GNU Lesser General Public License (LGPL)**, which permits its use in proprietary applications.

Installation

To install and deploy JFreeChart, perform the following steps:

1. Visit <http://www.jfree.org/jfreechart>.
2. Download the latest version from Source Forge at <http://sourceforge.net/projects/jfreechart/files>.
3. Unzip and install the .jar file.
4. Add `jfreechart-1.0.17.jar` (for version 1.0.17) to classpath as follows:
 - For Mac OS, update the classpath by using export `CLASSPATH=$CLASSPATH:/JFreeChart_path/ jfreechart-1.0.17.jar`
 - For Windows, go to **System property | Advanced system settings | Advanced | Environment variables...** and then edit the entry of the CLASSPATH variable
5. Add the `jfreechart-1.0.17.jar` file to your IDE environment, if needed.

Other libraries and frameworks

Libraries and tools that are specific to a single chapter are introduced along with the topic. Scalable frameworks are presented in the last chapter along with the instructions to download them. Libraries related to the conditional random fields and support vector machines are described in the respective chapters.



Why not use Scala algebra and numerical libraries

Libraries such as **Breeze**, **ScalaNLP**, and **Algebird** are great Scala frameworks for linear algebra, numerical analysis, and machine learning. They provide even the most seasoned Scala programmer with a high-quality layer of abstraction. However, this book is designed as a tutorial that allows developers to write algorithms from the ground up using simple common Java libraries [1:8].

Source code

The Scala programming language is used to implement and evaluate the machine learning techniques presented in this book. Only a subset of the source code used to implement the techniques are presented in the book. The formal implementation of these algorithms is available on the website of Packt Publishing (<http://www.packtpub.com>).



Downloading the example code

You can download the example code files for all Packt books you have purchased from your account at <http://www.packtpub.com>. If you purchased this book elsewhere, you can visit <http://www.packtpub.com/support> and register to have the files e-mailed directly to you.

Context versus view bounds

Most Scala classes discussed in the book are parameterized with the type associated to the discrete/categorical value (`Int`) or continuous value (`Double`). Context bounds would require that any type used by the client code has `Int` or `Double` as upper bounds:

```
class MyClassInt[T <: Int]
class MyClassFloat[T <: Double]
```

Such a design introduces constraints on the client to inherit from simple types and to deal with covariance and contravariance for container types [1:9].

For this book, view bounds are used instead of context bounds only where they require an implicit conversion to the parameterized type to be defined:

```
Class MyClassFloat[T <% Double]
implicit def T2Double(t : T): Double
```

Presentation

For the sake of readability of the implementation of algorithms, all nonessential code such as error checking, comments, exceptions, or imports are omitted. The following code elements are discarded in the code snippet presented in the book:

- Code comments
- Validation of class parameters and method arguments:

```
class BaumWelchEM(val lambda: HMMLambda ...) {
  require( lambda != null, "Lambda model is undefined")
```

- Exceptions and an exception handler:

```
  try { .. }
  catch {
    case e: ArrayIndexOutOfBoundsException =>println(e.
toString)
  }
```

- Nonessential annotation:
`@inline def mean = ..`
- Logging and debugging code:
`m_logger.debug(...)`
- Private and nonessential methods

Primitives and implicits

The algorithms presented in this book share the same primitive types, generic operators, and implicit conversions.

Primitive types

For the sake of readability of the code, the following primitive types will be used:

```
type XY = (Double, Double)
type XYTSeries = Array[(Double, Double)]
type DMatrix[T] = Array[Array[T]]
type DVector[T] = Array[T]
type DblMatrix = DMatrix[Double]
type DblVector = Array[Double]
```

The types have the behavior (methods) of their primitive counterpart (array). However, adding a new functionality to vectors, matrices, and time series requires classes of their own right. These classes will be introduced in the next chapter.

Type conversions

Implicit conversion is an important feature of the Scala programming language because it allows developers to specify a type conversion for an entire library in a single place. Here are a few of the implicit type conversions used throughout the book:

```
implicit def int2Double(n: Int): Double = n.toDouble
implicit def vectorT2DblVector[T <% Double](vt: DVector[T]): DblVector =
  vt.map( t => t.toDouble)
implicit def double2DblVector(x: Double): DblVector = Array[Double](x)
implicit def dblPair2DblVector(x: (Double, Double)): DblVector =
  Array[Double](x._1,x._2)
implicit def dblPairs2DblRows(x: (Double, Double)): DblMatrix =
  Array[Array[Double]](Array[Double](x._1, x._2))
...
```



Library-specific conversion

The conversion between the primitive type listed here and types introduced in a particular library (such as Apache Commons Math) is declared in future chapters the first time those libraries are used.

Operators

Lastly, some operations are applied by multiple machine learning or preprocessing algorithms. They need to be defined implicitly. The operation on a pair of a vector of arbitrary type and vector of `Double` is defined as follows:

```
def Op[T <% Double](v: DVector[T], w: DblVector, op: (T, Double) =>
Double): DblVector =
  v.zipWithIndex.map(x => op(x._1, w(x._2)))
```

It is also convenient to define the following operators that are included in the Scala standard library:

```
implicit def /(v: DblVector, n: Int):DblVector = v.map( x => x/n)
implicit def /(m: DblMatrix, col: Int, z: Double): DblMatrix = { (0
until m(n).size).foreach(i => m(n) (i) /= z) }
```

We won't have to redefine the types, conversions, and operators from now on.

Immutability

It is usually a good idea to reduce the number of states of an object. Method invocation transitions an object from one state to another. The larger the number of methods or states, the more cumbersome the testing process becomes.

There is no point in creating a model that is not defined (trained). Therefore, making the training of a model as part of the constructor of the class it implements makes a lot of sense. Therefore, the only public methods of a machine learning algorithm are:

- Classification or prediction
- Validation
- Retrieval of model parameters (weights, latent variables, hidden states, and so on), if needed

Performance of Scala iterators

The evaluation of the performance of Scala high-order iterative methods is beyond the scope of this book. However, it is important to be aware of the trade-off of each method.

The `for` loop construct is to be avoided as a counting iterator except if it is used in conjunction with `yield`. It is designed to implement the for-comprehension monad (`map-flatMap`). The source code presented in this book uses the `while` and `foreach` constructs.

Scala reducer methods `reduce` and `fold` are also frequently used for their efficiency.

Let's kick the tires

This final section introduces the key elements of the training and classification workflow. A test case using a simple logistic regression is used to illustrate each step of the computational workflow.

Overview of computational workflows

In its simplest form, a computational workflow to perform runtime processing of a dataset is composed of the following stages:

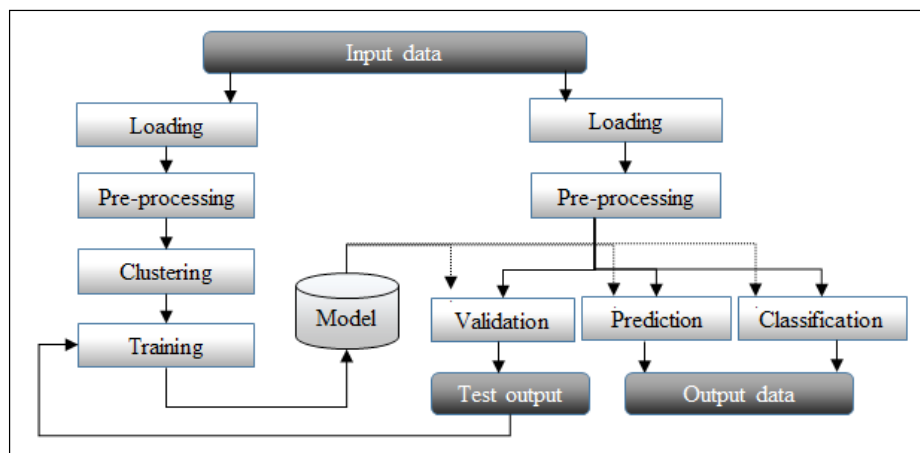
1. Loading the dataset from files, databases, or any streaming devices.
2. Splitting the dataset for parallel data processing.
3. Preprocessing data using filtering techniques, analysis of variance, and applying penalty and normalization functions whenever necessary.
4. Applying the model, either a set of clusters or classes to classify new data.
5. Assessing the quality of the model.

A similar sequence of tasks is used to extract a model from a training dataset:

1. Loading the dataset from files, databases, or any streaming devices.
2. Splitting the dataset for parallel data processing.
3. Applying filtering techniques, analysis of variance, and penalty and normalization functions to the raw dataset whenever necessary.
4. Selecting the training, testing, and validation set from the cleansed input data.
5. Extracting key features, establishing affinity between a similar group of observations using clustering techniques or supervised learning algorithms.

6. Reducing the number of features to a manageable set of attributes to avoid overfitting the training set.
7. Validating the model and tuning the model by iterating steps 5, 6, and 7 until the error meets criteria.
8. Storing the model into the file or database to be loaded for runtime processing of new observations.

Data clustering and data classification can be performed independent of each other or as part of a workflow that uses clustering techniques as a preprocessing stage of the training phase of a supervised learning algorithm. Data clustering does not require a model to be extracted from a training set, while classification can be performed only if a model has been built from the training set. The following image gives an overview of training and classification:




A generic data flow for training and running a model

This diagram is an overview of a typical data mining processing pipeline. The first phase consists of extracting the model through clustering or training of a supervised learning algorithm. The model is then validated against test data, for which the source is the same as the training set but with different observations. Once the model is created and validated, it can be used to classify real-time data or predict future behavior. In reality, real-world workflows are more complex and require being dynamically configurable to allow experimentation of different models. Several alternative classifiers can be used to perform a regression and different filtering algorithms are applied against input data depending of the latent noise in the raw data.

Writing a simple workflow

This book relies on financial data to experiment with a different learning strategy. The objective of the exercise is to build a model that can discriminate between volatile and nonvolatile trading sessions. For this first example, we select a simplified version of the logistic regression as our classifier as we treat a stock-price-volume action as a continuous or pseudo-continuous process.



Logistic regression

Logistic regression is treated in depth in *Chapter 6, Regression and Regularization*. The model treated in this example is a simple binary classifier using logistic regression for two-dimensional observations.

The classification of trading sessions according to their volatility is as follows:

- Select a dataset
- Load the dataset
- Preprocess the dataset
- Display data
- Create the model through training
- Classify new data

Selecting a dataset

Throughout the book, we will rely on financial data to evaluate and discuss the merit of different data processing and machine learning methods. In this example, the data is extracted from Yahoo! Finances using the CSV format with the following fields:

- Date
- Price at open
- Highest price in session
- Lowest price in session
- Price at session close
- Volume
- Adjust price at session close

Let's create a simple program that loads the content of the file, executes some simple preprocessing functions, and creates a simple model. We selected the CSCO stock price between January 1, 2012 and December 1, 2013 as our data input.

Let's consider two variables, price and volume, as illustrated by the following screenshot. The top graph displays the variation of the price of Cisco stock over time and the bottom bar chart represents the daily trading volume on Cisco stock over time:



Price-Volume action for the Cisco stock


Loading the dataset

The first step is loading the dataset from a local file. Typically, large datasets are loaded from a database or distributed filesystem such as **Hadoop Distributed File System (HDFS)**, as shown here:

```
def load(fileName: String): Option[XYTSeries] = {
  val src = Source.fromFile(fileName)
  val fields = src.getLines.map( _.split(CSV_DELIM) ).toArray //1
  val cols = fields.drop(1) //2
  val data = transform(cols)
  src.close //3
  Some(data)
}
```

The `transform` method will be described in the next section.

The data file is extracted through an invocation of the `Source.fromFile` static method, and then the fields are extracted through a `map` (line 1). The header (first) row is removed with a call to `drop` (line 2).



Data extraction

The `Source.fromFile.getLines.map` invocation pipeline method returns an iterator, which needs to be converted into an array to store the information into memory.

The file has to be closed to avoid leaking of the file handle (line 3).

Code readability

A long pipeline of Scala high-order methods make the code and underlying code quite difficult to read. It is recommended to break down long chains of method calls. The following code is an example of a long chain of method calls:

```
val cols = Source.fromFile.getLines.map(  
  _.split(CSV_DELIM).toArray.drop(1)
```



We can break down such method calls into several steps as follows:

```
val lines = Source.fromFile.getLines  
val fields = lines.map(_.split(CSV_DELIM).toArray)  
val cols = fields.drop(1)
```

We strongly encourage you to consult the excellent guide *Effective Scala*, written by Marius Eriksen from Twitter. This is definitively a must read for any Scala developer [1:10].

Preprocessing the dataset

The next step is to normalize the data in the range $[-0.5, 0.5]$ to be trained by the logistic binary classifier. It is time to introduce a non-sense statistics class.

Basic statistics

We select the computation of mean and standard deviation of the two time series as the first step of the preprocessing phase. The computation of these statistics can be implemented by the reduce methods `reduceLeft` and `foldLeft`:

```
val mean = price.reduceLeft(_ + _) / price.size  
val s2 = price.foldLeft(0.0)((s, x) => s + (x - mean) * (x - mean))  
val stdDev = Math.sqrt(s2 / (price.size - 1))
```

However, this implementation has one major drawback: the dataset (price in this example) has to be traversed for each method (mean, stdDev, min, max, and so on).

One of the solutions is to create a class that computes the counters and the statistics on demand using, once again, the lazy values:

```
class Stats[T <% Double](private values: DVector[T]) {  
  class _Stats(var minValue: Double, var maxValue: Double, var sum:  
    Double, var sumSqr: Double)  
  val stats = {  
    val _stats = new _Stats(Double.MaxValue, Double.MinValue, 0.0, 0.0)
```

```

    values.foreach(x => {
      if(x < _stats.minValue) x else _stats.minValue
      if(x > _stats.maxValue) x else _stats.maxValue
      _stats.sum + x
      _stats.sumSqr + x*x
    })
    _stats
  }

  lazy val mean = _stats.sum/values.size
  lazy val variance = (_stats.sumSqr - mean*mean*values.size)/(values.size-1)
  lazy val stdDev = if(variance < ZERO_EPS) ZERO_EPS else Math.sqrt(variance)
  lazy val min = _stats.minValue
  lazy val max = _stats.mazValue
}

```

We made the statistics object generic by using the view bounds `T <% Double`, which assumes a conversion from type `T` to `Double`. By defining the statistics as tuple counters (minimum value, maximum value, sum of values, and sum of square values) and folding these values into a statistics object, we limit the number of invocations of the `foldLeft` reducer method to 1, and therefore, avoid the recomputation of these statistics for the existing dataset each time new data is added.

The code illustrates the use and benefit of lazy values in Scala. The mean is computed only if and when needed.

Normalization and Gauss distribution

Statistics are usually used to normalize data into a probability value $[0, 1]$ as required by most classification or clustering algorithms. It is logical to add the normalization method to the `Stats` class, as we have already extracted the `min` and `max` values:

```

def normalize: DblVector = {
  val range = max - min; values.map(x => (x - min)/range)
}

```

The same approach is used to compute the multivariate normal distribution:

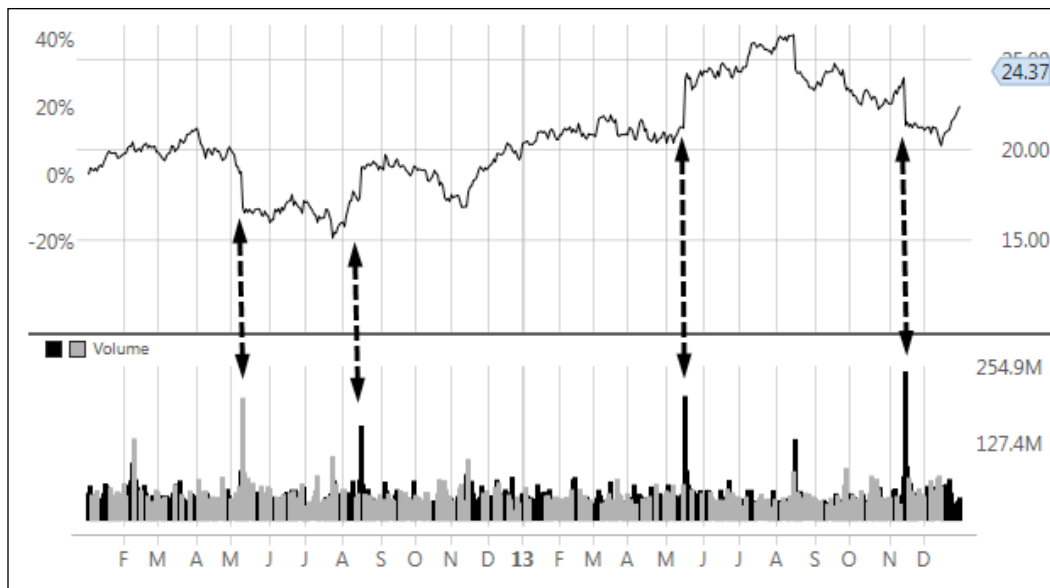
```

def gauss: DblVector =
  values.map(x =>{
    val y=x-mean
    INV_SQRT_2PI/stdDev*Math.exp(-0.5*y*y/stdDev)})

```

The price action chart has a very interesting characteristic. At a closer look, a sudden change in price and increase in volume occurs about every three months or so. Experienced investors will undoubtedly recognize that those price-volume patterns are related to the release of quarterly earnings of Cisco. Such regular but unpredictable patterns can be a source of concern or opportunity if risk can be managed. The strong reaction of the stock price to the release of corporate earnings may scare some long-term investors while enticing day traders.

The following graph visualizes the potential correlation between sudden price change (volatility) and heavy trading volume:



Correlation price-volume action for the Cisco stock

Let's try to correlate the volatility of the stock price with volume. For the sake of this exercise, we define the volatility as the maximum variation of the stock price within each trading session: the relative difference between the highest price during the trading session and the lowest price during the session.

The `YahooFinancials` enumeration extracts historical stock prices and session volume from a CSV file. For example, the volatility is extracted from the CSV fields of each line in the CSV file as follows:

```
object YahooFinancials extends Enumeration {  
  type YahooFinancials = Value  
  val DATE, OPEN, HIGH, LOW, CLOSE, VOLUME, ADJ_CLOSE = Value
```

```

    val volatility = (fs: Array[String]) => fs(HIGH.id).toDouble - fs(LOW.
id).toDouble
    ...
}

```

The transform method uses the `YahooFinancials` enumeration to generate the input data for the model:

```

def transform(cols: Array[Array[String]]): XYTSeries = {
  val volatility = Stats[Double](cols.map(YahooFinancials.
volatility)).normalize
  val volume = Stats[Double](cols.map(YahooFinancials.volume)
).normalize
  volatility.zip(volume)
}

```

The volatility and volume data is normalized using the `Stats.normalize` method defined earlier.

Plotting data

Although charting is not the primary goal of this book, we thought that you will benefit from a brief introduction to JFreeChart. The skeleton code to generate a scatter plot is rather simple. The most relevant code is the transformation of the `XYTSeries` into graphical JFreeChart's `XYSeries`:

```

val xLegend = "Session Volatility"
val yLegend = "Session Volume"
def display(xy: XYTSeries, w: Int, h: Int): Unit = {
  val series = new XYSeries("CSCO 2012-2013 Stock")
  xy.foreach(x => series.add(x._1, x._2))
  val seriesCollection = new XYSeriesCollection
  seriesCollection.addSeries(series)
  ... // plot rendering code
  val chart = ChartFactory.createScatterPlot(xLegend, xLegend,
yLegend, seriesCollection, PlotOrientation.VERTICAL, true, false,
false)
  createFrame("Logistic Regression", chart)
}

```

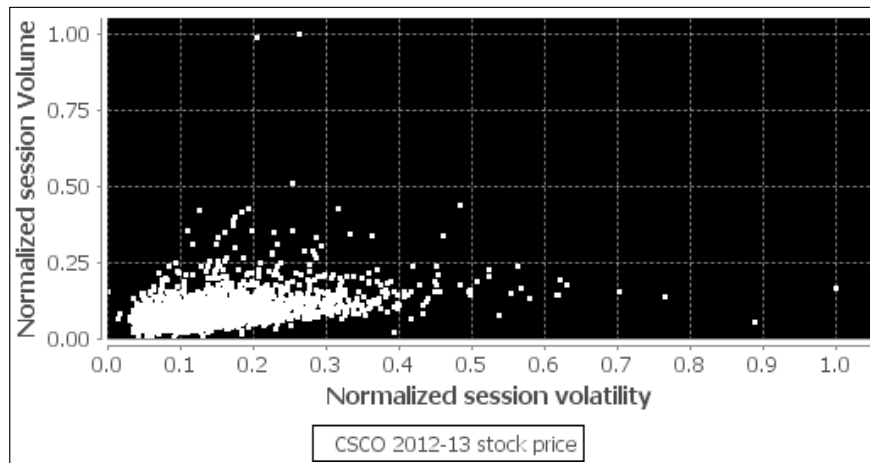


Visualization

The JFreeChart library is introduced as a robust charting tool. The visualization of the results of a computation is beyond the scope of this book. The code related to plots and charts is omitted from the book in order to keep the code snippets concise and dedicated to machine learning. In a few occasions, output data is formatted as a CSV file to be simply imported into a spreadsheet.

Here is an example of a plot using the `ScatterPlot.display` method:

```
val plot = new ScatterPlot(("CSCO 2012-2013", "Session High - Low",  
"Session Volume"), new BlackPlotTheme)  
plot.display(volatility_vol.filter( _.1 < 0.5), 250, 340)
```



Scatter plot of volatility and volume for the Cisco stock

There is a level of correlation between session volume and session volatility. We can use this information to classify trading sessions by their volatility.

Creating a model (learning)

The objective of the training is to build a model that can discriminate between volatile and nonvolatile trading sessions. For the sake of the exercise, session volatility has been defined as session price high and session price low coupled with heavy trading volume, which constitute the two parameters of the model.

Logistic regression is commonly used in statistics inference. The following implementation of the binary logistic regression classifier exposes a single method, `classify`, to comply with our desire to reduce the complexity and life cycle of objects. The model parameters, `weights`, are computed during training when the `LogBinRegression` class/model is instantiated. As mentioned earlier, the sections of the code nonessential to the understanding of the algorithm are omitted:

```
class LogBinRegression(val labels: DVector[(XY, Double)], val
  maxIters: Int, val eta: Double, val eps: Double) {
  val dim = 3
  val weights = train

  def classify(xy: XY): Option[(Boolean, Double)] = {
    if(weights != None) {
      val likelihood = sigmoid(w(0) + xy._1*w(1) + xy._2*w(2))
      Some(likelihood > 0.5, likelihood)
    }
    else None
  }
}
```

The training method, `train`, consists of iterating through the computation of the weight using a simple descent gradient. The method computes the weights and returns an option, so the model is either trained and ready for runtime classification or nonexistent (`None`):

```
def train: Option[DblVector] = {
  val w = Array.fill(dim) ( x=> Random.nextDouble-1.0)

  Range(0, maxIters).find(_ => {
    val deltaW = labels.foldLeft(Array.fill(dim)(0.0))((dw, lbl) => {
      val y = sigmoid(w(0) + w(1)*lbl._1._1 + w(2)*lbl._1._2)
      dw.map(dx => dx + (lbl._2 - y)*(lbl._1._1 + lbl._1._2))
    })
    val nextW = Array.fill(dim)(0.0)
      .zipWithIndex
      .map(nw => w(nw._2)+eta*deltaW(nw._2))
    val diff = Math.abs(nextW.sum - w.sum)
    nextW.copyToArray(w); diff < eps
  }) match {
    case Some(iters) => Some(w)
    case None => { ... }
  }
}

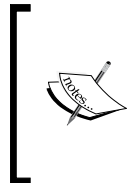
def sigmoid(x: Double):Double = 1.0/(1.0 + Math.exp(-x))
```

The iteration is encapsulated in the Scala `find` method that exists if the algorithm converges (`diff < eps`). The model parameters, `weights`, are set to `None` if the maximum number of iterations is reached.

The training method, `train`, iterates across the set of observations by computing the gradient between the predicted and observed values. In our simplistic approach, the gradient is computed as a linear function of the sigmoid of the sum of the product of the weight and training observations. As for any optimization problem, the initialization of the solution vector, `weights`, is critical. We choose to initialize the weight with random values, although in practice, you would use a more deterministic approach to initialize the model parameters.

In order to train the model, we need to label data. The process consists of tagging every trading session as **volatile** and **non volatile** according to the observations (relative session volatility and session volume). The labeling process is usually quite cumbersome; therefore, let's generate the label automatically. A trading session is considered volatile if a volatility and volume are both greater than 60 percent of the maximum relative volatility and volume:

```
val labels = volatilityVol.zip(volatilityVol.map(x =>if( x._1>0.3 &&
x._2>0.3) 1.0 else 0.0))
```



Automated labeling

Although quite convenient, automated creation of training labels is not without risk because it may mislabel singular observations. This technique is used in this test for convenience but it is not recommended unless a domain expert reviews the labels manually.

The model is created (trained) by a simple instantiation of the logistic binary classifier:

```
val logit = new LogBinRegression(labels, 300, 0.00005, 0.02)
```

The training run is configured with a maximum of 300 iterations, a gradient slope of 0.00005, and convergence criteria of 0.02.

Classify the data

Finally, the model can be tested with a new fresh dataset, not related to the training set:

```
Date,Open,High,Low,Close,Volume,Adj Close
3/9/2011,14.78,15.08,14.20,14.91,4.79E+08,14.88
11/17/2009,10.78,10.90,10.62,10.84,3901987,10.85
```

It is just a matter of executing the classification method (exceptions, conditions on method arguments, and returned values are omitted):

```
val testData = load("resources/data/chap1/CSC02.csv")
logit.classify(testData(0)) match {
  case Some(topCategory) => Display.show(topCategory)
  case None => { ... }
}
logit.classify(testData(1)) match {
  case Some(topCategory) => Display.show(topCategory)
  case None => { ... }
}
```

The result of the classification is `(true, 0.516)` for the first sample and `(false, 0.1180)` for the second sample.



Validation

The simple classification, in this test case, is provided for illustrating the runtime application of the model. It does not constitute a validation of the model by any stretch of imagination. The next chapter digs into validation metrics and methodology.

Summary

We hope you enjoyed this introduction to machine learning and how to leverage your existing skills in Scala programming to create a simple regression program to predict stock price/volume action. Here are the highlights of this introductory chapter:

- From monadic composition and high-order collection methods for parallelization to configurability to reusability patterns, Scala is the perfect fit to implement and leverage data mining and machine learning algorithms for large-scale projects
- There are many steps to create and apply a machine learning model
- The implementation of the logistic binary classifier presented as part of the test case is simple enough to encourage you to learn how to write and apply more advanced machine learning algorithms

To the delight of Scala programming aficionados, the next chapter will dig deeper into building a flexible workflow by leveraging traits and dependency injection.

2

Hello World!

In the first chapter, you were acquainted with some rudimentary concepts regarding data processing, clustering, and classification. This chapter is dedicated to the creation and maintenance of a flexible end-to-end workflow to train and classify data. The first section of the chapter introduces a data-centric (functional) approach to create number-crunching applications.

You will learn how to:

- Apply the concept of monadic design to create dynamic workflows
- Leverage some of Scala's advanced functional features, such as dependency injection, to build portable computational workflows
- Take into account the bias-variance trade-off in selecting a model
- Overcome overfitting in modeling
- Break down data into training, test, and validation sets
- Implement model validation in Scala using precision, recall, and F score

Modeling

Data is the lifeline of any scientist, and the selection of data providers is critical in developing or evaluating any statistical inference or machine learning algorithm.

A model by any other name

We briefly introduced the concept of a model in the *Model categorization* section in *Chapter 1, Getting Started*.

What constitutes a model? Wikipedia provides a reasonably good definition of a model as understood by scientists [2:1]:

A scientific model seeks to represent empirical objects, phenomena, and physical processes in a logical and objective way.

...

Models that are rendered in software allow scientists to leverage computational power to simulate, visualize, manipulate and gain intuition about the entity, phenomenon, or process being represented.

In statistics and the probabilistic theory, a model describes data that one might observe from a system to express any form of uncertainty and noise. A model allows us to infer rules, make predictions, and learn from data.

A model is composed of **features**, also known as **attributes** or **variables**, and a set of relation between those features. For instance, the model represented by the function $f(x, y) = x \cdot \sin(2y)$ has two features, x and y , and a relation, f . These two features are assumed to be independent. If the model is subject to a constraint such as $f(x, y) < 20$, then the *conditional independence* is no longer valid.

An astute Scala programmer would associate a model to a monoid for which the set is a group of observations and the operator is the function implementing the model. If it walks like a monoid and quacks like a monoid, then it is a monoid.

Models come in a variety of shapes and forms:

- **Parametric:** This consists of functions and equations (for example, $y = \sin(2t + w)$)
- **Differential:** This consists of ordinary and partial differential equations (for example, $dy = 2x \cdot dx$)
- **Probabilistic:** This consists of probability distributions (for example, $p(x | c) = \exp(k \cdot \log x - x) / x!$)
- **Graphical:** This consists of graphs that abstract out the conditional independence between variables (for example, $p(x, y | c) = p(x | c) \cdot p(y | c)$)
- **Directed graphs:** This consists of temporal and spatial relationships (for example, a scheduler)
- **Numerical method:** This consists of finite elements and methods such as Newton-Raphson
- **Chemistry:** This consists of formula and components (for example, H_2O , $\text{Fe} + \text{C}_{12} = \text{FeC}_{13}$, and so on)

- **Taxonomy:** This consists of a semantic definition and relationship of concepts (for example, APG/Eudicots/Rosids/Huaceae/Malvales)
- **Grammar and lexicon:** This consists of a syntactic representation of documents (for example, Scala programming language)
- **Inference logic:** This consists of a distribution pattern such as `IF (stock vol > 1.5 * average) AND rsi > 80 THEN...`

Model versus design

The confusion between model and design is quite common in Computer Science, the reason being that these terms have different meanings for different people depending on the subject. The following metaphors should help with your understanding of these two concepts:

- **Modeling:** This is describing something you know. A model makes the assumption, which becomes an assertion if proven correct (for example, the US population, p , increases by 1.2 percent a year, $dp/dt = 1.012$).
- **Designing:** This is manipulating representation for things you don't know. Designing can be seen as the exploration phase of modeling (for example, what are the features that contribute to the growth of the US population? Birth rate? Immigration? Economic conditions? Social policies?).

Selecting a model's features

The selection of a model's features is the process of discovering and documenting the minimum set of variables required to build the model. Scientists make the assumption that data contains many redundant or irrelevant features. Redundant features do not provide information already given by the selected features, and irrelevant features provide no useful information.

Selecting features consists of two consecutive steps:

1. Searching for new feature subsets.
2. Evaluating these feature subsets using a scoring mechanism.

The process of evaluating each possible subset of features to find the one that maximizes the objective function or minimizes the error rate is computationally intractable for large datasets. A model with n features requires $2^n - 1$ evaluations.

Extracting features

An **observation** is a set of indirect measurements of hidden, also known as latent, variables, which may be noisy or contain a high degree of correlation and redundancies. Using raw observations in a classification task would very likely produce inaccurate classes. Using all features from the observation also incurs a high computation cost.

The purpose of **extracting features** is to reduce the number of variables or dimensions of the model by eliminating redundant or irrelevant features. The features are extracted by transforming the original set of observations into a smaller set at the risk of losing some vital information embedded in the original set.

Designing a workflow

A data scientist has many options in selecting and implementing a classification or clustering algorithm.

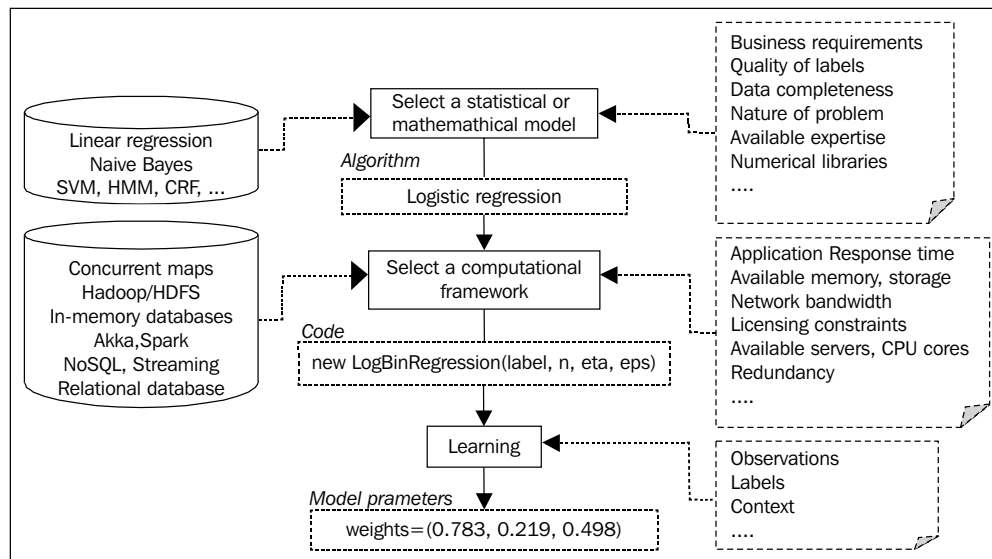
Firstly, a mathematical or statistical model is to be selected to extract knowledge from the raw input data or the output of a data upstream transformation. The selection of the model is constrained by the following parameters:

- Business requirements such as accuracy of results
- Availability of training data and algorithms
- Access to a domain or subject-matter expert

Secondly, the engineer has to select a computational and deployment framework suitable for the amount of data to be processed. The computational context is to be defined by the following parameters:

- Available resources such as machines, CPU, memory, or I/O bandwidth
- Implementation strategy such as iterative versus recursive computation or caching
- Requirements for the responsiveness of the overall process such as duration of computation or display of intermediate results

The following diagram illustrates the selection process to define the data transformation for each computation in the workflow:



Statistical and computation modeling for machine-learning applications

Domain expertise, data science, and software engineering

A domain or **subject-matter expert** is a person with authoritative or credited expertise in a particular area or topic. A chemist is an expert in the domain of chemistry and possibly related fields.



A **data scientist** solves problems related to data in a variety of fields such as biological sciences, health care, marketing, or finances. Data and text mining, signal processing, statistical analysis, and modeling using machine learning algorithms are some of the activities performed by a data scientist.

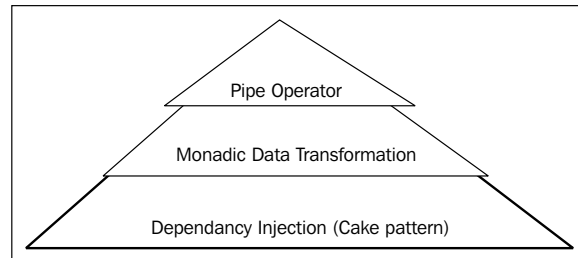
A **software developer** performs all the tasks related to creation of software applications, including analysis, design, coding, testing, and deployment.

The parameters of a data transformation may need to be reconfigured according to the output of the upstream data transformation. Scala's higher-order functions are particularly suitable for implementing configurable data transformations.

The computational framework

The objective is to create a framework flexible and reusable enough to accommodate different workflows and support all types of machine learning algorithms from preprocessing, data smoothing, and classification to validation.

Scala provides us with a rich toolbox that includes monadic design, design patterns, and dependency injections using traits. The following diagram describes the three levels of complexity for creating the framework:



Hierarchical design of a monadic workflow

The first step is to define a trait and a method that describes the transformation of data by a computation unit (element of the workflow).

The pipe operator

Data transformation is the foundation of any workflow for processing and classifying a dataset, training and validating a model, and displaying results.

The objective is to define a symbolic representation of the transformation of different types of data without exposing the internal state of the algorithm implementing the data transformation. The pipe operator is used as the signature of a data transformation:

```
trait PipeOperator[-T, +U] {  
  def |> (data: T): Option[U]  
}
```



F# reference

The notation `|>` as the signature of the transform or pipe operator is borrowed from the F# language [2:2]. The data transformation indeed implements a function, and therefore, has the same variance signature as `Function[-T, +R]` of Scala.

The `|>` operator transforms a data of the type `T` into a data of the type `U` and returns an option to handle internal errors and exceptions.

Advanced Scala idioms



The next two sections introduce a monadic representation of the data transformation and one implementation of the dependency injection to create a dynamic workflow as an alternative to the delimited continuation pattern. Although these topics may interest advanced Scala developers, they are not required to understand any of the techniques or procedures described in this book.

Monadic data transformation

The next step is to create a **monadic design** to implement the pipe operator. Let's use a monadic design to wrap `_fct`, a data transformation function (also known as operator), with the most commonly used Scala higher-order methods:

```
class _FCT[+T] (val _fct: T) {
  def map[U] (c: T => U): _FCT[U] = new _FCT[U] ( c(_fct))
  def flatMap[U] (f: T => _FCT[U]): _FCT[U] = f(_fct)
  def filter(p: T => Boolean): _FCT[T] = if( p(_fct) ) new _FCT[T] (_fct) else zeroFCT(_fct)
  def reduceLeft[U] (f: (U,T) => U) (implicit c: T=> U): U = f(c(_fct), _fct)
  def foldLeft[U] (zero: U) (f: (U, T) => U) (implicit c: T=> U): U = f(c(_fct), _fct)
  def foreach(p: T => Unit): Unit = p(_fct)
}
```

The methods of the `_FCT` class represent a subset of the traditional Scala higher methods for collections [2:3]. The `_FCT` class is to be used internally. Arguments are validated by subclasses or containers.

Finally, the `Transform` class takes a `PipeOperator` instance as an argument and automatically invokes its operator:

```
class Transform[-T, +U] (val op: PipeOperator[T, U]) extends _FCT[Function[T, Option[U]]] (op.|>) {
  def |>(data: T): Option[U] = _fct(data)
}
```


You may wonder about the reason behind the monadic representation of a data transformation, `Transform`. You can create any algorithm by just implementing the `PipeOperator` trait, after all. The reason is that `Transform` has a richer protocol (methods) and enables developers to create a complex workflow as an alternative to the delimited continuation. The following code snippet illustrates a generic function composition or data transformation composition using the monadic approach:

```
val op = new PipeOperator[Int, Double] {
  def |> (n: Int): Option[Double] = Some(Math.sin(n.toDouble))
}
def g(f: Int => Option[Double]): (Int => Long) = {
  (n: Int) => {
    f(n) match {
      case Some(x) => x.toLong
      case None => -1L
    }
  }
}
val gof = new Transform[Int, Double](op).map(g(_))
```

This code extends `op`, an existing transformation, with another function, `g`. As stated in the *Presentation* section under *Source code* in *Chapter 1, Getting Started*, code related to exceptions, error checking, and validation of arguments is omitted (refer to the *Format of code snippets* section in *Appendix A, Basic Concepts*).

Dependency injection

This section presents the key constructs behind the Cake pattern. A workflow composed of configurable data transformations requires a dynamic modularization (substitution) of the different stages of the workflow. The Cake pattern is an advanced class composition pattern that uses mix-in traits to meet the demands of a configurable computation workflow. It is also known as stackable modification traits [2:4].

This is not an in-depth analysis of the stackable trait injection and self-reference in Scala. There are few interesting articles on dependencies injection that are worth a look [2:5].

Java relies on packages tightly coupled with the directory structure and prefix to modularize the code base. Scala provides developers with a flexible and reusable approach to create and organize modules: traits. Traits can be nested, mixed with classes, stacked, and inherited.

Dependency injection is a fancy name for a reverse look up and binding to dependencies. Let's consider a simple application that requires data preprocessing, classification, and validation. A simple implementation using traits looks like this:

```
val myApp = new Classification with Validation with PreProcessing {
  val filter = .. }

```

If, at a later stage, you need to use an unsupervised clustering algorithm instead of a classifier, then the application has to be rewired:

```
val myApp = new Clustering with Validation with PreProcessing { val
  filter = .. }

```

This approach results in code duplication and lack of flexibility. Moreover, the `filter` class member needs to be redefined for each new class in the composition of the application. The problem arises when there is a dependency between traits used in the composition of the application. Let's consider the case for which the filter depends on the validation methodology.

Mixins linearization [2:6]

The linearization or invocation of methods between mixins follows a right-to-left pattern:

- Trait B extends A
- Trait C extends A
- Class M extends N with C with B

The Scala compiler implements the linearization as follows:
M => B => C => A => N

Although you can define `filter` as an abstract value, it still has to be redefined each time a new validation type is introduced. The solution is to use the `self` type in the definition of the newly composed `PreProcessingWithValidation` trait:

```
trait PreProcessingWithValidation extends PreProcessing {
  self: Validation =>
  val filter = ..
}

```

The application can then be simply composed as:

```
val myApp = new Classification with PreProcessingWithValidation {
  val validation: Validation
}

```



Overriding val with def

It is advantageous to override the declaration of a value with a definition of a method with the same signature. Contrary to a value that locks the implementation of the value, a method can return a different value for each invocation:

```
trait PreProcessor { val validation = ... }
trait MyValidator extends Validator { def validation
= ... }
```

In Scala, a value declaration can be overridden by the method definition, not vice versa.

Let's adapt and generalize this pattern to construct a boilerplate template in order to create dynamic computational workflows.

The first step is to generate different modules to encapsulate different types of data transformation.

Workflow modules

The data transformation defined by the `PipeOperator` instance is dynamically injected into the module by initializing the abstract value. Let's define three parameterized modules representing the preprocessing, processing, and post-processing stages of a workflow:

```
trait PreprocModule[-T, +U] { val preProc: PipeOperator[T, U] }
trait ProcModule[-T, +U] { val proc: PipeOperator[T, U] }
trait PostprocModule[-T, +U] { val postProc: PipeOperator[T, U] }
```

The modules (traits) contain only a single abstract value. One characteristic of the Cake pattern is to enforce strict modularity by initializing the abstract values with the type encapsulated in the module, as follows:

```
trait ProcModule[-T, +U] {
  val proc: PipeOperator [T, U]
  class Classification[-T, +U] extends PipeOperator [T,U] { }
}
```

One of the objectives in building the framework is allowing developers to create data transformation (inherited from `PipeOperator`) independently from any workflow. Under these constraints, strict modularity is not an option.



Scala traits versus Java packages

There is a major difference between Scala and Java in terms of modularity. Java packages constrain developers into following a strict syntax requirement; for instance, the source file has the same name as the class it contains. Scala modules based on stackable traits are far more flexible.

The workflow factory

The next step is to *write* the different modules into a workflow. This is achieved by using the `self` reference to the stack of the three traits defined in the previous paragraph. Here is an implementation of the said `self` reference:

```
class Workflow[T, U, V, W] {
  self: PreprocModule[T,U] with ProcModule[U,V] with
  PostprocModule[V,W] =>
  def |> (data: T): Option[W] = {
    preProc |> data match {
      case Some(input) => {
        proc |> input match {
          case Some(output) => postProc |> output
          case None => { ... }
        }
      }
      case None => { ... }
    }
  }
}
```

Quite simple indeed! If you need only two modules, you can either create a workflow with a stack of two traits or initialize the third with the `PipeOperator` identity:

```
def identity[T] = new PipeOperator[T,T] {
  override def |> (data:T): Option[T] = Some(data)
}
```

Let's test the wiring with the following simple data transformations:

```
class Sampler(val samples: Int) extends PipeOperator[Double => Double,
DblVector] {
  override def |> (f: Double => Double): Option[DblVector] =
```

Hello World!

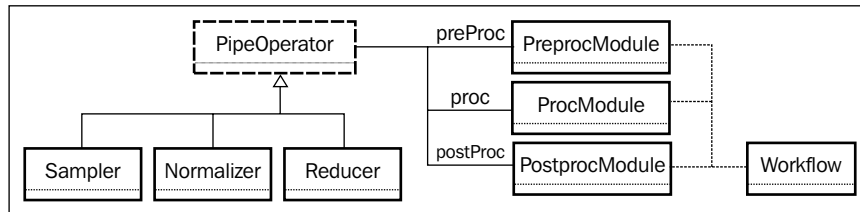
```
        Some(Array.tabulate(samples)(n => f(n.toDouble/samples)) )
    }

class Normalizer extends PipeOperator[DblVector, DblVector] {
    override def |> (data: DblVector): Option[DblVector] =
        Some(Stats[Double](data).normalize)
}

class Reducer extends PipeOperator[DblVector, Int] {
    override def |> (data: DblVector): Option[Int] =
        Range(0, data.size) find(data(_) == 1.0)
}
```

The first operator, *Sampler*, samples a function, *f*, with a frequency *1/samples* over the interval *[0, 1]*. The second operator, *Normalizer*, normalizes the data over the range *[0, 1]* using the *Stats* class introduced in the *Basic statistics* section in *Chapter 1, Getting Started*. The last operator, *Reducer*, extracts the index of the large sample (value *1.0*) using the Scala collection method, *find*.

A picture is worth a thousand words; the following UML class diagram illustrates the workflow factory design pattern:



Finally, the workflow is instantiated by dynamically initializing the abstract values, *preProc*, *proc*, and *postProc*, with a transformation of the type *PipeOperator* as long as the signature (input and output types) matches the parameterized types defined in each module (lines marked as *1*):

```
val dataflow = new Workflow[Double => Double, DblVector, DblVector,
Int]
    with PreprocModule[Double => Double, DblVector]
        with ProcModule[DblVector, DblVector]
            with PostprocModule[DblVector, Int] {

    val preProc: PipeOperator[Double => Double, DblVector] = new
    Sampler(100) //1
```

```

    val proc: PipeOperator[DblVector,DblVector]= new Normalizer //1
    val postProc: PipeOperator[DblVector,Int] = new Reducer//1
  }
  dataflow |> ((x: Double) => Math.log(x+1.0)+Random.nextDouble) match {
    case Some(index) => ...
  }

```

Scala's strong type checking catches any inconsistent data types at compilation time. It reduces the development cycle because runtime errors are more difficult to track down.

Examples of workflow components

It is difficult to build an example of workflow using classes and algorithms introduced later in the book. The modularization of the preprocessing and clustering stages is briefly described here to illustrate the encapsulation of algorithms described throughout the book within a workflow.

The preprocessing module

The following examples of a workflow module use the time series class, *XTSeries*, which is used throughout the book:

```
class XTSeries[T](label: String, arr: Array[T])
```

The *XTSeries* class takes an identifier, a label, and an array of parameterized values, *arr*, as parameters, and is formally described in *Chapter 3, Data Preprocessing*.

The preprocessing algorithms such as moving average or discrete Fourier filters are encapsulated into a preprocessing module using a combination of abstract value and inheritance:

```

trait PreprocessingModule[T] {
  val preprocessor: Preprocessing[T] //1

  abstract class Preprocessing[T] { //2
    def execute(xt: XTSeries[T]): Unit
  }

  abstract class MovingAverage[T] extends Preprocessing[T] with
PipeOperator[XTSeries[T], XTSeries[Double]] { //3
    override def execute(xt: XTSeries[T]): Unit = this |> xt match {
      case Some(filteredData) => ...
    }
  }

```

```
        case None => ...
      }
    }

    class SimpleMovingAverage[@specialized(Double) T <% Double] (period:
    Int) (implicit num: Numeric[T]) extends MovingAverage[T] {
    override def |> (xt: XTSeries[T]): Option[XTSeries[Double]] =
    ...
    }
    class DFTFir[T <% Double] (g: Double=>Double) extends Preprocessing[T]
    extends PreProcessing[T] with PipeOperator[XTSeries[T],
    XTSeries[Double]] {
      override def execute(xt: XTSeries[T]): Unit = this |> xt match {
        case Some(filteredData) => ...
        case None => ...
      }
      override def |> (xt: XTSeries[T]) : Option[XTSeries[Double]]
      }
    }
```

The preprocessing module, `PreprocessingModule`, defines `preprocessor`, an abstract value, that is initialized at runtime (line 1). The `PreProcessing` class is defined as a high-level abstract class with a generic execution function: `execute` (line 2). The preprocessing algorithms; filtering techniques moving average, `MovingAverage`; and discrete Fourier, `DFTFir` in this case, are defined as a class hierarchy with the base type `PreProcessing`. Each filtering class also implements `PipeOperator` so it can be weaved into a simpler data transformation workflow (line 3).

The preprocessing algorithms are described in the next chapter.

The clustering module

The encapsulation of clustering techniques is the second example of a module for dependency-injection-based workflow:

```
trait ClusteringModule[T] {
  type EMOutput = List[(Double, DblVector, DblVector)]
  val clustering: Clustering[T]

  abstract class Clustering[T] {
```

```

    def execute(xt: XTSeries[Array[T]]): Unit
  }

  class KMeans[T <% Double](K: Int, maxIters: Int, distance:
    (DbVector, Array[T]) => Double)(implicit order: Ordering[T], m:
    Manifest[T]) extends Clustering[T] with PipeOperator[XTSeries[Array
    [T]], List[Cluster[T]]] {

    override def |> (xt: XTSeries[Array[T]]): Option[List[Cluster[T]]]

    override def execute(xt: XTSeries[Array[T]]): Unit = this |> xt
  match {
    case Some(clusters) => ...
    case None => ...
  }
}

  class MultivariateEM[T <% Double](K: Int) extends Clustering[T] with
PipeOperator[XTSeries[Array[T]], EMOutput] {
    override def |> (xt: XTSeries[Array[T]]): Option[EMOutput] =
      override def execute(xt: XTSeries[Array[T]]): Unit = this |> xt
  match {
    case Some(emOutput) => ...
    case None => ...
  }
}
}

```

The `ClusteringModule` clustering module defines an abstract value, `clustering`, which is initialized at runtime (line 1). The two clustering algorithms, `KMeans` and `Expectation-Maximization`, `MultivariateEM`, inherits the `Clustering` base class. The clustering technique can be used in:

- A dependency-injection-based workflow by overriding `execute`
- A simpler data transformation flow by overriding `PipeOperator(|>)`

The clustering techniques are described in *Chapter 4, Unsupervised Learning*.



Dependency-injection-based workflow versus data transformation

The data transformation `PipeOperator` trades flexibility for simplicity. The design proposed for preprocessing and clustering techniques allows you to use both approaches. The techniques presented in the book implement the basic data transformation, `PipeOperator`, in order to keep the implementation of these techniques as simple as possible.

Assessing a model

Evaluating a model is an essential part of the workflow. There is no point in creating the most sophisticated model if you do not have the tools to assess its quality. The validation process consists of defining some quantitative reliability criteria, setting a strategy such as an N-Fold cross-validation scheme, and selecting the appropriate labeled data.

Validation

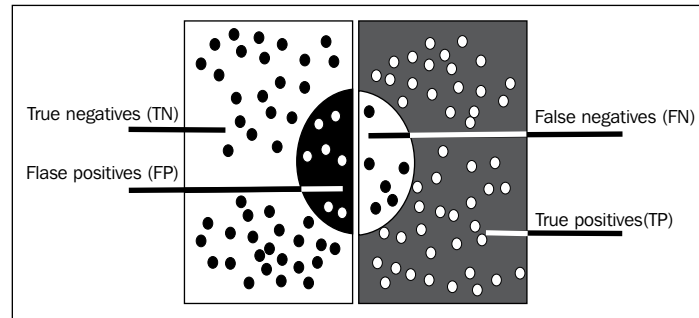
The purpose of this section is to create a Scala class to be used in future chapters for validating models. For starters, the validation process relies on a set of metrics to quantify the fitness of a model generated through training.

Key metrics

Let's consider a simple classification model with two classes defined as positive (with respect to negative) represented with Black (with respect to White) color in the following diagram. Data scientists use the following terminology:

- **True positives (TP)**: These are observations that are correctly labeled as belonging to the positive class (white dots on a dark background)
- **True negatives (TN)**: These are observations that are correctly labeled as belonging to the negative class (black dots on a light background)
- **False positives (FP)**: These are observations incorrectly labeled as belonging to the positive class (white dots on a dark background)

- **False negatives (FN):** These are observations incorrectly labeled as belonging to the negative class (black dots on a light background)



Categorization of validation results

This simplistic representation can be extended to classification problems that involve more than two classes. For instance, false positives are defined as observations incorrectly labeled that belong to any class other than the correct one. These four factors are used for evaluating accuracy, precision, recall, and F and G measures:

- **Accuracy:** Represented as ac , this is the percentage of observations correctly classified.
- **Precision:** Represented as p , this is the percentage of observations correctly classified as positive in the group that the classifier has declared positive.
- **Recall:** Represented as r , this is the percentage of observations labeled as positive that are correctly classified.
- **F-Measure or F-score F1:** This is the score of a test's accuracy that strikes a balance between precision and recall. It is computed as the harmonic mean of the precision and recall with values ranging between 0 (worst score) and 1 (best score).
- **G-measure:** Represented as G , this is similar to the F-measure but is computed as the geometric mean of precision p and recall r .

$$ac = \frac{TP+TN}{TP+TN+FP+FN} \quad p = \frac{TP}{TP+FP} \quad r = \frac{TP}{TP+FN}$$

$$F1 = \frac{2pr}{p+r} \quad G = \sqrt{pr}$$

Implementation

Let's implement the validation formula using the same trait-based modular design used in creating the preprocessor and classifier modules. The `Validation` trait defines the signature for the validation of a classification model: the computation of the *F1* statistics and the precision-recall pair:

```
trait Validation {
  def f1: Double
  def precisionRecall: (Double, Double)
}
```

Let's provide a default implementation of the `Validation` trait of the `F1Validation` class. In the tradition of Scala programming, the class is immutable; it computes the counters for TP, TN, FP, and FN when the class is instantiated. The class takes two parameters:

- The array of actual versus expected class: `actualExpected`
- The target class for true positive observations: `tpClass`

```
class F1Validation(actualExpected: Array[(Int, Int)], tpClass:
Int) extends Validation {
  val counts = actualExpected.foldLeft(new Counter[Label])((cnt,
oSeries) => cnt + classify(oSeries._1, oSeries._2))

  lazy val accuracy = {
    val num = counts(TP) + counts(TN)
    num.toDouble/counts.foldLeft(0)((s,kv) => s + kv._2)
  }

  lazy val precision = counts(TP).toDouble/(counts(TP) +
counts(FP))
  lazy val recall = counts(TP).toDouble/(counts(TP) +
counters(FN))

  override def f1: Double = 2.0*precision*recall/(precision +
recall)
  override def precisionRecall: (Double, Double) = (precision,
recall)

  def classify(actual: Int, expected: Int): Label = {
    if(actual == expected) { if(actual == tpClass) TP else TN }
    else { if (actual == tpClass) FP else FN }
  }
}
```

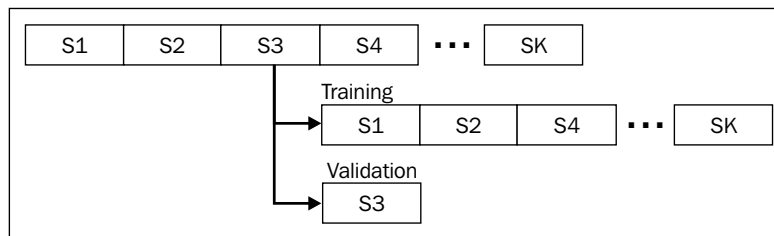
The `precision` and `recall` variables are defined as lazy so they are computed only once, when they are either accessed for the first time or the `f1` and `precisionRecall` functions are invoked. The class is independent of the selected machine learning algorithm, the training, the labeling process, and the type of observations.

Contrary to Java, which defines an enumerator as a class of types, Scala requires enumerators to be singletons that inherit the functionality of the `Enumeration` class:

```
object Label extends Enumeration {  
  type Label = Value  
  val TP, TN, FP, FN = Value  
}
```

K-fold cross-validation

It is quite common that the labeled dataset used for both training and validation is not large enough. The solution is to break the original labeled dataset into K data groups. The data scientist creates K training-validation datasets by selecting one of the groups as a validation set then combining all other remaining groups into a training set as illustrated in the next diagram. The process is known as the K -fold cross validation [2:7].



The third segment is used as validation data and all other dataset segments except **S3** are combined into a single training set. This process is applied to each segment of the original labeled dataset.

Bias-variance decomposition

There is an obvious challenge in creating a model that fits both the training set and subsequent observations to be classified during the validation phase.

If the model tightly fits the observations selected for training, there is a high probability that new observations may not be correctly classified. This is usually the case when the model is complex. This model is characterized as having a low bias with a high variance. Such a scenario can be attributed to the fact that the scientist is overly confident that the observations he or she selected for training are representative to the real world.

The probability of a new observation being classified as belonging to a positive class increases as the selected model fits loosely the training set. In this case, the model is characterized as having a high bias with a low variance.

The mathematical definition for the **bias**, **variance**, and **mean squared error (MSE)** of the distribution are defined by the following formulas:

$$\left[\begin{array}{l} \text{Variance and bias for a true model, } \theta: \\ \text{var } \hat{\theta} = E \left[\left(\hat{\theta} - E[\tilde{\theta}] \right)^2 \right] \quad \text{bias}(\hat{\theta}) = \hat{\theta} - \theta \quad (\hat{\theta}: \theta \text{ estimate}) \\ \text{Mean square error:} \\ \text{MSE} = \text{var}(\hat{\theta}) + \text{bias}(\hat{\theta})^2 \end{array} \right]$$

Let's illustrate the concept of bias, variance, and mean square error with an example. At this stage, most of the machine learning techniques have not been introduced yet. Therefore, the example will emulate a multiple models *fEst: Double => Double* generated from non-overlapping training sets.

These models are evaluated against a test/validation datasets that are emulated by a model, *emul*. The `BiasVarianceEmulator` emulator class takes the emulator function and the size of the `nValues` validation test as parameters. It merely implements the formula to compute the bias and variance for each of the *fEst* models:

```
class BiasVarianceEmulator[T <% Double](emul: Double => Double,
nValues: Int) {

  def fit(fEst: List[Double => Double]): Option[XYSeries] = {
    val rf = Range(0, fEst.size)
    val meanFEst = Array.tabulate(nValues)( x =>
```

```

rf.foldLeft(0.0)((s, n) => s+fEst(n)(x))/fEst.size) // 1

val r = Range(0, nValues)
Some(fEst.map(fe => {
  r.foldLeft(0.0, 0.0)((s, x) => {
    val diff = (fe(x) - meanFEst(x))/ fEst.size // 2
    (s._1 + diff*diff, s._2 + Math.abs(fe(x)-emul(x)))})
  }).toArray)
})
}

```

The `fit` method computes the variance and bias for each of the `fEst` models generated from training. First, the mean of all the models are computed (line 1), and then used in the computation of the variance and bias. The method returns a tuple (variance, bias) for each of the `fEst` model.

Let's apply the emulator to three nonlinear regression models evaluated against validation data:

$$y = \frac{x}{5}, y = 0.0003 \cdot x^2 + 0.18x \text{ and } y = x \left(1 + \frac{\sin\left(\frac{x}{20}\right)}{5} \right)$$

The client code for the emulator consists of defining the `emul` emulator function, and a list, `fEst`, of three models defined as tuples of (function, descriptor) of type `(Double=>Double, String)`. The `fit` method is call on the model functions extracted through a map, as shown in the following code:

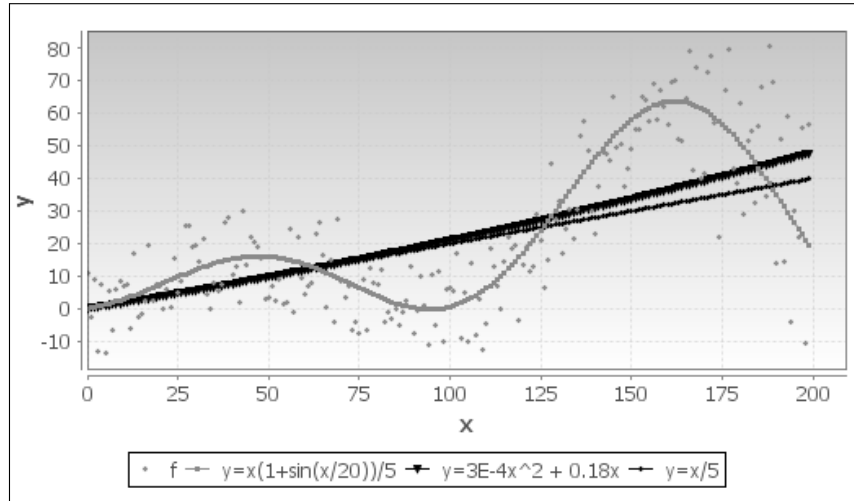
```

val emul = (x: Double) => 0.2*x*(1.0 + Math.sin(x*0.05))
val fEst = List[(Double=>Double, String)] (
  ((x: Double) => 0.2*x, "y=x/5"),
  ((x: Double) => 0.0003*x*x + 0.18*x, "y=3e-4.x^2-0.18x"),
  ((x: Double) =>0.2*x*(1+Math.sin(x*0.05),
    "y=x(1+sin(x/20))/5"))
val emulator = new BiasVarianceEmulator[Double](emul, 200)
emulator.fit(fEst.map(_._1)) match {
  case Some(varBias) => show(varBias)
  case None => ...
}

```

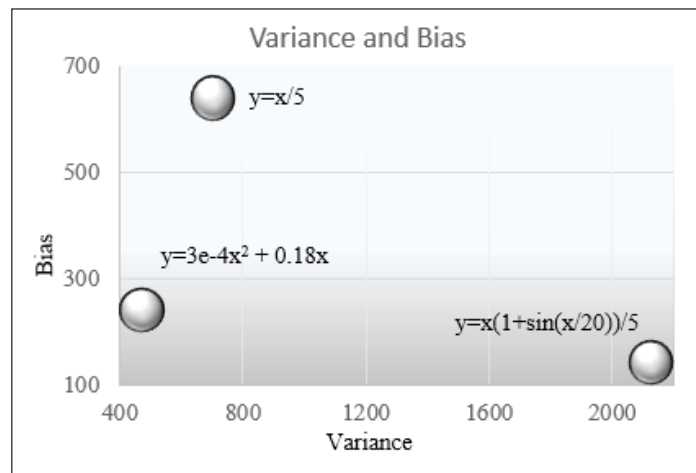
Hello World!

The JFreeChart library is used to display the test dataset and the three model functions.

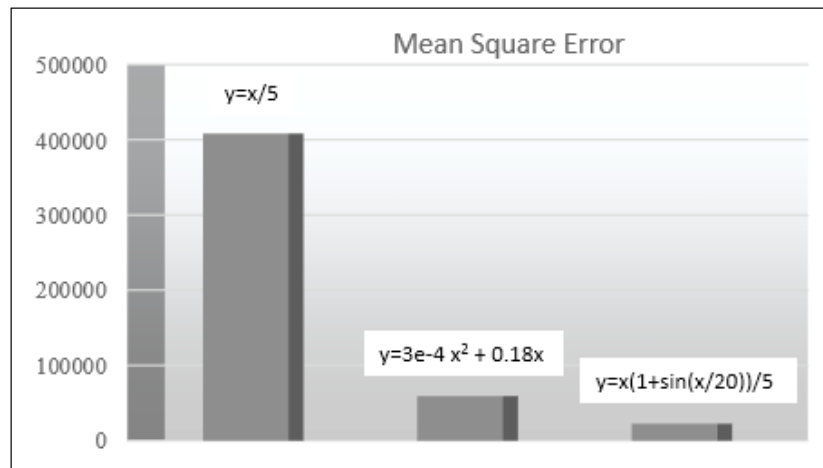


Fitting models to dataset

The variance-bias trade-off is illustrated in the following scatter chart using the absolute value of the bias:



The more complex the function, the lower the bias is. It is usually, but not always related to, a high variance. The most complex function $y=x(1+\sin(x/20))/5$ has by far the highest variance and the lowest bias. The more complex model matches fairly well with the training dataset. As expected, the mean square error reflects the ability of each of the three models to fit the test data.



Mean square error bar chart

The low bias of the complex model reflects in its ability to predict new observations correctly. Its MSE is therefore low, as expected.

Complex models with low bias and high variance are known as **overfitting**. Models with high bias and low variance are characterized as **underfitting**.

Overfitting

The methodology presented in the example can be applied to any classification and regression model. The list of models with low variance includes constant function and models independent of the training set. High degree polynomial, complex functions, and deep neural networks have high variance. Linear regression applied to linear data has a low bias, while linear regression applied to nonlinear data has a higher bias [2:8]

Overfitting affects all aspects of the modeling process negatively, for example:

- It is a sure sign of an overly complex model, which is difficult to debug and consumes computation resources
- It makes the model representing minor fluctuations and noise
- It may discover irrelevant relationships between observed and latent features
- It has poor predictive performance

However, there are well-proven solutions to reduce overfitting [2:9]:

- Increasing the size of the training set whenever possible
- Reducing noise in labeled and input data through filtering
- Decreasing the number of features using techniques such as principal components analysis
- Modeling observable and latent noised using filtering techniques such as Kalman or autoregressive models
- Reducing inductive bias in a training set by applying cross-validation
- Penalizing extreme values for some of the model's features using regularization techniques

Summary

In this chapter, we established the framework for the different data processing units that will be introduced in this book. There is a very good reason why the topics of model validation and overfitting are explored early on in this book. There is no point in building models and selecting algorithms if we do not have a methodology to evaluate their relative merits.

In this chapter, you were introduced to:

- The versatility and cleanness of the Cake pattern in Scala as an effective scaffolding tool for data processing
- The concept of pipe operator for data conversion
- A robust methodology to validate machine learning models
- The challenge in fitting models to both training and real-world data

The next chapter will address the problem of overfitting by penalizing outliers, modeling, and eliminating noise in data.

3

Data Preprocessing

Real-world data is usually noisy and inconsistent with missing observations. No classification, regression, or clustering model can extract relevant information from unprocessed data.

Data preprocessing consists of cleaning, filtering, transforming, and normalizing raw observations using statistics in order to correlate features or groups of features, identify trends and model, and filter out noise. The purpose of cleansing raw data is twofold:

- Extract some basic knowledge from raw datasets
- Evaluate the quality of data and generate clean datasets for unsupervised or supervised learning

You should not underestimate the power of traditional statistical analysis methods to infer and classify information from textual or unstructured data.

In this chapter, you will learn how to:

- Apply commonly used moving average techniques to detect long-term trends in a time series
- Identify market and sector cycles using discrete Fourier series
- Leverage the Kalman filter to extract the state of a dynamic system from incomplete and noisy observations

Time series

The overwhelming majority of examples used to illustrate the different machine algorithms in this book process time series or sequential, ordered, or unordered data.

Each library has its own container type to manipulate datasets. The challenge is to define all possible conversions between types from different libraries needed to implement a large variety of machine learning models. Such a strategy may result in a combinatorial explosion of implicit conversion. A solution consists of creating a generic class to manage conversion from and to any type used by a third-party library.



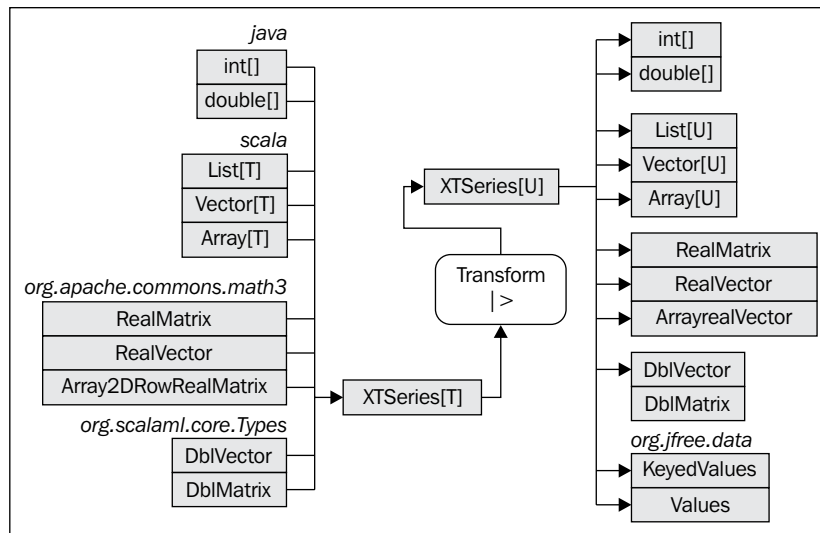
Scala.collection.JavaConversions _

Scala provides a standard package to convert collection types from Scala to Java and vice versa.

The generic data transformation, *DT*, can be used to transform any *XTSeries* time series:

```
class DT[T,U] extends PipeOperator[XTSeries[T], XTSeries[U]] {
  override def |> : PartialFunction[XTSeries[T], XTSeries[U]]
}
```

Let's consider the simple case of using a Java library, the Apache Commons Math framework, and JFreeChart for visualization, and define a parameterized time series class, *XTSeries* [T]. The *|>* data transformation converts a time series of values of type *T*, *XTSeries* [T], into a time series of values of type *U*, *XTSeries* [U]. The following diagram provides an overview of type conversion in data transformation:



Let's create the `XTSeries` class. As a container, the class should be an implementation of the Scala higher-order collections functions such as `map`, `foreach`, or `zip`. The class should support at least conversion to `DblVector` and `DblMatrix` types introduced in the first chapter.

Here is a partial implementation of the `XTSeries` class. Comments, exceptions, argument validations, and debugging code are omitted in the code:

```
class XTSeries[T](label: String, arr: Array[T]) { // 1
  def apply(n: Int): T = arr.apply(n)

  @implicitNotFound("Undefined conversion to DblVector") // 2
  def toDblVector(implicit f: T=>Double):DblVector =arr.map(f(_))

  @implicitNotFound("Undefined conversion to DblMatrix") // 2
  def toDblMatrix(implicit fv: T => DblVector): DblMatrix = arr.map(
    fv( _ ) )

  def + (n: Int, t: T)(implicit f: (T,T) => T): T = f(arr(n), t)

  def head: T = arr.head //3
  def drop(n: Int):XTSeries[T] = XTSeries(label,arr.drop(n))
  def map[U: ClassTag](f: T => U): XTSeries[U] = XTSeries[U](label,
    arr.map( x =>f(x)))
  def foreach( f: T => Unit) = arr.foreach(f) //3
  def sortWith(lt: (T,T)=>Boolean):XTSeries[T] = XTSeries[T](label,
    arr.sortWith(lt))
  def max(implicit cmp: Ordering[T]): T = arr.max //4
  def min(implicit cmp: Ordering[T]): T = arr.min
  ...
}
```

The class takes an optional label and an invariant array of the parameterized type `T`. The annotation `@specialized` (line 1) instructs the compiler to generate two versions of the class:

- A generic `XTSeries[T]` class that exploits all the implicit conversions required to perform operations on time series of a generic type
- An optimized `XTSeries[Double]` class that bypasses the conversion and offers the client code with a faster implementation

The conversion to `DblVector` (resp. `DblMatrix`) relies on the implicit conversion of elements to type `Double` (resp. `DblVector`) (line 2). The `@implicitNotFound` annotation instructs the compiler to omit an error if no implicit conversion is detected. The conversion methods are used to implement the implicit conversion introduced in the previous section. These methods are defined in the singleton `org.scalaml.core.Types.CommonsMath` library. The following code shows the implementation of the conversion methods:

```
object Types {
  object CommonsMath {
    implicit def series2DblVector[T](xt: XTSeries[T])(implicit f:
      T=>Double):DblVector = xt.toDblVector(f)
    implicit def series2DblMatrix[T](xt: XTSeries[T])(implicit f:
      T=>DblVector): DblMatrix = xt.toDblMatrix(f)
    ...
  }
}
```

This code snippet exposes a subset of the Scala higher-order collections methods (line 3) applied to the time series. The computation of the minimum and maximum values in the time series required that the `cmp` ordering/compare method be defined for the elements of the type `T` (line 4).

Let's put our versatile `XTSeries` class to use in creating a basic preprocessing data transformation starting with the ubiquitous moving average techniques.

Moving averages

Moving averages provide data analysts and scientists with a basic predictive model. Despite its simplicity, the moving average method is widely used in the technical analysis of financial markets to define a dynamic level of support and resistance for the price of a given security.



Let's consider a time series $x_t = x(t)$ and a function $f(x_{t-p}, \dots, x_t)$ that reduces the last p observations into a value or average. The prediction or estimation of the observation at $t+1$ is defined by the following formula:


$$\tilde{x}_{t+1} = f(x_{t-p}, \dots, x_t)$$

Here, f is an average reducing function from the previous p data points.

The simple moving average

Simple moving average, a smoothing method, is the simplest form of the moving averages algorithms [3:1]. The simple moving average of period p estimates the value at time t by computing the average value of the previous p observations using the following formula:

The simple moving average of a time series $\{x_t\}$ with a period p is computed as the average of the last p observations:

$$\tilde{x}_t = \frac{1}{p} \sum_{j=t-p}^t x_j$$


The computation is implemented iteratively using the following formula (1):

$$\tilde{x}_t = \tilde{x}_{t-1} + \frac{x_t - x_{t-p}}{p} \quad \forall t \geq p; 0 \forall t \leq p$$

Here, \tilde{x}_t is the estimate or simple moving average value at time t .

Let's build a class hierarchy of moving average algorithms, with the abstract parameterized class `MovingAverage[T <% Double]` as its root. We use the generic time series class, `XTSeries[T]`, introduced in the first section and the generic pipe operator, `|>`, introduced in the previous chapter:

```
abstract class MovingAverage[T <% Double] extends
  PipeOperator[XTSeries[T], XTSeries[Double]]
```

The pipe operator for the `SimpleMovingAverage` class implements the iterative formula (1) for the computation of the simple moving average. The override keyword is omitted:

```
class SimpleMovingAverage[@specialized(Double) T <% Double] (val
  period: Int) (implicit num: Numeric[T]) extends MovingAverage[T] {

  def |> : PartialFunction[XTSeries[T], XTSeries[Double]] {
    case xt: XTSeries[T] if (xt != null && xt.size > 0) => {
      val slider = xt.take(data.size-period)
                        .zip(data.drop(period)) //1
      val a0 = xt.take(period).toArray.sum/period //2
      var a: Double = a0
      val z = Array[Array[Double]] (
```

```

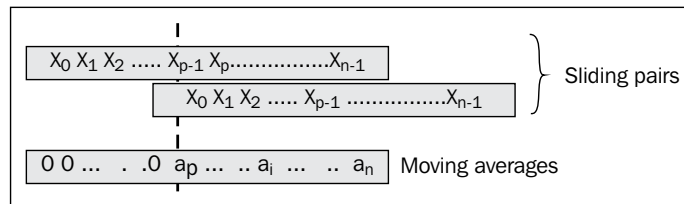
    Array.fill(period)(0.0), a, slider.map(x => {
      a += (x._2 - x._1)/period
      a})
  ).flatten //3
  XTSeries[Double](z)
}

```

The class is parameterized for the type of elements of the input time series. After all, we do not have control over the source of the input data. The type for the elements of the output time series is `Double`.

The class has a type `T` and is specialized for the `Double` type for faster processing. The implicitly defined `num: Numeric[T]` is required by the arithmetic operators `sum` and `/` (line 2).

The implementation has a few interesting elements. First, the set of observations is duplicated and the index in the clone is shifted by p observations before being zipped with the original to the array of a pair of values: `slider` (line 1):



The sliding algorithm to compute moving averages

The average value is initialized with the average of the first p data points. The first p values of the trends are initialized as an array of p zero values. It is concatenated with the first average value and the array containing the remaining average values. Finally, the array of three arrays is flattened (`flatten`) into a single array containing the average values (line 3).

The weighted moving average

The weighted moving average method is an extension of the simple moving average by computing the weighted average of the last p observations [3:2]. The weights a_j are assigned to each of the last p data points x_j and are normalized by the sum of the weights.



The weighted moving average of a series $\{x_t\}$ with a period p and a normalized weights distribution $\{a_j\}$ is given by the following formula (2):

$$\tilde{x}_t = \frac{1}{P} \sum_{j=t-p}^t \alpha_{j-p} x_j; \sum_{j=0}^{p-1} \alpha_j = 1$$

Here, \tilde{x}_t is the estimate or simple moving average value at time t .

The implementation of the `WeightedMovingAverage` class requires the computation of the last p data points. There is no simple iterative formula to compute the weighted moving average at time $t+1$ using the moving average at time t :

```
class WeightedMovingAverage[@specialized(Double) T <% Double] (val
  weights: DblVector) extends MovingAverage[T] {
  def |> : PartialFunction[XTSeries[T], XTSeries[Double]] = {
    case xt: XTSeries[T] if (xt != null && xt.size > 1) => {
      val smoothed = Range(weights.size, xt.size).map(i => {
        xt.toArray.slice(i- weights.size , i)
          .zip(weights)
          .foldLeft(0.0) ((s, x) => s + x._1*x._2) }) //1
      XTSeries[Double] (Array.fill(weights.size) (0.0) ++ smoothed) //2
    }
  }
}
```

As with the simple moving average, the array of the initial p moving average with the value 0 is concatenated (line 2) with the first moving average value and the remaining weighted moving average computed using a map (line 1). The period for the weighted moving average is implicitly defined as `weights.size`.

The exponential moving average

The exponential moving average is widely used in financial analysis and marketing surveys because it favors the latest values. The older the value, the less impact it has on the moving average value at time t [3:3].



The exponential moving average on a series $\{x_t\}$ and a smoothing factor α is computed by the following iterative formula:

$$\tilde{x}_t = (1 - \alpha) \tilde{x}_{t-1} + \alpha x_t \quad \forall t > 0; x_0 \text{ if } t = 0$$

Here, \tilde{x} is the value of the exponential average at t .

The implementation of the `ExpMovingAverage` class is rather simple. There are two constructors, one for a user-defined smoothing factor and one for the Nyquist period, p , used to compute the smoothing factor $\alpha = 2/(p+1)$:

```
class ExpMovingAverage[@specialized(Double) T <% Double](val alpha:
Double) extends MovingAverage[T] {
  def |> : PartialFunction[XTSeries[T], XTSeries[Double]] = {
    case xt: XTSeries[T] if(xt != null && xt.size > 1) => {
      val alpha_1 = 1-alpha
      var y: Double = data(0)
      xt.map( x => {
        val z = x*alpha + y*alpha_1; y=z; z })
      }
    }
  }
}
```

The version of the constructor that uses the Nyquist period p is implemented using the Scala `apply` method:

```
def apply[T <% Double](nyquist: Int): ExpMovingAverage[T] = new
ExpMovingAverage[T](2/( nyquist + 1))
```

Let's compare the results generated from these three moving averages methods with the original price. We use a data source (with respect to sink), `DataSource` (with respect to `DataSink`) to load the historical daily closing stock price of **Bank of America (BAC)**. The `DataSource` and `DataSink` classes are defined in the *Data extraction* section in *Appendix A, Basic Concepts*. The comparison of results can be done using the following code:

```
val p_2 = p >>1
val w = Array.tabulate(p)(n =>if(n==p_2) 1.0 else 1.0/(Math.
abs(n-p_2)+1)) //1
val weights = w map { _ / w.sum } //2

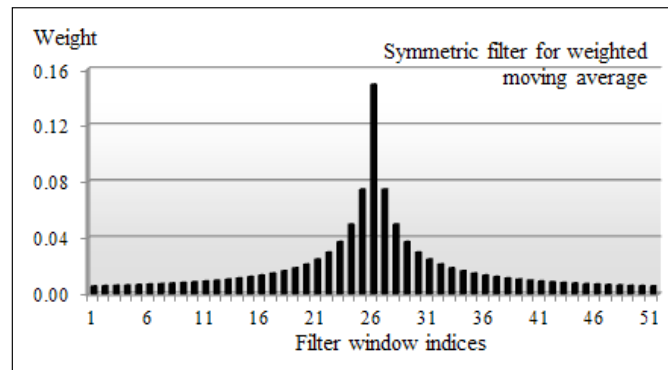
val src = DataSource("resources/data/chap3/BAC.csv, false)//3

val price = src |> YahooFinancials.adjClose //4
val sMvAve = SimpleMovingAverage(p)
val wMvAve = WeightedMovingAverage(weights)
val eMvAve = ExpMovingAverage(p)

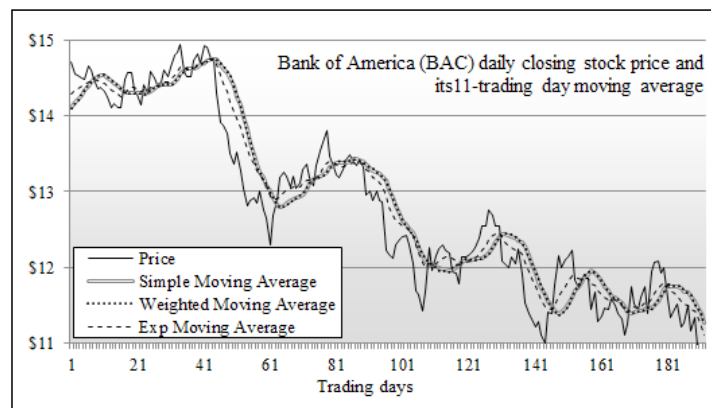
val results = price :: sMvAve.|>(price) :: wMvAve.|>(price) ::
eMvAve.|>(price) :: List[XTSeries[Double]]() //5
Val outFile = "output/chap3/mvaverage" + p.toString + ".csv"
DataSink[Double]( outFile) |> results //6
```

The coefficients for the weighted moving average are generated (line 1) and normalized (line 2). The trading data regarding the ticker symbol, BAC, is extracted from the Yahoo! finances CSV file (line 3), `YahooFinancials`, using the `adjClose` extractor (line 4). The smoothed data generated by each of the moving average techniques are concatenated into a list of time series (line 5). Finally, the content is formatted and dumped into a file, `outFile`, using a `DataSink` instance (line 6).

The weighted moving average method relies on a symmetric distribution of normalized weights computed by a function passed as an argument of the generic `tabulate` method. Note that the original price time series is generated if a specific moving average cannot be computed. The following graph is an example of a symmetric filter for weighted moving averages:

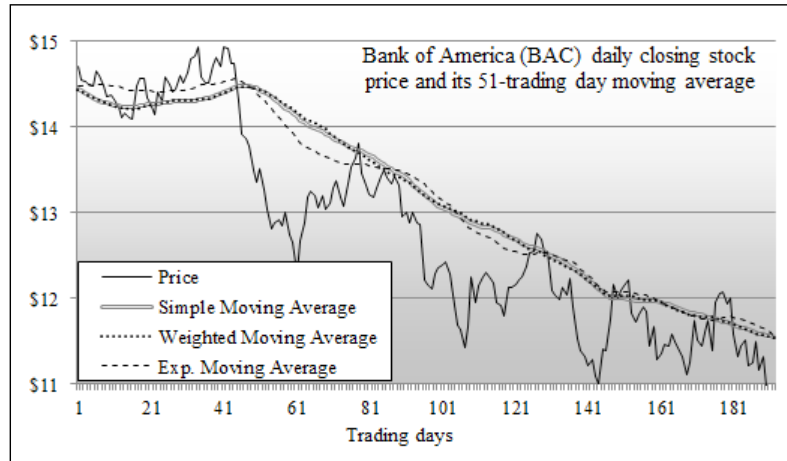


The three moving average techniques are applied to the price of the stock of Bank of America (BAC) over 200 trading days. Both the simple and weighted moving average uses a period of 11 trading days. The exponential moving average method uses a scaling factor of $2/(11+1) = 0.1667$.



11-day moving averages of the historical stock price of Bank of America

The three techniques filter the noise out of the original historical price time series. The exponential moving average reacts to a sudden price fluctuation despite the fact that the smoothing factor is low. If you increase the period to 51 trading days or two calendar months, the simple and weighted moving averages generate a smoothed time series compared to the exponential moving average with a smoothing factor of $2/(p+1) = 0.038$.



51-day moving averages of the historical stock price of Bank of America

You are invited to experiment further with different smooth factors and weight distributions. You will be able to confirm the following basic rule: as the period of the moving average increases, noise with decreasing frequencies is eliminated. In other words, the window of allowed frequencies is shrinking. The moving average acts as a low-band filter that allows only lower frequencies. Fine-tuning the period or smoothing factor is time consuming. Spectral analysis, or more specifically, Fourier analysis, transforms the time series into a sequence of frequencies, which is a time series in the frequency domain.

Fourier analysis

The purpose of **spectral density estimation** is to measure the amplitude of a signal or a time series according to its frequency [3:4]. The spectral density is estimated by detecting periodicities in the dataset. A scientist can better understand a signal or time series by analyzing its harmonics.



The spectral theory

Spectral analysis for time series should not be confused with spectral theory, a subset of linear algebra that studies Eigenfunctions on Hilbert and Banach spaces. Harmonic and Fourier analyses are regarded as a subset of spectral theory.

The **fast Fourier transform (FFT)** is the most commonly used frequency analysis algorithm [3:5]. Let's explore the concept behind the discrete Fourier series and the Fourier transform as well as their benefits as applied to financial markets. The Fourier analysis approximates any generic function as the sum of trigonometric functions, sine and cosine. The decomposition in a basic trigonometric function is known as a **Fourier transform** [3:6].

Discrete Fourier transform (DFT)

A time series $\{x_k\}$ can be represented as a discrete real-time domain function $f, x=f(t)$. In the 18th century, Jean Baptiste Joseph Fourier demonstrated that any continuous periodic function f could be represented as a linear combination of sine and cosine functions. The **discrete Fourier transform (DFT)** is a linear transformation that converts a time series into a list of coefficients of a finite combination of complex or real trigonometric functions, ordered by their frequencies.

The frequency ω of each trigonometric function defines one of the harmonics of the signal. The space that represents signal amplitude versus frequency of the signal is known as the **frequency domain**. The generic DFT transforms a time series into a sequence of frequencies defined as complex numbers $\omega = a + j.\varphi$ ($j_2 = -1$), for which a is the amplitude of the frequency and φ is the phase.

This section is dedicated to the real DFT that converts a time series into an ordered sequence of frequencies with real values.

Real discrete Fourier transform

A periodic function f can be represented as an infinite combination of sine and cosine functions:

$$f(t) = \frac{a_0}{2} + \sum_1^{\infty} a_k \cos(nx) = \sum_1^{\infty} b_k \sin(nx)$$

The Fourier cosine transform of a function f is defined as:

$$F^c(f, k) = \int_{-\infty}^{\infty} \cos(2\pi kx) f(x) dx$$



The discrete real cosine series of a function $f(-x) = f(x)$ is defined as:

$$f(x) = f(-x) = \frac{a_0}{2} + \sum_{k=1}^{2N-3} a_k \cos(kx) \text{ where } a_k = \frac{2}{\pi} \int_0^{\pi} f(t) \cos(kt) .dt$$

The Fourier sine transform of a function is defined as:

$$F^s(f, k) = \int_{-\infty}^{\infty} \sin(2\pi kx) f(x) dx$$

The discrete real sine series of a function $f(-x) = f(x)$ is defined as:

$$f(x) = f(-x) = \sum_{k=1}^{2N-3} b_k \sin(kx) \text{ where } b_k = \frac{2}{\pi} \int_0^{\pi} f(t) \sin(kt) .dt$$

The computation of the Fourier trigonometric series is time consuming with an asymptotic time complexity of $O(n^2)$. Several attempts have been made to make the computation as effective as possible. The most common numerical algorithm used to compute the Fourier series is the fast Fourier transform created by J. W. Cooley and J. Tukey [3:7]. The algorithm, called Radix-2, recursively breaks down the Fourier transform for a time series of N data points into any combination of $N1$ and $N2$ sized segments such as $N = N1 N2$. Ultimately, the discrete Fourier transform is applied to the deepest-nested segments.



The Cooley-Tukey algorithm

I encourage you to implement the Radix-2 Cooley-Tukey algorithm in Scala using a tail recursion.

The Radix-2 implementation requires that the number of data points is $N=2n$ for even functions (sine) and $N = 2n+1$ for cosine. There are two approaches to meet this constraint:

- Reduce the actual number of points to the next lower radix, $2n < N$
- Extend the original time series by padding it with 0 to the next higher radix, $N < 2n+1$

Padding the original time series is the preferred option because it does not affect the original set of observations.

Let's define a base class, `DTransform[T]`, for all the fast Fourier transforms, parameterized with a view bounded to the `Double` type (`Double`, `Float`, and so on). The first step is to implement the padding method, common to all the Fourier transforms:

```
trait DTransform[T] extends PipeOperator[XTSeries[T],
  XTSeries[Double]] {
  def padSize(xtSz: Int, even: Boolean=true): Int = {
    val sz = if( even ) xtSz else xtSz-1
    if( (sz & (sz-1)) == 0) 0
    else {
      var bitPos = 0
      do {
        bitPos += 1
      } while( (sz >> bitPos) > 0)
      (if(even) (1<<bitPos) else (1<<bitPos)+1) - xtSz
    }
  }

  def pad(xt: XTSeries[T], even: Boolean=true)
    (implicit f: T => Double): DblVector = {
    val newSize = padSize(xt.size, even)
    val arr: DblVector = xt
    if( newSize > 0) arr ++ Array.fill(newSize)(0.0) else arr
  }
}
```

The while loop



Scala developers prefer Scala higher-order methods on collection to implement iterative computation. However, nothing prevents you from using a traditional while loop if either readability or performance is an issue.

The fast implementation of the padding method, `pad`, consists of detecting the number of observations, N , which is a power of 2 using the bit operator `&` by evaluating whether $N \& (N-1)$ is null. The next highest radix is extracted by computing the number of bits shift in N . The code illustrates the effective use of implicit conversion to make the code readable. The `arr: DblVector = series` conversion triggers a conversion defined in the `XTSeries` companion object.

The next step is to write the `DFT` class for the real discrete transforms, sine and cosine, by subclassing `DTransform`. The purpose of the class is to select the appropriate Fourier series, pad the time series to the next power of 2 if necessary, and invoke the `FastSineTransformer` and `FastCosineTransformer` classes of the Apache Commons Math library [3:8] introduced in the first chapter:

```
class DFT[@specialized(Double) T<%Double] extends DTransform[T] {
  def |> : PartialFunction[XTSeries[T], XTSeries[Double]] = {
    case xt: XTSeries[T] if (xt != null && xt.length > 0) =>
      XTSeries[Double](fwrд(xt)._2)
  }
  def fwrд(xt:XTSeries[T]): (RealTransformer, DblVector) = {
    val rdt = if(Math.abs(xt.head) < DFT_EPS)
      new FastSineTransformer(DstNormalization.STANDARD_DST_I)
    else new FastCosineTransformer(DctNormalization.STANDARD_DCT_I)

    (rdt, rdt.transform( pad(xt,xt.head==0.0),TransformType.FORWARD))
  }
}
```

The discrete Fourier sine series requires that the first value of the time series is 0.0. This implementation automates the selection of the appropriate series by evaluating `series.head`. This example uses the standard formulation of the cosine and sine transformation, defined by the `DctNormalization.STANDARD_DCT_I` argument. The orthogonal normalization, which normalizes the frequency by a factor of $1/\sqrt{2(N-1)}$, where N is the size of the time series, generates a cleaner frequency spectrum for a higher computation cost.



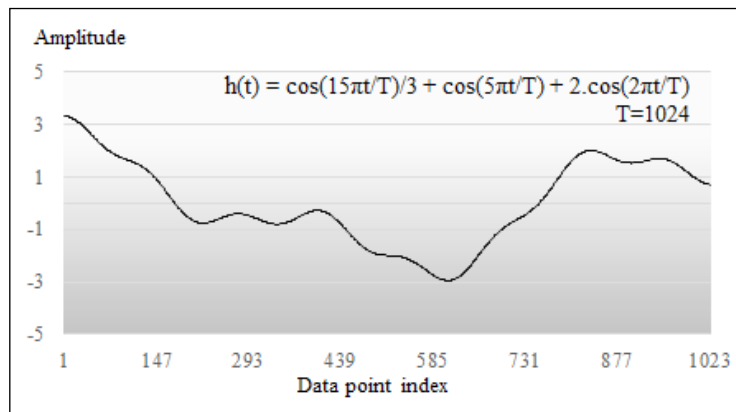
@specialized

The `@specialized(Double)` annotation is used to instruct the Scala compiler to generate a specialized and more efficient version of the class for the type `Double`. The drawback of specialization is the duplication of byte code as the specialized version coexists with the parameterized classes [3:9].

In order to illustrate the different concepts behind DFTs, let's consider the case of a time series generated by a sequence h of sinusoidal functions:

```
val _T= 1.0/1024
val h = (x:Double) =>2.0*Math.cos(2.0*Math.PI*_T*x) +
  Math.cos(5.0*Math.PI*_T*x) + Math.cos(15.0*Math.PI*_T*x)/3
```

As the signal is synthetically created, we can select the size of the time series to avoid padding. The first value in the time series is not null, so the number of observations is $2n+1$. The data generated by the function h is plotted as follows:



Example of the sinusoidal time series


Let's extract the frequencies spectrum for the time series generated by the function h . The data points are created by tabulating the function h . The frequencies spectrum is computed with a simple invocation of the pipe operator on the instance of the DFT class:

```
val rawOut = "output/chap3/raw.csv"
val smoothedOut = "output/chap3/smoothed.csv"
val values = Array.tabulate(1025)(x =>h(x/1025))
DataSink[Double](rawOut) |> values //1

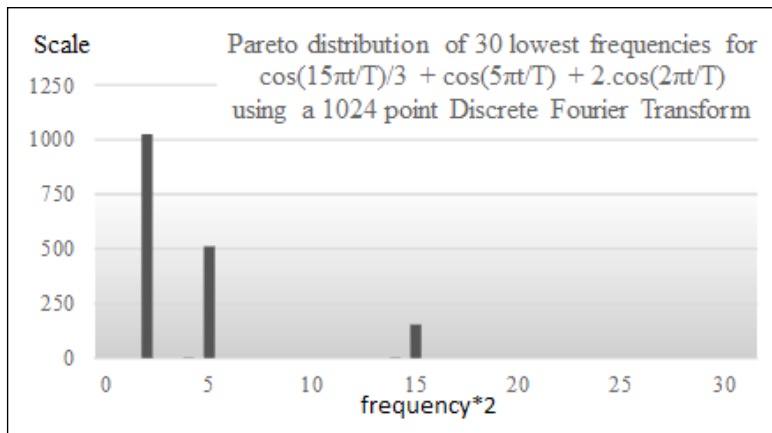
val smoothed = DFT[Double] |> XTSeries[Double](values) //2
DataSink[Double]("output/chap3/smoothed.csv") |> smoothed
```


The first data sink (the type `DataSink`) stores the original time series into a CSV file (line 1). The `DFT` instance extracts the frequencies spectrum and formats it as time series (line 2). Finally, a second sink saves it into another CSV file.

Data sinks and spreadsheets

 In this particular case, the results of the discrete Fourier transform are dumped into a CSV file so that it can be loaded into a spreadsheet. Some spreadsheets support a set of filtering techniques that can be used to validate the result of the example. A simpler alternative would be to use `JFreeChart`.

The spectrum of the time series, plotted for the first 32 points, clearly shows three frequencies at $k=2, 5, \text{ and } 15$. This is expected because the original signal is composed of three sinusoidal functions. The amplitude of these frequencies are $1024/1, 1024/2,$ and $1024/6,$ respectively. The following plot represents the first 32 harmonics for the time series:



Frequency spectrum for a three-frequency sinusoidal

The next step is to use the frequencies spectrum to create a low-pass filter using DFT. There are many algorithms to implement a low or pass band filter in the time domain from autoregressive models to the Butterworth algorithm. However, the fast Fourier transform is still a very popular technique to smooth signals and extract trends.



Big Data

A DFT for a large time series can be very computation intensive. One option is to treat the time series as a continuous signal and sample it using the Nyquist frequency. The Nyquist frequency is half of the sampling rate of a continuous signal.

DFT-based filtering

The purpose of this section is to introduce, describe, and implement a noise filtering mechanism that leverages the discrete Fourier transform. The idea is quite simple: the forward and inverse Fourier transforms are used sequentially to convert the time series from the time domain to the frequency domain and back. The only input you need to supply is a function G that modifies the sequence of frequencies. This operation is known as the convolution of the filter G and the frequencies spectrum. A convolution is similar to an inner product of two time series in the frequencies domain. Mathematically, the convolution is defined as follows:

Convolution

The convolution of two functions f and g is defined as:

$$\langle f, g \rangle = \int_{-\infty}^{\infty} f(t) \cdot g(x-t) dt$$

DFT convolution

One important property of the Fourier transform is that convolution of two signals is implemented as the inner product of their relative spectrums:

$$F(f * g) = F(f)F(g)$$

Let's apply the property to the discrete Fourier transform. If a time series $\{x^i\}$ has a frequency spectrum $\{\omega_f\}$ and a filter f in a frequency domain defined as $\{\omega_g\}$, then the convolution is defined as:

$$F(f * g) = \sum_0^{N-1} \omega_{x,j} \omega_{f,k-j}$$

Let's apply the convolution to our filtering problem. The filtering algorithm using the discrete Fourier transform consists of five steps:

1. Pad the time series to enable the discrete sine or cosine transform.
2. Generate the ordered sequence of frequencies using the forward transform.
3. Select the filter function g in the frequency domain and a cutoff frequency.
4. Convolute the sequence of frequency with the filter function g .
5. Generate the filtered signal in the time domain by applying the inverse DFT transform to the convoluted frequencies.

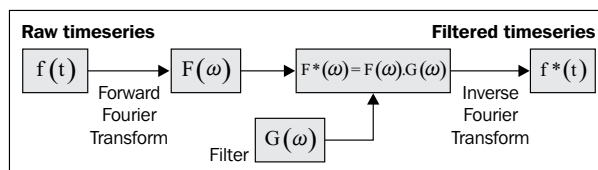


Diagram of a discrete Fourier filter

The most commonly used low-pass filters are known as the `sinc` and `sinc2` functions, defined as a rectangular function and a triangular function, respectively. The simplest low-pass filter is implemented by a `sinc` function that returns 1 for frequencies below a cutoff frequency, f_c , and 0 if the frequency is higher:

```

def sinc(f: Double, fc: Double): Double = if(Math.abs(f) < fc) 1.0
  else 0.0
def sinc2(f: Double, fc: Double): Double = if(f*f < fc) 1.0 else 0.0
  
```

The filtering computation is implemented as a data transformation (pipe operator `|>`). The `DFTFIR` class inherits from the `DFT` class in order to reuse the `fwrdd` forward transform function. As usual, exception and validation code is omitted. The frequency domain function `g` is an attribute of the filter. The `g` function takes the frequency cutoff value `fc` as the second argument. The two filters `sinc` and `sinc2` defined in the previous section are examples of filtering functions.

```

class DFTFIR[T <% Double](val g: (Double, Double) =>Double, val fc:
  Double) extends DFT[T]
  
```

The pipe operator implements the filtering functionality:

```

def |> : PartialFunction[XTSeries[T], XTSeries[Double]] = {
  case xt: XTSeries[T] if(xt != null && xt.size > 2) => {
    val spectrum = fwrdd(xt) //1
    val cutOff = fc*spectrum._2.size
  }
}
  
```

```

    val filtered = spectrum._2.zipWithIndex.map(x => x._1*g(x._2,
        cutOff)) //2
    XTSeries[Double](spectrum._1.transform(filtered, TransformType.
        INVERSE)) //3
}

```

The filtering process follows three steps:

1. Computation of the discrete Fourier forward transformation (sine or cosine), `fwrд`.
2. Apply the filter function through a Scala `map` method.
3. Apply the inverse transform on the frequencies.

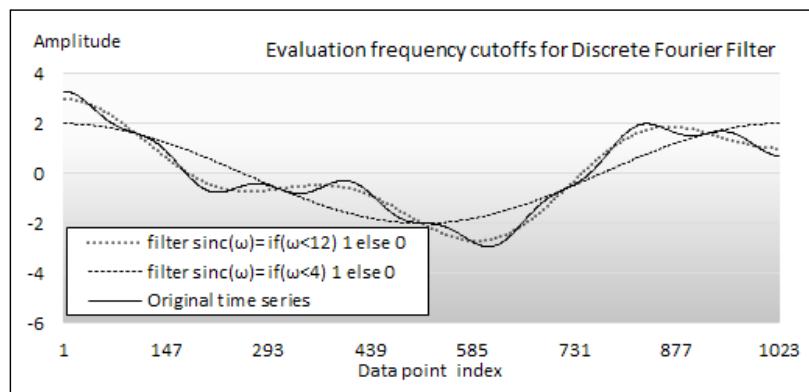
Let's evaluate the impact of the cutoff values on the filtered data. The implementation of the test program consists of invoking the DFT filter pipe operator and writing results into a CSV file. The code reuses the generation function `h` introduced in the previous paragraph:

```

val price = src |> YahooFinancials.adjClose
val filter = new DFTFir[Double](sinc, 4.0)
val filteredPrice = filter |> price

```

Filtering out the noise is accomplished by selecting the cutoff value between any of the three harmonics with the respective frequencies of 2, 5, and 15. The original and the two filtered time series are plotted on the following graph:



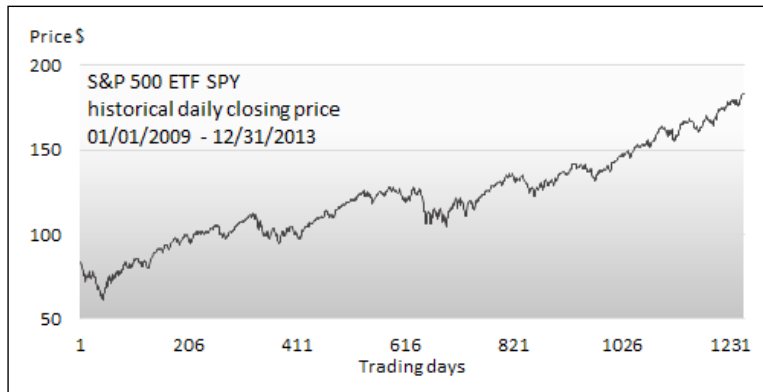
Plotting of the discrete Fourier filter-based smoothing

As you would expect, the low-pass filter with a cutoff value of 12 removes the noise with the highest frequencies. The filter (with the cutoff value 4) cancels out the second harmonic (low-frequency noise), leaving out only the main trend cycle.

Detection of market cycles

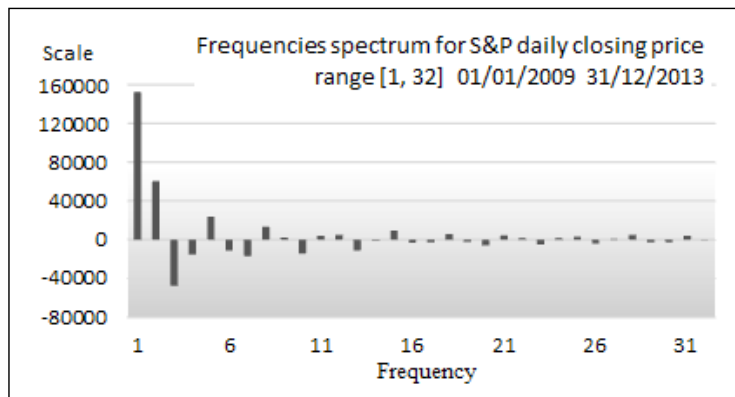
Using the discrete Fourier transform to generate the frequencies spectrum of a periodical time series is easy. However, what about real-world signals such as the time series representing the historical price of a stock?

The purpose of the next exercise is to detect, if any, the long term cycle(s) of the overall stock market by applying the discrete Fourier transform to the quote of the S&P 500 index between January 1, 2009, and December 31, 2013, as illustrated in the following graph:



Historical S&P 500 index prices

The first step is to apply the DFT to extract a spectrum for the S&P 500 historical prices, as shown in the following graph, with the first 32 harmonics:



Frequencies spectrum for historical S&P index

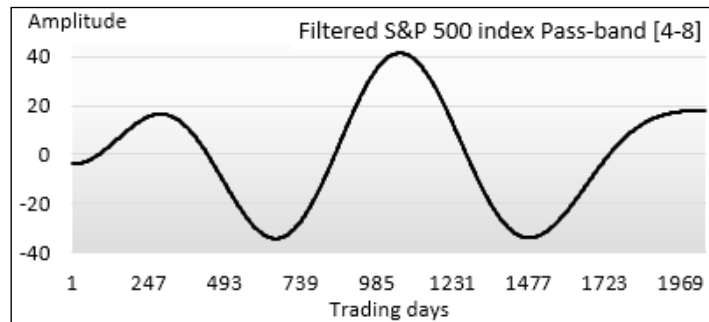
The frequency domain chart highlights some interesting characteristics regarding the S&P 500 historical prices:

- Both positive and negative amplitudes are present, as you would expect in a time series with complex values. The cosine series contributes to the positive amplitudes while the sine series affects both positive and negative amplitudes, ($\cos(x+\pi) = \sin(x)$).
- The decay of the amplitude along the frequencies is steep enough to warrant further analysis beyond the first harmonic, which represents the main trend. The next step is to apply a pass-band filter technique to the S&P 500 historical data in order to identify short-term trends with lower periodicity.

A low-pass filter is limited to reduce or cancel out the noise in the raw data. In this case, a passband filter using a range or window of frequencies is appropriate to isolate the frequency or the group of frequencies that characterize a specific cycle. The `sinc` function introduced in the previous section to implement a low-band filter is modified to enforce the passband within a window, $[w1, w2]$, as follows:

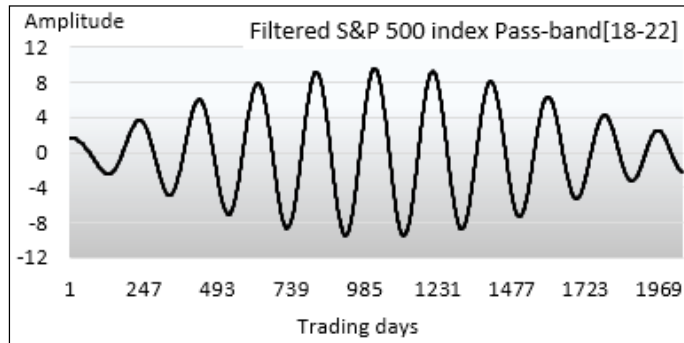
```
def sinc(f: Double, w: (Double, Double)): Double = if (Math.abs(f) >
  w._1 && Math.abs(f) < w._2) 1.0 else 0.0
```

Let's define a DFT-based pass-band filter with a window of width 4, $w=(i, i+4)$, with i ranging between 2 and 20. Applying the window $[4, 8]$ isolates the impact of the second harmonic on the price curve. As we eliminate the main upward trend with frequencies less than 4, all filtered data varies within a short range relative to the main trend. The following graph shows output of this filter:



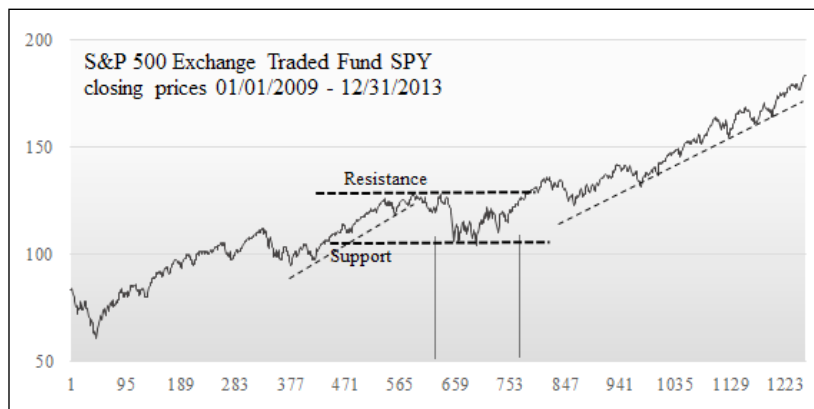
The output of a pass-band DFT filter range 4-8 on the historical S&P index

In this case, we filter the S&P 500 index around the third group of harmonics with frequencies ranging from 18 to 22; the signal is converted into a familiar sinusoidal function, as shown here:



The output of a pass-band DFT filter range 18-22 on the historical S&P index

There is a possible rational explanation for the shape of the S&P 500 data filtered by a passband with a frequency of 20, as illustrated in the previous plot; the S&P 500 historical data plot shows that the frequency of the fluctuation in the middle of the uptrend (trading sessions 620 to 770) increases significantly. This phenomenon can be explained by the fact that the S&P 500 index reaches a resistance level around the trading session 545 when the existing uptrend breaks. A tug-of-war starts between the bulls, betting the market nudges higher, and the bears, who are expecting a correction. The back and forth between the traders ends when the S&P 500 index breaks through its resistance and resumes a strong uptrend characterized by a high amplitude and low frequency, as shown in the following graph:



One of the limitations of using the Fourier transform to clean up data is that it requires the data scientist to extract the frequencies spectrum and modify the filter on a regular basis, as he or she is never sure that the most recent batch of data does not introduce noise with a different frequency. The Kalman filter addresses this limitation.

The Kalman filter

The Kalman filter is a mathematical model that provides an accurate and recursive computation approach to estimate the previous states and predict the future states of a process for which some variables may be unknown. R. E. Kalman introduced it in the early 60s to model dynamics systems and predict trajectory in aerospace [3:10]. Today, the Kalman filter is used to discover a relationship between two observed variables that may or may not be associated with other hidden variables. In this respect, the Kalman filter shares some similarities with the **Hidden Markov models (HMM)** described in *Chapter 6, Regression and Regularization* [3:11].

The Kalman filter is used as:

- A predictor of the next data point from the current observation
- A filter that weeds out noise by processing the last two observations
- A smoother that computes trends from a history of observations



Smoothing versus filtering

Smoothing is an operation that removes high-frequency fluctuations from a time series or signal. Filtering consists of selecting a range of frequencies to process the data. In this regard, smoothing is somewhat similar to low-pass filtering. The only difference is that a low-pass filter is usually implemented through linear methods.

Conceptually, the Kalman filter estimates the state of a system from noisy observations. The Kalman filter has two characteristics:

- **Recursive:** A new state is predicted and corrected using the input of a previous state
- **Optimal:** This is an optimal estimator because it minimizes the mean square error of the estimated parameters (against actual values)

The Kalman filter is one of the stochastic models that are used in adaptive control [3:12].



Kalman and nonlinear systems

The Kalman filter estimates the internal state of a linear dynamic system. However, it can be extended to a model nonlinear-state space using linear or quadratic approximation functions. These filters are known as, you guessed it, **extended Kalman filters (EKF)**, the theory of which is beyond the scope of this book.

The following section is dedicated to discrete Kalman filters for linear systems, as applied to financial engineering. A continuous signal can be converted to a time series using the Nyquist frequency.

The state space estimation

The Kalman filter model consists of two core elements of a dynamic system—a process that generates data and a measurement that collects data. These elements are referred to as the state space model. Mathematically speaking, the state space model consists of two equations:

- **Transition equation:** This describes the dynamics of the system including the unobserved variables
- **Measurement equation:** This describes the relationship between the observed and unobserved variables

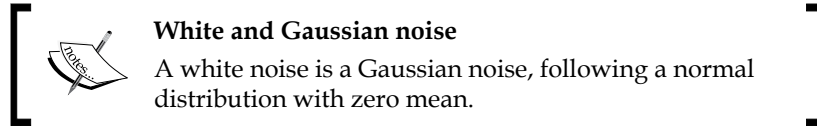
The transition equation

Let's consider a system with a linear state x_t of n variables and a control input vector u_t . The prediction of the state at time t is computed by a linear stochastic equation:

$$x_t = A_t \cdot x_{t-1} + B_t \cdot u_t + w_t$$

- A is the square matrix of dimension n that represents the transition from state x at $t-1$ to state x at t . The matrix is intrinsic to the dynamic system under consideration.
- B is an n by n matrix that describes the control input model (external action on the system or model). It is applied to the control vector u .
- w represents the noise generated by the system or from a probabilistic point of view, the uncertainty on the model. It is known as the process white noise.

The control input vector represents the external input (or control) to the state of the system. Most systems, including our financial example later in this chapter, have no external input to the state of the model.



The measurement equation

The measurement of m values z_t of the state of the system is defined by the following equation:

$$z_t = H_t \cdot x_t + v_t$$

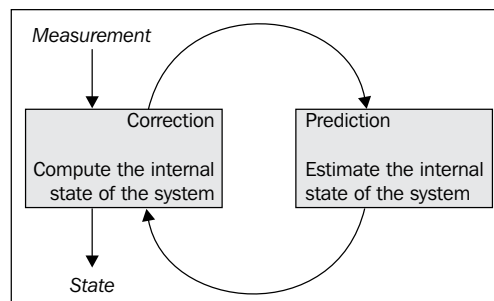
- H is a matrix m by n that models the dependency of the measurement to the state of the system.
- v is the white noise introduced by the measuring devices. Similar to the process noise, v follows a Gaussian distribution with zero mean and a variance R , known as the measurement noise covariance.

The recursive algorithm

The set of equations for the discrete Kalman filter are implemented as recursive computation with two distinct steps:

- The algorithm uses the transition equations to estimate the next observation
- The estimation is created with the actual measurement for this observation

The recursion is visualized in the following diagram:




An overview diagram of the recursive Kalman algorithm

Let's illustrate the prediction and correction phases in the context of filtering financial data, in a manner similar to the moving average and Fourier transform. The objective is to extract the trend and the transitory component of the yield of the 10-year Treasury bond. The Kalman filter is particularly suitable for the analysis of interest rates for two reasons:

- Yields are the results of multiple factors, some of which are not directly observable
- Yields are influenced by the policy of the Federal Reserve that can be easily modeled by the control matrix

The 10-year Treasury bond has a higher trading volume than bonds with longer maturity, making trends in interest rates a bit more reliable [3:13].

Applying the Kalman filter to clean raw data requires you to define a model that encompasses both observed and non-observed states. In the case of the trend analysis, we can safely create our model with a two-variable state: the current yield x_t and the previous yield x_{t-1} .

	<p>State in dynamic systems</p> <p>The term "state" refers to the state of the dynamic system under consideration. This is a different term for observation, data, or value vector. A state or observation is a set of values, one for each variable of the model.</p>	
--	---	--

This implementation of the Kalman filter uses the Apache Commons Math library, which defines and manipulates specific types. The first step is to define the implicit type conversion required to interface with the `KalmanFilter` class:

```
type DblMatrix = Array[Array[Double]]
type DblVector = Array[Double]
implicit def double2RealMatrix(x: DblMatrix): RealMatrix = new
Array2DRowRealMatrix(x)
implicit def double2RealRow(x: DblVector): RealMatrix = new
Array2DRowRealMatrix(x)
implicit def double2RealVector(x: DblVector): RealVector = new
ArrayRealVector(x)
```

The implicit type conversion has to be defined in the scope of the client code.

The Kalman model assumes that process and measurement noise follow a Gaussian distribution, also known as white noise. For the sake of maintainability, the generation or simulation of the white noise is encapsulated in the `QRNoise` class with `qr` as the tuple of scale factors for the process noise matrix `Q` and the measurement noise `R`. The two create methods execute the user-defined noise function `white`:

```
class QRNoise(qr: XY, white: Double=> Double) {
  def q = white(qr._1)
  def r = white(qr._2)
  def noisyQ = Array[Double](q,q)
  def noisyR = Array[Double](r,r)
}
```

The easiest approach to manage the matrices and vectors used in the recursion is to define them as parameters of the main class, `DKalman`:

```
class DKalman(A:DblMatrix, B:DblMatrix, H:DblMatrix, P:DblMatrix)
  (implicit val qrNoise: QRNoise) extends PipeOperator[XY,XY] {

  val Q = new DblMatrix(A.size).map(_ => Array.fill(A.size)(qrNoise.qr.1))

  var x: RealVector = _
  var filter: KalmanFilter = _
}
```

The matrix used in the prediction and correction phase is defined as an argument of the `DKalman` class. The matrices for the covariance of the process noise `Q` and the measurement noise `R` are also initialized during the instantiation of the Kalman filter class. The key elements of the filter are now in place and it's time to implement the prediction-correction cycle portion of the Kalman algorithm.

Prediction

The prediction phase consists of estimating the x state (yield of the bond) using the transition equation. We assume that the Federal Reserve has no material effect on the interest rates, making control input matrix B null. The transition equation can be easily resolved using simple operations on matrices.

$$\begin{bmatrix} \hat{x}_t \\ \hat{x}_{t-1} \end{bmatrix} = \begin{bmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{bmatrix} \cdot \begin{bmatrix} \hat{x}_t \\ \hat{x}_{t-1} \end{bmatrix} + \begin{bmatrix} 0 & 0 \\ 0 & 0 \end{bmatrix} \cdot \begin{bmatrix} u_t \\ u_{t-1} \end{bmatrix} + \begin{bmatrix} w_t \\ w_{t-1} \end{bmatrix}$$

Visualization of the transition equation of the Kalman filter

The purpose of this exercise is to evaluate the impact of the different parameters of the transition matrix A in terms of smoothing.



The control input matrix B

In this example, the control matrix B is null because there is no known deterministic external action on the yield of the 10-year Treasury bond. However, the yield can be affected by unknown parameters that we represent as hidden variables. The matrix B would be used to model the decision of the Federal Reserve regarding asset purchases and federal fund rates.

The mathematics behind the Kalman filter presented as reference to its implementation in Scala use the same notation for matrices and vectors. It is absolutely not a prerequisite to understand the Kalman filter and its implementation in the next section. If you have a natural inclination toward linear algebra, the following note describes the two equations for the prediction step.



The prediction step

The prediction of the state at time $t+1$ is computed by extrapolating the state estimate:

$$\hat{x}_t' = A_t \cdot \hat{x}_{t-1} + B_t \cdot u_t$$

- A is the square matrix of dimension n that represents the transition from state x at $t-1$ to state x at time t .
- \hat{x}_t' is the predicted state of the system based on the current state and the model A
- B is the vector of n dimension that describes the input to the state

The mean square error matrix P , which is to be minimized, is updated through the following formula:

$$P_t' = A_t \cdot P_{t-1} \cdot A_t^T + Q_t$$

- AT is the transpose of the state transition matrix.
- Q is the process white noise described as a Gaussian distribution with a zero mean and a variance Q , known as the noise covariance.

The state transition matrix is implemented using the matrix and vector classes included in the Apache Commons Math library. The types of matrices and vectors are automatically converted into `RealMatrix` and `RealVector` classes. The implementation of the equation is as follows:

```
x = A.operate(x).add(qrNoise.noisyQ)
```

The new state is predicted (or estimated), and then used as an input to the correction step.

Correction

The second and last step of the recursive Kalman algorithm is the correction of the estimated yield of the 10-year Treasury bond with the actual yield. In this example, the white noise of the measurement is negligible. The measurement equation is simple because the state is represented by the current and previous yield, and their measurement z :

$$\begin{bmatrix} z_t \\ z_{t-1} \end{bmatrix} = \begin{bmatrix} h_{11} & h_{12} \\ h_{21} & h_{22} \end{bmatrix} \cdot \begin{bmatrix} \hat{x}_t \\ \hat{x}_{t-1} \end{bmatrix} + \begin{bmatrix} v_t \\ v_{t-1} \end{bmatrix}$$

Visualization of the measurement equation of the Kalman filter

The sequence of mathematical equations of the correction phase consists of updating the estimation of the state x using the actual values z , computing the Kalman gain K , and estimating the matrix of the error covariance P .

Correction step

The state of the system x is estimated from the actual measurement z through the following formula:

$$\hat{x}_t = \hat{x}'_t + K_t (z_t - H_t \cdot \hat{x}'_t) \quad r_t = z_t - H_t \cdot \hat{x}'_t$$

- r is the residual between the predicted measurement and the actual measured values
- K is the Kalman gain for the correction factor Kr



The Kalman gain is computed using the estimated error covariance matrix P'_t :

$$K_t = P'_t \cdot H_t^T (H_t \cdot P'_t \cdot H_t^T + R_t)^{-1}$$

- HT is the matrix transpose of H

Finally, the estimate of the error covariance matrix P'_t is corrected to the value P_t through the following formula:

$$P_t = (I_d - K_t \cdot H_t) \cdot P'_t$$

- I_d is the identity matrix.

Kalman smoothing

It is time to put our knowledge of the transition and measurement equations to the test. The Apache Commons Library defines two classes, `DefaultProcessModel` and `DefaultMeasurementModel`, to encapsulate the components of the matrices and vectors. The historical values for the yield of the 10-year Treasury bond is loaded through the `DataSource` method and mapped to the smoothed series that is the output of the filter.

```
def |> : PartialFunction[XTSeries[XY], XTSeries[XY]] = {
  case xt: XTSeries[XY] if (xt.size > 0) => xt.map( y => {
    initialize(Array[Double](y._1, y._2)) //1
    val nState = newState //2
    (nState(0), nState(1)) }) //3
  ...
}
```

The data transformation for the Kalman filter initializes the process and measurement model for each data point (line 1), updates the state using the transition and correction equations iteratively (line 2), and returns the filtered series (line 3).

Exception handling



The code to catch and process exceptions thrown by the Apache Commons Math library is omitted as the standard practice in the book. As far as the execution of the Kalman filter is concerned, the following exceptions have to be handled:

- `NonSquareMatrixException`
- `DimensionMismatchException`
- `MatrixDimensionMismatchException`

The model is a **2-step lag smoothing** algorithm using a single smoothing factor a with a state, S_t :

$$S_t = \{x_{t+1}, x_t\} \text{ with } x_{t+1} = \alpha \cdot x_t + (1 - \alpha) \cdot x_{t-1} \text{ and } x_t = x_t$$

Following the Scala standard to return errors to the client code, the exceptions thrown by the Commons Math API are caught and processed through the `Option` monad. The iterative prediction and correction of the smoothed yields is implemented by the `newState` method. The method iterates through four steps:

1. Filter an estimate of the state x at time t .
2. The new state is computed using the transition equation.
3. The measured value z of the state is computed using the measurement equation.
4. The original estimate x is corrected with the measured value.

The `newState` method is defined as follows:

```

val PROCESS_NOISE_Q = 0.03
val PROCESS_NOISE_R = 0.1
val MEASUREMENT_NOISE = 0.4

def newState: DblVector = {
  Range(0, maxIters) foreach( _ => {
    filter.predict //1
    val w = qrNoise.create(PROCESS_NOISE_Q, PROCESS_NOISE_R)
    x = A.operate(x).add(qrNoise.noisyQ) //2
    val v = qrNoise.create(MEASUREMENT_NOISE)
    val z = H.operate(x).add(qrNoise.noisyR) //3
    filter.correct(z) // 4
  })
  filter.getStateEstimation
}

```

The `PROCESS_NOISE` factor (with respect to `MEASUREMENT_NOISE`) used in the creation of the process noise w and measurement noise v are somewhat arbitrary. Their purpose is to simulate the white noise for the model. The `newState` method returns the filtered state as a `DblVector` instance for this particular state.



The exit condition

In the code snippet for the `newState` method, the iteration for specific data points exits when the maximum number of iterations is reached. A more elaborate implementation consists of either evaluating the matrix P at each iteration or estimation converged within a predefined range.

Experimentation

The objective is to smoothen the yield of the 10-year Treasury bond and quantify the impact of the elements of the state-transition matrix A on the smoothing process. The state equation updates the values of the state $[x_t, x_{t-1}]$ using the previous state $[x^{t-1}, x_{t-2}]$, where x represents the yield at time t . This is accomplished by shifting the values of the original time series $\{x_0, \dots, x_n\}$ by 1 using the `drop` method, $X1 = \{x_1, \dots, x_n\}$, creating a copy of the original time series without the last element $X2 = \{x_0, \dots, x_{n-1}\}$ and zipping $X1$ and $X2$. The resulting sequence of pair $\{(x_k, x_{k-1})\}$ is processed by the Kalman algorithm, as shown in the following code:

```

implicit val qrNoise = QRNoise((0.2, 0.4), (m: Double) => m * (new
Random(System.currentTimeMillis).nextGaussian) //1
val A: DblMatrix = ((0.9, 0.0), (0.0, 0.1))

```



```
val B: DblMatrix = (0.0, 0.0)
val H: DblMatrix = (1.0, 1.0)
val P0: DblMatrix = ((0.4, 0.5), (0.4, 0.5))
val x0: DblVector = (175.0, 175.0)

val dKalman = new DKalman(A, B, H, P0) //2
val output = "output/chap3/kalman.csv"
val zt_1 = zSeries.drop(1)
val zt = zSeries.take(zSeries.size-1)
val filtered = dKalman |> XTSeries[(Double, Double)](zt_1.zip(zt)) //3
DataSink[Double](output) |> filtered.map(_._1) //4
```

The process and measurement noise `qrNoise` is implicitly initialized with the respective factors, 0.2 and 0.4 (line 1). The Kalman filter is initialized with the prediction-correction equation matrices `A`, `B`, `H`, and `P0`, and the initial state x_0 (line 2). A time series $\{(x_t, x_{t-p})\}_i$ is generated by zipping two copies of the historical 10 Treasury bond yield series, with the second one being shifted by `p` data. The Kalman filter is applied to the time series of tuples and the result is dumped into an output file using a `DataSink` instance (line 4)

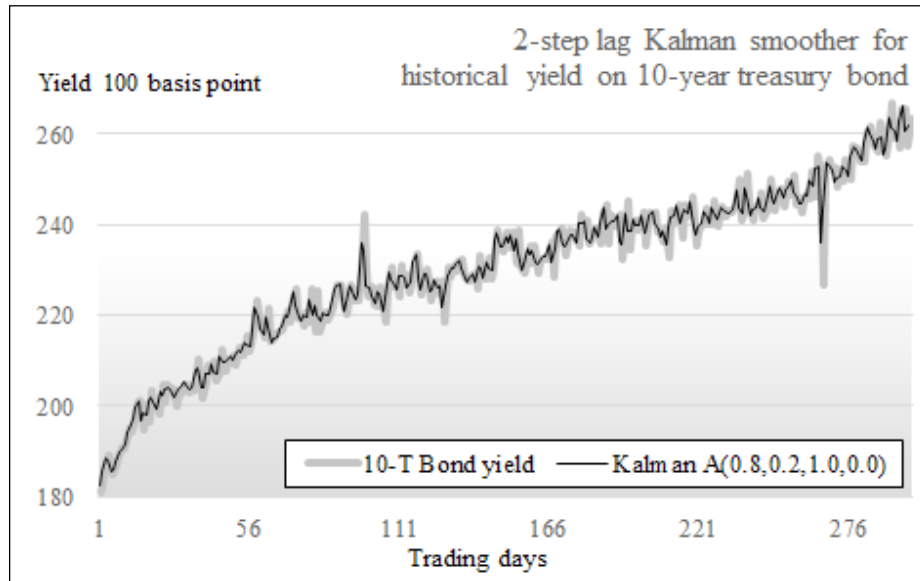
The test is performed over a period of one year, and the results are plotted using a basis point or 100th of a percentage. The quality of the output is evaluated using two different values for the state transition matrix `A`: `[0, 8, 0.2, 1.0, 0.0]` and `[0.5, 0.5, 1.0, 0.0]`.



Modeling state transition and noise

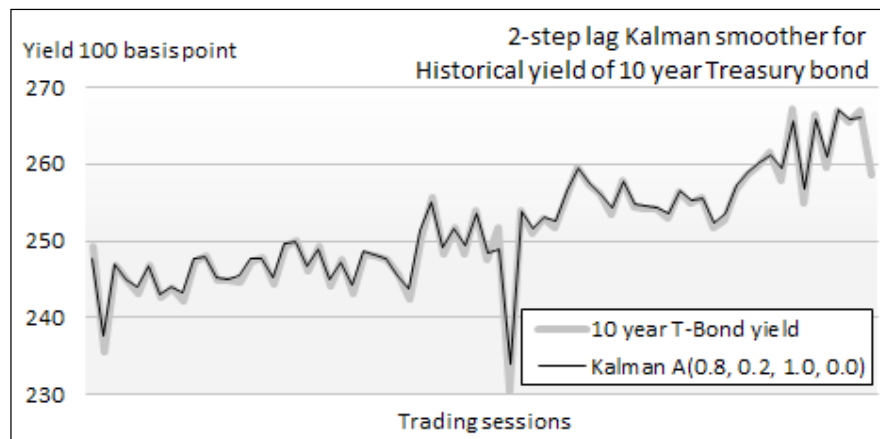
The state transition and the noise related to the process have to be selected carefully. The resolution of the state equations relies on the **QR decomposition**, which requires a non-negative definite matrix. The implementation in the Apache common library throws a `NonPositiveDefiniteMatrixException` if the principle is violated.

The smoothed yield is plotted along the raw data as follows:



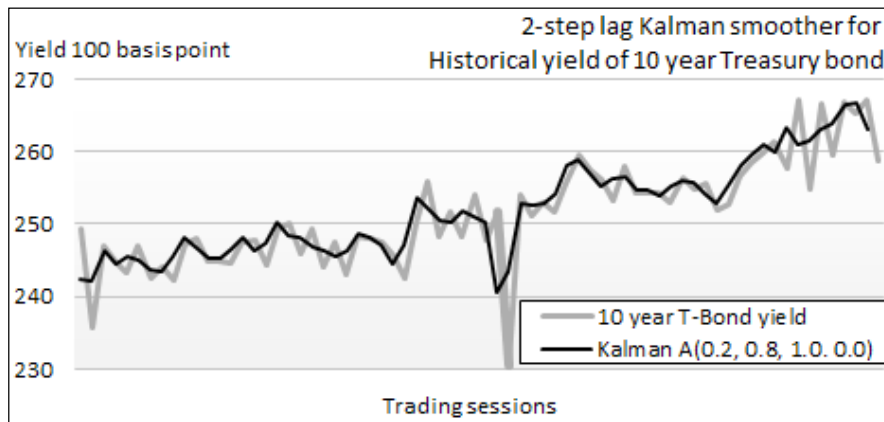
The output of the Kalman filter for the 10-year Treasury bond historical prices

Clearly, the yield time series has been smoothed. However, the amplitude of the underlying trend is significantly higher than any of the noise or the spikes. Consequently, the Kalman filter has a limited impact. Let's analyze the data for a shorter period during which the noise is the strongest, between the 190th and the 275th trading days.



The output of the Kalman filter for the 10-year Treasury bond prices 0.8-0.2

The high frequency noise has been significantly reduced without cancelling the actual spikes. The distribution 0.8-0.2 takes into consideration the previous state and favors the predicted value. Contrarily, a run with a state transition matrix A [0.2, 0.8, 0.0, 1.0] that favors the latest measurement will preserve the noise, as seen in the following graph:



The output of the Kalman filter for the 10-year Treasury bond price 0.2-0.8

The Kalman filter is a very useful and powerful tool in understanding the distribution of the noise between the process and observation. Contrary to the low or pass-band filters based on the fast Fourier transform, the Kalman filter does not require computation of the frequencies spectrum or assume the range of frequencies of the noise.

However, the linear Kalman filter has its limitations:

- The noise generated by both the process and the measurement has to be Gaussian. Processes with non-Gaussian noise can be modeled with techniques such as a Gaussian Sum filter or adaptive Gaussian mixture [3:14].
- It requires that the underlying process is linear. Researchers have been able to formulate extensions to the Kalman filter, known as the **extended Kalman filter (EKF)** to filter signals from non-linear dynamic systems, at the cost of significant computational complexity.

Alternative preprocessing techniques

For the sake of space and your time, this chapter introduced and applied three filtering and smoothing classes of algorithms. Moving averages, Fourier series, and the Kalman filter are far from being the only techniques used in cleaning raw data. The alternative techniques can be classified into two categories:

- Autoregressive models that encompass **autoregressive moving average (ARMA)**, **autoregressive integrated moving average (ARIMA)**, **generalized autoregressive conditional heteroskedasticity (GARCH)**, and Box-Jenkins that relies on some form of autocorrelation function
- Curve-fitting algorithms that include the polynomial and geometric fit with the ordinary least squares method, non-linear least squares using the Levenberg-Marquardt optimizer, and probability distribution fitting

Summary

This completes the overview of the most commonly used data filtering and smoothing techniques. There are other types of data preprocessing algorithms such as normalization, analysis, and reduction of variance; the identification of missing values is also essential to avoid the **garbage-in garbage-out** conundrum that plagues so many projects that use machine learning for regression or classification.

Scala can be effectively used to make the code understandable and avoid cluttering methods with unnecessary arguments.

The three techniques presented in this chapter, from the simplest moving averages and Fourier transform to the more elaborate Kalman filter, go a long way in setting up data for the next concepts introduced in the next chapter – unsupervised learning and more specifically, clustering.

4

Unsupervised Learning

Labeling a set of observations for classification or regression can be a daunting task, especially in the case of a large feature set. In some cases, labeled observations are either not available or not possible to create. In an attempt to extract some hidden association or structures from observations, the data scientist relies on unsupervised learning techniques to detect patterns or similarity in data.

The goal of unsupervised learning is to discover patterns of regularities and irregularities in a set of observations. These techniques are also applied in reducing the solution space or feature set similarly to the divide-and-conquer approach commonly used in Computer Science.

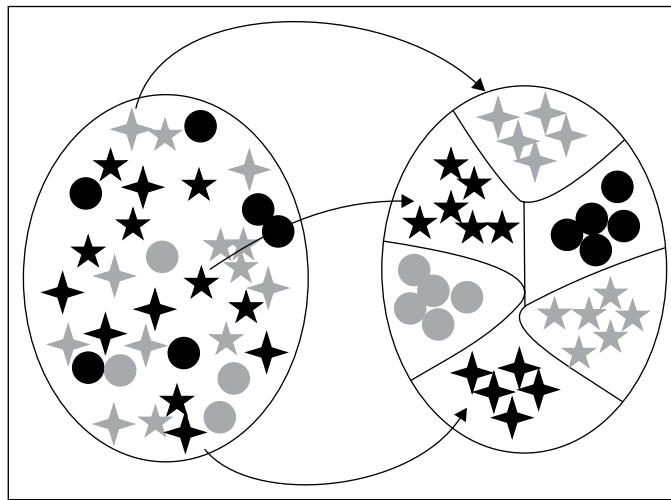
There are numerous unsupervised algorithms; some are more appropriate to handle dependent features while others generate more relevant groups in the case of hidden features [4:1]. In this chapter, you will learn three of the most common unsupervised learning algorithms:

- **K-means:** Clustering observed features
- **Expectation-maximization (EM):** Clustering observed and latent features
- **Principal components analysis (PCA):** Reducing the dimension of the model

Any of these algorithms can be applied to technical analysis or fundamental analysis. Fundamental analysis of financial ratios and technical analysis of price movements are described in the *Technical analysis* section under *Finances 101* in *Appendix A, Basic Concepts*. The K-means algorithm is fully implemented in Scala while expectation-maximization and principal components analysis leverage the Apache Commons Math library.

Clustering

Problems involving a large number of features for large datasets become quickly intractable, and it is quite difficult to evaluate the independence between features. Any computation that requires some level of optimization and, at a minimum, computation of first order derivatives requires a significant amount of computing power to manipulate high-dimension matrices. As with many engineering fields, a divide-and-conquer approach to classifying very large datasets is quite effective. The objective is to reduce continuous, infinite, or very large datasets into a small group of observations that share some common attributes.



Visualization of data clustering

This approach is known as vector quantization. **Vector quantization** is a method that divides a set of observations into groups of similar size. The main benefit of vector quantization is that the analysis using a representative of each group is far simpler than an analysis of the entire dataset [4:2].

Clustering, also known as **cluster analysis**, is a form of vector quantization that relies on a concept of distance or similarity to generate groups known as clusters.



Learning vector quantization (LVQ)

Vector quantization should not be confused with learning vector quantization. Learning vector quantization is a special case of artificial neural networks that relies on a winner-take-all learning strategy to compress signals, images, or videos.

This chapter introduces two of the most commonly applied clustering algorithms:

- K-means, which is used for quantitative types and minimizes the total error (known as the reconstruction error) given the number of clusters and the distance formula.
- Expectation-maximization (EM), which is a two-step probabilistic approach that maximizes the likelihood estimates of a set of parameters. EM is particularly suitable to handle missing data.

K-means clustering

K-means is a popular iterative clustering algorithm. The representative of each cluster is computed as the center of the cluster, known as the **centroid**. The similarity between observations within a single cluster relies on the concept of distance between observations.

Measuring similarity

There are many ways to measure the similarity between observations. The most appropriate measure has to be intuitive and avoid computational complexity. This section reviews three similarity measures:

- The Manhattan distance
- The Euclidean distance
- Cosine of value observations

The Manhattan distance is defined by the absolute distance between two variables or vectors, $\{x_i\}$ and $\{y_i\}$, of the same size:

$$d(x, y) = \sum |x_i - y_i|$$

The implementation is generic enough to compute the distance between two arrays of elements of different types as long as an implicit conversion between each of these types to `Double` values is already defined, as shown here:

```
def manhattan[T <% Double, U <% Double](x: Array[T], y: Array[U]):
  Double = (x, y).zipped.foldLeft(0.0)((s, t) => s + Math.abs(t._1 -
  t._2))
```


The ubiquitous Euclidean distance is defined as the square of the distance between two vectors, $\{x_i\}$ and $\{y_i\}$, of the same size:

$$d(x, y) = \sum (x_i - y_i)^2$$

```
def euclidean[T <% Double, U <% Double](x: Array[T], y: Array[U]):  
Double = Math.sqrt((x, y).zipped.foldLeft(0.0)((s, t) => { val d =  
t._1 - t._2; s + d*d } ))
```

The cosine distance is defined as the cosine of an angle between two vectors, $\{x_i\}$ and $\{y_i\}$, of the same size:

$$d(x, y) = \frac{\sum x_i y_i}{(\sum x_i^2 \sum y_i^2)^{1/2}}$$

In this implementation, the computation of the dot product and the norms for each dataset is done simultaneously using the tuple within the fold method:

```
def cosine[T <% Double, U <% Double](x: Array[T], y: Array[U]): Double  
= {  
  val zeros = (0.0, 0.0, 0.0)  
  val norms = (x, y).zipped.foldLeft(zeros)((s, t) =>  
    (s._1 + t._1*t._2, s._2 + t._1*t._1, s._3 + t._2*t._2))  
  norms._1/Math.sqrt(norms._2*norms._3)  
}
```

Performance of zip

The scalar product of two vectors is one of the most common operations. It is tempting to implement the dot product using the generic zip method:



```
def dot(x: Array[Double], y: Array[Double]):  
Array[Double] =  
  x.zip(y).map( x => f(x._1, x._2) )
```

An functional alternative is to use the Tuple2.zipped method.

```
def dot(x: Array[Double], y: Array[Double]):  
Array[Double] = (x, y).zipped map ( _ * _ )
```

If readability is not a primary issue, you can always implement the dot method with a while loop.

Overview of the K-means algorithm

The main advantage of the K-means algorithm (and the reason for its popularity) is its simplicity [4:3].



Let's consider K clusters $\{C_k\}$ with means $\{m_k\}$. The K-means algorithm is indeed an optimization problem, the objective of which is to minimize the reconstruction or the total error defined as the total sum of distance.

$$\min_{C_k} \sum_1^K \sum_{x_i \in C_k} d(x_i, m_k)$$

The steps of the iterative algorithm are:

1. Initialize the centroids or means m_k of the K clusters.
2. Assign observations to the nearest cluster given m_k .
3. Iterate until no observations are reassigned to a cluster:
 - Compute centroids m_k that minimize the total error reconstruction for the current assignment
 - Reassign the observations given the new centroids m_k

Step 1 – cluster configuration

The configuration of the K clusters consists of defining the following parameters for the K-means algorithm: number of K clusters, the distance metrics, the maximum number of iterations, and the initial value of the cluster's centroid.

Defining clusters

The first step is to define a cluster. A cluster is defined by the following parameters:

- Centroid: `center`
- The indices of the observations that belong to this cluster: `members`

The following code shows the definition of a cluster:

```
class Cluster[T <% Double] (val center: DblVector) {
  val members = new ListBuffer[Int]
```

The cluster is responsible for managing its members (data points) at any point of the iterative computation of the K-means algorithm. It is assumed that a cluster will never contain the same data points twice.

The constructor of the `Cluster` class is implemented by the `apply` method in the companion object (for convenience, refer to the *Class constructor template* section in *Appendix A, Basic Concepts*):

```
object Cluster {
  def apply[T <% Double] (c:DblVector):Cluster[T] = new Cluster[T] (c)
}
```

At a minimum, a cluster should be able to manage its membership of observations, update its center, and compute the variance or standard deviation of all its member observations:

```
def += (n:Int): Unit = members.append(n)
def moveCenter(xt: XTSeries[Array[T]]): Cluster[T] ={
  val sums = members.map(xt(_).map(_.toDouble)).toList
    .transpose
    .map( _.sum)
  Cluster[T] (sums.map( _ / members.size).toArray)
}

def stdDev(xt: XTSeries[Array[T]], distance: (DblVector, Array[T]) =>
Double): Double = {
  Stats[Double] (members.map(xt( _))
    .map( distance(center, _)).toArray).stdDev
}
```

The three important methods that define the behavior of a cluster instance are as follows:

- `+=`: Add a member (index of an observation in the original time series).
- `moveCenter`: Create a new cluster with the existing members and a new centroid computed as the mean of all the observations contained in the cluster.
- `stdDev`: Compute the standard deviation (or density) of all the observations contained in the cluster relative to its center. The distance between each member and the centroid is extracted through a `map`, and then folded to generate the statistics. The function to compute the distance between the center and an observation is an argument of the method. The default distance is Euclidean.



Cluster selection

There are different ways to select the most appropriate cluster when reassigning an observation (updating its membership). In this implementation, we will select the cluster with the larger spread or lowest density. An alternative is to select the cluster with the largest membership.

Defining K-means

Let's declare the K-means algorithm class, `KMeans`, with its public methods.

The `KMeans` class takes the number of clusters, `K`, and the maximum number of iterations, `maxIters`, as parameters. The implicit conversion of type `T` to a `Double` is specified by the `T <% Double` view bound. The `Ordering` class has to be passed implicitly as a parameter because it is required by the `sortBy` method in the `initialize` and `maxBy` methods. The `Manifest` method is required to preserve the type erasure for `Array[T]` in the JVM:

```
class KMeans[T <% Double](K: Int, maxIters: Int, distance:
  (DblVector, Array[T]) => Double)(implicit order: Ordering[T],
  m: Manifest[T]) extends PipeOperator[XTSeries[Array[T]],
  List[Cluster[T]]] {
  def |> : PartialFunction[XTSeries[Array[T]], List[Cluster[T]]]
  def initialize(xt: XTSeries[Array[T]]): List[Cluster[T]]
```

As with other data processing units, the extraction of K-means clusters is encapsulated by the pipe operator `|>`, so clustering can be integrated into a workflow using dependency injection described in the *Dependency injection* section in *Chapter 2, Hello World!*. The initialization of the centroids of each of the `K` clusters is performed by the private `initialize` method.

Initializing clusters

The initialization of the cluster centroids is important to ensure fast convergence of K-means. Solutions range from the simple random generation of centroids to the application of genetic algorithms to evaluate the fitness of centroid candidates. We selected an efficient and fast initialization algorithm developed by M. Agha and W. Ashour [4:4].

The steps of the initialization are as follows:

1. Compute the standard deviation of the set of observations.
2. Select the dimension $k \{x_{k'0}, x_{k'1} \dots x_{k'n}\}$ with maximum standard deviation.
3. Rank the observations by their increasing value of standard deviation for the dimension k .
4. Divide the ranked observations set equally into K sets $\{S_m\}$.
5. Find the median values, size $(S_m)/2$.
6. Use the corresponding observations as centroids.

The initialization algorithm is implemented by the private `initialize` method:

```
def initialize(xt:XTSeries[Array[T]]): List[Cluster[T]]={
  val stats = statistics(xt) //1
  val maxSDevDim = Range(0,stats.size).maxBy (stats( _ ).stdDev)//2
  val rankedObs = xt.zipWithIndex
    .map(x=> (x._1(maxSDevDim), x._2)) //2
    .sortWith( _._1 < _._1) //3
  val halfSegSize = ((rankedObs.size>>1)/K).floor.toInt //4
  val centroids = rankedObs.filter(isContained( _, halfSegSize,
rankedObs.size) ).map(n => xt(n._2)) //6
  Range(0, K).foldLeft(List[Cluster[T]]())((xs, i) => Cluster[T]
(centroids(i)) :: xs) //7
}
```

Let's deconstruct the implementation of the Agha-Ashour algorithm in the `initialize` method.

The `statistics` function is applied to the input time series to extract the standard deviation for each dimension in the observations set (line 1). The dimension with the `maxSDevDim` maximum variance or standard deviation is computed by using the `maxBy` method on a `Stats` instance (line 2). Then, the observations are ranked by the increasing value of the standard deviation, `rankedObs` (line 3).

The ordered sequence of observations is then broken into $xt.size/K$ segments (line 4) and the indices of the `centroids` are selected as the midpoint (or median) observations of those segments using the filtering condition, `isContained`:

```
def isContained(t: (T,Int), hSz: Int, dim: Int): Boolean =
  ((t._2 % hSz == 0) && (t._2 % (hSz<<1) != 0))
```

The indices of the centroid in the time series are converted to actual observations using a map method (line 6). Finally, the list of clusters is generated using a fold (`foldLeft`) method on the range of cluster indices ($0, K-1$) (line 7).

Step 2 – cluster assignment

The second step in the K-means algorithm is the assignment of the observations to the clusters for which the centroids have been initialized in step 1. This feat is accomplished by the private `assignToClusters` method:

```
def assignToClusters(xt: XTSeries[Array[T]], clusters:
List[Cluster[T]], membership: Array[Int]): Int = {
  xt.toArray
    .zipWithIndex
    .filter(x => { //1
      val nearestCluster = getNearestCluster(clusters, x._1)//2
      val reassigned = nearestCluster != membership(x._2)
      clusters(nearestCluster) += x._2 //3
      membership(x._2) = nearestCluster //4
      reassigned
    }).size
}
```

The core of the assignment of observations to each cluster is the filter on the time series (line 1). The filter computes the index of the closest cluster and checks whether the observation is to be reassigned (line 2). The observation at the index `x._2` is added to the nearest cluster, `clusters(nearestCluster)` (line 3). The current membership of the observations is then updated (line 4).

The cluster closest to an observation data is computed by the `getNearestCluster` method as follows:

```
def getNearestCluster(clusters: List[Cluster[T]], x:Array[T]): Int={
  clusters.zipWithIndex.foldLeft((Double.MaxValue,0))((p,c) => {
    val measure = distance(c._1.center, x)
    if(measure < p._1) (measure, c._2) else p
  })._2
}
```

A fold is used to extract from the list of clusters the cluster that is closest to the observation `x` using the `distance` metric defined in the K-means constructor.

Step 3 – iterative reconstruction

The final step is to implement the iterative computation of the reconstruction error. In this implementation, the iteration terminates when no more observations are reassigned to different clusters. As with other data processing units, the extraction of K-means clusters is encapsulated by the pipe operator `|>`, so that clustering can be integrated into a workflow using dependency injection described in the *Dependency Injection* section in *Chapter 2, Hello World!*.

The generation of the K clusters is executed by the data transformation `|>`:

```
def |> :PartialFunction[XTSeries[Array[T]], List[Cluster[T]]] = {
  case xt: XTSeries[Array[T]] if(xt.size>2 && xt(0).size>0) => {
    val clusters = initialize(xt) //1

    if( clusters.isEmpty) List.empty
    else {
      val membership = Array.fill(xt.size)(0)
      val reassigned = assignToClusters(xt,clusters,membership)//2
      var newClusters: List[Cluster[T]] = List.empty
      Range(0, maxIters).find( _ => {
        newClusters = clusters.map( c => {
          if( c.size > 0) c.moveCenter(xt, dimension(xt))
          else clusters.filter( _.size > 0)
                        .maxBy( _.stdDev(xt, distance))
        }) //3
        assignToClusters(xt, newClusters, membership) == 0
      }) match {
        case Some(index) => newClusters
        case None => { ... }
      } //4
    }
  }
}
```

As described in the algorithm overview section, the main method initializes the membership for all the observations (line 1), creates and initializes the clusters, and assigns the observations to clusters using the `assignToClusters` method (line 2). The iteration updates the content of each cluster using the `moveCenter` method, by assigning new observations to the cluster with the highest standard deviation (line 3). The iterative loop exits when no more reassignment is needed (line 4).



K-means algorithm exit condition

In some rare instances, the algorithm may reassign the same few observations between clusters, preventing its convergence toward a solution in a reasonable time. Therefore, it is recommended to add a maximum number of iterations as an exit condition. If K-means does not converge with the maximum number of iterations, then the cluster centroids need to be reinitialized and the iterative process needs to be executed once again.

The companion object for `KMeans` implements the `apply` constructor and the computation of the `stdDev` standard deviation for each cluster. The default constructor uses the Euclidean distance:

```
def apply[T <% Double](K: Int, maxIters: Int)(implicit order:
  Ordering[T], m: Manifest[T]): KMeans[T] = new KMeans[T](K, maxIters,
  euclidean)
def stdDev[T](c: List[Cluster[T]], xt: XTSeries[Array[T]]):
  List[Double] = c.map( _.stdDev(xt))
```

The `stdDev` method computes the standard deviation of the distances between each data point that belongs to a `c` cluster and its centroid.



Centroid versus mean

The terms centroid and mean refer to the same entity: the center of a cluster. This chapter uses these two terms interchangeably.

Note that ordering a trait and `Manifest` have to be provided in the `apply` constructor because there is no guarantee that such capabilities are provided in runtime by the client code.

Curse of dimensionality

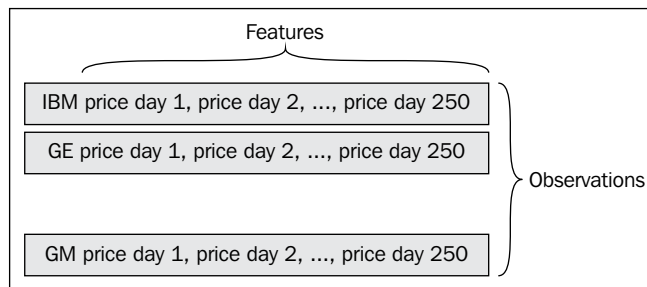
A model with a significant number of features (high dimensions) requires a larger number of observations in order to extract robust clusters. K-means clustering with very small datasets, of size less than 50, produces models with high bias and a limited number of clusters that are affected by the order of observations [4:5]. I have been using the following simple empirical rule of thumb for a training set of size n , expected K clusters, and N features: $n < K.N$.



Dimensionality versus size of training set

The issue with the dimensionality of models versus the number of observations is not specific to unsupervised learning algorithms. All supervised learning techniques face the same challenge to set up a viable training plan.

Whichever empirical rule you follow, such a restriction is particularly an issue for analyzing stocks using historical quotes. Let's consider our examples of using technical analysis to categorize stocks according to their price behavior over a period of 1 year (or approximately 250 trading days). The dimension of the problem is 250 (250 daily closing prices). The number of stocks (observations) would have exceeded several hundred!



Price model for K-means clustering

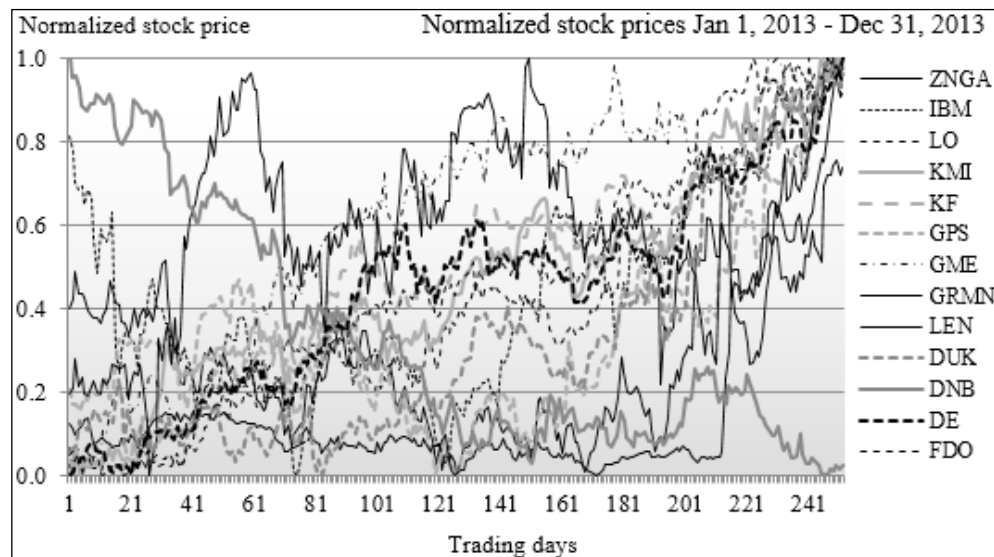
There are options to get around this limitation and shrink the number of observations; among them are:

- Sampling the trading data without losing a significant amount of information from the raw data, assuming the distribution of observations follows a known probability density function.
- Smoothing the data to remove the noise as seen in *Chapter 3, Data Preprocessing*, assuming the noise is Gaussian. In our test, a smoothing technique will remove the price outliers for each stock and therefore reduce the number of features (trading session). This approach differs from the sampling approach because it does not require an assumption that the dataset follows a known density function. On the other hand, the reduction of features will be less significant.

These approaches are workaround solutions at best, used for the sake of this tutorial, but they are not recommended for actual commercial analytical applications. The principal component analysis introduced in the last section of this chapter is one of the most reliable dimension reduction techniques.

Experiment

The objective is to extract clusters from a set of stock price actions during a period of time between January 1 and Dec 31, 2013 as features. For this test, 127 stocks are randomly selected from the S&P 500 list. The following chart visualizes the behavior of the normalized price of a subset of these 127 stocks:



Price action of stocks used in K-means clustering

The key is to select the appropriate features prior to clustering and the time window to operate on. It would make sense to consider the entire historical price over the 252 trading days as a feature. However, the number of observations (stocks) is too limited to use the entire price range. The (`SAMPLES = 50`) observations are the stock closing price for each trading session between the 80th and 130th days. The adjusted daily closing prices are normalized using the minimum and maximum values.

First, let's create a simple function to execute the K-means algorithm:

```

Val MAX_ITERS = 150
def run(K: Int, obs: DblMatrix): Unit = {
  val kmeans = KMeans[Double](K, MAX_ITERS) //1

  val clusters = kmeans |> XTSeries[DblVector](obs) //2
  clusters.foreach( _.center.foreach( show( _ ) ) ) //3
  clusters.map( _.stdDev(XTSeries[DblVector](obs, euclidean)) ).
  foreach( show( _ ) ) //4
}

```

The `KMeans` class is first initialized with a number of clusters, κ , and a maximum number of iterations, `MAX_ITERS` (line 1). These two parameters are domain and problem specific. The clustering algorithm is executed (line 2) returning a list of clusters. The clusters' centroid information is then displayed (line 3) and the standard deviation is computed for each of the clusters for a given number of clusters, κ , and observations, `obs` (line 4).

Let's load the data from CSV files using the `DataSource` class (refer to the *Data extraction* section in *Appendix A, Basic Concepts*):

```
final val path = "resources/data/chap4/"
val extractor = YahooFinancials.adjClose :: List[Array[String]
=>Double]() // 5
def symbols = DataSource.listSymbols(path) //6

final val START = 80
final val SAMPLES = 50
val normalize=true
val prices = symbols.map(s =>DataSource(s,path,normalize) |>
extractor) //7
prices.find(_.isEmpty) match { //8
  case Some(noPrice) = { ... }
  case None => {
    val values = prices. map(x => x(0))
                        .map(_.drop(START).take(SAMPLES))
    args.map(_.toInt) foreach( run(_, values)) //9
  }
}
```

As mentioned earlier, the cluster analysis applies to the closing price in the range between the 80th and 130th trading day. The extractor is defined to extract the adjusted closing price for a stock whose price information is retrieved from `YahooFinancials` (line 5). The list of stock symbols is used to extract price information from CSV files located at the path (line 6). For instance, the ticker symbol for General Electric Corp. is `GE` and the trading data is located in `GE.csv`.

The 50 daily prices for each stock are extracted by an instance of `DataSource` (line 7). The `run` method introduced earlier is invoked either for each stock or as soon as K-means fails through an exit condition in the `find` method (line 8). The normalized data `values.toArray` for the specific time window is extracted by the combination of calls to `drop` and `take` Scala array methods (line 9).

The first test run is executed with $K=3$ clusters. The mean (or centroid) vector for each cluster is plotted as follows:

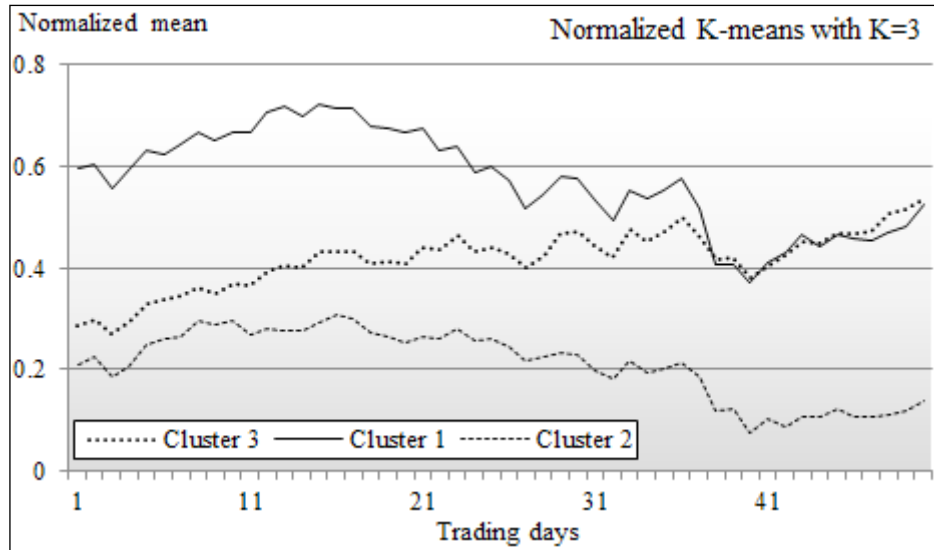


Chart of means of clusters using K-means $K=3$

The means vectors of the three clusters are quite distinctive. The top and bottom means 1 and 2 in the chart have the respective standard deviation of 0.34 and 0.27 and share a very similar pattern. The difference between the elements of the 1 and 2 cluster mean vectors is almost constant: 0.37. The cluster with a mean vector 3 represents the group of stocks that behave like the stocks in cluster 2 at the beginning of the time period, and behave like the stocks in cluster 1 towards the end of the time period.

This behavior can be easily explained by the fact that the time window or trading period, the 80th to 130th trading day, correspond to the shift in the monetary policy of the federal reserve in regard to the quantitative easing program. Here is the list of stocks for each of the clusters whose centroid values are displayed on the chart:

Cluster	List of stocks
Cluster 1	AET, AHS, BBY, BRCM, C, CB, CL, CLX, COH, CVX, CYH, DE, DG, DHI, DO, DUK, EA, EBAY, EXC, EXP, FE, GLW, GPS, IBM, JCP, JNJ, JWN, K, KF, KMI, KO, KRFT, LEN, LINC, LRCX, MSFT, NVMI, THC, XRT
Cluster 2	AA, AAPL, ADBE, ADSK, AFAM, AMZN, AU, BHI, BTU, CAT, CCL, CCMP, COP, CSC, CU, DOW, EMR, ENTG, ETFC, FCX, FDX, FFIV, FISV, FLIR, FLR, FLS, FTR, GLD, GRMN, GT, JCI, QCOM, QQQ, SIL, SLV, SLW
Cluster 3	ADM, ADP, AXP, BA, BBT, BEN, BK, BSX, CA, CBS, CCE, CELG, CHK, CI, CME, CMG, CSCO, CVS, DAL, DD, DNB, EMC, EXPE, F, FDO, FITB, FMC, GCI, GE, GM, GME, GS, HCA, JNPR, JPM, KLAC, LH, LLL, LM, LMT, LNC, LO, MKSI, MU, NEM, TRW, TXN, UNH, WDC, XLF, XLNX, ZNGA

Let's evaluate the impact of the number of clusters K on the characteristics of each cluster.

Tuning the number of clusters

We repeat the previous test on the 127 stocks and the same time window with the number of clusters varying from 2 to 15.

The mean (or centroid) vector for each cluster is plotted as follows for $K = 2$:

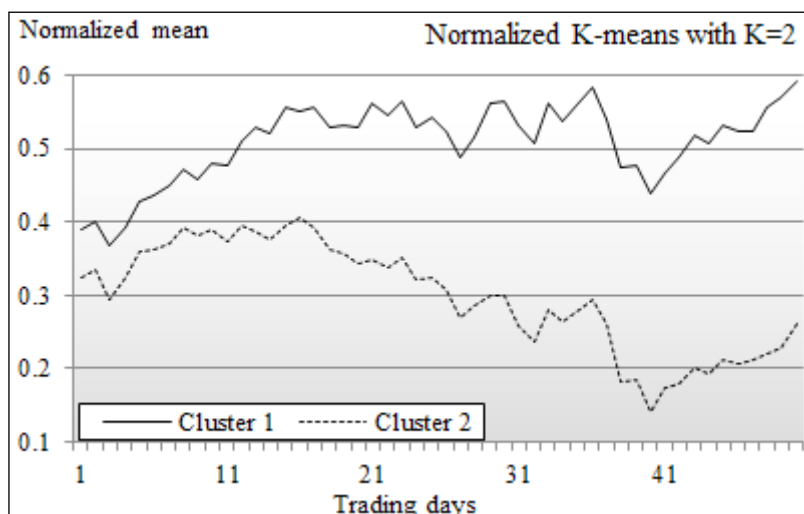


Chart of means of clusters using K-means $K=2$

The chart of the results of the K-means algorithms with 2 clusters shows that the mean vector for the cluster labeled 2 is similar to the mean vector labeled 3 on the chart with $K = 3$ clusters. However, the cluster with the mean vector 1 reflects somewhat the aggregation or summation of the mean vectors for the clusters 1 and 3 in the chart $K = 3$. The **aggregation effect** explains why the standard deviation for the cluster 1, 0.55, is twice as much as the standard deviation for the cluster 2, 0.28.

The mean (or centroid) vector for each cluster is plotted as follows for $K = 5$:

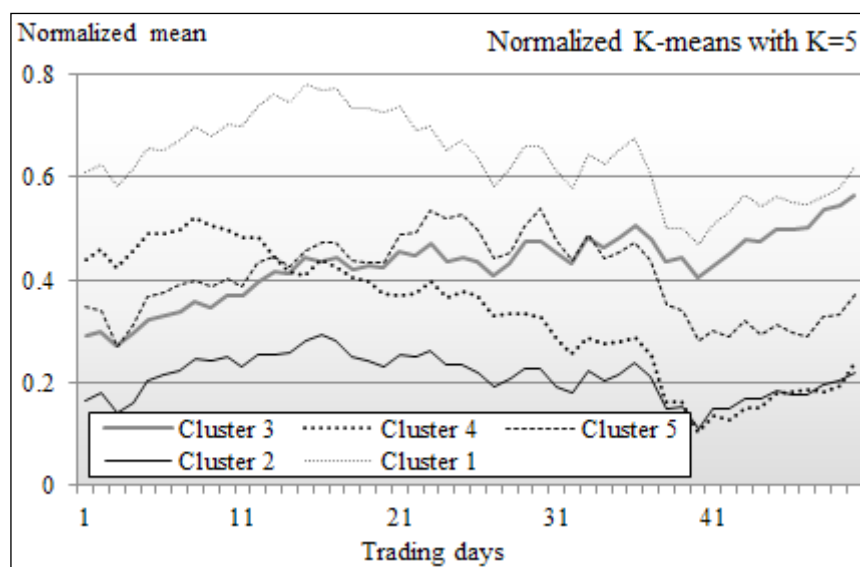


Chart of means of clusters using K-means $K=5$

In this chart, we can assess that the clusters 1 (with the highest mean), 2 (with the lowest mean), and 3 are very similar to the clusters with the same labels in the chart for $K = 3$. The cluster with the mean vector 4 contains stocks whose behaviors are quite similar to those in cluster 3, but in the opposite direction. In other words, the stocks in cluster 3 and 4 reacted in opposite ways following the announcement of the change in the monetary policy.

In the tests with high values of K , the distinction between the different clusters becomes murky, as shown in the following chart for $K = 10$:

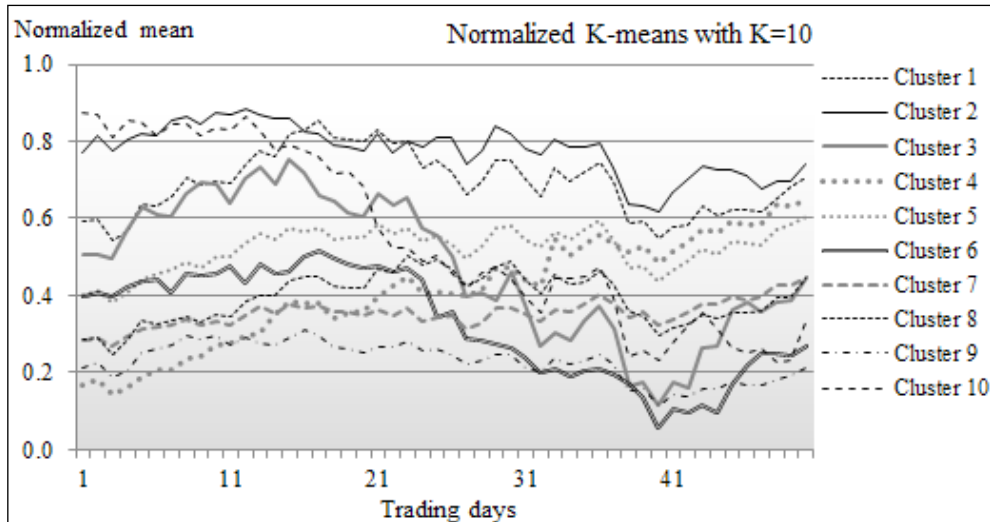


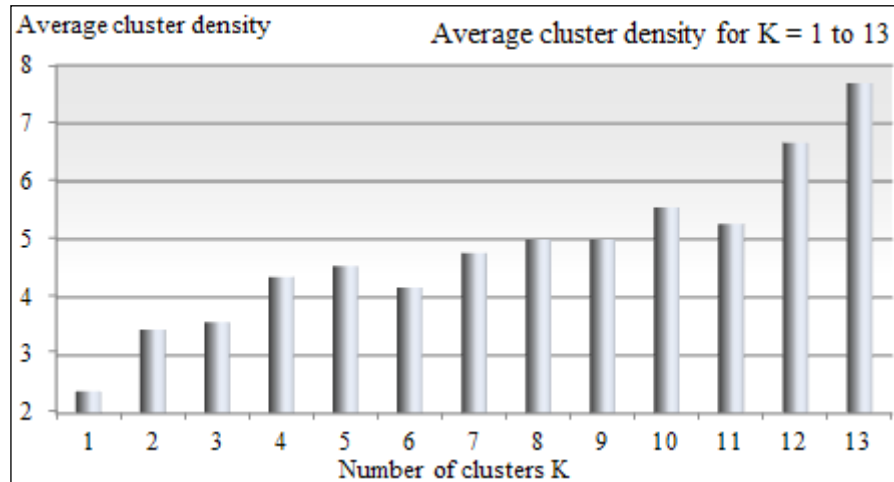
Chart of means of clusters using K-means $K=10$

The means for clusters 1, 2, and 3 seen in the first chart for the case $K = 3$ are still visible. It is fair to assume that these are very likely the most reliable clusters. These clusters happened to have a low standard deviation or high density.

Let's define the density of a cluster C_j with a centroid c_j as the inverse of the Euclidean distance between all members of each cluster and its mean (or centroid):

$$d(C_j) = 1 / \sum_{x \in C_j} (x - c_j)^2$$

The density of the cluster is plotted against the number of clusters with $K = 1$ to 13:



Bar chart of the average cluster density for $K = 1$ to 13

As expected, the average density of each cluster increases as K increases. From this experiment, we can draw the simple conclusion that the density of each cluster does not significantly increase in the test runs for $K = 5$ and beyond. You may observe that the density does not always increase as the number of clusters increases ($K = 6$ to $K = 11$). The anomaly can be explained by the following three factors:

- The original data is noisy
- The model is somewhat dependent on the initialization of the centroids
- The exit condition is too loose

Validation

There are several methodologies to validate the output of a K-means algorithm from purity to mutual information [4:6]. One effective way to validate the output of a clustering algorithm is to label each cluster and run those clusters through a new batch of labeled observations. For example, if during one of these tests you find that one of the clusters CC contains most of the commodity-related stocks, then you can select another commodity-related stock, SC , which is not part of the first batch, and run the entire clustering algorithm again. If SC is contained in CC , then the clustering has performed as expected. If this is the case, you should run a new set of stocks, some of which are commodity related, and measure the number of true positives, true negatives, false positives, and false negatives. The precision, recall, and F1 measures introduced in the *Assessing a model* section of *Chapter 2, Hello World!*, confirms whether the tuning parameters and labels you selected for your cluster are indeed correct.



Validation

The quality of the clusters, as measured by the F1 statistics, depends on the labeling of the cluster and the rule (that is, label a cluster with the industry with the highest relative percentage of stocks in the cluster) used to assign a label. This process is very subjective. The only sure way to validate a validation methodology is to evaluate several labeling schemes and select the one that generates the highest F1 statistics.

We reviewed some of the tuning parameters that impact the quality of the results of the K-means clustering. They are as follows:

- Initial selection of centroid
- Number of K clusters

In some cases, the similarity criterion (that is, Euclidean distance versus cosine value) can have an impact on the *cleanness* or density of the clusters.

The final and important consideration is the computational complexity of the K-means algorithm. The previous sections of the chapter described some of the performance issues with K-means and possible remedies.

Despite its many benefits, the K-means algorithm does not handle missing data or unobserved features very well. Features that depend on each other indirectly may in fact depend on a common hidden (also known as latent) variable. The expectation-maximization algorithm described in the next section addresses some of these limitations.

Expectation-maximization (EM) algorithm

The expectation-maximization algorithm was originally introduced to estimate the maximum likelihood in the case of incomplete data [4:7]. It is an iterative method to compute the model features that maximize the likely estimate for observed values, taking into account unobserved values.

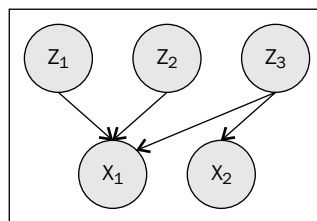
The iterative algorithm consists of computing:

- The expectation, E , of the maximum likelihood for the observed data by inferring the latent values (**E-step**)
- The model features that maximize the expectation E (**M-step**)

The expectation-maximization algorithm is applied to solve clustering problems by assuming that each latent variable follows a Normal or Gaussian distribution. This is similar to the K-means algorithm for which the distance of each data point to the center of each cluster follows a Gaussian distribution [4:8]. Therefore, a set of latent variables is a mixture of Gaussian distributions.

Gaussian mixture model

Latent variables Z can be visualized as the behavior (or symptoms) of a model (observed) X for which Z are the root causes of the behavior:



Visualization of observed and latent features

The latent values Z follow a Gaussian distribution. For the statisticians among us, the mathematics of a mixture model is described in the following information box.

The mixture model

If $\{x_i\}$ is a set of observed features associated with latent features $\{z_k\}$, the probability for the feature x_i given z_k has a value j :

$$p(x_i | Z_k = j)$$

The probability p is called the base distribution. If we extend to the entire model, $\theta = \{x_i, z_k\}$, the conditional probability is defined as follows:

$$p(x_i | \theta) = \sum_{j=1}^J \pi_j p(x_i | Z_k = j)$$



The most widely used mixture model is the Gaussian mixture model that represents the base distribution p as a Normal distribution and the conditional probability as a weighted Normal multivariate distribution:

$$p(x_i | \theta) = \sum_{j=1}^J \pi_j \frac{1}{2\pi^{d/2} \sqrt{|\Sigma_j|}} e^{-\frac{1}{2}(x_i - \mu_j)^T \Sigma_j^{-1} (x_i - \mu_j)}$$

EM overview

As far as the implementation is concerned, the expectation-maximization algorithm can be broken down into three stages:

1. The computation of the log likelihood for the model features given some latent variables (**LL**).
2. The computation of the expectation of the log likelihood at iteration t (E-step).
3. The maximization of the expectation at iteration t (M-step).

Log likelihood

- **LL:** Let's consider a set of observed variables $X=\{x_i\}$ and latent variables $Z=\{z_i\}$. The log likelihood for X for given Z is:

$$L(\theta) = \sum \log p(x_i, z_i | \theta)$$



- **E-step:** The expectation for the model variable θ at iteration t is computed as:

$$Q(\theta, \theta_t) = E[L(\theta) | X, \theta_t]$$

- **M-step:** The function Q is maximized for the model features θ as:

$$\theta^{t+1} = \arg \max_{\theta} Q(\theta, \theta^t)$$

A formal, detailed, but short mathematical formulation of the EM algorithm can be found in S. Borman's tutorial [4:9].

Implementation

Let's implement the three steps (LL, E-step, and M step) in Scala. The internal calculations of the EM algorithm are a bit complex and overwhelming. You may not benefit much from the details of a specific implementation such as computation of the eigenvalues of the covariance matrix of the expectation of the log likelihood. This implementation hides some complexities by using the Apache Commons Math library package [4:10].



Inner workings of EM

You may want to download the source code for the implementation of the EM algorithm in the Apache Commons Math library if you need to understand the condition for which an exception is thrown.

First, let's define convenient internal types:

```
type EM = MultivariateNormalMixtureExpectationMaximization
type EMOutput = List[(Double, DblVector, DblVector)]
import scala.collections.JavaConversions._ //1
```

The constructor of the `MultivariateEM` class uses the standard template for machine learning algorithm classes:

- Parameterized view bound type
- Implementation of EM as a data transformation by extending `PipeOperator`

Here is an implementation of the constructor of `MultivariateEM`:

```
class MultivariateEM[T <% Double](K: Int) extends PipeOperator[XTSeries[Array[T]], EMOutput]
```

The Apache Commons Math Java implementation of the EM uses Java container classes that need to be explicitly converted to Scala collections. Those conversions are defined in the `JavaConversions` package (line 1).

The implementation of the EM algorithm in the data transformation `|>` operator uses the Apache Commons Math `MultivariateNormalMixture` class for the Gaussian mixture model and the `MultivariateNormalMixtureExpectationMaximization` class for the EM algorithm:

```
def |> : PartialFunction[XTSeries[Array[T]], EMOutput] = {
  case xt: XTSeries[Array[T]] if (xt.size>0 && dimension(xt)>0) =>{
    val data: DblMatrix = xt //2
    val multivariateEM = new EM(data)
    val est = MultivariateNormalMixtureExpectationMaximization
      .estimate(data, K)
    multivariateEM.fit(est) //3

    val newMixture = multivariateEM.getFittedModel //4
    val components = newMixture.getComponents.toList //5
    components.map(p => (p.getKey.toDouble, p.getValue.getMeans,
      p.getValue.getStandardDeviations) )//6
    ....
```

Let's look at the main `|>` method of the `MultivariateEM` wrapper class. The first step is to convert the time series into a primitive matrix of `Double` with observations and historical quotes as rows and the stock symbols as columns (line 2).

The initial mixture of Gaussian distributions can be provided by the user or can be extracted from the dataset as an estimate (line 3). The `getFittedModel` method triggers the M-step (line 4).

The Apache library uses Java primitives that need to be converted to Scala types using the package `import scala.collection.JavaConversions`. An instance of `java.util.List` is converted to `scala.collection.immutable.List` using `toList`, which invokes the `asScalaIterator` method of `WrapAsScala`, one of the base traits of `JavaConversions` (line 5).

The `<Double, MultivariateNormalDistribution>` key-value pair, returned by the call to `getFittedModel` by the Apache `math` method, is to be converted to a tuple containing the mean and standard deviation for each cluster (line 6).

Third-party library exceptions

Scala does not enforce the declaration of exceptions as part of the signature of a method. Therefore, there is no guarantee that all types of exceptions will be caught locally. This problem occurs when exceptions are thrown from a third-party library in two scenarios:



- The documentation of the API does not list all the types of exceptions
- The library is updated and a new type of exception is added to a method

One easy workaround is to leverage the Scala exception-handling mechanism:

```
Try {  
  ..  
} match {  
  case Success(results) => ...  
  case Failure(exception) => ...  
}
```

Testing

Let's apply the `MultivariateEM` class to the clustering of the same 127 stocks used in evaluating the K-means algorithm.

As discussed in the paragraph related to the curse of dimensionality, the number of stocks (127) to analyze restricts the number of observations to be used by the EM algorithm. A simple option is to filter out some of the noise of the stocks and apply a basic sampling method. The maximum sampling rate is restricted by the frequencies in the spectrum of noises of different types in the historical price of every stock.

Filtering and sampling



The preprocessing of the data using a combination of a simple moving average and fixed interval sampling prior to clustering is very rudimentary in this example. For instance, we cannot assume that the historical quotes of all the stocks share the same noise characteristics. The noise pattern in the quotation of momentum and heavily traded stocks is certainly different from blue-chip securities with a strong ownership, and these stocks are held by large mutual funds.

The sampling rate should take into account the spectrum of frequency of the noise. It should be set as at least twice the frequency of the noise with the lowest frequency.

The object of the test is to evaluate the impact of the sampling rate, `samplingRate`, and the number κ of clusters used in the EM algorithm:

```
val extractor = YahooFinancials.adjClose :: List[Array[String]
=>Double]() //1

val period = 8
val samplingRate = 10
val smAv = SimpleMovingAverage[Double](period) //2
val obs = DataSource.listSymbols(path).map(sym => { //3
  val xs = DataSource(sym, path, true) |> extractor //2
  val values : XTSeries[Double] = XTSeries.|>(xs)).head //4
  val filtered = smAv |> values
  filtered.zipWithIndex //5
    .drop(period+1).toArray //6
    .filter( _._2%samplingRate==0)
    .map( _._1)
})
```

The first step is to extract the historical quotes for all the stocks using the same extractor as in the K-means test case (line 1).

The symbols of the stocks under consideration are extracted from the name of the files in the path directory. The historical data is contained in the CSV file named `path/STOCK_NAME.csv` (line 3). An implicit conversion is triggered by an assignment of values of the type `XTSeries[Double]` (line 4). The simple moving average algorithm zeroed out the first period values in the smoothed data, `filtered` (line 5). Those null values have to be dropped before applying the sampling (line 6).

The first test is to execute the EM algorithm with $K=3$ clusters and a sampling period of 10 on data smoothed by a simple moving average with a period of 8:

```
MultivariateEM[Double] (K) |> XTSeries[DblVector] (obs) foreach (...)
```

The driver prints the key (line 3), the mean (coordinates of the centroid vector) (line 4), and the standard deviation for each component (cluster).

The sampling of historical prices of the 127 stocks between January 1, 2013 and December 31, 2013 with a frequency of 0.1 hertz produces 24 data points. The following chart displays the mean or centroid of each of the 3 clusters:

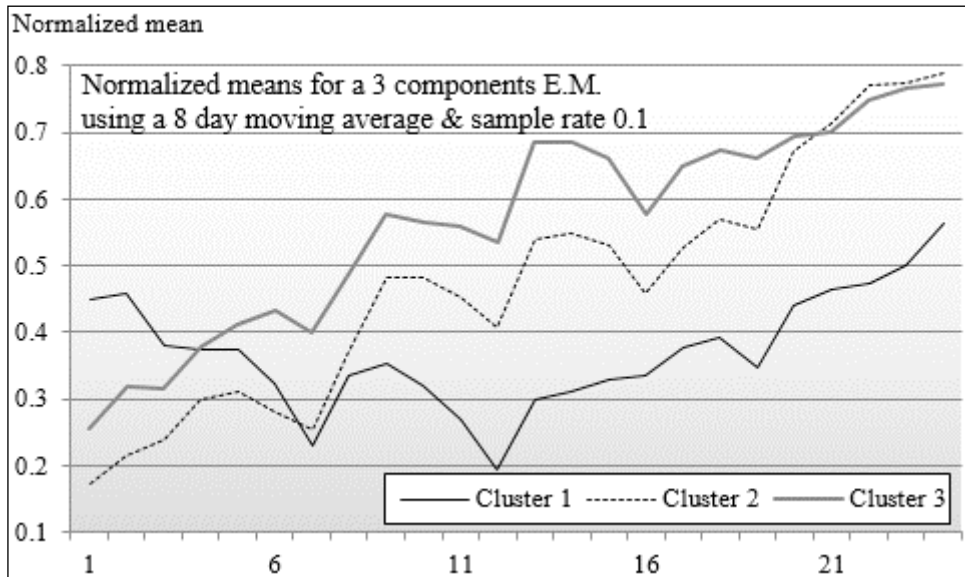


Chart of the normalized means per cluster using EM $K=3$

The mean vectors of clusters 2 and 3 have similar patterns, which may suggest that 2 components or clusters could provide a first insight into the similarity within groups of stocks. The following is a chart of the normalized standard deviation per cluster using EM $K = 3$:

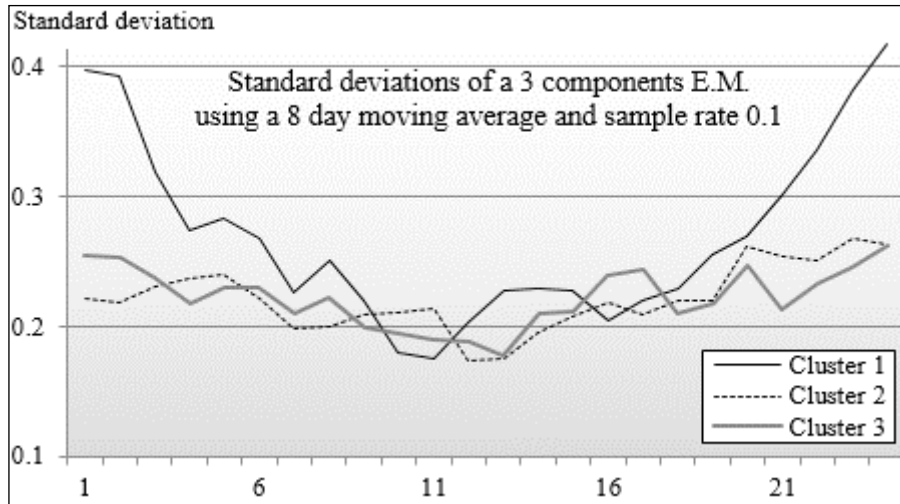


Chart of the normalized standard deviation per cluster using EM $K=3$

The distribution of the standard deviation along the mean vector of each cluster can be explained by the fact that the price of stocks from a couple of industries went down in synergy, while others went up as a semihomogenous group following the announcement from the Federal Reserve that the monthly quantity of bonds purchased as part of the quantitative easing program would be reduced in the near future.

Relation to K-means



You may wonder what is the relation between EM and K-means as both techniques address the same problem. The K-means algorithm assigns each observation uniquely to one and only one cluster. The EM algorithm assigns an observation based on posterior probability. K-means is a special case of the EM for Gaussian mixtures [4:11].

Online EM

Online learning is a powerful strategy for training a clustering model when dealing with very large datasets. This strategy has regained interest from scientists lately. The description of online EM is beyond the scope of this tutorial. However, you may need to know that there are several algorithms available for online EM if you ever have to deal with large datasets: **batch EM**, **stepwise EM**, **incremental EM**, and **Monte Carlo EM** [4:12].

Dimension reduction

Without prior knowledge of the data domain, data scientists include all possible features in their first attempt to create a classification, prediction, or regression model. After all, making assumptions is a poor and dangerous approach to reduce the search space. It is not uncommon for a model to use hundreds of features, adding complexity and significant computation costs to build and validate the model.

Noise-filtering techniques reduce the sensitivity of the model to features that are associated with sporadic behavior. However, these noise-related features are not known prior to the training phase, and therefore, cannot be discarded. As a consequence, training of the model becomes a very cumbersome and time-consuming task.

Overfitting is another hurdle that can arise from a large feature set. A training set of limited size does not allow you to create a model with a large number of features.

Dimension reduction techniques alleviate these problems by detecting features that have little influence on the overall model behavior.

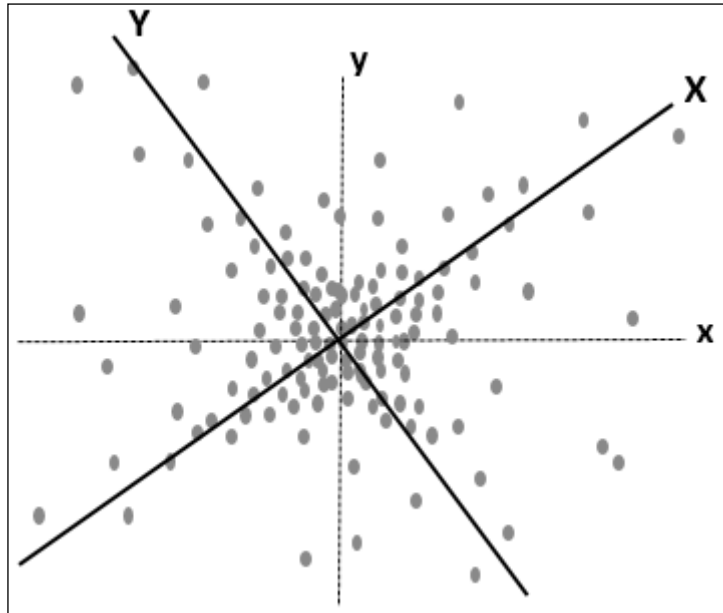
There are three approaches to reduce the number of features in a model:

- Statistical analysis solutions such as ANOVA for smaller feature sets
- Regularization and shrinking techniques, which are introduced in *Chapter 6, Regression and Regularization*
- Algorithms that maximize the variance of the dataset by transforming the covariance matrix

The next section introduces one of the most commonly used algorithms of the third category – principal component analysis.

Principal components analysis (PCA)

The purpose of principal components analysis is to transform the original set of features into a new set of ordered features by decreasing the order of variance. The original observations are transformed into a set of variables with a lower degree of correlation. Let's consider a model with two features $\{x, y\}$ and a set of observations $\{x_i, y_i\}$ plotted on the following chart:



Visualization of principal components for a 2-dimension model

The features x and y are converted into two variables X and Y (that is rotation) to more appropriately match the distribution of observations. The variable with the highest variance is known as the first principal component. The variable with the n^{th} highest variance is known as the n^{th} principal component.

Algorithm

I highly recommend the tutorial from Lindsay Smith [4:13] that describes the PCA algorithm in a very concrete and simple way using a 2-dimension model.

PCA and covariance matrix

The covariance of two features X and Y with the observations set $\{x_i, y_i\}$ is defined as:


$$\text{cov}(X, Y) = \frac{1}{n-1} \sum (x_i - \bar{x})(y_i - \bar{y})$$

Here, \bar{x} and \bar{y} are the respective mean values for the observations x and y .

The covariance is computed from the *zScore* of each observation:

$$x_i = (x_i - \bar{x}) / \sigma$$

For a model with n features, x_i , the covariance matrix is defined as:



$$\Sigma = \begin{bmatrix} \text{cov}(x_0, x_0) & \dots & \text{cov}(x_0, x_{n-1}) \\ \vdots & \text{cov}(x_i, x_j) & \vdots \\ \text{cov}(x_{n-1}, x_0) & \dots & \text{cov}(x_{n-1}, x_{n-1}) \end{bmatrix}$$

The transformation of x to X consists of computing the eigenvalues of the covariance matrix:

$$\Sigma' = W^T \Sigma W = \|\text{cov}(X_i, X_j)\| \text{ and } X = W^T x$$

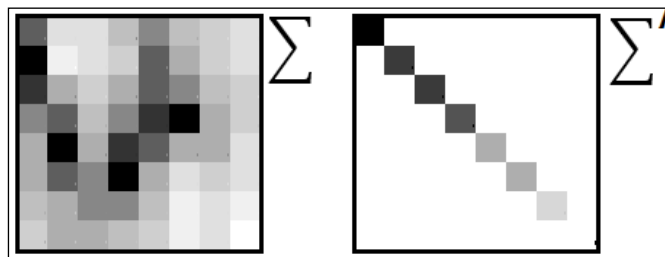
The eigenvalues are ranked by their decreasing order of variance and the cumulative variance for each eigenvalue is computed. Finally, the m top eigenvalues for which the cumulative of variance exceeds a predefined threshold (percentage of the trace of the matrix) are the principal components or reduced feature set.

$$Z = \left\{ X_i \mid m \mid \sum_{k=1}^m \text{cov}(x_k, x_k) > \in \cdot \text{Tr}(\text{cov}) \right\}$$

The algorithm is implemented in five steps:

1. Compute the *zScore* for the observations by standardizing the mean and standard deviation.
2. Compute the covariance matrix Σ for the original set of observations.
3. Compute the new covariance matrix Σ' for the observations with the transformed features by extracting the eigenvalues and eigenvectors.
4. Convert the matrix to rank eigenvalues by decreasing the order of variance. The ordered eigenvalues are the principal components.
5. Select the principal components for which the total sum of variance exceeds a threshold by as a percentage of the trace of the new covariance matrix.

The extraction of principal components by diagonalization of the covariance matrix Σ is visualized in the following diagram. The color used to represent the covariance value varies from white (lowest value) to black (highest value):



Visualization of the extraction of eigenvalues in PCA

The eigenvalues (variance of X) are ranked by the decreasing order of their values. The PCA algorithm succeeds when the cumulative value of the last eigenvalues (the right-bottom section of the diagonal matrix) becomes insignificant.

Implementation

PCA can be easily implemented by using the Apache Commons Math library methods that compute the eigenvalues and eigenvectors. Once again, the main routine is implemented as a pipe operator so that it can be used in a generic workflow as defined in the *The Pipe Operator* section under *Designing a workflow* in *Chapter 2, Hello World!*.

```
import types.ScalaML._, types.CommonMath._, //2

def |> : PartialFunction[XTSeries[Array[T]], (Db1Matrix, Db1Vector)]={
  case xt: XTSeries[Array[T]] if(xt !=null && xt.size>1) => {
```

```
zScoring(xt) match { //1
case Some(obs) => {
  val covariance = new Covariance(obs).getCovarianceMatrix //3
  val transf = new EigenDecomposition(covariance)
  val eigVectors = transf.getV //4
  val eigValues = new ArrayRealVector(transf.getRealEigenvalues)
  val cov = obs.multiply(eigVectors).getData
  (cov, eigValues.toArray) //5
...
}
```

PCA requires that the original set of observations is standardized using the z-score transformation. It is implemented using the `XTSeries.zScoring` function introduced in the *Normalization and Gauss distribution* section in *Chapter 1, Getting Started* (line 1).

The assignment forces the implicit conversion of a time series of features of the type `T` into a matrix of the type `Double`. The implicit conversions between Scala primitives and ScalaML types such as `DblMatrix` (resp. between Apache Commons Math types and Scala ML) are defined in `Types.ScalaML`, as mentioned in the *Type conversions* section in *Chapter 1, Getting Started* (resp. `Types.CommonMath` in the *Time series* section in *Chapter 3, Data Preprocessing*) (line 2). The covariance matrix is computed based on the `zScore` created from the original observations (line 3). The eigenvectors, `eigVectors`, are computed using the `getV` method in the Apache Commons Math `EigenDecomposition` class. The eigenvalues, `eigValues`, are extracted as principal components (line 4).

Finally, the data transformation returns the tuple (*covariance matrix, array of eigenvalues*) (line 5).

Test case

Let's apply the PCA algorithm to extract a subset of the features that represents some of the financial metrics ratios of 34 S&P 500 companies. The metrics under consideration are:

- Trailing Price-to-Earnings ratio (PE)
- Price-to-Sale ratio (PS)
- Price-to-Book ratio (PB)
- Return on Equity (ROE)
- Operation Margin (OM)

The financial metrics are described in the *Terminology* section under *Finances 101* in *Appendix A, Basic Concepts*.

The input data is specified with the following format as a tuple: the ticker symbol and an array of five financial ratios, PE, PS, PB, ROE, and OM:

```
val data = Array[(String, DblVector)] (
  // Ticker          PE      PS      PB      ROE      OM
  ("QCOM", Array[Double] (20.8, 5.32, 3.65, 17.65, 29.2)),
  ("IBM",  Array[Double] (13, 1.22, 12.2, 88.1, 19.9)),
  ...
)
```

The client code that executes the PCA algorithm is defined simply as follows:

```
val pca = new PCA[Double] //1
val input = data.map( _._2.take(3))
val cov = pca |> XTSeries[DblVector](input) //2
Display.show(toString(cov), logger) //3
```

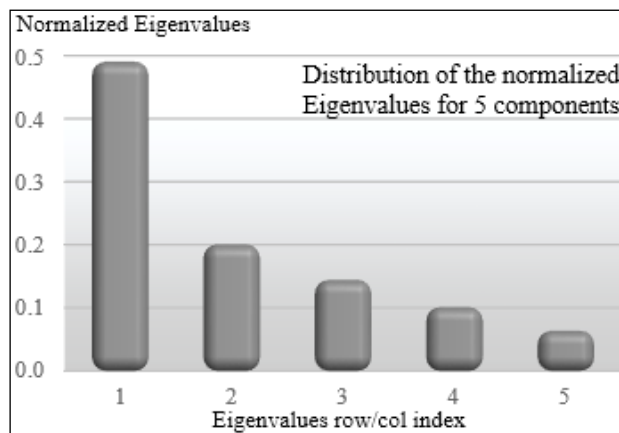
Once the `PCA` class is instantiated (line 1), the eigenvalues and covariance matrix, `cov`, are computed (line 2), and then displayed using the utility singleton `Display` that formats messages and appends to the logger (line 3).

Evaluation

The first test on the 34 financial ratios uses a model that has five dimensions. As expected, the algorithm produces a list of five ordered eigenvalues.

```
2.5321, 1.0350, 0.7438, 0.5218, 0.3284
```

Let's plot the relative value of the eigenvalues (that is, relative importance of each feature) on a bar chart:



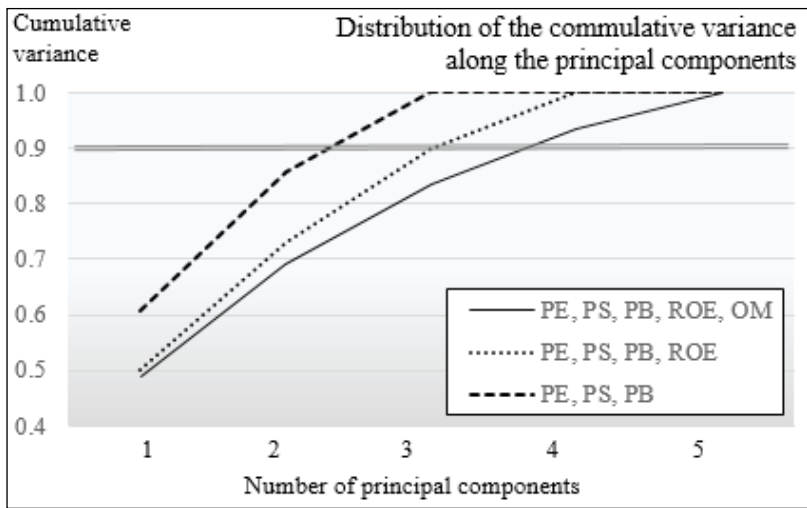
Distribution of eigenvalues in PCA for 5 dimensions

The chart shows that 3 out of 5 features account for 85 percent of total variance (trace of the transformed covariance matrix). I invite you to experiment with different combinations of these features. The selection of a subset of the existing features is as simple as applying Scala's take or drop methods:

```
val numFeatures = 4
val ts = XTSeries[DblVector](data.map(_.take(numFeatures)))
```

Let's plot the cumulative eigenvalues for the three different model configurations:

- **Five features:** PE, PS, PB, ROE, and OM
- **Four features:** PE, PS, PB, and ROE
- **Three features:** PE, PS, and PB



Distribution of eigenvalues in PCA for 3, 4, and 5 features

The chart displays the cumulative value of eigenvalues that are the variance of the transformed features X_i . If we apply a threshold of 90 percent to the cumulative variance, then the number of principal components for each test model is as follows:

- **{PE, PS, PB}: 2**
- **{PE, PS, PB, ROE}: 3**
- **{PE, PS, PB, ROE, OM}: 4**

In conclusion, the PCA algorithm reduced the dimension of the model by 33 percent for the 3-feature model, 25 percent for the 4-feature model, and 40 percent for the 5-feature model for a threshold of 90 percent.



Cross-validation of PCA

Like any other unsupervised learning technique, the resulting principal components have to be validated through a one or K-fold cross-validation using a regression estimator such as **partial least square regression (PLSR)** or the **predicted residual error sum of squares (PRESS)**. For those not afraid of statistics, I recommend *Fast Cross-validation in Robust PCA* by S. Engelen and M. Hubert [4:14]. You need to be aware, however, that the implementation of these regression estimators is not simple.

The principal components can be validated through a 1-fold or K-fold cross-validation, by performing some type of regression estimators or EM on the same dataset. The validation of the PCA is beyond the scope and space allocated to this chapter.

Principal components analysis is a special case of the more general factor analysis. The later class of algorithm does not require the transformation of the covariance matrix to be orthogonal.

Other dimension reduction techniques

Although quite popular, the principal components analysis is far from being the only dimension reduction method. Here are some alternative techniques, listed as reference: factor analysis, principal factor analysis, maximum likelihood factor analysis, independent component analysis (ICA), Random projection, nonlinear PCA, nonlinear ICA, Kohonen's self-organizing maps, neural networks, and multidimensional scaling, just to name a few [4:15].

Performance considerations

The three unsupervised learning techniques share the same limitation – a high computational complexity.

K-means

The K-means has the computational complexity of $O(iKnm)$, where i is the number of iterations, K the number of clusters, n the number of observations, and m the number of features. The algorithm can be improved through the use of other techniques by using the following techniques:

- Reducing the average number of iterations by seeding the centroid using an algorithm such as initialization by ranking the variance of the initial cluster as described at the beginning of this chapter.

- Using a parallel implementation of K-means and leveraging a large-scale framework such as Hadoop or Spark.
- Reducing the number of outliers and possible features by filtering out the noise with a smoothing algorithm such as a discrete Fourier transform or a Kalman filter.
- Decreasing the dimensions of the model by following a two-step process: a first pass with a smaller number of clusters K and/or a loose exit condition regarding the reassignment of data points. The data points close to each centroid are aggregated into a single observation. A second pass is then run on a smaller set of observations.

EM

The computational complexity of the expectation-maximization algorithm for each iteration ($E + M$ steps) is $O(m^2n)$, where m is the number of hidden or latent variables and n is the number of observations.

A partial list of suggested performance improvement includes:

- Filtering of raw data to remove noise and outliers
- Using a sparse matrix on a large feature set to reduce the complexity of the covariance matrix, if possible
- Applying the **Gaussian mixture model (GMM)** wherever possible: the assumption of Gaussian distribution simplifies the computation of the log likelihood
- Using a parallel data processing framework such as Apache Hadoop or Spark as explained in the *Apache Spark* section in *Chapter 12, Scalable Frameworks*
- Using a kernel method to reduce the estimate of covariance in the E-step

PCA

The computational complexity of the extraction of the principal components is $O(m^2n + n^3)$, where m is the number of features and n the number of observations. The first term represents the computational complexity for computing the covariance matrix. The last term reflects the computational complexity of the eigenvalue decomposition.

The list of potential performance improvements or alternative solutions for PCA includes:

- Assuming that the variance is Gaussian
- Using a sparse matrix to compute eigenvalues for problems with large feature sets and missing data
- Investigating alternatives to PCA to reduce the dimension of a model such as the **discrete Fourier transform (DFT)** or **singular value decomposition (SVD)** [4:16]
- Using the PCA in conjunction with EM (a research)
- Deploying a dataset on a parallel data processing framework such as Apache Spark or Hadoop as explained in the *Apache Spark* section in *Chapter 12, Scalable Frameworks*

Summary

This completes the overview of three of the most commonly used unsupervised learning techniques:

- K-means for clustering fully observed features of a model with reasonable dimensions
- Expectation-maximization for clustering a combination of observed and latent features
- Principal components analysis to transform and extract the most critical features in terms of variance

The key point to remember is that unsupervised learning techniques are used:

- By themselves to extract structures and associations from unlabelled observations
- As a preprocessing stage to supervised learning in reducing the number of features prior to the training phase

In the next chapter, we will address the second use case, and cover supervised learning techniques starting with generative models.

5

Naïve Bayes Classifiers

This chapter introduces the most common and simple generative classifiers – Naïve Bayes. As a reminder, generative classifiers are supervised learning algorithms that attempt to fit a **joint probability distribution**, $p(X, Y)$, of two events X and Y , representing two sets of observed and hidden (or latent) variables, x and y .

In this chapter, you will learn, and hopefully appreciate, the simplicity of the Naïve Bayes technique through a concrete example. Then, you will build a Naïve Bayes classifier to predict stock price movement, given some prior technical indicators in the analysis of financial markets.

Finally, you will apply Naïve Bayes to text mining by predicting stock prices, using financial news feed and press releases.

Probabilistic graphical models

Let's start with a refresher course in basic statistics.

Given two events or observations, X and Y , the joint probability of X and Y is defined as $p(X, Y) = p(X \cap Y)$. If the observations X and Y are not related, an assumption known as **conditional independence**, then $p(X, Y) = p(X).p(Y)$. The conditional probability of event Y , given X , is defined as $p(Y | X) = p(X, Y)/p(X)$.

These two definitions are quite simple. However, **probabilistic reasoning** can be difficult to read in the case of large numbers of variables and sequences of conditional probabilities. As a picture is worth a thousand words, researchers introduced graphical models to describe a probabilistic relation between random variables [5:1].

There are two categories of graphs, and therefore, graphical models:

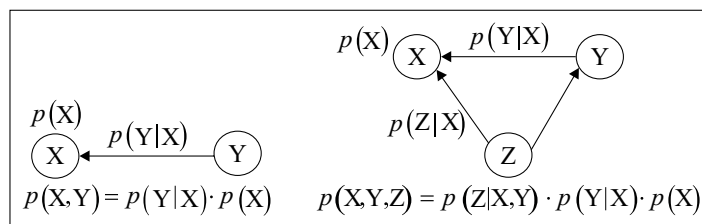
- Directed graphs such as Bayesian networks
- Undirected graphs such as conditional random fields (refer to the *Conditional random fields* section in *Chapter 7, Sequential Data Models*)

Directed graphical models are directed acyclic graphs that have been introduced to:

- Provide a simple way to visualize a probabilistic model
- Describe the conditional dependence (or independence) between variables
- Represent statistical inference in terms of graphical manipulation

A **Bayesian network** is a directed graphical model defining a joint probability over a set of variables [5:2].


The two joint probabilities, $p(X, Y)$ and $p(X, Y, Z)$, can be graphically modeled using Bayesian networks, as follows:



Examples of probabilistic graphical models

The conditional probability $p(Y | X)$ is represented by an arrow directed from the output (or symptoms) Y to the input (or cause) X . Elaborate models can be described as a large directed graph between variables.

[



Metaphor for graphical models

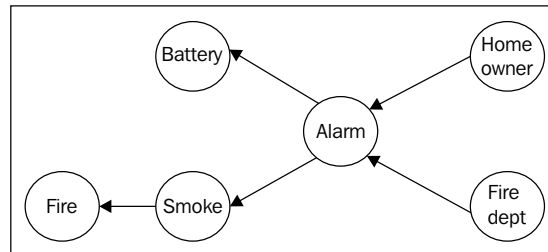
From a software engineering perspective, graphical models visualize probabilistic equations the same way the UML class diagram visualizes object-oriented source code.

]

Here is an example of a real-world Bayesian network; the functioning of a smoke detector:

1. A fire may generate smoke.
2. Smoke may trigger an alarm.
3. A depleted battery may trigger an alarm.

4. The alarm may alert the homeowner.
5. The alarm may alert the fire department.



A Bayesian network for smoke detectors

This representation may be a bit counterintuitive, as the vertices are directed from the symptoms (or output) to the cause (or input). Directed graphical models are used in many different models, besides Bayesian networks [5:3].




Plate models

There are several alternate representations of probabilistic models, besides the directed acyclic graph, such as the plate model commonly used for the **latent Dirichlet allocation (LDA)** [5:4].

The Naïve Bayes models are probabilistic models based on the Bayes's theorem under the assumption of features independence, as mentioned in the *Generative models* section in *Chapter 1, Getting Started*.

Naïve Bayes classifiers

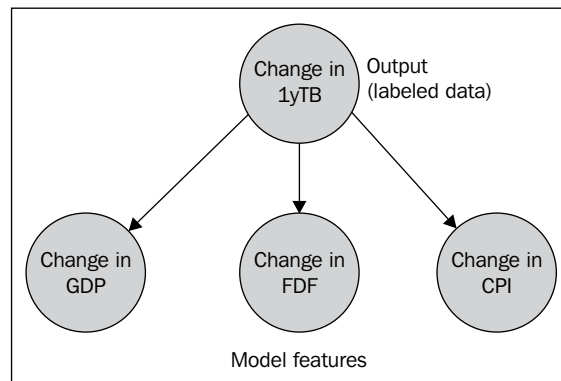
This conditional independence between X features is an essential requirement for the Naïve Bayes classifier. It also restricts its applicability. The Naïve Bayes classification is better understood through simple, concrete examples [5:5].

Introducing the multinomial Naïve Bayes

Let's consider the problem of how to predict change in interest rates. The first step is to list the factors that potentially may trigger or cause an increase or decrease in the interest rates. For the sake of illustrating Naïve Bayes, we will select the **consumer price index (CPI)**, change in the **Federal fund rate (FDF)** and the **gross domestic product (GDP)** as a first set of features. The terminology is described in the *Terminology* section under *Finances 101* in *Appendix A, Basic Concepts*.

The use case is to predict direction of the change in the yield of the **1-year Treasury bill (1yTB)**, taking into account the change in the current CPI, FDF, and GDP. The objective is, therefore, to create a predictive model using a combination of these three features.

It is assumed that there is no available financial investment expert who can supply rules or policies to predict interest rates. Therefore, the model depends highly on the historical data. Intuitively, if one feature is always increasing when the yield of the 1-year Treasury bill increases, then we can conclude that there is a strong correlation of causal relationship between the features and the output variation in interest rates.



The Naïve Bayes model for predicting the change in the yield of the 1-year T-bill

The correlation (or cause-effect relationship) is derived from historical data. The methodology consists of counting the number of times each feature either increases (UP) or decreases (DOWN), and recording the corresponding output (or labeled data), as illustrated in the following table:

ID	GDP	FDF	CPI	1yTB
1	UP	DOWN	UP	UP
2	UP	UP	UP	UP
3	DOWN	UP	DOWN	DOWN
4	UP	DOWN	DOWN	DOWN
...				
256	DOWN	DOWN	UP	DOWN

First, let's tabulate the number of occurrence of each change $\{UP, DOWN\}$ for the three features and the output value (the 1-year Treasury bill):

Number	GDP	FDI	CPI	1yTB
UP	169	184	175	159
DOWN	97	72	81	97
Total	256	256	256	256
UP/Total	0.66	0.72	0.68	0.625

Next, let's compute the number of positive directions for each of the features when the yield 1-year Treasury bill increases (159 occurrences):

Number	GDP	Fed funds	CPI
UP	110	136	127
DOWN	49	23	32
Total	159	159	159
UP/Total	0.69	0.85	0.80

For this table, we conclude that the yield of the 1-year Treasury bill increases when the GDP is increasing (69 percent of the time), the rate of the Federal funds increases (85 percent of the time) and the CPI increases (80 percent of the time).

Let's formalize the Naïve Bayes model before turning these findings into a probabilistic model.

Formalism

Let's start by clarifying the terminology used in the Bayesian model:

- **Class prior probability** or **class prior** is the probability of a class
- **Likelihood** is the probability of an observation given a class, also known as the probability of the predictor given a class
- **Evidence** is the probability of observations occurring, also known as the prior probability of the predictor
- **Posterior probability** is the probability of an observation x being in a given class

No model can be simpler! The log likelihood, $\log(p(x | C))$, is commonly used instead of the likelihood, $p(x | C)$, (probability of an observation given a class) in order to reduce the impact of the features y that have a low likelihood, $p(y | C)$.

The objective of the Naïve Bayes classification of a new observation, is to compute the class that has the higher log likelihood. The mathematical notation for the Naïve Bayes model is also straightforward.

The posterior probability, $p(C_j | x)$:

$$p(C_j | x) = \frac{p(x | C_j) \cdot p(C_j)}{p(x)}$$

- $x = \{x_i\}$ ($0, n-1$), with a set of n features
- $\{C_j\}$, a set of classes with their class prior $p(C_j)$
- $p(x)$, the evidence of new observation
- $p(x | C_j)$, the likelihood for each feature

Posterior probability, $p(C_j | x)$, with conditional independence:



$$p(C_j | x) = \prod_{i=0}^{n-1} p(x_i | C_j) \cdot p(C_j)$$

- x_i are independent and the probabilities are normalized for evidence $p(x) = 1$

Log-likelihood:

$$\log p(C_j | x) = \sum_{i=0}^{n-1} \log p(x_i | C_j) + \log p(C_j)$$

Naïve Bayes classification:

$$C_m = \arg \max_j (\log p(C_j | x))$$

This particular use case has a major drawback – the GDP statistics are provided quarterly, while the CPI data is made available once a month and a change in the FDF rate is rather infrequent.

The frequentist perspective

The ability to compute the posterior probability depends on the formulation of the likelihood using historical data. A simple solution is to count the occurrences of observations for each class and compute the frequency.

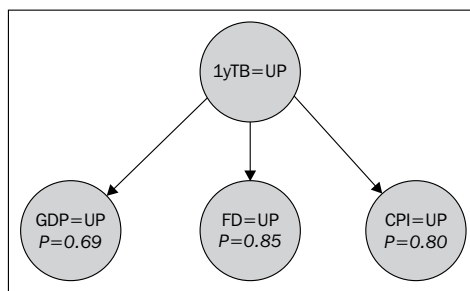
Let's consider the first example that predicts the direction of change in the yield of the 1-year Treasury bill given changes in the GDP, FDF, and CPI.

The results are expressed with simple probabilistic formulas and a directed graphical model:

$$P(\text{GDP=UP} | 1\text{yTB=UP}) = 110/159$$

$$P(1\text{yTB=UP}) = \text{num occurrences } (1\text{yTB=UP}) / \text{total num of occurrences} = 159/256$$

$$\begin{aligned} p(1\text{yTB=UP} | \text{GDP=UP}, \text{FDF=UP}, \text{CPI=UP}) &= p(\text{GDP=UP} | 1\text{yTB=UP}) \times \\ & p(\text{FDF=UP} | 1\text{yTB=UP}) \times \\ & p(\text{CPI=UP} | 1\text{yTB=UP}) \times \\ p(1\text{yTB=UP}) &= 0.69 \times 0.85 \times \\ & 0.80 \times 0.625 \end{aligned}$$



The Bayesian network for the prediction of the change of the yield of the 1-year Treasury bill



Overfitting

The Naïve Bayes model is not immune to overfitting, in case the number of observations is not large enough relative to the number of features. One approach to address this problem is to perform a feature selection, using the mutual information exclusion [5:6].

This problem is not a good candidate for a Bayesian classification for two reasons:

- The training set is not large enough to compute accurate prior probabilities and generate a stable model; decades of quarterly GDP data is needed to train and validate the model
- The features have different rates of change, which predominately favor the feature with the highest frequency; in this case, the CPI

Let's select another use case for which a large historical data set is available and can be automatically labeled.

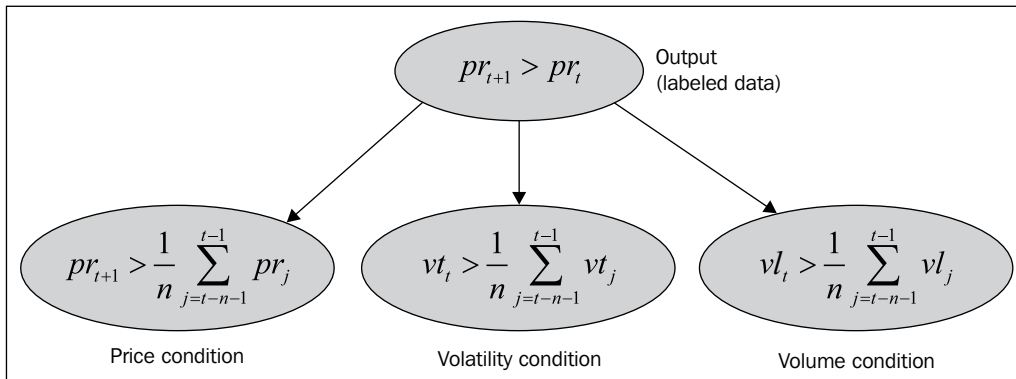
The predictive model

The predictive model is the second use case that consists of predicting the direction of the closing price of a stock, $pr(t+1) = \{UP, DOWN\}$, at trading day $t+1$, given the history of its direction of the price, volume, and volatility for the previous t days, $pr(i), i=1, t$. The features volume and volatility have been already used in the *Creating a model (learning)* section under *Let's kick the tires* in *Chapter 1, Getting Started*.

Therefore, the three features under consideration are:

- The closing price, $pr(t)$, of the last trading session, t , is above or below the average closing price over the n previous trading days, $[t-n, t]$
- The volume of the last trading day, $vl(t)$, is above or below the average volume of the n previous trading days
- The volatility on the last trading day, $vt(t)$, is above or below the average volatility of the previous n trading days

The directed graphic model can be expressed using one output variable (price at session $t+1$ is greater than price at session t) and three features: price condition (1), volume condition (2), and volatility condition (3).



A Bayesian model for predicting the future direction of the stock price

This model works under the assumption that there is at least one observation, and ideally few observations for each feature and for each labeled output.


The zero-frequency problem

It is possible that the training set does not contain any data actually observed for a feature for a specific label or class. In this case, the mean is $0/N = 0$, and therefore, the likelihood is null, making classification unfeasible. The case for which there are only few observations for a feature in a given class is also an issue, as it skews the likelihood.

There are a couple of correcting or smoothing formulas for unobserved features or features with a low number of occurrences that address this issue, such as the Laplace and Lidstone smoothing formula.


The smoothing factor for counters

Laplace smoothing of the mean k/N out of N observations of features of dimension n :



$$\mu' = \frac{k+1}{N+n}$$

Lidstone smoothing with a factor α :



$$\mu' = \frac{k+\alpha}{N+\alpha \cdot n}$$

The two formulas are commonly used in natural language processing applications, for which occurrence of a specific word or tag is a feature [5:7].

Implementation

I think it is time to write some Scala code and toy around with Naïve Bayes. Let's start with an overview of the software components.

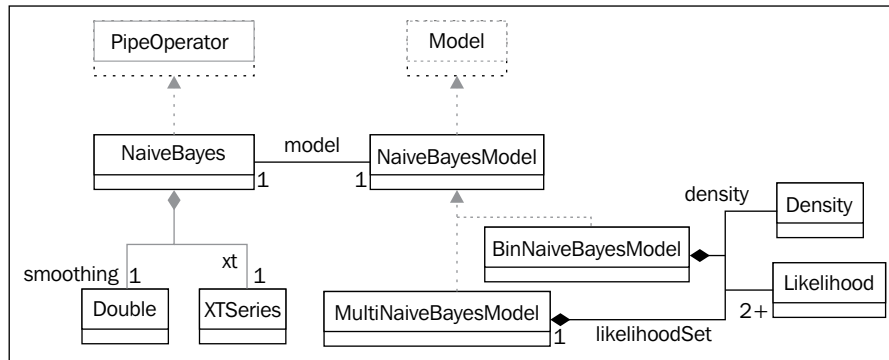
Software design

Our implementation of the Naïve Bayes classifier uses the following components:

- A generic model, `NaiveBayesModel`, of the type `Model`, which is initialized through training during the instantiation of the class.
- A model for the binomial classification, `BinNaiveBayesModel`, which subclasses `NaiveBayesModel`. The model consists of a density function of the type `Density`, and a pair of positive and negative `Likelihood` instances.
- A model for the multinomial classification `MultiNaiveBayesModel`.
- The predictive or classification routine is implemented as a data transformation extending the `PipeOperator` trait.
- The `NaiveBayes` classifier class has two parameters: a smoothing function such as Laplace and a labeled training set of the `XTSeries` type.

The principle of software architecture applied to the implementation of classifiers is described in the *Design template for classifiers* section in *Appendix A, Basic Concepts*.

The key software components of the Naïve Bayes classifier are described in the following UML class diagram:



The UML class diagram for the Naïve Bayes classifier


Training

The objective of the training phase is to build a model consisting of the likelihood for each feature and the class prior. The likelihood for a feature is identified as:

- The number of occurrences k of this features for $N > k$ observations in case of binary features or counters
- The mean value for all the observations for this features in the case of numeric or continuous features

It is assumed for the sake of this test case that the features, technical analysis indicators price, volume, and volatility are conditionally independent. This assumption is not actually correct.

[



Conditional dependency

Recent models, known as **Hidden Naïve Bayes (HNB)**, relax the restrictions on the independence between features. The HNB algorithm uses conditional mutual information to describe the interdependency between some of the features [5:8].

]

Let's write the code to train the multinomial Naïve Bayes. The first step is to define the likelihood for each feature using historical data. The `Likelihood` class has the following attributes:

- The label for the observation, `label`
- An array of tuple Laplace or Lidstone smoothed mean and standard deviation, `muSigma`
- The prior class `prior` that computes $p(c)$

As with any code snippet presented in this book, the validation of class parameters and method arguments are omitted in order to keep the code readable. The `Likelihood` class is defined as follows:

```

type Density = (Double*) => Double //1
type XYTSeries = Array[(Double, Double)]
val MINLOGARG = 1e-32
val MINLOGVALUE = -MINLOGARG
class Likelihood[T <% Double](val label: Int, val muSigma: XYTSeries,
prior: Double) { //2
  def score(obs: Array[T], density: Density): Double =
    (obs, muSigma).zipped
      .foldLeft(0.0)((post, xms) => {
        val mean = xms._2._1
        val stdDev = xms._2._2
        val _obs = xms._1
        val prob = density(mean, stdDev, _obs)
        post + Math.log(if(prob < MINLOGARG) MINLOGVALUE else prob)
      }) + Math.log(prior) //3
}

```

The functions of the `Density` type compute the probability density for the values of a feature (line 1). The method takes an undefined number of arguments: the mean, the standard deviation, and the input value for the Gaussian distribution, the mean and input value $\{0, 1\}$ for the Bernoulli distribution. The default probability density function is the normal distribution implemented by `Stats.gauss`.

The parameterized, view-bounded class, `Likelihood`, has two purposes:

- Define the model extracted from training (likelihood for each feature and the class prior) in the constructor (line 2)
- Compute the score of a new observation as part of the classification process score (line 3). The computation of the log of the likelihood uses a `density` method of the type `Density`, which is an argument of the `score` method. As seen in the next section, the density can be either a Gaussian or a Bernoulli distribution. The `score` method uses the Scala's `zipped` method to merge the observation values with the labeled output.

The next step is to define the `BinNaiveBayesModel` model for a two-class classification scheme. The two-class model consists of the two `Likelihood` instances: positives for the label UP (`value==1`) and negatives for the label DOWN (`value==0`). In order to make the model generic, we created `NaiveBayesModel`, an abstract class that can be extended as needed to support both the Binomial and Multinomial Naïve Bayes models, as follows:

```
abstract class NaiveBayesModel [T <% Double] (density: Density) {
  def classify(values: DblVector): Int
}
class BinNaiveBayesModel [T <% Double] (positives: Likelihood,
negatives: Likelihood, density: Density) extends NaiveBayesModel [T] (
density) {
  override def classify(x: Array[T]): Int =
    if (positives.score(x,density) > negatives.score(x,density)) 1
    else 0
}
```

The classification is executed by the `classify` method called by the `|>` operator in the Naïve Bayes classifier. It returns 1 for the class containing the positive cases and 0 for the negative.



Model validation

The parameters of the Naïve Bayes model (likelihood) are computed through training and the `model` value is instantiated regardless of whether the model is actually validated in this example. A commercial application would require the model to be validated using a methodology such as the K-fold validation and F1 measure. (Refer to the *Design template for classifiers* section in *Appendix A, Basic Concepts*.)

The multinomial Naïve Bayes model, defined by the `MultiNaiveBayesModel` class is very similar to the `BinNaiveBayesModel` class:

```
class MultiNaiveBayesModel[T <% Double](likelihoodXs:
List[Likelihood[T]], density: Density) extends NaiveBayesModel[T]
(density) {
  override def classify(x: Array[T]): Int =
    likelihoodXs.sortWith((p1,p2) => p1.score(x, density) >
p2.score(x, density)).head.label
}
```

The multinomial Naïve Bayes model differs from the binomial version in the following ways:

- The likelihood is defined as a list, `likelihoodXs` (one likelihood per class)
- The runtime classification sorts the class by the log likelihood (`sortWith`), selects the class with the highest `score`, and returns the class ID

Finally, the Naïve Bayes classifier is implemented by the `NaiveBayes` class. It implements the training and runtime classification using the Naïve Bayes formula. Any supervised learning model needs to be validated. In order to force the developer to define a validation for any new supervised learning technique, the class inherits from the `Supervised` trait that declares the validation method, `validate`:

```
trait Supervised[T] {
  def validate(xt: XTSeries[(Array[T],Int)], tpClass: Int): Double
}
```

The `validate` method takes a labeled time series `xt` as an array of tuples (observation, class label) and the `tpClass` index that contains the true positives (that is, increase in the stock price) outcome. The method returns an F1-measure.

Besides inheriting the `Supervised` trait, the `NaiveBayes` class inherits the `PipeOperator` trait so that it can be integrated into a generic workflow as one of the computation units.

The attributes of the multinomial Naïve Bayes are as follows:

- The smoothing formula (Laplace, Lidstone, and so on): `smoothing`
- The labeled training set defined as a time series: `xt`
- The probability density function: `density`

The NaiveBayes class is defined as follows:

```

Class NaiveBayes[T <% Double](smoothing: Double, xt:
XTSeries[(Array[T], Int)], density: Density) extends PipeOperator[XTSeries
ries[(Array[T]), Array[Int]] with Supervised[T] {

  val model = BinNaiveBayesModel[T](train(1), train(0), density) //1
  def train(label: Int)(implicit f: Array[T] => DblVector):
Likelihood[T] = { //2
    val xi = xt.toArray
    val values = xi.filter( _. _2 == label ).map(x => f(x._1) )
    val dim = xi(0)._1.size
    val vt = XTSeries[DblVector](values.toArray) //3
    val muStdDev = statistics(vt).map(stat =>
      (stat.lidstoneMean(smoothing, dim), stat.stdDev))
    Likelihood(label, muStdDev, values.size.toDouble/xi.size) //4
  }
  ...

```

The classifier uses the binomial Naïve Bayes model, `BinNaiveBayesModel` (line 1). The training process is implemented in the constructor by invoking the private `train` method (line 2). The method relies on an implicit conversion, `f: Array[T] => DblVector`, because of the `Array` type erasure. The main reason for this is to hide the details of the model and its training from the client code. We cannot assume that the user of the model is the same person as the creator of the model.



Training and class instantiation

There are several benefits of allowing the instantiation of the Naïve Bayes mode only once when it is trained. It prevents the client code from invoking the algorithm on an untrained or partially trained model, and it reduces the number of states of the model (untrained and trained). It is an elegant way to hide the details of the training of the model from the user.

The `train` method takes the labeled observations (observations or label) as input. The `vt` time series is extracted (line 3) and the likelihoods are calculated by counting the positive and negative labels, computing the mean, corrected with the Lidstone smoothing formula (line 4). The `lidstoneMean` method and standard deviation, `stdDev`, use the `statistics` method of the `XTSeries` singleton instance.

The `NaiveBayes` class also defined the runtime classification method `|>` and the F1-validation methods. Both methods are described in the next section.

Handling missing data



Naïve Bayes has a no-nonsense approach to handling missing data. You just ignore the attribute in the observations for which the value is missing. In this case, the prior for this particular attribute for these observations is not computed. This workaround is obviously made possible because of the conditional independence between features.

Classification

The likelihood and class prior that have been computed through training is used for validating the model and classifying new observations.

The score represents the log of likelihood estimate (or the posterior probability), which is computed as the summation of the log of the Gaussian distribution using the mean and standard deviation, extracted from the training phase and the log of the likelihood class.

The Naïve Bayes classification using Gaussian distribution is illustrated using two classes, c_1 and c_2 , and a model with two features (x and y):

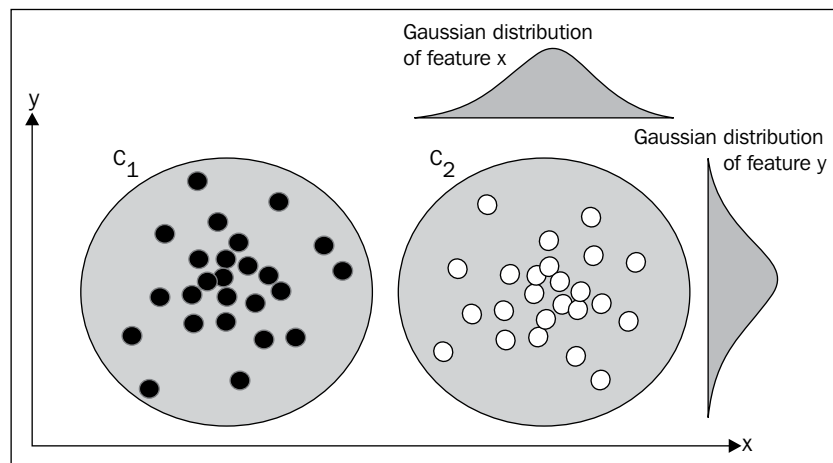


Illustration of the Gaussian Naive Bayes using a 2-dimensional model

The **Gaussian mixture** is particularly suited for modeling datasets for which the features have large sets of discrete values or are continuous variables. The conditional probabilities for the feature x is described by the normal probability density function [5:9].

Naïve Bayes classification using Gaussian density

For a Lidstone or Laplace smoothed mean μ' and a standard deviation σ , the log likelihood of a posterior probability is defined as:



$$\log p(C_j | x) = \sum_{i=0}^{N-1} \log \left(\frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{(x_j - \mu')^2}{2\sigma^2}} \right) + \log p(C_j)$$

In this example, we used the Gaussian distribution as our probability density function as defined in the `Stats` object, which was introduced in *Chapter 2, Hello World!*. The implementation of the computation of the **Gaussian** probability density is quite simple, shown as follows:

```
object Stats {
  final val INV_SQRT_2PI = 1.0/Math.sqrt(2.0*Math.PI)
  def gauss(mu: Double, sigma: Double, x:Double) : Double = {
    val y = x - mu
    INV_SQRT_2PI/sigma * Math.exp(-0.5*y*y/sigma*sigma)
  }
  def gauss(x: Double*): Double = gauss(x(0), x(1), x(2))
  ...
}
```

The second version of the Gaussian density is required to handle the `Density` type: `(Double, Double, Double) => Double`.

Finally, the classification method is implemented as the pipe operator `|>` of the `NaiveBayes` class. The classification model and the density function are provided at runtime as attributes of the class:

```
def |> : PartialFunction[XTSeries[Array[T]], Array[Int]] = {
  case xt: XTSeries[Array[T]] if(xt != null && xt.size > 0 && model !=
  None) => xt.toArray.map(model.classify(_))
}
```

Labeling

The most critical element in the training of a supervised learning algorithm is the creation of labeled data. Fortunately, in this case, the label (or expected class) can be automatically generated. The objective is to predict the direction of the price of a stock for the next trading day, taking into account the average price, volume, and volatility over the last n days.

The first step is to extract the average price, volume, and volatility for each stock during the period of Jan 1, 2000 and Dec 31, 2014 with daily and weekly closing prices. Let's use the simple moving average to compute these averages for the $[t-n, t]$ window.

First, the `extractor` function extracts the closing, high, and low prices, and volume for each trading day, using the `toDouble` and `%` operators described in the *Data extraction* and *Data sources* section in *Appendix A, Basic Concepts*, as follows:

```
val extractor = toDouble(CLOSE) //stock closing price
               :: ratio(HIGH, LOW) //volatility (HIGH-LOW)/HIGH
               :: toDouble(VOLUME) //daily stock trading volume
               :: List[Array[String] => Double] ()
```

Secondly, the data source extractor outputs the four statistics for each stock (line 1) for which the average for a window period is computed (line 3) using a simple moving average `mv` (line 2):

```
val xs = DataSource(symbol, path, true) |> extractor //1
val mv = SimpleMovingAverage(period) //2

val ratios = xs.map(x => { //3
  val xt = mv get x, toArray
  val zValues = x.drop(period).zip(xt.drop(period))
  zValues.map(z => if(z._1 > z._2) 1 else 0).toArray //4
})
var prev = xs(0)(period)
val label = xs(0).drop(period+1).map( x => { //5
  val y = if( x > prev) 1 else 0
  prev = x; y
}).toArray
ratios.transpose.take(label.size).zip(label) //6
```

The Scala's `drop` method is used to shift the time series to compute the average of the three variables: price, `toDouble(CLOSE)`; volume, `toDouble(VOLUME)`; and volatility, `ratio(HIGH, LOW)` (line 4). The labeled data, direction of the price action for the next trading day, is added to the three ratios (line 5). Finally, the array is transposed to extract the list of tuples (list of UP/DOWN values for each feature and price direction for next trading day/labeled data) (line 6).

The labeled data extracted from the input CSV file is used in the training and validation of the time series using the Naïve Bayes classifier:

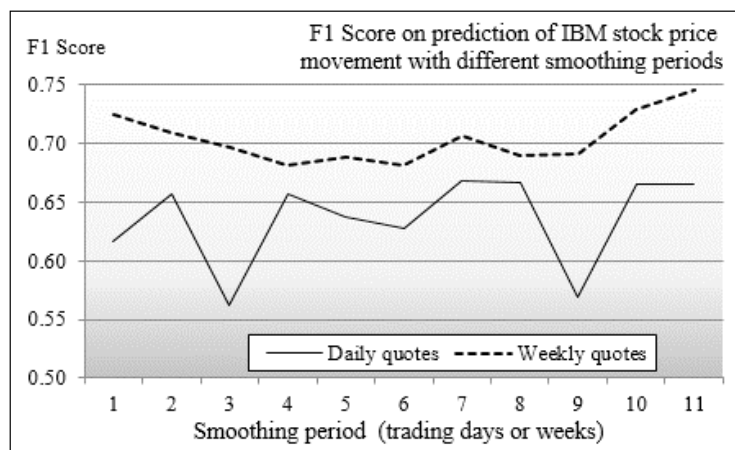
```
val trainValidRatio = 0.8
val period = 10

val labels = XTSeries[(Array[Int], Int)](input.map(x =>
    (x._1.toArray, x._2)).toArray) //7
val numObsToTrain = (trainValidRatio*labels.size).floor.toInt //8
val nb = NaiveBayes[Int](labels.take(numObsToTrain)) //9
validate(labels.drop(numObsForTrains+1), nb) //10
```

The original labeled dataset, `labels`, is split between training and validation labeled data (line 7) using the `trainValidRatio` ratio (line 8). The `NaiveBayes` constructor initializes the model through training (line 9). Finally, the `validate` method returns the F1 measure for the validation test (line 10).

Results

The next chart plots the value of the F1 measure of the predictor of the direction of the IBM stock using price, volume, and volatility over the previous n trading days, with n varying from 1 to 12 trading days:



A graph of the F1-measure for the validation of the Naïve Bayes model

The preceding chart illustrates the impact of the value of the averaging period (number of trading days) on the quality of the multinomial Naïve Bayesian prediction, using the value of stock price, volatility, and volume relative to their average over the averaging period.

From this experiment, we conclude that:

- The prediction of the stock movement using the average price, volume, and volatility is not very good. The F1 measure for the models using weekly (with respect to daily) closing prices varies between 0.68 and 0.74 (with respect to 0.56 and 0.66).
- The prediction using weekly closing prices is more accurate than the prediction using the daily closing prices. In this particular example, the distribution of the weekly closing prices is more reflective of an intermediate term trend than the distribution of daily prices.
- The prediction is somewhat independent of the period used to average the features.

Multivariate Bernoulli classification

The previous example uses the Gaussian distribution for features that are essentially binary, $\{UP=1, DOWN=0\}$, to represent the change in value. The mean value is computed as the ratio of the number of observations for which $x_i = UP$ over the total number of observations.

As stated in the first section, the Gaussian distribution is more appropriate for either continuous features or binary features for very large labeled datasets. The example is the perfect candidate for the Bernoulli model.

Model

The Bernoulli model differs from Naïve Bayes classifier in that it penalizes the features x , which do not have any observations; the Naïve Bayes classifier ignores them [5:10].



The Bernoulli mixture model

For a feature function f_i , with $f_i = 1$ if the feature is observed, and a value of 0 if the feature is not observed:

$$p(f_i | C_j) = \prod_{k=0}^{n-1} (f_k \cdot p(x_k | C_j) + (1 - f_k)(1 - p(x_k | C_j)))$$

Implementation

The implementation of the Bernoulli model consists of modifying the `Likelihood`.score scoring function by using the Bernoulli density defined in the `Stats` object:

```
object Stats {  
  def bernoulli(mean: Double, p: Int): Double = mean*p +  
  (1-mean)*(1-p)  
  def bernoulli(x: Double*): Double = bernoulli(x(0), x(1).toInt)  
  ...  
}
```

The first version of the Bernoulli algorithm is the direct implementation of the mathematical formula. The second version uses the signature of the *Density* (`Double*`) => `Double` type.

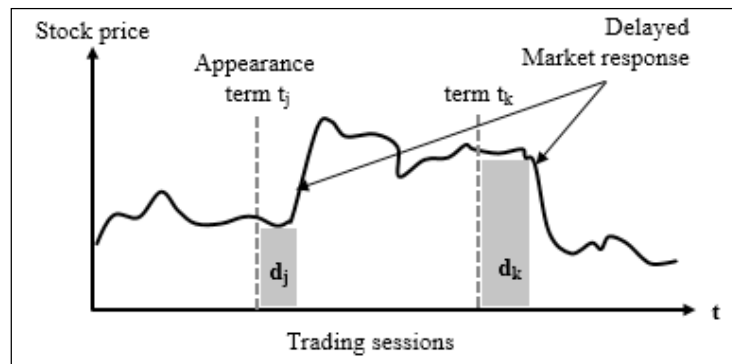
The mean value is the same as in the Gaussian version. The binary feature is implemented as an `Int` type with the value `UP = 1` (with respect to `DOWN = 0`) for the upward (with respect to downward) direction of the financial technical indicator.

Naïve Bayes and text mining

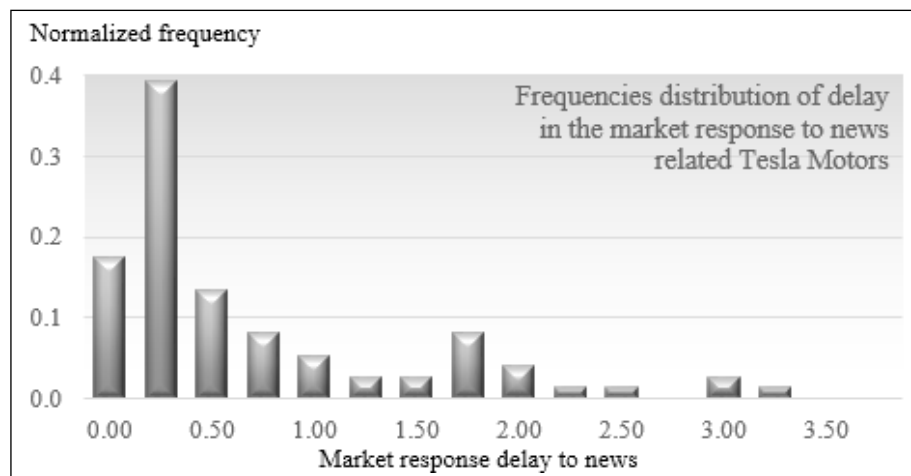
The multinomial Naïve Bayes classifier is particularly suited for **text mining**. Naïve Bayes is used to classify the following entities:

- E-mails as legitimate versus spam
- Business news stories
- Movie reviews and scoring
- Technical papers as per field of expertise

This third use case consists of predicting the direction of a stock, Tesla Motors Inc, (ticker symbol: TSLA) give the financial news. The features are the frequency of occurrence of some specific terms related to the stock. It is unclear how fast the investor or trader reacts to the news and influence, if any, of the value of a stock. Therefore, the delayed response time, as depicted in the following chart, should be a feature of the proposed model:



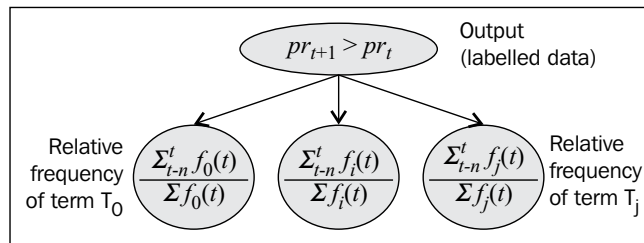
The feature market response delay would play a role in the training, only if the variance of the observations is significant. The distribution of the frequencies of the delay in the market response to any newsworthy articles regarding TSLA shows that the stock prices react within the same day in 82 percent of the case, as seen here:



The frequency peak for a market response delay of 1.75 days can be explained by the fact that some news are released over the weekend and investors have to wait till the following Monday to impact the stock price. The second challenge is to assign any shift of stock price to a specific news release, taking into account that some news can be redundant and simultaneous.

Therefore, the model features for predicting the stock price, pr_{t+1} , are the relative frequency, f_i , of occurrence of a term T_i within a time window $[t-n, t]$, where t and n are trading days.

The following graphical model formally describes the causal relation or conditional dependency of the direction of the stock price between two consecutive trading sessions t and $t+1$, given the relative frequency of appearance of some terms in the media:



The Bayesian model for the prediction of stock movement given financial news

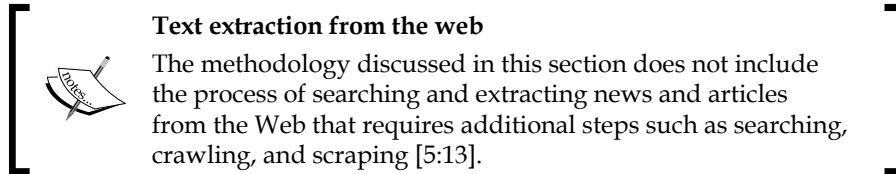
For this exercise, the observation sets are the corpus of news feeds and articles released by the most prominent financial news organizations, such as Bloomberg or CNBC. The first step is to devise a methodology to extract and select the most relevant terms associated with a specific stock.

Basics of information retrieval

A full discussion of information retrieval and text mining is beyond the scope of this book [5:11]. For the sake of simplicity, the model will rely on a very simple model for extracting relevant terms and computing their relative frequency. The following 10-step sequence of actions describe one of numerous methodologies to extract the most relevant terms from a corpus:

1. Create or extract the timestamp for each news article.
2. Extract the title, paragraph, and sentences of each article using a Markovian classifier.
3. Extract the terms from each sentence using **regular expressions**.
4. Correct terms for typos using a dictionary and metric such as the **Levenstein** distance.
5. Remove the nonstop words.
6. Perform **stemming** and **lemmatization**.

7. Extract bags of words and generate a list of **n-grams** (as a sequence of n terms).
8. Apply a **tagging model** build using a maximum entropy or conditional random field to extract nouns and adjectives (such as NN, NNP, and so on).
9. Match the terms against a dictionary that supports senses, hyponyms, and synonyms, such as **WordNet**.
10. **Disambiguate** word sense using **DBpedia** [5:12].



Implementation

Let's apply the text mining methodology template to predict the direction of a stock, given the financial news. The algorithm relies on a sequence of 8 simple steps:

1. Extracting all news with a reference to a specific stock or company in the news feed.
2. Extracting the timestamp or date of the article using a regular expression.
3. Grouping all the news articles related to the stock for a specific date t into a document \mathcal{D}_t .
4. Ordering the documents \mathcal{D}_t as per the timestamp.
5. Extracting the terms $\{T_{i,D}\}$ from each sentence of the document \mathcal{D}_t and ranking them by their relative frequency.
6. Aggregating the terms $\{T_{t,i}\}$ for all the documents sharing the same release date t .
7. Computing the relative frequency, rtf , of each term, $\{T_{t,i}\}$, for the date t , as the ratio of number of its occurrences in all the articles released at t to the total number of its occurrences of the term in the entire corpus.
8. Normalizing the relative frequency for the average number of articles per date, $nrtf$.

The relative term frequency for term t_i with n_{ia} occurrences in article a released on the date Dt is given as:

$$ntrf(t_i) = \frac{\sum_{a \in Dt} n_{ia}}{\sum_{a \in Corpus} n_{ia}}$$



The relative term frequency normalized by the average number of articles per day, Na/D is given as:

$$ntrf(t_i) = \frac{rtf(t_i)}{Na/D}$$

Extraction of terms

First, let's define the features set for the financial terms as the `NewsArticles` class parameterized for the date type `T`. For the sake of simplicity, the type of date value is explicitly viewbounded to `Long`. The `NewsArticles` class is a container of the news articles and press releases relevant to a specific stock. At its core, a news article is defined by its release or publication, and the list of tuple of terms and their relative frequency. The `NewsArticles` class is defined as follows:

```
@implicitNotFound("NewsArticles. Ordering not explicitly defined")
class NewsArticles[T <% Long](implicit val order: Ordering[T]) {
  val articles = new HashMap[T, Map[String, Double]]
  ...
}
```



The `@implicitNotFound` annotation

I recommend using the `implicitNotFound` annotation for every implicit class and method parameter. A declaration may be obvious to one software developer but not obvious to another developer.

The `NewsArticles` class uses the mutable `HashMap` data structure to manage the set of articles. An article is defined by:

- Its release date (type `T`)
- Its map of tuples $\{term\ contained\ in\ the\ article,\ relative\ frequency\ (or\ weight)\ of\ the\ term\}$, `wTerms`

The weight of a term is computed as the ratio of the number of occurrences of this term in the article, to the total number of occurrences in the entire corpus of articles related to the stock.

The implicit `Ordering` class parameter is required for sorting.

The `map articles` is populated with the overloaded operator `+=`:

```
def += (date: T, wTerms: Map[String, Double]): Unit = { //1
  def merge(m1: Map[String, Double], m2: Map[String, Double]):
  Map[String, Double] = { //2
    (m1.keySet ++ m2.keySet).foldLeft(new HashMap[String, Double])((m,
  x) => {
      var wt = 0.0
      if(m1.contains(x)) wt += m1(x)
      if(m2.contains(x)) wt += m2(x)
      m.put(x, wt)
      m
    }).toMap
  }
  articles.put(date, if(articles.contains(date))
    merge(articles(date), wTerms) else wTerms) //3
}
```

The `+=` method adds new sets (mutable hash map) of pairs (terms, relative frequency), `wTerms`, released at a specific date, to the existing map of news articles (line 1). The terms related to different articles from the same date are merged using the local merge function (line 2). Finally, the list of key-value pairs (term, frequency) is ordered by their timestamp of the type `T`.

The second method, `toOrderedArray`, consists of ordering the articles per their release date:

```
def toOrderedArray: Array[(T, Map[String, Double])] = articles.
  toArray.sortWith( _._1 < _._1)
```

Scoring of terms

The scoring of the terms is actually performed by the `TermsScore` class, parameterized by date and the `score` method:

```
class TermsScore[T <% Long](toDate: String =>T, toWords: String =>
  Array[String], lexicon: Map[String, String])(implicit val order:
  Ordering[T]) {
  def score(corpus: Corpus): Option[NewsArticles[T]]
}
```

The `TermsScore` class parameterized for the type of release date has three parameters:

- A `toDate` function to extract the date from each news article. The function can be implemented as a regular expression or a group of regular expressions.
- A `toWords` function to extract the nonstop terms from the content of the article. The function can be quite elaborate, as described in the previous section. It may require creating classifiers to extract sentences, n-grams, and tags.
- A `lexicon` function that simulates the lemmatization and stemming of the most common terms. The `lexicon` function is implemented as a map that attaches a semantic equivalent to each term as a poor man's lemmatization. For example, "China", "Chinese", and "Shanghai" are semantically associated to the term "China".

The type for date `T` is view bounded by the `Long` type because it is assumed that any date can be potentially converted into time in milliseconds. The `Ordering[T]` class is provided as an implicit attribute to order the news articles as per their release date.

The relative frequency of a term t is computed arbitrarily, as the ratio of the number of occurrences of t for a specific date to the total number of terms.

Let's look at the scoring method:

```
type Corpus = (String, String, String) //1
def score(corpus: Corpus): Option[NewsArticles[T]] = { //2
  val docs = rank(corpus)

  val cnts = docs.map(doc => (doc._1, count(doc._3)) ) //3
  val totals = cnts
    .map(_._2) //4
    .foldLeft(Counter[String])((s, cnt) => s ++ cnt)
  val articles = NewsArticles[T]
  cnts.foreach(cnt => articles += (cnt._1, (cnt._2/totals).toMap))
  articles
  ...
}
```

The `score` method processes the training set or corpus of the news articles related to a stock and returns a set of `NewsArticles` instances.

The `corpus` type (line 1) defines the three essential components of a news article: a timestamp, a title, and a body or content. The `rank` method (line 2) extracts the release date from each news article and orders them as per increasing date.

The frequency of terms is computed for each document or group of news articles associated with a date (line 3) using the `count` method. The `count` method matches each term extracted from the news article to the entries of the lexicon map. The counters of the `Counter: Map[String, Int]` type collect the number of occurrences of each term. The next instruction (line 4) aggregates the counts for the entire corpus that is used to compute the relative frequencies (line 5).

The `rank` method uses a sequence of Scala methods `map` and `sortWith` to order the articles as per date (line 6):

```
def rank(corpus: Corpus): Option[CorpusType[T]] = {
  corpus.map(doc => (toDate(doc._1.trim), doc._2, doc._3))
    .sortWith( _._1 < _._1) //6
}
```

The scoring method is protected by a Scala exception handler (line 7). Finally, the `count` method matches a term with an entry in the lexicon and updates the count if a match is found (line 8):

```
def count(term: String): Counter[String] =
  toWords(term).foldLeft(new Counter[String])((cnt, w) =>
    if( lexicon.contains(w)) cnt + lexicon(w) //8
    else cnt
  )
```

Testing

For testing purpose, let's select the news articles mentioning Tesla Motors and its ticker symbol TSLA over a period of two months.

Retrieving textual information

First, you need to define the three parameters of the scoring `TermsScore` class: `toDate`, `toWords`, and `lexicon`.

The private `toDate` method converts a string into a date defined as a `Long` data type:

```
def toDate(date: String): Long = {
  val idx1 = date.indexOf(".")
  val idx2 = date.lastIndexOf(".")
  if(idx1 != -1 && idx2 != -1)
    (date.substring(0, idx1) + date.substring(idx1+1, idx2)).toLong
  else -1L
}
```

The `toWords` method uses simple regular expressions, `regExpr`, to replace any punctuation into a `.` character (line 1), used as a word delimiter (line 2). All words shorter than three characters are discounted (line 3):

```
def toWords(txt: String): Array[String] = {  
  val regExpr = "[',|,|.!?|!|:|\\]"  
  txt.trim.toLowerCase  
    .replace(regExpr, "&@") //1  
    .split("&@") //2  
    .filter(_.length > 2) //3  
}
```

Finally, the lexicon contains the terms that need to be monitored. In this particular period of time, the news media were looking for any announcement regarding Tesla Motors' foray into the Chinese market, issues with the batteries, and any plan to deploy electrical vehicle charger stations. The set of terms regarding these issues is limited, and therefore, the lexicon can be built manually:

```
val LEXICON = Map[String, String] (  
  "tesla"->"Tesla", "tsla"->"TSLA", "china"->"China", "chinese"->  
  "China", ....)
```

The semantic analysis



This example uses a very primitive semantic map (lexicon) for the sake of illustrating the benefits and inner workings of the multinomial Naïve Bayes algorithm. Commercial applications involving sentiment analysis or topic analysis require a deeper understanding of semantic associations and extraction of topics using advanced generative models, such as the latent Dirichlet allocation.

The client code to train and validate the model executes the entire workflow, from extracting and scoring the news articles and press releases to generating the normalized labeled data and computing the F1 measure.

The output (or labeled data) `TSLA_QUOTES` consists of the stock price for Tesla Motors:

```
val TSLA_QUOTES = Array[Double] (250.56, 254.84, ... )
```

The first step is to load and clean all the articles (`corpus`) defined in the `pathname` directory (line 1). This task is performed by the `DocumentsSource` class (described in the *Extraction of documents* section under *Scala programming in Appendix A, Basic Concepts*):

```

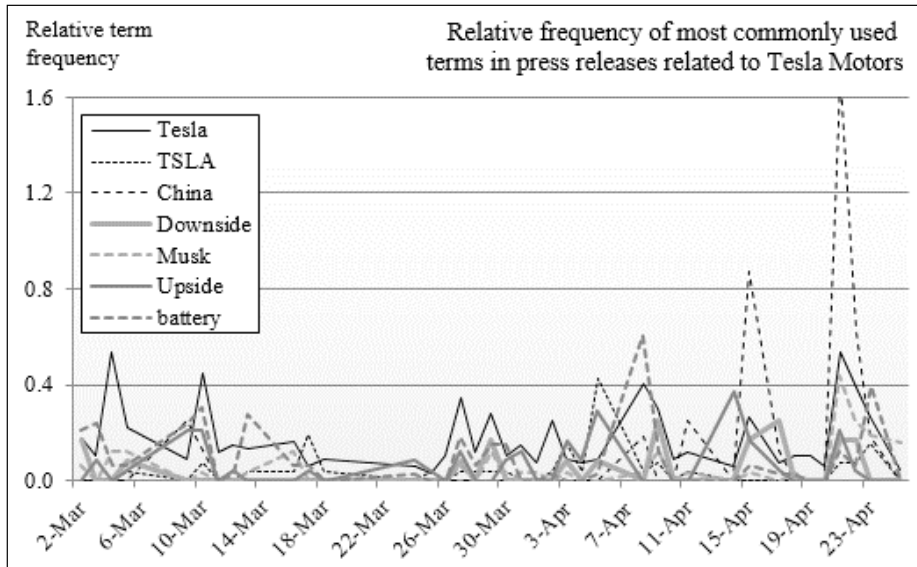
val corpus: Corpus = DocumentsSource(pathName) |> { //1
val ts = new TermsScore[Long](toDate, toWords, LEXICON)
ts.score(corpus) match { //2
  case Some(terms) => {
    var prevQ = 0.0
    val diff = TSLA_QUOTES.map( q => {
      val delta = if(q > prevQ) 1 else 0
      prevQ = q; delta
    })
    val columns = LEXICON.values.foldLeft(new HashSet[String])((hs,
key) => {hs.add(key); hs}).toArray
    val fqLabels = terms.toOrderedArray //3
      .zip(diff) //4
      .map( x => (x._1._2, x._2))
      .map(lbl => (columns //5
      .map(f => if( lbl._1.contains(f) ) lbl._1(f)
      else 0.0), lbl._2))
    val xt = XTSeries[(Array[Double], Int)](fqLabels)
    val nb = NaiveBayes[Double](xt) //6
    ...

```

Next, the `TermsScore.score` method extracts and scores the more relevant terms from the corpus, using the normalized relative frequency defined in steps 7 and 8 of the information retrieval process (line 2). The `terms` are then ordered by date (line 3) and zipped with the labels (direction of the next trading day's stock price) (line 4). The lexicon is used to generate the final labeled observations (*features = terms relative frequency, label = direction of stock price*) (line 5). Finally, the model is built by invoking the `NaiveBayes.apply` constructor (line 6), which consists of running the algorithm through the training set.

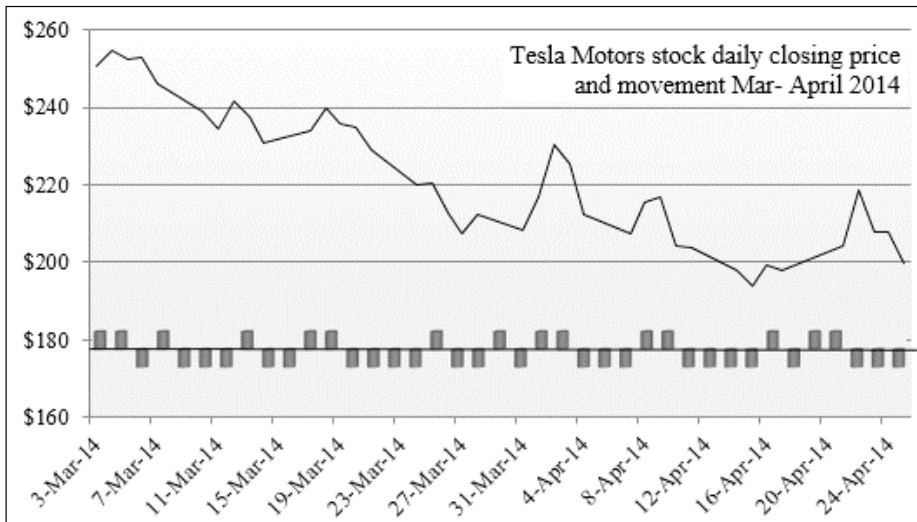
Evaluation

The following chart describes the frequency of occurrences of some of the terms related to either Tesla Motors or its stock ticker TSLA:



Plot of the relative frequency of a partial list of stock-related terms

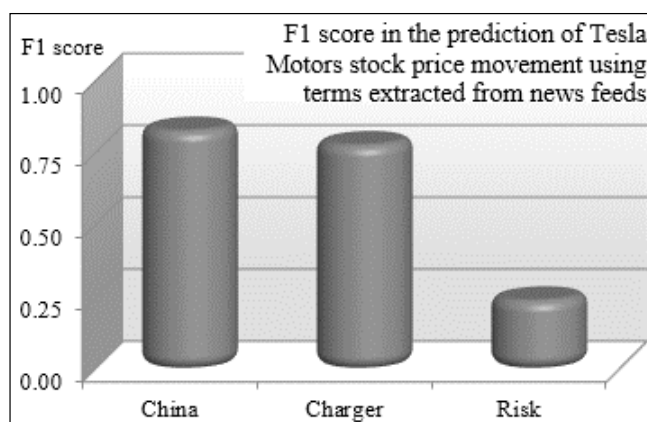
The next chart plots the labeled data, which is the direction of the stock price for the day following the press release(s) or news article(s):



Plot of the stock price and movement for Tesla Motors stock

This chart displays the historical price of the stock TSLA with the direction (UP or DOWN). The classification of 15 percent of the labeled data selected for validation has an F1 measure of 0.71. You need to keep in mind that no preprocessing or clustering was performed to isolate the most relevant features/keywords. The keywords were selected according the frequency of their occurrence in the financial news.

It is fair to assume that some of the keywords have a more significant impact on the direction of the stock price than others. One simple but interesting exercise is to record the value of the F1 score for a validation for which only the observations that have a high number of occurrences of a specific keyword are used, as shown here:



Bar chart representing predominant keywords in predicting TSLA stock movement

The bar chart shows that the terms **China**, representing all the mentions of the activities of Tesla Motors in China, and **Charger**, which covers all the references to the charging stations, have a significant positive impact on the direction of the stock with a probability averaging 75 percent. The terms under the category **Risk** have a negative impact on the direction of the stock with a probability of 68 percent, or a positive impact of the direction of the stock with a probability of 32 percent. Within the remaining eight categories, 72 percent of them were unusable as a predictor of the direction of the stock price.

This approach can be used for selecting features as an alternative to mutual information for using more elaborate classifiers. However, it should not be regarded as the primary methodology for the features selection, but instead as a by-product of the Naïve Bayes in case a very small number of features (less than 10 percent) are predominant in the model. This result can always be validated by computing the principal components, for which the normalized cumulative variance (eigenvalues) of the most predominant features is 90 percent or more.

Pros and cons

The examples selected in this chapter do not do justice to the versatility and accuracy of the Naïve Bayes family of classifiers.

Naïve Bayes classifiers are simple and robust generative classifiers that rely on prior conditional probabilities to extract a model from a training dataset. The Naïve Bayes has its benefits, as mentioned here:

- Simple implementation and easy to parallelize
- Very low computational complexity: $O((n+c)*m)$, where m is the number of features, C the number of classes, and n the number of observations
- Handles missing data
- Supports incremental updates, insertions, and deletions

However, Naïve Bayes is not a silver bullet. It has the following disadvantages:

- The assumption of the independence of features is not practical in the real world
- It requires a large training set to achieve reasonable accuracy
- It contains a zero-frequency problem for counters

Summary

There is a reason why the Naïve Bayes model is the first supervised learning technique you learned: it is simple and robust. As a matter of fact, this is the first technique that should come to mind when you are considering creating a model from a labeled dataset, as long as the features are conditionally independent.

This chapter also introduced you to the basics of text mining as an application of Naïve Bayes.

Despite all its benefits, the Naïve Bayes classifier assumes that the features are conditionally independent, a limitation that cannot be always overcome. In the case of document classification, Naïve Bayes assumes incorrectly that terms are semantically independent: the two entities' age and date of birth are highly correlated. The discriminative classifiers described in the next few chapters attempt to address some of the Naïve Bayes's disadvantages [5:14].

However, this chapter does not address temporal dependencies, sequence of events, or conditional dependencies between observed and hidden features. These types of dependencies necessitate a different approach to modeling that is the subject of the next chapter.

6

Regression and Regularization

In the first chapter, we briefly introduced the binary logistic regression (binomial logistic regression for a single variable) as our first test case. The purpose was to illustrate the concept of discriminative classification. There are many more regression models, starting with the ubiquitous ordinary least-square linear regression and the logistic regression [6:1].

The purpose of regression is to minimize a loss function, with the **residual sum of squares (RSS)** being one that is commonly used. The problem of overfitting described in the *Overfitting* section of *Chapter 2, Hello World!*, can be addressed by adding a **penalty term** to the loss function. The penalty term is an element of the larger concept of **regularization**.

The first section of this chapter will describe and implement the linear least-squares regression. The second section will introduce the concept of regularization with an implementation of the **Ridge regression**.

Finally, the logistic regression will be revisited in detail from the perspective of a classification model.

Linear regression

Linear regression is by far the most widely used, or at least the most commonly known, regression method. The terminology is usually associated with the concept of fitting a model to data. Linear regression can be implemented using the least squares method. Practically, the least squares method entails the minimization of the sum of the squares of the error between the observed data and the actual model.

The least squares problems fall into two categories:

- Ordinary least squares
- Nonlinear least squares

One-variate linear regression

Let's start with the simplest form of linear regression, which is the single variable regression, in order to introduce the terms and concepts behind linear regression. In its simplest interpretation, the one-variate linear regression consists of fitting a line to a set of data points $\{x, y\}$.



Single variable linear regression is given by the following formula:

$$\hat{w} = \arg \min_{w,r} \sum_{j=0}^{n-1} (y_j - f(x_j | w))^2 \quad f(x | w) = w_0 + w_1 \cdot x$$

Here, w_1 is the slope, w_0 is the intercept, f is the linear function that minimizes the RSS, and (x_j, y_j) is a set of n observations.

The RSS is also known as the **sum of squared errors (SSE)**. The **mean squared error (MSE)** for n observations is defined as the ratio RSS/n .



Terminology

The terminology used in the scientific literature regarding regression is a bit confusing at times. Regression weights are also known as regression coefficients or regression parameters. The weights are referred to as w in formulas and the source code throughout the chapter, although β is also used in reference books.

Implementation

Let's create a parameterized class `SingleLinearRegression[T]` to implement the formula described in the previous section. The class implements the data transformation `PipeOperator` (refer to the *Design template for classifiers* section in *Appendix A, Basic Concepts*).

```
class SingleLinearRegression[T <% Double](xt: XTSeries[(T, T)])
  (implicit g: Double => T) extends PipeOperator[Double, T] {
    type XY = (Double, Double)
    ...
  }
```

Model instantiation



The model parameters are computed through training and the value model is instantiated regardless of whether the model is actually validated. A commercial application requires the model to be validated using a methodology such as the K-fold validation. (Refer to the *Design template for classifiers* section *Appendix A, Basic Concepts*.)

The application code must provide an implicit conversion `g` from `Double` to the class type parameter, `T`. The training generates the model defined as the regression weights, the tuple (slope, intercept), in the case of single variable linear regression:

```
val model: Option[XY] = {
  val data = xt.toArray
    .map(x => Array[Double](x._1, x._2)) //1
  val regr = new SimpleRegression(true)
  regr.addData(data) //2
  Some((regr.getSlope, regr.getIntercept)) //3
}
```

The tuple of regression weights or coefficients for the model are computed using the `SimpleRegression` class from the `stats.regression` package of the Apache Commons Math library. The time series is converted to a matrix of double values, `data` (line 1), which is used to initialize the instance of `SimpleRegression` (line 2). The model is initialized with the slope and intercept computed during the training (line 3).

private vs. private[this]



A private value or variable can be accessed only by all the instances of a class. A value declared `private[this]` can be manipulated only by *this* instance. For example, the value `model` can be accessed only by *this* instance of `SingleLinearRegression`.

Test case

For our first test case, we compute the single variate linear regression of the price of the copper ETF (the ticker symbol: CU) over a period of 6 months (January 1, 2013 to June 30, 2013):

```
val price = DataSource(path, false, true, 1) |> adjClose //1
val xy = price.zipWithIndex
    .map(x => (x._2.toDouble, x._1.toDouble)) //2

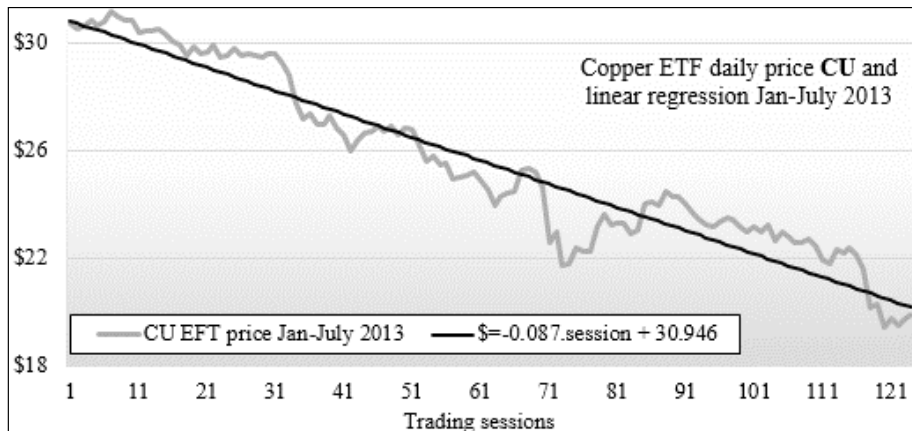
val linRegr = SingleLinearRegression(xy) //3
val w1 = linRegr.slope
```

```
val w0 = linRegr.intercept
if( w1 != None ) //4
  Display.show(lsErr(xy.toArray, w1.get, w0.get), logger)
...
```

The closing price for the CU ETF is extracted from a CSV file (line 1) using a DataSource instance (refer to the *Data extraction* section *Appendix A, Basic Concepts*). The 2-dimension time series is generated by converting the indexes of the time series into the x values using the zipWithIndex Scala method (line 2). The regression model, linRegr, is trained during instantiation of the SingleLinearRegression class (line 3). Once the model is created successfully, the least squared error lsErr of the predicted values and the actual values is computed, as follows:

```
def lsErr(xyt: Array[XY], w1: Double, w0: Double): Double =
  Math.sqrt(xyt.foldLeft(0.0)((err, xy) => {
    val diff = xy._2 - w1*xy._1 - w0; err + diff*diff
  })/xyt.size)
```

The original stock price and the linear regression equation are plotted in the following chart:




Single variable linear regression - Copper ETF daily price

Although the single variable linear regression is convenient, it is limited to scalar time series. Let's consider the case of multiple variables.

Ordinary least squares (OLS) regression

The **ordinary least squares regression** computes the parameters w of a linear function, $y = f(x_1, x_2, \dots, x_d)$, by minimizing the residual sum of squares. The optimization problem is solved by performing vector and matrix operations (transposition, inversion, and substitution).

Minimization of the loss function is given by the following formula:



$$\hat{w} = \arg \min_w \sum_{i=0}^{n-1} \left(y_i - f(x_i | w) \right)^2 \quad f(x | w) = \sum_{d=1}^{D-1} w_d x_d$$

where $w_{j,0,D}$ is the D regression (or model) parameters (or weights), $(x_i, y_i)_{i=0,n-1}$ is n observations of vector x and output value y , and f is the linear multivariate function, $y = f(x_1, x_2, \dots, x_d, \dots)$.

There are several methodologies to minimize the residual sum of squares (RSS) for a linear regression:

- Resolution of the set of n equations with d variables (weights) using the **QR decomposition** of the n by d matrix representing the time series of n observations of vector of d dimension (d features) with $n > d$ [6:2]
- **Singular value decomposition** on the observations-features matrix, in the case where the dimension d exceeds the number of observations n [6:3]
- **Gradient descent** [6:4]
- **Stochastic gradient descent** [6:5]

An overview of these matrix decompositions and optimization techniques can be found in the *Linear algebra* and *Summary of optimization techniques* sections in *Appendix A, Basic Concepts*.

The QR decomposition generates the smallest relative error MSE for the most common least squares problem. The technique is used in our implementation of the least squares regression.

Design

The following implementation of the least squares regression leverages the Apache Commons Math library implementation of the ordinary least squares regression [6:6].

Let's create a class, `MultiLinearRegression`, which inherits the implementation of the ordinary least square computation of the Apache Commons Math library `OLSMultipleLinearRegression`. The class is defined as a data transformation implementing the `PipeOperator`, as follows:

```
class MultiLinearRegression[T <% Double](xt: XTSeries[Array[T]],
y: DbVector) extends OLSMultipleLinearRegression with
PipeOperator[Array[T], Double]
```

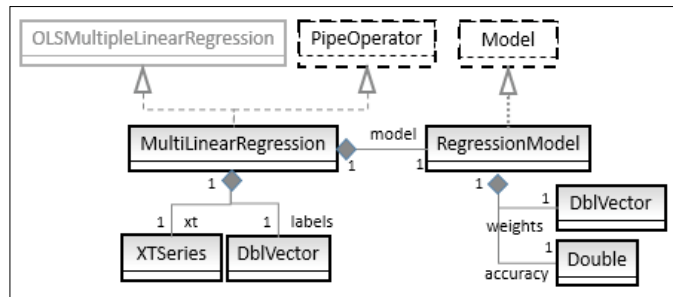
The parameterized class takes the following two parameters:

- The time series of the variables vector `xt` (input matrix)
- The labeled output values, `y`, used in training

The model for the linear regression is defined by its `weights` (or parameters) and its residual sum of squares, `rss`. The RSS is included in the model because it provides the client code with important information regarding the accuracy of the underlying technique used to minimize the loss function:

```
case class RegressionModel(val weights: DbVector, val rss: Double)
```

The relationship between the different components of the least squares regression is described in the following UML class diagram:



Implementation

The training is performed during the instantiation of the class `MultiLinearRegression` (refer to the *Design template for classifiers* section in *Appendix A, Basic Concepts*):

```
val model: Option[RegressionModel] = {
  newSampleData(labels, xt.toDbMatrix) //1
  val weights = estimateRegressionParameters
  val wRss = (weights, calculateResidualSumOfSquares) //2
  Some(RegressionModel(wRss._1, wRss._2))
}
```

The least squares algorithm is initialized with the feature observations, `xt`, and the target data, `labels`, using the `newSampleData` method of `OLSMultipleLinearRegression` (line 1).

The model `weights` are retrieved using `estimateRegressionParameters` (similarly, `rss` using `calculateResidualSumOfSquares`) (line 2).



Exception handling

Wrapping up invocation of methods in a third party with a Scala exception handler matters for a couple of reasons: it makes debugging easier by segregating your code from the third party and it allows your code to recover from the exception by re-executing the same function with alternative third-party library methods, whenever possible.

The predictive algorithm for the ordinary least squares regression is implemented by the data transformation `|>`. The method predicts the output value given `model` and an input value `x`:

```
def |> : PartialFunction[Feature, Double] = {
  case x: Feature if (model != None && x.size == model.get.size - 1) => {
    val w = model.get.weights
    x.zip(w.drop(1)).foldLeft(w(0))((s, z) => s + z._1 * z._2)
  }
}
```

The predictive value is computed by zipping the weight w_1 to w_n with the input vector `x` and then folding the zipped array.

Test case 1 – trending

Trending consists of extracting the long-term movement in a time series. Trend lines can be identified using a multivariate least squares regression. The objective of this first test is to evaluate the filtering capability of the ordinary least squares regression.

The regression is performed on the relative price variation of the Copper ETF (ticker symbol: CU). The selected features are volatility and volume, and the label or target variable is the price change between two consecutive trading sessions y . The volume, volatility, and price variation for CU between January 1, 2013 and June 30, 2013 are plotted in the following chart:

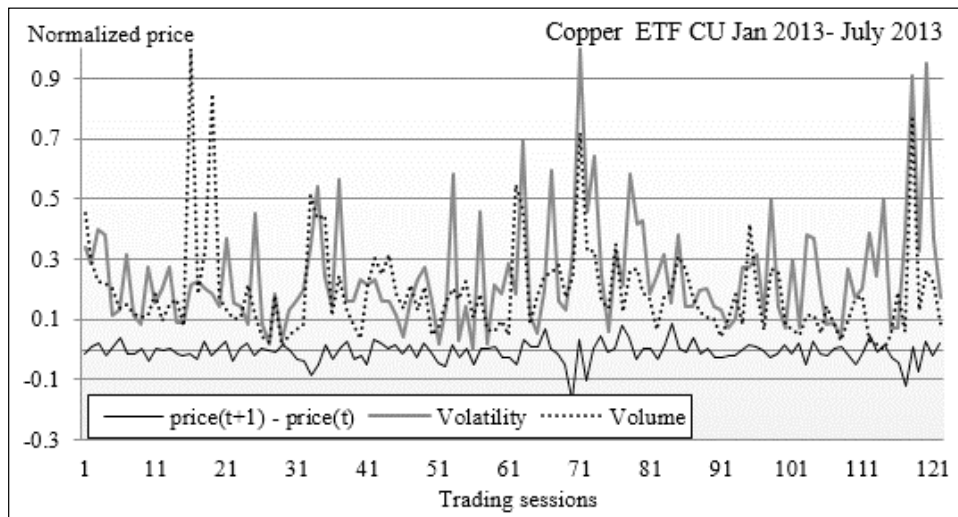


Chart for price variation, volatility, and trading volume for Copper ETF

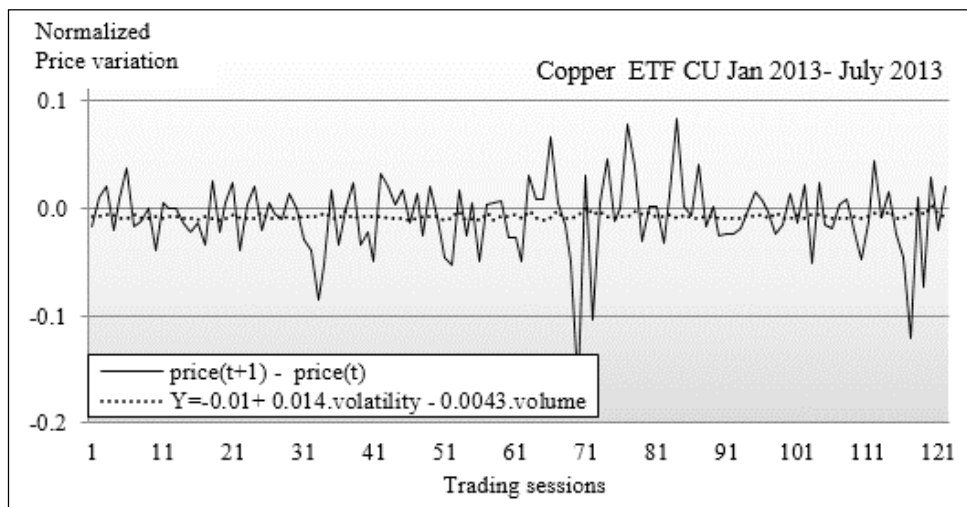
Let's write the client code to compute the multivariate linear regression, *price change* = $w_0 + volatility.w_1 + volume.w_2$:

```
val path = "resources/data/chap6/CU.csv"
val src = DataSource(path, true, true, 1) //2
val price = (src |> YahooFinancials.adjClose).toArray //1
val volatility = src |> YahooFinancials.volatility //1
val volume = src |> YahooFinancials.volume //1

val deltaPrice = price.drop(1)
                    .zip(price.take(price.size - 1))
                    .map(z => z._1 - z._2) //3
val data = volatility.zip(volume)
                    .map(z => Array[Double](z._1, z._2))
val features = XTSeries[DblVector](data.dropRight(1)) //4
val regression = MultiLinearRegression[Double](features, deltaPrice)
//5
regression.weights match {
  case Some(w) => Display.show(w, logger)
  ...
}
```

The daily session adjusted closing price, the session volatility, and the session volume for the CU ETF is extracted from a CSV file (line 1) using the `DataSource` transformation (line 2). The array, `priceChange`, which is the daily price change between two consecutive trading sessions is computed by duplicating, shifting, and zipping the session closing prices (line 3). The features are computed by zipping volatility and the volume time series (line 4). The regression model is trained by instantiating the `MultiLinearRegression` class (line 5) and the model weights are displayed using an auxiliary `display` method (to the logger or standard output) (line 6).

The original price change time series and the data predicted by the regression are plotted in the following chart:



Price variation and the least squares regression for copper ETF according to volatility and volume

The least squares regression model is defined by the linear function for the estimation of price variation as follows:

$$\text{price}(t+1) - \text{price}(t) = -0.01 + 0.014 \text{ volatility} - 0.0042 \text{ volume}$$

The estimated price change (the dotted line in the preceding chart) represents the long term trend from which the noise is filtered out. In other words, the least squares regression operates as a simple low-pass filter as an alternative to some of the filtering techniques such as discrete Fourier transform or the Kalman filter for dynamic systems (refer to *Chapter 3, Data Preprocessing*) [6:7].

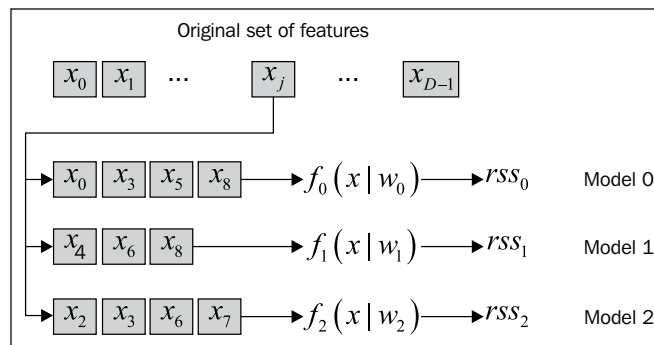
Although trend detection is an interesting application of the least squares regression, the method has limited filtering capabilities for time series [6:8]:

- It is sensitive to outliers
- It put a greater weight to the first and last few observations that need to be discarded
- As a deterministic method, it does not support noise analysis (distribution, frequencies, and so on)

Test case 2 – features selection

The second test case is related to features selection. The objective is to discover which subset of initial features generates the most accurate regression model, that is, the model with the smallest residual sum of squares (RSS) on the training set.

Let's consider an initial set of D features $\{x_i\}$. The objective is to estimate the subset of features $\{x_i^d\}$ that are the most relevant to the set of observations using a least squares regression. Each subset of features is associated to an $f_j(x | w_j)$ model:



The OLS can be used to select the model parameters w if the original set of features is small. Performing the regression of each subset of a large original features set is not practical.

The features selection can be expressed mathematically as follows:

$$\left[\begin{array}{l} \text{✍️} \\ \tilde{f} = \arg \min_{f_j} \left\{ \sum_{i=0}^{n-1} (y_j - f(x_j | w))^2 \right\} \quad f(x | w) = w_{j0} + \sum_{d=1}^{D_j-1} w_{jd} x_d \end{array} \right]$$

Let's consider the following four financial time series over the period from January 1, 2009 to December 31, 2013:

- The exchange rate of Chinese Yuan to US Dollar
- The S&P 500 index
- The spot price of gold
- The 10-year treasury bond price

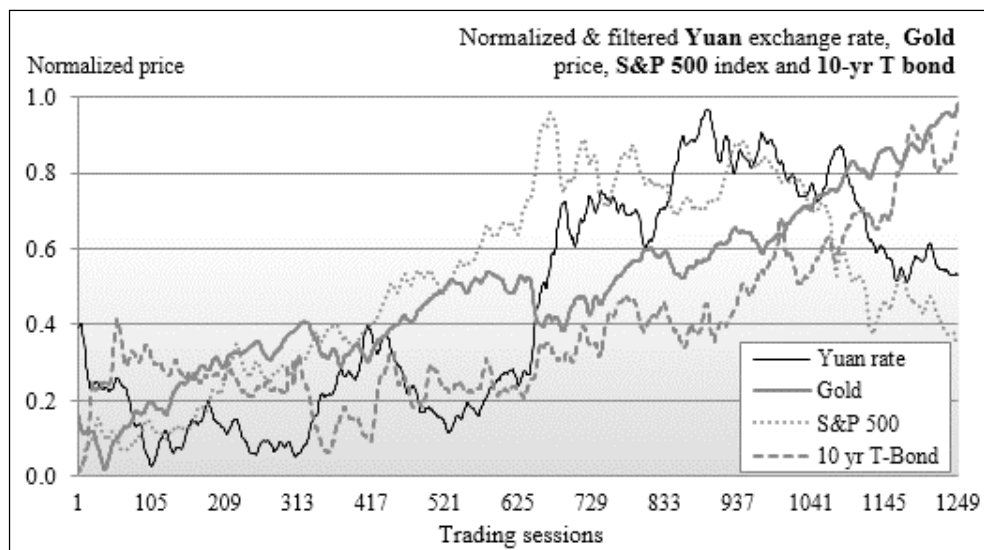
The problem is to estimate which combination of the three variables S&P 500 index, gold price, and 10-year treasury bond price is the most correlated to the exchange rate of the Yuan. For practical reasons, we use the Exchange Trade Funds CYN as the proxy for the Yuan/US dollar exchange rate (similarly, SPY, GLD, and TLT for S&P 500 index, the spot price of gold, and the 10-year treasury bond price respectively).



Automation of features extraction

The code in this section implements an ad hoc extraction of features with an arbitrary fixed set of models. The process can be easily automated with an optimizer (gradient descent, genetic algorithm, and so on) using $1/\text{RSS}$ as the objective function to be maximized.

The number of models to evaluate is relatively small, so an ad hoc approach to compute the RSS for each combination is acceptable. Have a look at the following graph:



Graph of the Chinese Yuan exchange rate, gold, 10-year treasury bond price, and S&P 500 index

The `getRss` method implements the computation of the RSS value given a set of observations `xt` and labeled values `y`:

```
def getRss(xt: XTSeries[DblVector], y: DblVector): String = {
  val regression = MultiLinearRegression[Double](xt, y) //1
  val buf = new StringBuilder
  regression.weights.get
    .zipWithIndex //2
    .foreach(w => {
      if(w._2 == 0) buf.append(w._1)
      else buf.append(s" + ${w._1}.x${w._2}") //3
    })
  buf.append(s"RSS: ${regression.rss.get}").toString
}
```

The `getRss` method merely trains the model by instantiating the multilinear regression class (line 1), indexes the array of weights (line 2), and creates a text representation of the linear regression equation (line 3).

Once the regression model is trained during the instantiation of the `MultiLinearRegression` class, the coefficients of the regression weights and the RSS value are printed. The `rss` method is invoked for any combination of the variables `ETF`, `GLD`, `SPY`, and `TLT` against the label `CNY`:

```
val symbols = Array[String]("CNY", "GLD", "SPY", "TLT")
val smoothingPeriod = 16
val movAvg = SimpleMovingAverage[Double](smoothingPeriod) //4

val input= symbols.map(s=>DataSource(path+s+".csv",true,true, 1))
                  .map(_ |> YahooFinancials.adjClose ) //5
                  .map(x=> movAvg |> XTSeries[Double](x))
val features = input.drop(1)
val featuresList = List[(String, DblMatrix)](
  ("CNY=f(SPY,GLD,TLT)", features.map(_._1.toArray).transpose), //6
  ("CNY=f(GLD,TLT)", features.drop(1).map(_._1.toArray).transpose),
  ...
)
featuresList.foreach(x => Display.show(x._1 +
  getRss(XTSeries[DblVector](x._2), input(0)), logger)) //7
```

The dataset is large (1,260 trading sessions) and noisy enough to warrant filtering using a simple moving average with a period of 16 trading sessions, `movAvg` (line 4). The time series are extracted from CSV files using the `DataSource` class, then smoothed using a sequence of `Array.map` invocations (line 5). The first map extracts the content of the files associated to the stock ticker symbol, assuming that the names of the files are formatted as `path/symbol.csv`.

For the sake of simplicity, the option type returned by the pipe operator is not validated.

The first model using the three variables `SPY`, `GLD`, and `TLT` is created by transposing them by the `xt.size` matrix (line 6). The RSS value is computed by invoking the `rss` method (line 7). The second model using two variables, `SPY` and `TLT`, is created by filtering out the `GLD` time series. The process is repeated for all other models. Have a look at the following screenshot:

```
CNY = f(SPY, GLD, TLT)
0.16089780923264457 + -0.21189413823325406.x1 + 0.26299169969099795.x2 + 0.3556562652009136.x3
RSS: 3.681353535940423

CNY = f(SPY, TLT)
0.2039015515038045 + -0.03796334296279046.x1 + 0.26219728078589966.x2
RSS: 3.8589613138639227

CNY = f(GLD, TLT)
0.19290917330324198 + 0.015507174710195552.x1 + 0.2204800144601237.x2
RSS: 3.8849688539396317

CNY = f(SPY, GLD)
0.22242202699107552 + 0.17842973203100937.x1 + -0.12099602178260839.x2
RSS: 4.6681933948464645

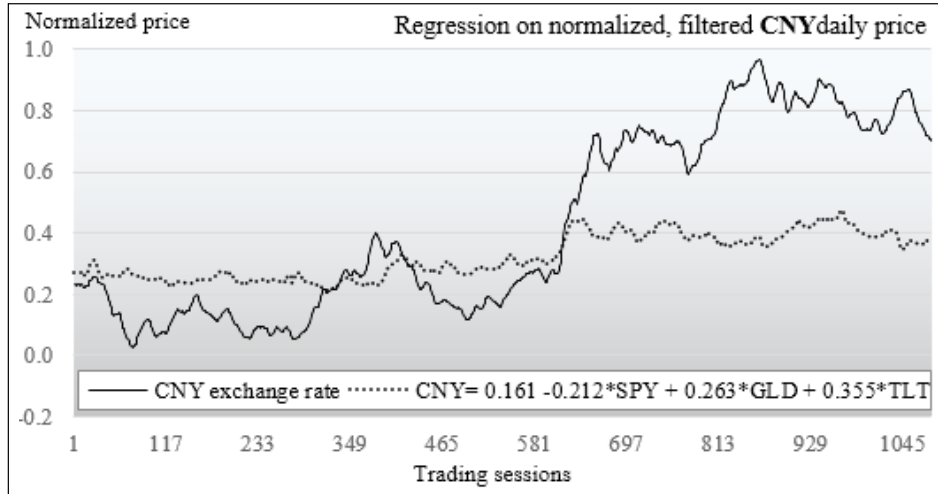
CNY = f(SPY)
0.20238901847764892 + 0.1251591898720694.x1
RSS: 4.7291908591838405

CNY = f(TLT)
0.19724352413716711 + 0.22501420632545652.x1
RSS: 3.8876824376753705

CNY = f(GLD)
0.198195293931846 + 0.16413676262473123.x1
RSS: 5.149661975952835
```

The output results clearly show that the three variable regression $CNY=f(SPY, GLD, TLT)$ is the most accurate or fittest model for the `CNY` time series, followed by $CNY=f(SPY, TLT)$. Therefore, the feature selection process generates the features set, `{SPY, GLD, TLT}`.

Let's plot the model against the raw data:



Ordinary least regression on the Chinese Yuan ETF (CNY)

The regression model smoothed the original CNY time series. It weeded out all but the most significant price variation.

However, the RSS does not always provide an accurate visualization of the fitness of the regression model. The fitness of the regression model is commonly assessed using **r^2 statistics**. The r^2 value is a number that indicates how well data fits a statistical model.

RSS and r^2 statistics are related by the following formulae:

$$r^2 = 1 - \frac{RSS}{TSS} \quad TSS = \sum_{i=0}^{n-1} (y_j - \bar{f}(x|w))^2 \quad \bar{f} = \sum_j f_j$$

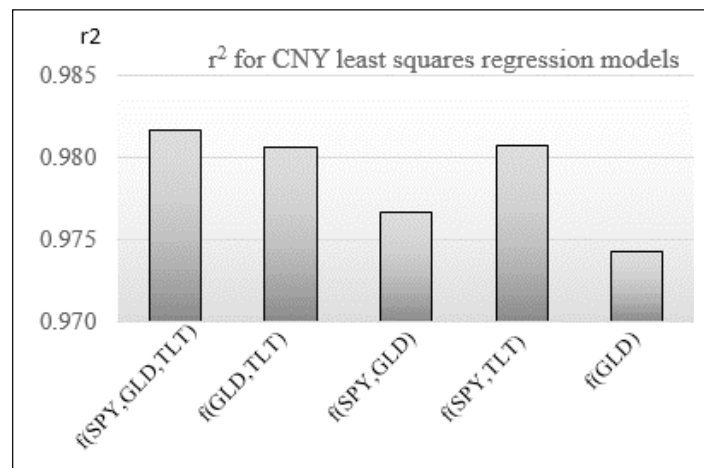
The implementation of the computation of the r_2 statistics is fairly simple. For each model f_j , the `rssSum` method computes the tuple {`rss`, sum of predicted values}:

```
def rssSum(xt: XTSeries[DblVector], y: DblVector): XY = {
  val regression = MultiLinearRegression[Double](xt, y)
  (regression.rss.get,
   xt.toArray.zip(y).foldLeft(0.0) (s,x) =>
    val d = (x._2 - (regression |> x._1))
    s + d*d
  })
```

Finally, the process is repeated for each model and the sum of the predicted values for each model is summed (line 8), averaged (line 9), and then used in the r_2 formula (line 10):

```
var xsRss = new ListBuffer[Double] ()
val tss = featuresList.foldLeft(0.0)((s, x) => { //8
  val _tss = rssSum(XTSeries[DblVector](x._2), input(0))
  xsRss.append(_tss._1)
  s + _tss._2 //9
})/xsRss.size
xsRss.map( 1.0 - _/tss) //10
```

The graph plotting the r^2 value for each model confirms that the three features model is the most accurate:



General linear regression



The concept of linear regression is not restricted to polynomial fitting models such as $y = w_0 + w_1x + w_2x^2 + \dots + w_nx^n$. Regression models can also be defined as a linear combination of **basis functions** as $\phi_j: y = w_0 + w_1\phi_1(x) + w_2\phi_2(x) + \dots + w_n\phi_n(x)$ [6:9].

Regularization

The ordinary least squares method for finding the regression parameters is a specific case of the maximum likelihood. Therefore, regression models are subject to the same challenge in terms of overfitting as any other discriminative model. You are already aware that regularization is used to reduce model complexity and avoid overfitting as stated in the *Overfitting* section of *Chapter 2, Hello World!*.

L_n roughness penalty

Regularization consists of adding a penalty function $J(w)$ to the loss function (or RSS in the case of a regressive classifier) in order to prevent the model parameters (or weights) from reaching high values. A model that fits a training set very well tends to have many features variable with relatively large weights. This process is known as **shrinkage**. Practically, shrinkage involves adding a function with model parameters as an argument to the loss function:

$$\hat{w} = \arg \min_{w_d} \left\{ \sum_{i=0}^{n-1} (y_i - f(x_i | w))^2 + \lambda J(w) \right\}$$

The penalty function is completely independent from the training set $\{x, y\}$. The penalty term is usually expressed as a power to the function of the norm of the model parameters (or weights), w_d . For a model of D dimensions, the generic **L_p -norm** is defined as follows:

$$J_{pq}(w) = \|w\|_p^q = \left[\sum_{d=1}^{D-1} |w_d|^p \right]^{q/p}$$



Notation

Regularization applies to parameters or weights associated to an observation. In order to be consistent with our notation, w_0 being the intercept value, the regularization applies to the parameters w_1, \dots, w_d .

The two most commonly used penalty functions for regularization are L_1 and L_2 .

Regularization in machine learning



The regularization technique is not specific to the linear or logistic regression. Any algorithm that minimizes the residual sum of squares, such as a support vector machine or feed-forward neural network, can be regularized by adding a roughness penalty function to the RSS.

The L_1 regularization applied to the linear regression is known as the **Lasso regularization**. The **Ridge regression** is a linear regression that uses the L_2 regularization penalty.

You may wonder which regularization makes sense for a given training set. In a nutshell, L_2 and L_1 regularization differ in terms of computation efficiency, estimation, and features selection: [6:10] [6:11]

- **Model estimation:** L_1 generates a sparser estimation of the regression parameters than L_2 . For a large nonsparse dataset, L_2 has a smaller estimation error than L_1 .
- **Feature selection:** L_1 is more effective in reducing the regression weights for features with high value than L_2 . Therefore, L_1 is a reliable features selection tool.
- **Overfitting:** Both L_1 and L_2 reduce the impact of overfitting. However, L_1 has a significant advantage in overcoming overfitting (or excessive complexity of a model); for the same reason, it is more appropriate for selecting features.
- **Computation:** L_2 is conducive to a more efficient computation model. The summation of the loss function and the L_2 penalty, \mathbf{w}^2 , is a continuous and differentiable function for which the first and second derivative can be computed (**convex minimization**). The L_1 term is the summation of $|\mathbf{w}_i|$ and therefore not differentiable.

Terminology



The ridge regression is sometimes called the **penalized least squares regression**. The L_2 regularization is also known as the weight decay.

Let's implement the ridge regression, and then evaluate the impact of the L_2 -norm penalty factor.

The ridge regression


The ridge regression is a multivariate linear regression with an L_2 -norm penalty term:

$$\hat{w}_{Ridge} = \arg \min_{w_d} \sum_{j=0}^{n-1} (y - w_0 - w^T x)^2 + \lambda \|w\|_2^2 \quad \|w\|_2^2 = \sum_{d=1}^D w_d^2$$

The computation of the ridge regression parameters requires the resolution of a system of linear equations similar to the linear regression.

The matrix representation of the ridge regression closed form is as follows:

$$(X^T X - \lambda I) \hat{w}_{Ridge} = X^T y$$

 I is the identity matrix and uses the QR decomposition:

$$(X^T X - \lambda I) Q \begin{bmatrix} R \\ 0 \end{bmatrix} w_{Ridge} = Q_y^T \begin{bmatrix} R \\ 0 \end{bmatrix}^{-1}$$

Implementation

The implementation of the ridge regression adds the L2 regularization term to the multiple linear regression computation of the Apache Commons Math library.

The methods of `RidgeRegression` have the same signature as their ordinary least squares counterparts. However, the class has to inherit the abstract base class, `AbstractMultipleLinearRegression`, in the Apache Commons Math library and override the generation of the QR decomposition to include the penalty term:

```
class RidgeRegression[T <% Double] (xt: XTSeries[Array[T]], y:
DblVector, lambda: Double) extends AbstractMultipleLinearRegression
with PipeOperator[Array[T], Double] {
  var qr: QRDecomposition = _
  val model: Option[RegressionModel] = ...
  ...
}
```

Besides the input time series x_t and the labels y , the ridge regression requires the λ factor of the L_2 penalty term. The instantiation of the class trains the model. The steps to create the ridge regression models are as follows:

1. Extract the Q and R matrices for the input values, `newXSampleData` (line 1).
2. Compute the weights using `calculateBeta` defined in the base class (line 2).
3. Return the tuple regression weights, `calculateBeta`, and the residuals, `calculateResiduals`.

Consider the following code:

```
val model: Option[(DblVector, Double)] = {
  this.newXSampleData(xt.toDblMatrix) //1
  newYSampleData(y)
  val _rss = calculateResiduals.toArray.map(x => x*x).sum
  val wRss = (calculateBeta.toArray, _rss) //2
  Some(RegressionModel(wRss._1, wRss._2))
}
```

The QR decomposition in the base class, `AbstractMultipleLinearRegression`, does not include the penalty term (line 3); the identity matrix with the λ factor in the diagonal has to be added to the matrix to be decomposed (line 4):

```
override protected def newXSampleData(x: DblMatrix): Unit = {
  super.newXSampleData(x) //3
  val xtx: RealMatrix = getX
  val nFeatures = xt(0).size
  Range(0, nFeatures)
    .foreach(i =>xtx.setEntry(i,i,xtx.getEntry(i,i)+lambda)) //4
  qr = new QRDecomposition(xtx)
}
```

The regression weights are computed by resolving the system of linear equations using substitution on the Q.R matrices. It overrides `calculateBeta` from the base class:

```
override protected def calculateBeta: RealVector =
  qr.getSolver().solve(getY())
```

The test case

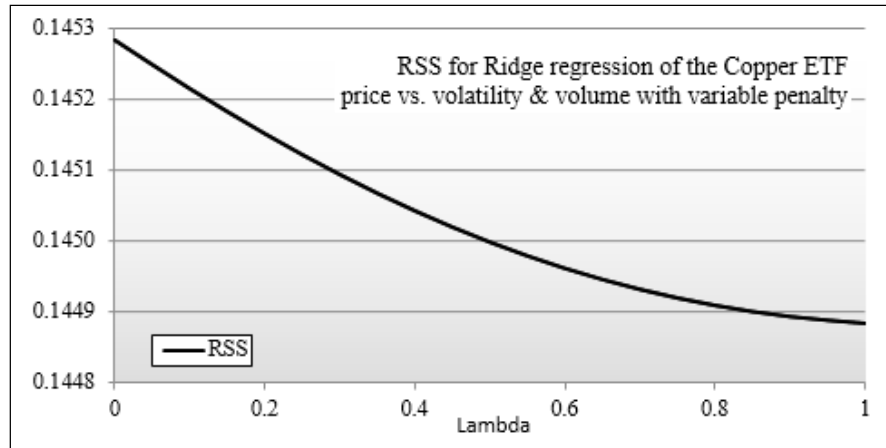
The objective of the test case is to identify the impact of the L_2 penalization on the RSS value and then compare the predicted values with the original values.

Let's consider the first test case related to the regression on the daily price variation of the Copper ETF (symbol: CU) using the stock daily volatility and volume as features. The implementation of the extraction of observations is identical to that of the least squares regression:

```
val lambda = 0.5
val src = DataSource(path, true, true, 1)
val price = src |> YahooFinancials.adjClose
val volatility = src |> YahooFinancials.volatility
val volume = src |> YahooFinancials.volume //1
val deltaPrice = XTSeries[Double] (price.drop(1)
                                   .zip(price.take(_price.size - 1))
                                   .map( z => z._1 - z._2)) //2
val data = volatility.zip(volume)
                                   .map(z => Array[Double] (z._1, z._2)) //3
val features = XTSeries[DblVector] (data.dropRight(1))
val regression = new RidgeRegression[Double] (features, deltaPrice,
lambda) //4
regression.rss match {
  case Some(rss) => Display.show(rss, logger)
  ...
```

The observed data, that is, the ETF daily price and the features (volatility and volume) are extracted from the `src` source (line 1). The daily price change `deltaPrice` is computed using a combination of Scala `take` and `drop` methods (line 2). The features vector is created by zipping `volatility` and `volume` (line 3). The model is created by instantiating the `RidgeRegression` class (line 4). The RSS value, `rss`, is finally displayed (line 5).

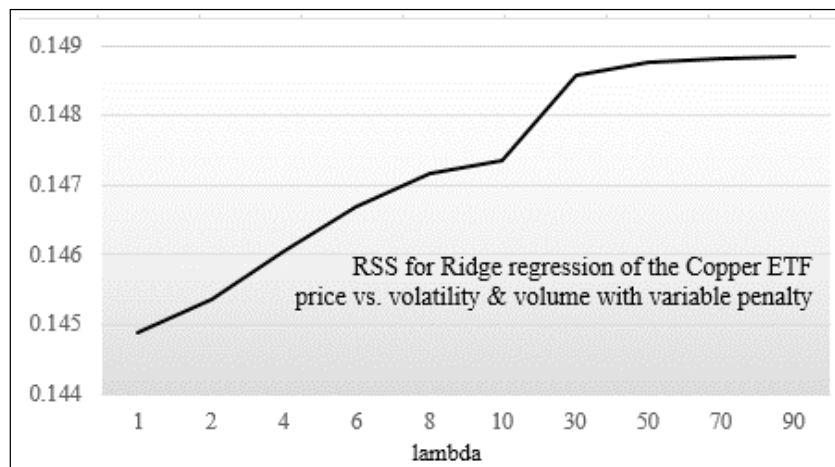
The RSS value, r_{SS} , is plotted for different values of lambda less than 1.0, as shown in the following chart:



Graph of RSS versus Lambda for Copper ETF

The residual sum of squares decreases as λ increases. The curve seems to be reaching for a minimum around $\lambda = 1$. The case of $\lambda = 0$ corresponds to the least squares regression.

Next, let's plot the RSS value for λ varying between 1 and 100:



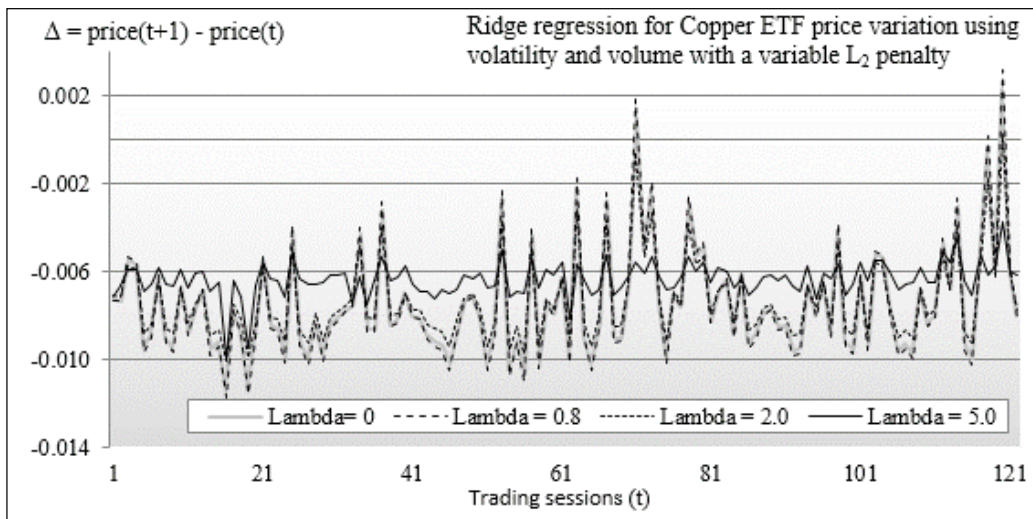
Graph of RSS versus large-value Lambda for Copper ETF

This time around, the value of RSS increases with λ before reaching a maximum of $\lambda > 60$. This behavior is consistent with other findings [6:12]. As λ increases, the overfitting gets more expensive and therefore, the RSS value increases.

The regression weights can be simply outputted as follows:

```
regression.weights.get
```

Let's plot the predicted price variation of the Copper ETF using the ridge regression with different values of lambda (λ):



The graph of ridge regression on Copper ETF price variation with variable lambda

The original price variation of the Copper ETF, $\Delta = price(t+1)-price(t)$, is plotted as $\lambda = 0$. The predicted values for $\lambda = 0.8$ is very similar to the original data. The predicted values for $\lambda = 2$ follow the pattern of the original data with a reduction of large variations (peaks and troves). The predicted values for $\lambda = 5$ correspond to a smoothed dataset. The pattern of the original data is preserved but the magnitude of the price variation is significantly reduced.

The logistic regression, briefly introduced in the *Let's kick the tires* section of *Chapter 1, Getting Started*, is the next logical regression model to discuss. The logistic regression relies on optimization methods. Let's go through a short refreshment course in optimization before diving into the logistic regression.

Numerical optimization

This section briefly introduces the different optimization algorithms that can be applied to minimize the loss function, with or without a penalty term. These algorithms are described in greater detail in the *Summary of optimization techniques* section in *Appendix A, Basic Concepts*.

First, let's define the **least squares problem**. The minimization of the loss function consists of nullifying the first order derivatives, which in turn generates a system of D equations (also known as gradient equations), D being the number of regression weights (parameters). The weights are iteratively computed by solving the system of equations using a numerical optimization algorithm.

The definition of the least squares-based loss function is as follows:

$$L(w) = \sum_{i=0}^{n-1} r_i(w) = y_i - f(x_i | w)$$

The generation of gradient equations with a Jacobian J matrix (refer to the *Jacobian and Hessian matrices* section in *Appendix A, Basic Concepts*) after minimization of the loss function L is described as follows:

$$\sum_{i=0}^{n-1} r_i(w) J_{id} = 0 \quad J_{id}(w) = -\frac{\partial r_i(w)}{\partial w_d}$$



Iterative approximation using the Taylor series is described as follows:

$$f(x_i | w) - ff(x_i | w^{(k)}) \sim \sum_{jd=0}^{D-1} \frac{\partial f(x_i | w^{(k)})}{\partial w_d} (w - w^{(k)})$$

Normal equations using the matrix notation and the Jacobian J matrix is described as follows:

$$(J^T J)(w^{(k+1)} - w^{(k)}) = J^T (y_i^{(k+1)} - y_i^{(k)})$$

The logistic regression is a nonlinear function. Therefore, it requires the nonlinear minimization of the sum of least squares. The optimization algorithms for the nonlinear least squares problems can be divided into the following two categories:

- **Newton (or 2nd order techniques):** These algorithms calculate the second order derivatives (the Hessian matrix) to compute the regression weights that nullify the gradient. The two most common algorithms in this category are the Gauss-Newton and the Levenberg-Marquardt methods (refer to the *Nonlinear least squares minimization* section in *Appendix A, Basic Concepts*). Both algorithms are included in the Apache Commons Math library.
- **Quasi-Newton (or 1st order techniques):** First order algorithms do not compute but estimate the second order derivatives of the least squares residuals from the Jacobian matrix. These methods can minimize any real-valued functions, not just the least squares summation. This category of algorithms includes the Davidon-Fletcher-Powell and the Broyden-Fletcher-Goldfarb-Shannon methods (refer to the *Quasi-Newton algorithms* section in *Appendix A, Basic Concepts*).

The logistic regression

Despite its name, *the logistic regression is a classifier*. As a matter of fact, the logistic regression is one of the most used discriminative learning techniques because of its simplicity and its ability to leverage a large variety of optimization algorithms. The technique is used to quantify the relationship between an observed target variable y and a set of variables x that it depends on. Once the model is created (trained), it is used to classify real-time data.

A logistic regression can be either binomial (two classes) or multinomial (three and more classes). In a binomial classification, the observed outcome is defined as {true, false}, {0, 1}, or {-1, +1}.

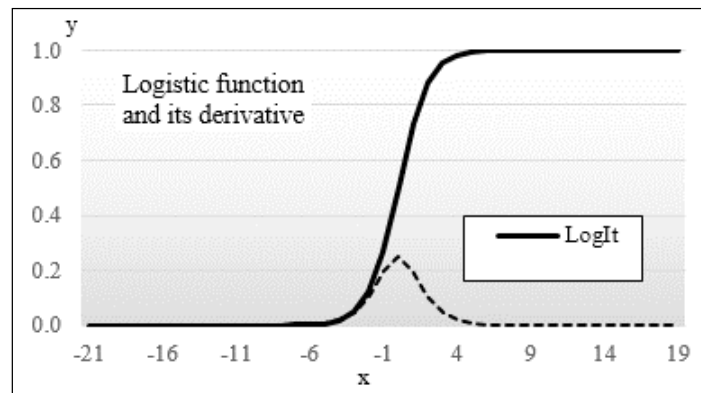
The logit function

The conditional probability in a linear regression model is a linear function of its weights [6:13]. The logistic regression model addresses the nonlinear regression problem by defining the logarithm of the conditional probability as a linear function of its parameters.

First, let's introduce the logistic function and its derivative, which are defined as follows:

$$f(x) = \frac{1}{1 + e^{-x}} \quad \frac{df}{dx} = f(x)(1 - f(x))$$

Have a look at the following graph:



The graph of the logistic function and its derivative

The remainder of this section is dedicated to the application of the multivariate logistic regression to a binary classification (two classes).

Binomial classification

The logistic regression is popular for several reasons; some are as follows:

- It is available with most statistical software packages and open source libraries
- Its S-shape describes the combined effect of several explanatory variables
- Its range of values $[0, 1]$ is intuitive from a probabilistic perspective

Let's consider the classification problem using two classes. As discussed in the *Validation* section of *Chapter 2, Hello World!*, even the best classifier produces false positives and false negatives. The training procedure for a binomial classification is illustrated in the following diagram:

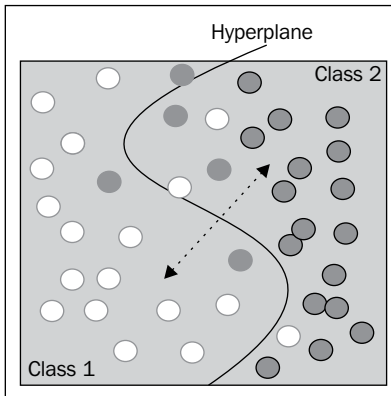


Illustration of the binomial classification for a 2-dimension dataset

The purpose of the training is to compute the **hyperplane** that separates the observations into two categories or classes. Mathematically speaking, a hyperplane in an n -dimensional space (number of features) is a subspace of $n-1$ dimensions. The separating hyperplane of a three-dimension space is a curved surface. The separating hyperplane of a two-dimension problem (plane) is a line. In our preceding example, the hyperplane segregates/separates a training set into two very distinct classes (or groups), class 1 and class 2, in an attempt to reduce the overlap (false positive and false negative).

The equation of the hyperplane is defined as the logistic function of the dot product of the regression parameters (or weights) and features.

The logistic function accentuates the difference between the two groups of training observations, separated by the hyperplane. It pushes the observations away from the separating hyperplane towards either of the classes.

In the case of two classes, c_1 and c_2 with their respective probabilities, $p(C=c_1 | X=x^i | w) = p(x^i | w)$ and $p(C=c_2 | X=x^i | w) = 1 - p(x^i | w)$, where w is the model parameters set or weights in the case of the logistic regression, the following functions can be defined:

The log likelihood:

$$L(w) = \sum_{i=0}^{N-1} \log p(x_i | w)$$

Conditional probabilities using the logit function:

$$x = [1, x_1, x_2 \dots x_d]^T \quad p(x | w) = \frac{e^{w^T x}}{1 + e^{w^T x}}$$



The log likelihood for the binomial logistic regression:

$$L(w) = \sum_{i=0}^{N-1} y_i w^T x_i - \log(1 + e^{w^T x_i}) \quad y \in \{0, 1\}$$

First order derivative for the log likelihood:


$$\frac{\partial L(w)}{\partial w_j} = \sum_{i=0}^{N-1} x_{ij} (y_i - p(x_i | w))$$

Let's implement the logistic regression without a penalty term using the Apache Commons Math library. The library contains several least squares optimizers, allowing you to specify the minimizing algorithm, `optimizer`, for the loss function in the logistic regression class `LogisticRegression`:

```
class LogisticRegression[T <% Double] (xt: XTSeries[Array[T]],
labels: Array[Int], optimizer: LogisticRegressionOptimizer) extends
PipeOperator[Array[T], Int] {
  val model: Option[RegressionModel] = { ... }
  ...
}
```

The parameters of the logistic regression class are the multivariate time series (features) `xt`, the target or labeled data, `labels`, and the `optimizer` algorithm used to minimize the loss function or residual sum of squares. In the case of the binomial logistic regression, `labels` are assigned the values of 1 for one class and 0 for the other.

The purpose of the training is to determine the regression coefficient, `model._1`, which minimizes the loss function. The **residual sum of squares (RSS)** is computed as `model._2`.

 **Target values**

There is no specific rule to assign the two values to the observed data for the binomial logistic regression: $\{-1, +1\}$, $\{0, 1\}$, or $\{\text{false}, \text{true}\}$. The values pair $\{0, 1\}$ is convenient because it allows the developer to reuse the code for multinomial logistic regression using normalized class values.

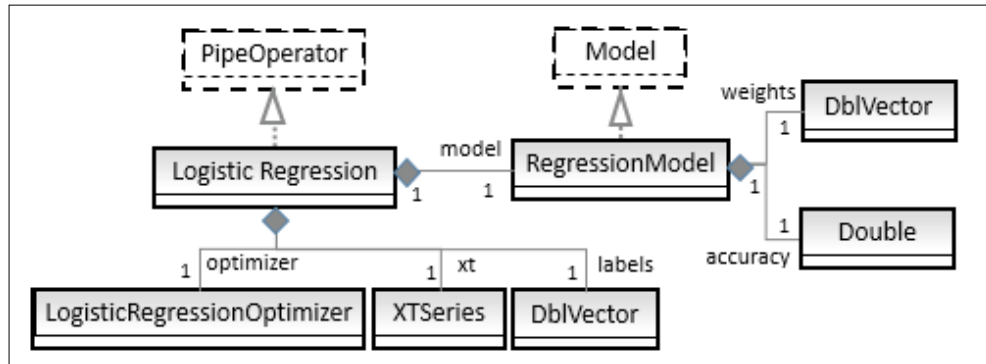
For convenience, the definition and the configuration of the optimizer are encapsulated in the `LogisticRegressionOptimizer` class.

Software design

The implementation of the logistic regression uses the following components:

- `RegressionModel` of the `Model` type, which is initialized through training during the instantiation of the classifier. We reuse the `RegressionModel` type introduced in the *Linear regression* section.
- The predictive or classification routine is implemented as a data transformation `|>` extending the `PipeOperator` trait.
- The logistic regression class, `LogisticRegression`, has three parameters: the least squares optimizer of the type `LogisticRegressionOptimizer` (used in training), a features set `XTSeries`, and a label vector `DbfVector`.

The key software components of the logistic regression are described in the following UML class diagram:



The UML class diagram for the logistic regression

The training workflow

Our implementation of the training of the logistic regression model leverages either the Gauss-Newton or the Levenberg-Marquardt nonlinear least squares optimizers, (refer to the *Nonlinear least squares minimization* section in *Appendix A, Basic Concepts*) packaged with the Apache Commons Math library.

The training of the logistic regression is performed by the `train` method:

```
val model: Option[RegressionModel] = train
```



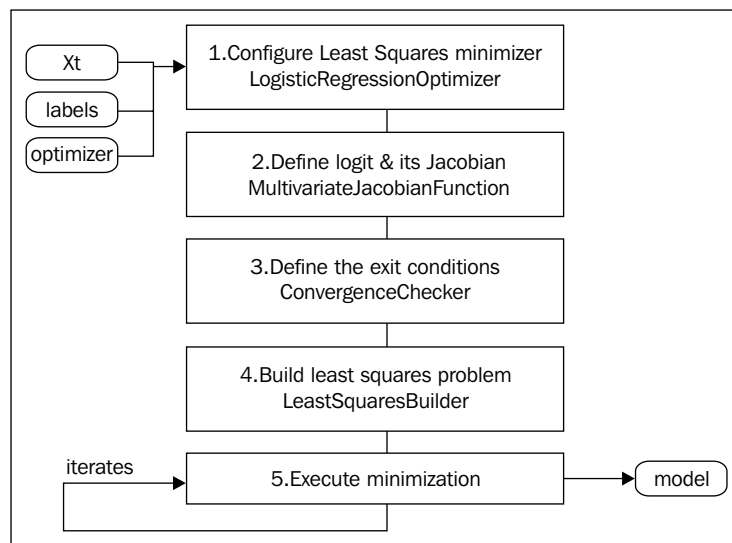
Handling exceptions from the Apache Commons Math library

The training of the logistic regression using the Apache Commons Math library requires handling `ConvergenceException`, `DimensionMismatchException`, `TooManyEvaluationsException`, `TooManyIterationsException`, and `MathRuntimeException`. Debugging is greatly facilitated by understanding the context of these exceptions in the Apache library source code.

The implementation of the training method, `train`, relies on the following five steps:

1. Select and configure the least squares optimizer.
2. Define the logit function and its Jacobian.
3. Specify the convergence and exit criteria.
4. Compute the residuals using the least squares problem builder.
5. Run the optimizer.

The workflow and the Apache Commons Math classes used in the training of the logistic regression are visualized by the following flow diagram:



The workflow for training the logistic regression using Apache Commons Math

The first four steps are required by the Apache Commons Math library to initialize the configuration of the logistic regression prior to the minimization of the loss function. Let's start with the configuration of the least squares optimizer.

Configuring the least squares optimizer

In this step, you have to specify the algorithm to minimize the residual of the sum of squares. The `LogisticRegressionOptimizer` class is responsible for configuring the optimizer. The class has the following two purposes:

- Encapsulating the configuration parameters for the optimizer
- Invoking the `LeastSquaresOptimizer` interface defined in the Apache Commons Math library

Consider the following code:

```
class LogisticRegressionOptimizer(maxIters: Int, maxEvals: Int, eps:
Double, lsOptimizer: LeastSquaresOptimizer) {
  def optimize(lsProblem: LeastSquaresProblem): Optimum = lsOptimizer.
optimize(lsProblem)
}}
```

The configuration of the logistic regression optimizer is defined using the maximum number of iterations (`maxIters`), the maximum number of evaluations (`maxEval`) for the logistic function and its derivative, the convergence criteria (`eps`) on the residual sum of squares, and the instance of the least squares problem (`org.apache.commons.math3.fitting.leastsquares.LeastSquaresProblem`).

Computing the Jacobian matrix

The next step consists of computing the value of the logistic function and its first order partial derivatives with respect to the weights by overriding the `value` method of the `fitting.leastsquares.MultivariateJacobianFunction` interface:

```
final val initWeight = 0.5
val weights0 = Array.fill(xt(0) + 1)(initWeight) //1

val lrJacobian = new MultivariateJacobianFunction {
  override def value(w:RealVector):Pair[RealVector,RealMatrix] = {
    val _w = w.toArray
    val gradient = xt.toArray
      .map( g => { //2
        val expn = g.zip(_w.drop(1))
          .foldLeft(_w(0))((s,z) => s + z._1*z._2)
        val logIt = 1.0/(1.0 + Math.exp(-expn)) //3
        (logIt, logIt *(1- logIt)) //4
      })

    val jacobian = Array.ofDim[Double](xt.size, weights0.size)//5
    xt.toArray.zipWithIndex.foreach(xi => { //6
      val df: Double = gradient(xi._2)._2
      Range(0, xi._1.size).foreach(j =>
        jacobian(xi._2)(j+1) = xi._1(j)*df)
      jacobian(xi._2)(0) = 1.0 //7
    })
    (new ArrayRealVector(gradient.map(_.1)),
     new Array2DRowRealMatrix(jacobian)) //8
  }
}
```

The regression weights, `weights0`, are initialized with the arbitrary value of 0.5.

The `value` method uses the primitives types `RealVector`, `RealMatrix`, `ArrayRealVector`, and `Array2DRowRealMatrix` defined in the `org.apache.commons.math3.linear` Apache Commons Math package.

It takes the regression weight, w , and computes the `gradient` (line 2) of the logistic function for each data point and returns the value of `logit` (line 3) and its derivative (line 4) as a tuple. The Jacobian matrix is created (line 5), and then initialized with `logit` and its derivative (line 6). The first element of each column of the Jacobian matrix is set to 1.0 to take into account the intercept (line 7). Finally, the vector of the `logit` values for each observation and the Jacobian matrix are returned (line 8) as a tuple to comply with the return type of the function value.

Defining the exit conditions

The third step defines the exit condition for the optimizer. It is accomplished by overriding the `converged` method of the parameterized `org.apache.commons.math3.optim.ConvergenceChecker` interface:

```
val exitCheck = new ConvergenceChecker[PointVectorValuePair] {
  override def converged(iteration: Int, prev: PointVectorValuePair,
    current: PointVectorValuePair): Boolean = {
    val delta = prev.getValue
      .zip(current.getValue)
      .foldLeft(0.0)((s, z) =>{
        val d = z._1 - z._2
        s + diff*diff
      })
    Math.sqrt(delta) < optimizer.eps && iteration >= optimizer.maxIters
  }
}
```

This implementation computes the convergence or exit condition as follows:

- Either the L_2 -norm of the difference between the weights of the current iteration and the weights of the previous iteration, `delta`, is smaller than the convergence criteria, `eps`
- Or the iteration exceeds the maximum number of iterations that `maxIters` allowed

Defining the least squares problem

The Apache Commons Math least squares optimizer package requires all the input to the nonlinear least squares minimizer to be defined as an instance of `LeastSquareProblem` generated by the factory `LeastSquareBuilder` class:

```
val builder = new LeastSquaresBuilder
val diagWeights0 = Array.fill(xt.size)(1.0) //1
val wMatrix = MatrixUtils.createRealDiagonalMatrix(diagWeights0)
val lsp = builder.model(lrJacobian) //2
                .weight(wMatrix)
                .target(labels) //7
                .checkerPair(exitCheck) //5
                .maxEvaluations(optimizer.maxEvals) //3
                .start(weights0) //6
                .maxIterations(optimizer.maxIters) //4
                .build
```

The diagonal elements of the weights matrix are initialized to 1.0 (line 1). Besides the initialization of the model with the Jacobian matrix, `lrJacobian` (line 2), the maximum number of evaluations (line 3), maximum number of iterations (line 4), and the exit condition (line 5) are also initialized.

The regression weights are initialized as 0.5 (`weights0`) (line 6). Finally, the labeled or target values are initialized (line 7).

Minimizing the loss function

The training is executed with a simple call to the least squares minimizer, `lsp`:

```
val optimum = optimizer.optimize(lsp)
(optimum.getPoint.toArray, optimum.getRMS)
```

The regression coefficients (or weights) and the residuals mean square (RMS) are returned by invoking the `getPoint` method on the `optimum` class of the Apache Commons Math library.

Test

Let's test our implementation of the binomial multivariate logistic regression using the example of the Copper ETF price variation versus volatility and volume, used in the previous two sections. The only difference is that we need to define the target values as 0 if the ETF price decreases between two consecutive trading sessions, and 1 otherwise. Therefore, the `deltaPrice` vector used in the linear and ridge regression is to be modified to support the binary outcome:

```
val deltaPrice = prices.drop(1).zip(prices).dropRight(1)
  .map(p => if(p._1>p._2) 1 else 0)
```

Executing the test case is just a matter of instantiating the `LogisticRegression` class with the appropriate configuration parameters. The implementation reuses the code already defined for the least squares and ridge regression to load data from CSV files (`src`, `price`, `volatility`, and `volume`) and normalize the observations:

```
val MAXITERS = 80; val MAXEVALS = 1000; val EPS = 1e-4

val lsOptimizer = LogisticRegressionOptimizer(MAXITERS, MAXEVALS, EPS,
  new LevenbergMarquardtOptimizer)
val xt = XTSeries[DblVector](features)
val regression = new LogisticRegression[Double](xt, deltaPrice,
  lsOptimizer)
val rms = regression.rms.get
val weights = regression.weights.get
```

In this example, the Levenberg-Marquardt algorithm is used to minimize the loss function.



Levenberg-Marquardt parameters

The driver code uses the `LevenbergMarquardtOptimizer` with the default tuning parameters configuration to keep the implementation simple. However, the algorithm has a few important parameters, such as relative tolerance for cost and matrix inversion, that are worth tuning for commercial applications (refer to the *Levenberg-Marquardt* section in *Appendix A, Basic Concepts*).

The execution of the test produces the following results:

- Residual mean square is 0.497
- Weights are -0.124 for intercept, 0.453 for ETF volatility, and -0.121 for ETF volume

The last step is the classification of the real-time data.

Classification

As mention earlier and despite its name, the binomial logistic regression is a binary classifier. The classification method is implemented as a data transformation by overriding the pipe operator:

```
type Feature = Array[T]
final val MARGIN = 0.01
def |> : PartialFunction[Feature, Int] = { //1
  case x: Feature if(model!=None && model.get.size-1==x.size) =>{
    val w = _model.get.weights
    val dot = x.zip(w.drop(1))
      .foldLeft(w(0))((s,xw) => s + xw._1*xw._2)//2
    if(logit(dot) > 0.5 + MARGIN) 1 else 0 //3
  }
}
```

The classification method, `|>`, checks if the number of model parameters (weights) is equal to the number of features plus 1 (line 1) and throws an exception if the test fails. The dot product of the weights and the features is computed using a fold. Finally, the method returns 1 (class 1, which signifies that the price variation of the ETF is positive) if the value of the sigmoid is greater than 0.5. It returns 0 otherwise (class 2, which signifies that the price variation of the ETF is negative) (line 3).

Class identification

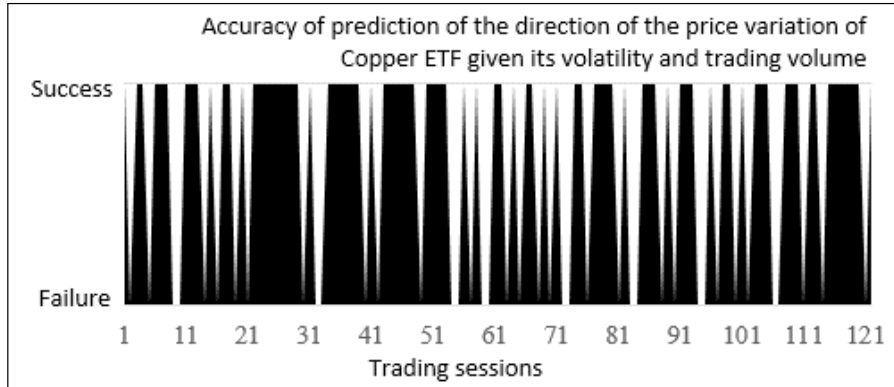


The class that the new data x belongs to is determined by the $\text{logit}(\text{dot}) > 0.5$ test, where dot is the product of the features and the regression weights ($w_0 + w_1 \cdot \text{volatility} + w_2 \cdot \text{volume}$). This test is equivalent to $\text{dot} > 0.0$. You may find either condition in the literature.

Let's apply the classification to the original training set, `features`, to validate our model (weights):

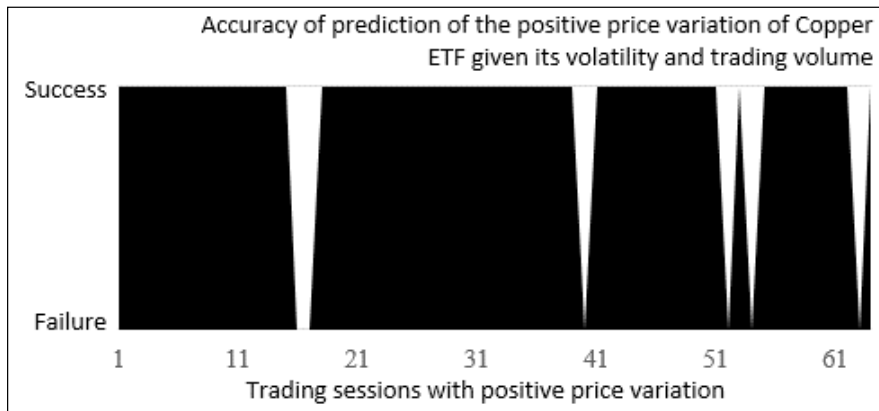
```
val predicted = features.map(x => regression |> x)
```

The direction of the price variation of the Copper ETF, $\text{price}(t+1) - \text{price}(t)$, is compared to the direction predicted by the logistic regression. The result is plotted with the success value if the positive or negative direction is correctly classified, otherwise, it is plotted with the failure value:



The logistic regression was able to classify 78 out of 121 trading sessions (65 percent accuracy).

Now, let's use the logistic regression to predict the positive price variation for the Copper ETF, given its volatility and trading volume. This trading or investment strategy is known as being *long on the market*. This use case ignores the trading sessions for which the price was either flat or declined:



The logistic regression was able to correctly predict the positive price variation for 58 out of 64 trading sessions (90.6 percent accuracy). What is the difference between the first and second test cases?

In the first case, the separating hyperplane equation, $w_0 + w_1 \cdot \text{volatility} + w_2 \cdot \text{volume}$, is used to segregate both the features generating either positive or negative price variation. The overall accuracy of the classification is negatively impacted by the overlap of the features from the two classes.

In the second case, the classifier has to consider only the observations *located on one side* of the hyperplane equation, without taking into account the false negatives.



Impact of rounding errors

Under some circumstances, the generation of the rounding errors during the computation of the Jacobian matrix has an impact on the accuracy of the separating hyperplane equation: $w_0 + w_1 \cdot \text{volatility} + w_2 \cdot \text{volume}$. This negatively impacts the prediction of both the positive and negative price variation.

The accuracy of the binary classifier can be further improved by considering the positive variation of price as $\text{price}(t+1) - \text{price}(t) > EPS$.



Validation methodology

The validation set is generated by randomly selecting data points from the original labeled set. A formal validation requires the use of a K-fold validation methodology to compute the recall, precision, and F_1 measure for the logistic regression model.

Summary

This concludes the description and implementation of linear and logistic regression and the concept of regularization to reduce overfitting. Your first analytical projects using machine learning will (or did) likely involve a regression model of some type. Regression models, along with the Naïve Bayes classification, are the most understood techniques for those without a deep knowledge of statistics or machine learning.

At the completion of this chapter, you hopefully have a grasp on the following:

- The concept of linear and nonlinear least squares-based optimization
- The implementation of ordinary least square regression as well as logistic regression
- The impact of regularization with an implementation of the Ridge regression

The logistic regression is also the foundation of the conditional random fields introduced in the next chapter and artificial neural networks in *Chapter 9, Artificial Neural Networks*.

Contrary to the Naïve Bayes models (refer to *Chapter 5, Naïve Bayes Classifiers*), the least squares or logistic regression does not impose the condition that the features have to be independent. However, the regression models do not take into account the sequential nature of a time series such as asset pricing. The next chapter, *Chapter 7, Sequential Data Models*, describes two classifiers that take into account the time dependency in a time series.

7

Sequential Data Models

The universe of Markov models is vast and encompasses computational concepts such as the **Markov decision process**, **discrete Markov**, **Markov chain Monte Carlo** for Bayesian networks, and **hidden Markov models**.

Markov processes, and more specifically, the hidden Markov model (HMM), are commonly used in speech recognition, language translation, text classification, document tagging, and data compression and decoding.

The first section of this chapter introduces and describes the hidden Markov model with the full implementation of the three canonical forms of the hidden Markov model using Scala. This section details the different dynamic programming techniques used in the evaluation, decoding, and training of the hidden Markov model. The design of the classifier follows the same pattern as the logistic and linear regression.

The second and last section of the chapter is dedicated to a discriminative (labels conditional to observation) alternative to the hidden Markov model: conditional random fields. The open source CRF Java library authored by Sunita Sarawagi from the Indian Institute of Technology, Bombay, is used to create a predictive model using conditional random fields [7:1].

Markov decision processes

This first section also describes the basic concepts you need to know in order to understand, develop, and apply the hidden Markov model. The foundation of the Markovian universe is the concept known as the **Markov property**.

The Markov property

The Markov property is a characteristic of a stochastic process where the conditional probability distribution of a future state depends on the current state and not on its past states. In this case, the transition between the states occurs at a discrete time, and the Markov property is known as the **discrete Markov chain**.

The first-order discrete Markov chain

The following example is taken from *Introduction to Machine Learning* by E. Alpaydin [7:2].

Let's consider the following use case. N balls of different colors are hidden in N boxes (one each). The balls can have only three colors $\{Blue, Red, and Green\}$. The experimenter draws the balls one by one. The state of the discovery process is defined by the color of latest ball drawn from one of the boxes: $S_0 = Blue$, $S_1 = Red$, and $S_2 = Green$.

Let $\{\pi_0, \pi_1, \pi_2\}$ be the initial probabilities for having an initial set of color in each of the boxes.

Let q_t denote the color of the ball drawn at the time t . The probability of drawing a ball of color S_k at the time k after drawing a ball of the color S_j at the time j is defined as $p(q_t = S_k | q_{t-1} = S_j) = a_{jk}$. The probability to draw a red ball in the first attempt is $p(q_{10} = S_1) = \pi_1$. The probability to draw a blue ball in the second attempt is $p(q_1 = S_0 | q_0 = S_1) = \pi_1 a_{10}$. The process is repeated to create a sequence of the state $\{S_t\} = \{Red, Blue, Blue, Green, \dots\}$ with the following probability:

$$p(q_0 = S_1) \cdot p(q_1 = S_0 | q_0 = S_1) \cdot p(q_2 = S_0 | q_1 = S_0) \cdot p(q_3 = S_2 | q_2 = S_0) \dots = \pi_1 \cdot a_{10} \cdot a_{00} \cdot a_{02} \dots$$

The sequence of states/colors can be represented as follows:

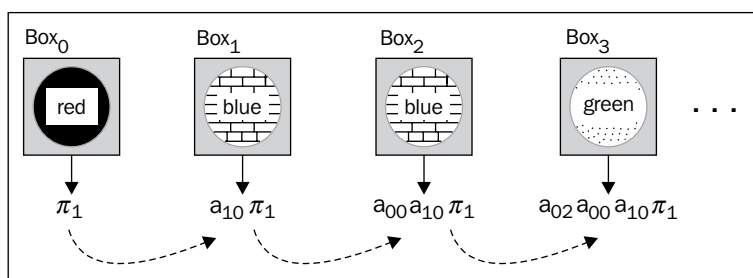


Illustration of the ball and boxes example

Let's estimate the probabilities p using historical data (learning phase):

1. The estimation of the probability to draw a red ball (S_1) in the first attempt is π_1 , which is computed as the number of sequences starting with S_1 (red) / total number of balls.
2. The estimation of the probability of retrieving a blue ball in the second attempt is a_{10} , the number of sequences for which a blue ball is drawn after a red ball / total number of sequences, and so on.

Nth-order Markov



The Markov property is popular mainly because of its simplicity. As you will discover while studying the Hidden Markov model, having a state solely dependent on the previous state allows us to apply efficient dynamic programming techniques. However, some problems require dependencies between more than two states. These models are known as Markov random fields.

Although the discrete Markov process can be applied to trial and error types of applications, its applicability is limited to solving problems for which the observations do not depend on hidden states. Hidden Markov models are a commonly applied technique to meet such a challenge.

The hidden Markov model (HMM)

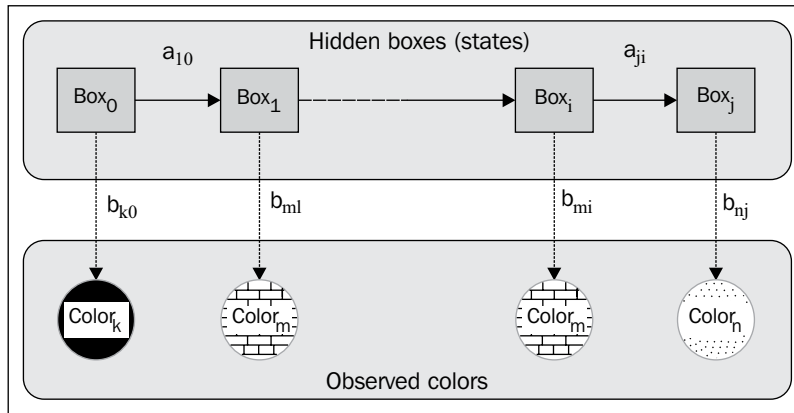
The hidden Markov model has numerous applications related to speech recognition, face identification (biometrics), and pattern recognition in pictures and video [7:3].

A hidden Markov model consists of a Markov process (also known as a Markov chain) for observations with a discrete time. The main difference with the Markov processes is that the states are not observable. A new observation is emitted with a probability known as the emission probability each time the state of the system or model changes.

There are now two sources of randomness:

- Transition between states
- Emission of an observation when a state is given


Let's reuse the boxes and balls example. If the boxes are hidden states (non-observable), then the user draws the balls whose color is not visible. The emission probability is the probability $b_{ik} = p(o_t = color_k | q_t = S_i)$ to retrieve a ball of the color k from a hidden box i , as described in the following diagram:



The hidden Markov model for the balls and boxes example

In this example, we do not assume that all the boxes contain balls of different colors. We cannot make any assumptions on the order as defined by the transition a_{ij} . The HMM does not assume that the number of colors (observations) is identical to the number of boxes (states).

[



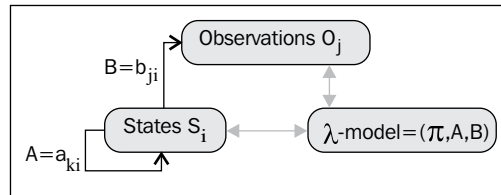
Time invariance
 Contrary to the Kalman filter, for example, the hidden Markov model requires that the transition elements, a_{ij} , are independent of time. This property is known as stationary or homogeneous restriction.

]

It must be kept in mind that the observations, in this case the color of the balls, are the only tangible data available to the experimenter. From this example, we can conclude that a formal HMM has three components:

- A set of observations
- A sequence of hidden states
- A model that maximizes the joint probability of the observations and hidden states, known as the Lambda model

A Lambda model, λ , is composed of initial probabilities π , the probabilities of state transitions as defined by the matrix A , and the probabilities of states emitting one or more observations:



Visualization of the HMM key components

This diagram illustrates that, given a sequence of observations, HMM tackles three problems known as canonical forms:

- **CF1 – evaluation:** Evaluate the probability of a given sequence of observations O , given a model $\lambda = (\pi, A, B)$
- **CF2 – training:** Identify (or learn) a model $\lambda = (\pi, A, B)$ given a set of observations O
- **CF3 – decoding:** Estimate the state sequence Q with the highest probability to generate a given set of observations O and a model λ

The solution to these three problems uses dynamic programming techniques. However, we need to clarify the notations prior to diving into the mathematical foundation of the hidden Markov model.


Notation

One of the challenges of describing the hidden Markov model is the mathematical notation that sometimes differs from author to author. From now on, we will use the following notation:

	Description	Formulation
N	The number of hidden states	
S	A finite set of N hidden states	$S = \{S_0, S_1, \dots, S_{N-1}\}$
M	The number of observation symbols	
q_t	The state at time or step t	
Q	Time sequence of states	$Q = \{q_0, q_1, \dots, q_{n-1}\} = Q_{0:n-1}$
T	The number of observations	
o_t	The observation at time t	
O	A finite sequence of T observations	$O = \{o_0, o_1, \dots, o_{T-1}\} = O_{0:T-1}$

	Description	Formulation
A	The state transition probability matrix	$a_{ji} = p(q_{t+1}=S_i q_t=S_j)$
B	The emission probability matrix	$b_{jk} = p(o_t=O_k q_t=S_j)$
π	The initial state probability vector	$\pi_i = p(q_0=S_i)$
λ	The hidden Markov model	$\lambda = (\pi, A, B)$

[

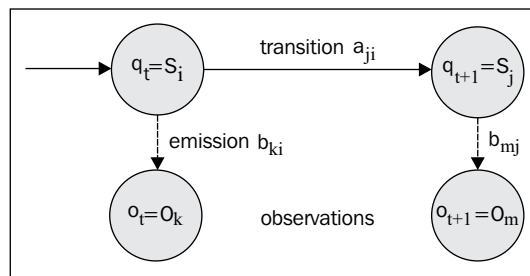


Variance in notation

Some authors use the symbol z to represent the hidden states instead of q and x to represent the observations O .

]

For convenience, let's simplify the notation of the sequence of observations and states using the following condensed form: $p(O_{0:T}, q_t | \lambda) = p(O_0, O_1, \dots, O_T, q_t | \lambda)$. It is quite common to visualize a hidden Markov model with a lattice of states and observations similar to our description of the boxes and balls examples, as shown here:



The formal HMM-directed graph

The state S_i is observed as O_k at time t , before being transitioned to the state S_j observed as O_m at the time $t+1$. The first step in the creation of our HMM is the definition of the class that implements the lambda model $\lambda = (\pi, A, B)$ [7:4].

The lambda model

The three canonical forms of the hidden Markov model rely heavily on manipulation and operations on matrices and vectors. For convenience, let's define an `HMMConfig` class that contains the dimensions used in the HMM:

```
class HMMConfig(val _T: Int, val _N: Int, val _M: Int) extends Config
```

The input parameters for the class are:

- `_T`: The number of observations
- `_N`: The number of hidden states
- `_M`: The number of observation symbols or features

Consistency with mathematical notation



The implementation uses `_T` (with respect to `_N`, `_M`) to represent programmatically the number of observations `T` (with respect to hidden states `N` and features `M`). As a general rule, the implementation reuses the mathematical symbols as much as possible. Although the practice does not always make the code elegant, it improves its readability.

The `HMMConfig` companion object defines the operations on ranges of index of matrix rows and columns. The `foreach`, `foldLeft`, and `maxBy` methods are regularly used in each of the three canonical forms:

```
object HMMConfig {
  def foreach(i: Int, f: Int => Unit): Unit = Range(0, i).foreach(f)
  def foldLeft(i: Int, f: (Double, Int) => Double, zero: Double) =
    Range(0, i).foldLeft(zero)(f)
  def maxBy(i: Int, f: Int => Double): Int = Range(0, i).maxBy(f)
  ...
}
```

Notation




The λ model in HMM should not be confused with the regularization factor discussed in the L_n roughness penalty section in *Chapter 6, Regression and Regularization*.

As mentioned earlier, the lambda model is defined as a tuple of the transition probability matrix A , emission probability matrix B , and the initial probability π . It is easily implemented as a case class, `HMMLambda`, using the `Matrix` class defined in the *Matrix class* section in *Appendix A, Basic Concepts*. The simplest constructor for the `HMMLambda` class is invoked in the case where the state-transition probability matrix, the emission probability matrix, and the initial states are known, as shown here:

```
class HMMLambda(val A: Matrix[Double], val B: Matrix[Double], var pi:
  DblVector, val numObs: Int) {
  def getT: Int = numObs
  def getN: Int = A.nRows
  def getM: Int = B.nCols
  val d1 = numObs - 1
  ...
}
```


The implementation reflects the mathematical notation, with p_i being the initial state probability, A the state transition matrix, and B the emission matrix. The `numObs` value is the number of observations in the sequence. The `getT`, `getN`, and `getM` methods are used to keep the implementation consistent with the initial configuration, `HMMConfig`. The section related to the training of HMM introduces a different constructor for `HMMLambda` using the configuration as a parameter.

The initial probabilities are unknown, and therefore, initialized with a random generator of values $[0, 1]$.



Normalization

Input states and observations data may have to be normalized and converted to probabilities before initializing the matrices A and B .

The two other components of the HMM are the sequence of observations and the sequence of hidden states.

HMM execution state

The canonical forms of the HMM are implemented through dynamic programming techniques. These techniques rely on variables that define the state of the execution of the HMM for any of the canonical forms:

- **Alpha** (the forward variable): The probability of observing the first $t < T$ observations for a specific state at S_i for the observation t , $\alpha_t(i) = p(O_{0:t}, q_t = S_i | \lambda)$
- **Beta** (the backward variable): The probability of observing the remainder of the sequence qt for a specific state $\beta_t(i) = p(O_{t+1:T-1} | q_t = S_i, \lambda)$
- **Gamma**: The probability of being in a specific state given a sequence of observations and a model $\gamma_t(i) = p(q_t = S_i | O_{0:T-1}, \lambda)$
- **Delta**: The sequence to have the highest probability path for the first i observations defined for a specific test $\delta_t(i)$
- **Qstar**: The optimum sequence q^* of states $Q_{0:T-1}$
- **DiGamma**: The probability of being in a specific state at t and another defined state at $t+1$ given the sequence of observations and the model $\gamma_t(i, j) = p(q_t = S_i, q_{t+1} = S_j | O_{0:T-1}, \lambda)$

Each of the parameters is described in the section related to each canonical form. Let's create a class `HMMState` that encapsulates the variables used in the implementation of the three canonical cases.

For convenience, all the parameters related to the three canonical cases and listed in the previous notation section are encapsulated into a single outer class, `HMMState`:

```
class HMMState(lambda: HMLambda, maxIters:Int) extends Config {
  val delta = Matrix[Double]( lambda.getT, lambda.get N) //  $\delta_t(i)$ 

  object QStar { ... } //  $q^*$ 
  object DiGamma { ... } //  $\gamma_t(i, j)$ 
  object Gamma { ... } //  $\gamma_t(i)$ 
}
```

Once again, we use the same notation as for the configuration of the HMM; `lambda.getT`, being the number of observations, and `lambda.getN`, the number of hidden states. The HMM state parameters have self-descriptive names that strictly follow the notation introduced earlier. The λ model, the HMM state, and the sequence of observations are all the elements needed to implement the three canonical cases.

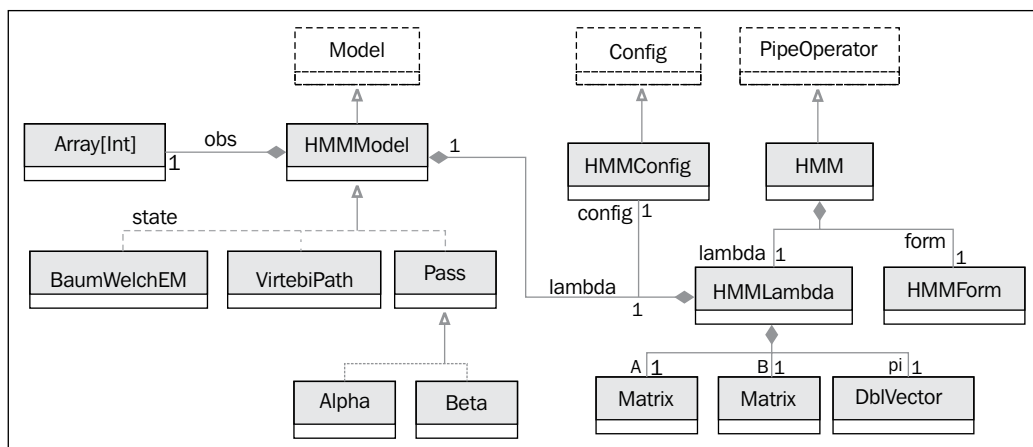
The `Gamma` and `DiGamma` singletons are used and described in the evaluation canonical form. The `DiGamma` singleton is described as part of the Viterbi algorithm to extract the sequence of states with the highest probability given a λ model and a set of observations.

The execution of any of the three canonical forms relies on dynamic programming techniques (refer to the *Overview of dynamic programming* section in *Appendix A, Basic Concepts*) [7:5]. The simplest of the dynamic programming techniques is a single traversal of the observations/state chain.

Therefore, it makes sense to define a base class, `HMMModel`, that has all the algorithms that manipulate the λ model, `lambda`, and the observed states, `obs`:

```
abstract class HMMModel(lambda: HMLambda, obs: Array[Int])
```

The list of dynamic-programming-related algorithms used in any of the three canonical forms is visualized through the class hierarchy of our implementation of the HMM:



Scala classes' hierarchy for HMM (UML class diagram)

Each class is described as needed in the description of the three canonical forms of HMM. It is time to dive into the implementation details of each of the canonical forms, starting with the evaluation.

Evaluation (CF-1)

The objective is to compute the probability (or likelihood) of the observed sequence O_t given a λ model. A dynamic programming technique is used to break down the probability of the sequence of observations into two probabilities:

$$p(O_{0:T-1} | \lambda) \propto p(O_{0:t} | \lambda) \cdot p(O_{t+1:T-1} | \lambda)$$

The likelihood is computed by marginalizing over all the hidden states $[7:6]\{S_i\}$:

$$p(O_{0:T-1} | \lambda) = \sum_{i=0}^{N-1} p(O_{0:T-1}, q_t = S_i | \lambda)$$

If we use the notation introduced in the previous chapter for alpha and beta variables, the probability for the observed sequence O_t given a λ model can be expressed as:


$$p(O_{0:T-1} | \lambda) = \sum_i \alpha_t(i) \cdot \beta_t(i)$$

The product of the probabilities α and β can potentially underflow. Therefore, it is recommended to use the log of the probabilities instead of the probabilities.

Alpha class (the forward variable)

The computation of the probability of observing a specific sequence given a sequence of hidden states and a λ model relies on a two-pass algorithm. The alpha algorithm consists of the following steps:

1. Compute the initial alpha value [M1]. The value is then normalized by the sum of alpha values across all the hidden states [M2].
2. Compute the alpha value iteratively for the time 0 to time t , then normalize by the sum of alpha values for all states [M3].
3. The final step is the computation of the log of the probability of observing the sequence [M4].



Performance consideration
A direct computation of the probability of observing a specific sequence requires $2TN^2$ multiplications. The iterative alpha and beta classes reduce the number of multiplications to N^2T .

For those with some inclination toward mathematics, computation of the alpha matrix is defined in the following information box. Each formula has an identifier [Mx], which is referenced in the Scala source code implementing it.

Alpha-class (forward variable)

- **M1:** Initialization:

$$\alpha_0(i) = \pi_i \cdot b_i(O_0)$$

- **M2:** Normalization of initial values:

$$\hat{\alpha}_0(i) = \alpha_0(i) / \sum_{j=0}^{N-1} \alpha_0(j)$$



- **M3:** Normalized summation:

$$\alpha_t(i) = \sum_{j=0}^{N-1} \alpha_{t-1}(j) a_{ji} b_i(O_t) \quad c_t = 1 / \sum_{i=0}^{N-1} \alpha_t(i) \quad \hat{\alpha}_t(i) = \alpha_t(i) \cdot c_t$$

- **M4:** Probability of observing a sequence given a lambda model and states:


$$\log p(O | \lambda) = - \sum_{j=0}^{T-1} \log \left(\frac{1}{\sum_{i=0}^{N-1} \hat{\alpha}_t(i)} \right)$$

Let's look at the implementation of the alpha class in Scala, using the referenced number of the mathematical expressions of the alpha class. The alpha and beta values have to be normalized [M3], and therefore, we define a base class, `Pass`, for the alpha and beta algorithms that implements the normalization:

```
class Pass(_lambda: HMMLambda, _obs: Array[Int]) extends HMMModel(_
lambda, _obs) { //1
  var alphaBeta: Matrix[Double] = _
  val ct = Array.fill(lambda.getT) (0.0) //2

  def normalize(t: Int): Unit = {
    ct.update(t, foldLeft(lambda.getN, (s, n) => s + alphaBeta(t,
n))) //3
    alphaBeta /= (t, ct(t))
  }
}
```

As with any algorithm used in the hidden Markov model, the `Pass` base class of the alpha and beta classes is a composition of the attributes of the model (`HMMLambda`), the computation parameters (`HMMParams`), and the sequence of observations `obs` (line 1). The `alphaBeta` matrix represents either the alpha or beta matrix manipulated in the subclasses (line 2). The scale factor, `ct`, is computed as the summation of the alpha or beta row matrix over all the states using a fold (line 3).



Computation efficiency

Scala's `reduce`, `fold`, and `foreach` methods are far more efficient iterators than the `for` loop. You need to keep in mind that the main purpose of the `for` loop in Scala is the monadic chaining of `map` and `flatMap` operations.

The computation of the `alpha` variable in the `Alpha` class follows the same computation flow as defined in the mathematical expression:

```
class Alpha(lambda: HMMLambda, obs: Array[Int]) extends Pass(lambda, obs)
```

The `alpha` value is initialized [M1] (line 4), then normalized [M2] using the current sequence order (line 5). The value of `alpha` is then updated [M3] by summation of the previous `alpha` value at $t-1$ and the transition from the state j to the state i (line 6), as shown here:

```
import HMMConfig._
val alpha = {
  alphaBeta = lambda.initAlpha(obs) //4
  normalize(0) //5
  sumUp //6
}

def sumUp: Double = { //M2
  foreach(lambda.getT, t => {
    updateAlpha(t) //7
    normalize(t) //8
  })
  foldLeft(lambda.getN, (s, k) => s + alphaBeta(lambda.dim_1, k))
}

def updateAlpha(t: Int): Unit =
  HMMConfig.foreach(lambda.getN, i =>
    alphaBeta += (t, i, lambda.alpha(alphaBeta(t-1, i), i, obs(t)))
  )
}
```

The value of `alpha` is updated by the `updateAlpha` method (line 7) before normalization (line 8). The implementation that relies on the `fold` method is omitted, but can be easily written.

Finally, the computation of the logarithm of the probability to observe a specific sequence, given the sequence of states and a predefined λ model, [M4] can be performed by the following code (line 9):

```
def logProb: Double = foldLeft(lambda.getT, (s, t)
    => s + Math.log(ct(t)), Math.log(alpha))//9
```

The method computes the logarithm of the probability instead of the probability itself. The summation of the logarithm of probabilities is less likely to cause an underflow than the product of probabilities.

Beta class (the backward variable)

The recursive computation of beta values is similar to the Alpha class except that the iteration executes backward on the sequence of states.

The implementation of Beta is similar to the alpha class:

1. Compute [M5] and normalize [M6] the value of beta at $t=0$ across states.
2. Compute and normalize iteratively the beta at the time $T-1$ to t updated from its value at $t+1$ [M7].

Beta class (the backward variable)

- **M5:** Initialization of beta: $\beta_{T-1}(t)=1$
- **M6:** Normalization of initial beta values:

$$\hat{\beta}_{T-1}(i) = \beta_{T-1}(i) / \sum_{j=0}^{N-1} \beta_{T-1}(j)$$

- **M7:** Normalized summation of beta:

$$\beta_t(i) = \sum_{j=0}^{N-1} \beta_{t+1}(j) \cdot a_{ij} \cdot b_j(O_{t+1}) \quad c_t = 1 / \sum_{j=0}^{N-1} \beta_t(j) \quad \hat{\beta}_t(i) = \beta_t(i) \cdot c_t$$



The definition of the class for the Beta class is identical to the Alpha class:

```
class Beta(lambdaB: HMMLambda, _obs: Array[Int]) extends Pass(lambdaB,
  _obs)
```

The implementation of the Beta class is similar to the Alpha class with computation (line 1) and normalization (line 2) of beta at $t=0$. As expected, the summation routine `sumUp` (line 3) is implemented as updating and normalizing beta at the time t , as shown here:

```
val complete = { //4
  alphaBeta = Matrix[Double](lambda.getT, lambda.getN)
  alphaBeta += (lambda.dim_1, 1.0) //1
  normalize(lambda.dim_1) //2
  sumUp; true
}

def sumUp: Unit = //3
  (lambda.getT-2 to 0 by -1).foreach( t =>{
    updateBeta(t)
    normalize(t)
  })

def updateBeta(t: Int): Unit =
  foreach(lambda.config.getN, i => {
    alphaBeta += (t, i, lambda.beta(alphaBeta(t+1, i), i, obs(t+1)))
  })
```

The recursive method updates and normalizes the beta matrix by traversing the sequence of observations backward from before the last observation to the first. Contrary to the Alpha class, the Beta class does not generate an output value. Therefore, we need to flag the state of the class using a ready Boolean value, which is set to true if the instantiation succeeds and false otherwise.



Constructors

The alpha and beta values are computed within the constructors of their respective class, so no public or protected method needs to verify if these values are already computed. The design pattern reduces the complexity of implementation by ensuring that a class instance has only one state: computation completed.

What is the value of a model if it cannot be created? The next canonical form CF2 leverages dynamic programming and recursive functions to extract the λ model.

Training (CF-2)

The objective of this canonical form is to extract the λ model given a set of observations and a sequence of states. It is similar to the training of a classifier. The simple dependency of a current state on the previous state enables an implementation using an iterative procedure, known as the **Baum-Welch estimator** or expectation-maximization (EM).

Baum-Welch estimator (EM)

At its core, the algorithm has three steps and an iterative method, similar to the evaluation canonical form:

1. Compute the probability π (the gamma value at $t=0$) [M9].
2. Compute and normalize the state's transition probabilities matrix A [M10].
3. Compute and normalize the matrix of emission probabilities B [M11].
4. Repeat steps 2 and 3 until the change of likelihood is insignificant.

The algorithm uses the digamma and summation gamma variables defined in the `HMMConfig` class.

The Baum-Welch algorithm

- **M8:** Joint probability of the state q_t at t and q_j at $t+1$:

$$\gamma_t(i, j) = p(q_t = S_i, q_{t+1} = S_j | \mathbf{O}, \lambda)$$

$$\gamma_t(i, j) = \frac{\alpha_t(i) a_{ij} b_j(O_{t+1}) \beta_{t+1}(j)}{\sum_{j=0}^{N-1} \alpha_t(i) \beta_t(j)}$$

- **M9:** The initial probabilities vector:

$$\hat{\pi}_i = \gamma_0(i) \quad \gamma_t(i) = \sum_{j=0}^{N-1} \gamma_t(i, j)$$

- **M10:** Update of the transition probabilities matrix:

$$\hat{a}_{ij} = \frac{\sum_{t=0}^{T-1} (\gamma_t(i, j))}{\sum_{t=0}^{T-1} \gamma_t(i)}$$

- **M11:** Update of the emission probabilities matrix :

$$\hat{b}_{ij} = \frac{\sum_{t=0}^{0j} \gamma_t(i)}{\sum_{t=0}^{T-1} \gamma_t(i)}$$



The Baum-Welch algorithm requires the following three inputs:

- The λ model, `_lambda`, initialized with random values uniformly distributed
- The current state of the training, `state`
- The labeled observed data, `_obsIdx`

The implementation of the Baum-Welch algorithm illustrates the elegance and conciseness of the Scala programming language. The constructor requires a fourth parameter to describe the minimum rate of change of the estimate of the likelihood between iterative calls, as shown in the following code snippet:

```
class BaumWelchEM config: HMMConfig, obs: Array[Int], numIters:
  Int, eps: Double) extends HMMModel(HMMLambda(config), obs) {
  val state = HMMState(lambda, numIters)
}
```

The λ model has to be initialized with the configuration parameters (number of observations, number of states, and number of symbols). The matrices *A* and *B* and the initial state probabilities *pi* are initialized with a uniform random generator [0, 1], `Matrix.fillRandom`, as shown here:

```
object HMMLambda {
  def apply(config: HMMConfig): HMMLambda = {
    val A = Matrix[Double](config._N)
    A.fillRandom(0.0)
    val B = Matrix[Double](config._N, config._M)
    B.fillRandom(0.0)
    val pi = Array.fill(config._N)(Random.nextDouble)
    new HMMLambda(A, B, pi, config._T)
  }
}
```

The maximum likelihood, `maxLikelihood`, is computed as part of the constructor to ensure a consistent state:

```
var likelihood = frwrdBckwrDLattice
Range(0, state.maxIters) find( _ => {
  lambda.estimate(state, obs) //1
  val _likelihood = frwrdBckwrDLattice //2
  val diff = likelihood - _likelihood //3
  likelihood = _likelihood
  diff < eps //4
}) match {
  case Some(index) => maxLikelihood
  ...
}
```

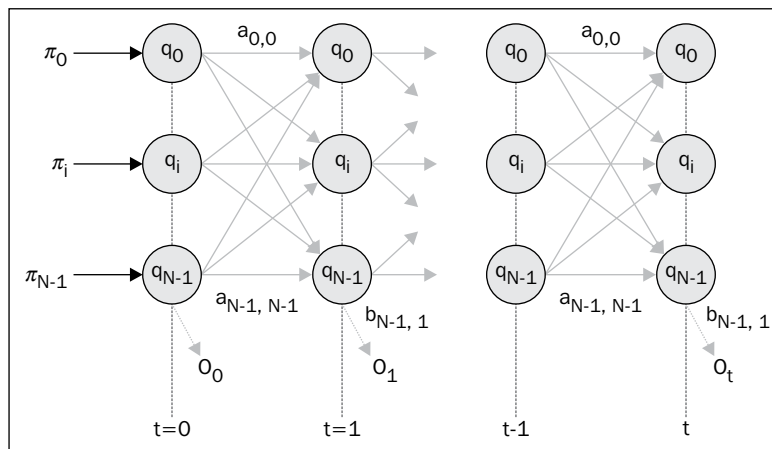
The computation of the likelihood requires the estimation of the transition matrix *A* and emission matrix *B* (line 1). The training process iterates by traversing the lattice forward and backward until the likelihood reaches a local or global maximum. The λ model is updated using the `estimate` method (line 1). The method computes the likelihood of the sequence of states (line 2) and then compares it with the likelihood computed in the previous iteration (line 3). The method exits if the difference between two consecutive likelihood values meets the convergence criteria `eps` (line 4).

The estimate method of the HMMLambda class updates the λ model (A , B , and π):

```
def estimate(state: HMMState, obsIdx: Array[Int]): Unit = {
  pi = Array.tabulate(config._N)(i => state.Gamma(0, i) )
  HMMConfig.foreach(config._N, i => {

    var denominator = state.Gamma.fold(dim_1, i)
    HMMConfig.foreach(config._N, k =>
      A += (i, k, state.DiGamma.fold(dim_1, i, k)/denominator)
    )
    denominator = state.Gamma.fold(config._T, i)
    HMMConfig.foreach(config._N, k => B += (i, k, state.Gamma.
      fold(config._T, i, k, obsIdx)/denominator))
  })
}
```

The core of the Baum-Welch expectation maximization is the iterative forward and backward update of the lattice of states and observations between time t and $t+1$. The lattice-based iterative computation is illustrated in the following diagram:



Visualization of HMM graph lattice for the Baum-Welch algorithm

The iteration across the lattice is implemented by the `frwrdBckwrDLattice` method (line 2). The lattice is traversed ahead using the `Alpha` instance class (line 1), and backward using the `Beta` instance class (line 2):

```
def frwrdBckwrDLattice: Double = {
  val _alpha = Alpha(lambda, obs).alpha //1
  val _beta = Beta(lambda, obs) //2
  val a = _alpha.alphaBeta
  val b = _beta.alphaBeta
}
```

```

Gamma.update(a, b) //3
DiGamma.update(a, b, A, B, obs) //4
_alpha.alpha
}

```

The method returns the alpha coefficient and computes the new values for the Gamma (line 3) vector and DiGamma (line 4) matrix. These HMMState methods are omitted for the sake of clarity.

Decoding (CF-3)

This last canonical form consists of extracting the most likely sequence of states $\{q_t\}$ given a set of observations O_t and a λ model. Solving this problem requires, once again, a recursive algorithm.

The Viterbi algorithm

The extraction of the best state sequence (the sequence of state that has the highest probability) is very time consuming. An alternative consists of applying a dynamic programming technique to find the best sequence $\{q_t\}$ through iteration. The algorithm is known as the **Viterbi algorithm**. Given a sequence of states $\{q_t\}$ and sequence of observations $\{o_t\}$, the probability $\delta_t(i)$ for any sequence to have the highest probability path for the first T observations is defined for the state S_i [7:7].

The Viterbi algorithm

M12: Definition of delta function:

$$\delta_t(i) = \max_{q_{1:T-1}} p(q_{0:T-1} = S_i, O_{0:T-1} | \lambda)$$

M13: Initialization of delta:

$$\delta_0(i) = \pi_i b_i(O_0) \quad \psi_0(i) = 0 \forall i$$

M14: Recursive computation of delta:

$$\delta_t(i) = \max_j (\delta_{t-1}(j) \cdot a_{ji} \cdot b_i(O_t)) \quad \psi_t(i) = \arg \max_j (\delta_{t-1}(j) \cdot a_{ji})$$

M15: Computation of the optimum state sequence Q :

$$q_t^* = \psi_{t+1}(q_{t+1}^*) \quad q_t^* = \arg \max_j \delta_t(j)$$



The constructor of the Viterbi algorithm, `ViterbiPath`, is similar to the algorithms of the first two canonical forms, and therefore, inherits `HMMInference`. The purpose of the Viterbi algorithm is to compute the optimum sequence given a set of observations and a λ model by maximizing the delta, `maxDelta`:

```
class ViterbiPath(_lambda: HMMLambda, _state: HMMState, _obs:
  Array[Int]) extends HMMInference(_lambda, _state, _obs) {
  val maxDelta = recurse(lambda.getT, 0)
  ...
}
```

The recursive method that implements [M14] and [M15] steps is invoked by the constructor:

```
def recurse(t: Int, j: Int): Double = {
  var maxDelta = initial((t, j)) //1
  if( maxDelta == -1.0) {
    if(t != obs.size) {
      maxDelta = maxBy(lambda.getN, //2 [M14]
        s => recurse(t-1, s)* lambda.A(s, j)* lambda.B(j, obs(t))
      )
      val idx = maxBy(lambda.getT, i =>recurse(t-1 ,i)*lambda.A(i,j))
      //3 [M14]

      state.psi += (t, j, idx) //4
      state.delta += (t, j, maxDelta) //5
    }
    else { //6
      maxDelta = 0.0
      val index = maxBy(lambda.getN, i => {
        val delta = recurse(t-1 ,i)
        if( delta > maxDelta) maxDelta = delta
        delta
      })
      state.QStar.update(t, index) //7
    }
  }
  maxDelta
}
```

Once initialized (line 1), the maximum value of delta, `maxDelta`, is computed recursively by applying the formula [M14] at each state, `s`, using Scala's `maxBy` method (line 2). Next, the index of the column of the transition matrix `A` corresponding to the maximum of delta is computed (line 3). The last step is to update the matrix `psi` (line 4) (with respect to delta (line 5)). Once the step `t` reaches the maximum number of observation labels (line 6), the optimum sequence of states q^* is computed [M15] (line 7). Ancillary methods are omitted.

This implementation of the decoding form of the hidden Markov model completes the description of the hidden Markov model and its implementation in Scala. Now, let's put this knowledge into practice.

Putting it all together

The main class `HMM` implements the three canonical forms. A view bound to an array of integers is used to parameterize the `HMM` class. We assume that a time series of continuous or pseudocontinuous values is converted (or categorized) into discrete symbol values.

The `@specialized` annotation ensures that the byte code is generated for the `Array[Int]` primitive without executing the conversion implicitly declared by the bound view. The `HMM` can be potentially used as part of a computation workflow, and therefore, has to implement the pipe operator (`PipeOperator`).

There are two different constructors for the `HMM` class. The first constructor uses the λ model as input (evaluation (CF1) and decoding (CF3)):

```
class HMM[@specialized T <% Array[Int]](lambda: HMMLambda, form:
  HMMForm, maxIters: Int) (implicit f: DblVector => T) extends
  PipeOperator[T, HMMPredictor] {
  val state = HMMState(lambda, maxIters)
  ...
}
```

The `HMMForm` enumerator is used to specify the canonical form of the HMM solution:

```
object HMMForm extends Enumeration {
  type HMMForm = Value
  val EVALUATION, DECODING = Value
}
```

The conversion of `DblVector` to a type `T` is required only if the evaluation and decoding canonical form uses actual observation values as argument. The `f` function is then used to discretize the double values into a sequence of index of the observations.

The `HMPredictor` type consists of a tuple log probability (or likelihood) of observations and index of sequence of observations:

```
type HMPredictor = (Double, Array[Int])
```

The HMM has three canonical forms instead of the two forms of most classifiers.

The second canonical form, training, is implemented by defining a second constructor for the HMM class, as follows:

```
object HMM {
  def apply[T <% Array[Int]](config: HMMConfig, obs: Array[Int],
    form: HMMForm, maxIters: Int, eps: Double)
    (implicit f: DblVector => T): HMM[T] = {
    val baumWelchEM = new BaumWelchEM(config, obs, maxIters, eps)
    new HMM[T](baumWelchEM.lambda, form, maxIters)
  }
}
```

The `decode` (with respect to `evaluate`) method implements the third (with respect to the first) canonical form of HMM. Both methods take a sequence of indices for observations as an argument.

```
def decode(obsIdx: Array[Int]): HMPredictor = (ViterbiPath(lambda,
  state, obsIdx).maxDelta, state.QStar())
def evaluate(obsIdx: Array[Int]): HMPredictor = (-Alpha(lambda,
  obsIdx).logProb, obsIdx)
}
```

The data transformation `|>` encapsulates the evaluation and decoding forms in order to preserve its meaning. The observation, `obs`, is automatically converted into a sequence of indices to each observation (line 1) by the `DblVector => T` discretization function, which is an implicit parameter of the `HMM` class.

```
def |> : PartialFunction[DblVector, HMPredictor] = {
  case obs: DblVector if (obs != null && obs.size > 2) => {
    form match {
      case EVALUATION => evaluate(obs) //1
      case DECODING => decode(obs) //1
    }
  }
  ...
}
```




Normalized probabilities input

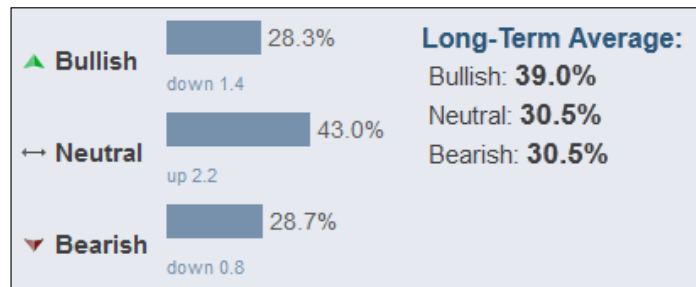
You need to make sure that the input probabilities for the λ model for evaluation and decoding canonical forms are normalized – the sum of the probabilities of all the states for the π vector and A and B matrices are equal to 1. This validation code is omitted in the example code.

Test case

Our test case is to train an HMM to predict the sentiment of investors as measured by the weekly sentiment survey of the members of the **American Association of Individual Investors (AAII)** [7:8]. The goal is to compute the transition probabilities matrix A , the emission probabilities matrix B , and the steady state probability distribution π , given the observations and hidden states (training canonical form).

We assume that the change in investor sentiments is independent of time, as required by the hidden Markov model.

The AAII sentiment survey grades the bullishness on the market in terms of percentage:



The weekly AAII market sentiment (reproduced by courtesy from AAII)

The sentiment of investors is known as a contrarian indicator of the future direction of the stock market. Refer to the *Terminology* section in *Appendix A, Basic Concepts*.

Let's select the ratio of percentage of investors that are bullish over the percentage of investors that are bearish. The ratio is then normalized. The following table lists this:

Time	Bullish	Bearish	Neutral	Ratio	Normalized ratio
t_0	0.38	0.15	0.47	2.53	1.0
t_1	0.41	0.25	0.34	1.68	0.53
t_2	0.25	0.35	0.40	0.71	0.0
....					

The sequence of non-normalized observations (ratio of bullish sentiment over bearish sentiment) is defined in a CSV file as follows:

```
final val OBS_PATH = "resources/data/chap7/obs.csv"

final val NUM_SYMBOLS = 6
final val NUM_STATES = 5
final val EPS = 1e-3
final val MAX_ITERS = 250

val srcObs = Source.fromFile(OBS_PATH)
val obs = srcObs.getLines.map(_.toDouble).toSeq //1
val config = new HMMConfig(obs.size, NUM_STATES, NUM_SYMBOLS)
val min = obs.min
val delta = obs.max - min
val obsSeq = obs.map( x => (x - min)/delta) //2
                .map(x =>(x*NUM_SYMBOLS).floor.toInt) //3
HMM[Array[Int]](config,obsSeq,EVALUATION,MAX_ITERS,EPS) match {
  case Some( hmm) => //4
    Display.show(s"Lambda: ${hmm.getModel.toString}", logger)
    ...
}
```

The sequence of observations is loaded from the CSV file (line 1) before being normalized (line 2). The discretization converts the normalized bullish sentiment/bearish sentiment ratio in six levels (integers) [0,-5] (line 3). The instantiation of the HMM class for the ratio levels (Array[Int]) generates the λ model (A, B, and pi) (line 4).

The following is a state-transition matrix:

A	1	2	3	4	5
1	0.090	0.026	0.056	0.046	0.150
2	0.094	0.123	0.074	0.058	0.0
3	0.093	0.169	0.087	0.061	0.056
4	0.033	0.342	0.017	0.031	0.147
5	0.386	0.47	0.314	0.541	0.271

The emission matrix is as follows:

B	1	2	3	4	5	6
1	0.203	0.313	0.511	0.722	0.264	0.307
2	0.149	0.729	0.258	0.389	0.324	0.471
3	0.305	0.617	0.427	0.596	0.189	0.186
4	0.207	0.312	0.351	0.653	0.358	0.442
5	0.674	0.520	0.248	0.294	0.259	0.03

The hidden Markov model for time series analysis

The evaluation form of the hidden Markov model is very suitable for filtering data for discrete states. Contrary to time series filters such as the Kalman filter introduced in the *The Kalman filter* section in *Chapter 3, Data Preprocessing*, HMM requires data to be somewhat stationary in order to create a reliable model. However, the hidden Markov model overcomes some of the limitations of analytical time series analysis. Filters and smoothing techniques assume that the noise (frequency mean, variance, and covariance) is known and usually follows a Gaussian distribution. The hidden Markov model does not have such a restriction. Moreover, moving averaging techniques, discrete Fourier transforms, and generic Kalman filters require the states to be continuous with linear dependencies, although the extended Kalman filter can approximate nonlinear states.

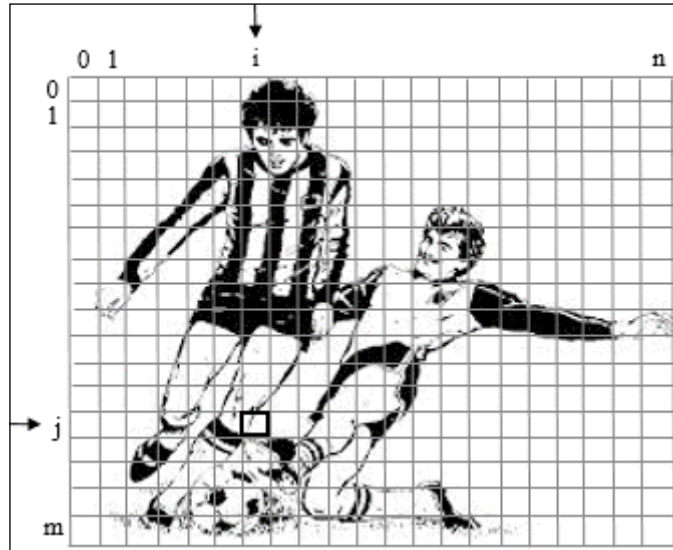
Conditional random fields

The **conditional random field (CRF)** is a discriminative machine learning algorithm introduced by John Lafferty, Andrew McCallum, and Fernando Pereira [7:9] at the turn of the century as an alternative to the HMM. The algorithm was originally developed to assign labels to a set of observation sequences as found.

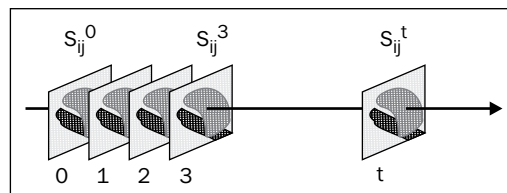
Let's consider a concrete example to understand the conditional relation between the observations and the label data.

Introduction to CRF

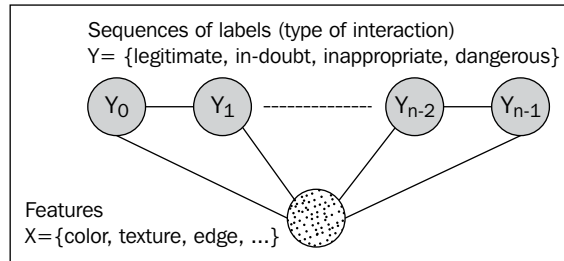
Let's consider the problem of detecting a foul during a soccer game using a combination of video and audio. The objective is to assist the referee and analyze the behavior of the players to determine whether an action on the field is dangerous (red card), inappropriate (yellow card), in doubt to be replayed, or legitimate. The following image is an example of segmentation of a video frame for image processing:



The analysis of the video consists of segmenting each video frame and extracting image features such as colors or edges [7:10]. A simple segmentation scheme consists of breaking down each video frame into tiles or groups of pixels indexed by their coordinates on the screen. A time sequence is then created for each tile S_{ij} , as represented in the following image:



The image segment S_{ij} is one of the labels that are associated with multiple observations. The same features extraction process applies to the audio associated with the video. The relation between the video/image segment and the hidden state of the alteration between the soccer players is illustrated by the following model graph:

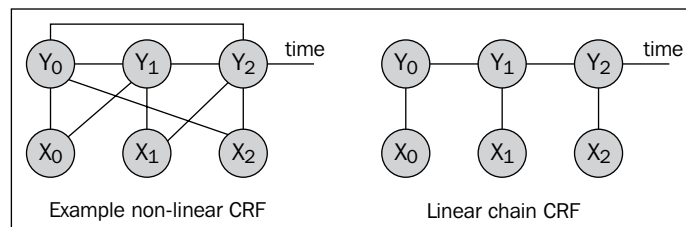


Undirected graph representation of CRF for soccer infraction detection

Conditional random fields (CRFs) are discriminative models that can be regarded as a structured output extension of the logistic regression. CRFs address the problem of labeling a sequence of data such as assigning a tag to each word in a sentence. The objective is to estimate the correlation among the output (observed) values Y conditional on the input values (features) X .

The correlation between the output and input values is described as a graph (also known as a **graph-structured CRF**). A good example of graph-structured CRF are cliques. Cliques are sets of connected nodes in a graph for which each vertex has an edge connecting it to every other vertex in the clique.

Such models are complex and their implementation is challenging. Most real-world problems related to time series or ordered sequences of data can be solved as a correlation between a linear sequence of observations and a linear sequence of input data much like HMM. Such a model is known as the **linear chain structured graph CRF** or **linear chain CRF** for short.




One main advantage of the linear chain CRF is that the maximum likelihood, $p(Y | X, w)$, can be estimated using dynamic programming techniques such as the Viterbi algorithm used in the HMM. From now on, the section focuses exclusively on the linear chain CRF to stay consistent with the HMM described in the previous section.

Linear chain CRF

Let's consider a random variable $X = \{x_i\}_{0:n-1}$ representing n observations and a random variable Y representing a corresponding sequence of labels $Y = \{y_j\}_{0:n-1}$. The hidden Markov model estimates the joint probability $p(X, Y)$ as any generative model requires the enumeration of all the sequences of observations.

If each element of Y , y_j , obeys the first order of the Markov property, then (Y, X) is a CRF. The likelihood is defined as a conditional probability $p(Y | X, w)$, where w is the model parameters vector.

[

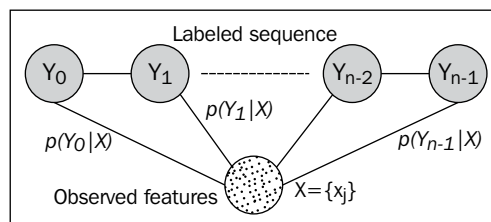


Observation dependencies
The purpose of CRF models is to estimate the maximum likelihood of $p(Y | X, w)$. Therefore, independence between observations X is not required.

]

A graphical model is a probabilistic model for which a graph denotes the conditional independence between random variables (vertices). The conditional and joint probabilities of random variables are represented as edges. The graph for generic conditional random fields can indeed be complex. The most common and simplistic graph is the linear chain CRF.

A first order linear chain conditional random field can be visualized as an undirected graphical model, which illustrates the conditional probability of a label Y_j given a set of observations X :



Linear, conditional, random field undirected graph

The Markov property simplifies the conditional probabilities of Y , given X , by considering only the neighbor labels $p(Y_1 | X, Y_j, j \neq 1) = p(Y_1 | X, Y_0, Y_2)$ and $p(Y_i | X, Y_j, j \neq i) = p(Y_i | X, Y_{i-1}, Y_{i+1})$.

The conditional random fields introduce a new set of entities and a new terminology:

- **Potential functions (f_i):** These are strictly positive, real value functions that represent a set of constraints on the configurations of random variables. They do not have any obvious probabilistic interpretation.
- **Identity potential functions:** These are potential functions $I(x, t)$ that take 1 if the condition on the feature x at time t is true, and 0 otherwise.
- **Transition feature functions:** Simply known as **feature functions**, t_i , are potential functions that take a sequence of features $\{X_i\}$, the previous label Y_{i-1} , the current label Y_i , and an index i . The transition feature function outputs a real value function. In a text analysis, a transition feature function would be defined by a sentence as a sequence of observed features, the previous word, the current word, and a position of a word in a sentence. Each transition feature function is assigned a weight that is similar to the weights or parameters in the logistic regression. Transition feature functions play a similar role as the state transition factors a_{ij} in HMM but without a direct probabilistic interpretation.
- State feature functions s_j are potential functions that take the sequence of features $\{X_i\}$, the current label Y_i , and the index i . They play a similar role as the emission factors in the HMM.

A CRF defines the log probability of a particular label sequence Y , given a sequence of observations X as the normalized product of the transition feature and state feature functions. In other words, the likelihood of a particular sequence Y , given the observed features X , is a logistic regression.

The mathematical notation to compute the conditional probabilities in the case of a first order linear chain CRF is described in the following information box.

CRF conditional distribution

- The log probability of a label's sequence y , given an observation x :

$$\log f_i(y_{i-1}, y_i, x, i) = w_c + \sum_{i=0}^{K-1} w_i t_i(y_{i-1}, y_i, x, i) + \sum_{j=0}^{K-1} \mu_j s_j(y_i, x, i)$$

- Transition feature functions with $I(a) = 1$ if a is true, 0 otherwise:

$$t_i(y_{i-1}, y_i, x, i) = I(y_{i-1} = l_1) \cdot I(y_i = l_2) \cdot I(x = 0)$$

- Using the notation:

$$F_i(y, x) = \sum_{j=0}^{K-1} f_j(y_{j-1}, y_j, x, i) \quad \log p(y | x, \lambda) \propto \sum_{j=0}^{K-1} w_j F_j(x, y)$$

- Conditional distribution of labels y , given x , using the Markov property:

$$p(y | x, w) = \frac{1}{Z(x)} e^{\sum_{j=0}^{K-1} w_j F_j(x, y)} \quad z(x) = \sum_{i=0}^{N-1} \sum_{j=0}^{K-1} w_j F_j(x, y)$$



The weights w_j are sometimes referred as λ in scientific papers, which may confuse the reader. w is used to avoid any confusion with the λ regularization factor.

Now, let's get acquainted with the conditional random fields algorithm and its implementation by Sunita Sarawagi.

CRF and text analytics

Most of the examples used to demonstrate the capabilities of conditional random fields are related to text mining, intrusion detection, or bioinformatics. Although these applications have a great commercial merit, they are not suitable as an introductory test case because they usually require a lengthy description of the model and the training process.

The feature functions model

For our example, we will select a simple problem: how to collect and aggregate an analyst's recommendation on any given stock from different sources with different formats.

Analysts at brokerage firms and investment funds routinely publish the list of recommendations or rating for any stock. These analysts used different rating schemes from buy/hold/sell; A, B, C rating; and stars rating to market perform/neutral/market underperform. For this example, the rating is normalized as follows:

- 0 for a strong sell, (or F or 1 star rating)
- 1 for sell (D, 2 stars, market underperform)
- 2 for neutral (C, hold, 3 stars, market perform, and so on)
- 3 for buy (B, 4 stars, market overperform, and so on)
- 4 from strong buy (A, 5 stars, highly recommended, and so on)

Here is an example of recommendations by stock analysts:

Macquarie upgraded AUJ from Neutral to Outperform rating

Raymond James initiates Ainsworth Lumber as Outperform

BMO Capital Markets upgrades Bear Creek Mining to Outperform

Goldman Sachs adds IBM to its conviction list

The objective is to extract the name of the financial institution that publishes the recommendation or rating, the stock rated, the previous rating, if available, and the new rating. The output can be inserted into a database for further trend analysis, prediction, or simply the creation of reports.



Scope of the application

Ratings from analysts are updated every day through different protocols (feed, emails, blogs, web pages, and so on). The data has to be extracted from HTML, JSON, plain text, or XML format before being processed. In this exercise, we assume that the input has already been converted into plain text (ASCII) using a regular expression or another classifier.

The first step is to define the labels Y representing the categories or semantics of the rating. A segment or sequence is defined as a recommendation sentence. After reviewing the different recommendations, we are able to specify the following seven labels:

- Source of the recommendation (Goldman Sachs and so on)
- Action (upgrades, initiates, and so on)
- Stock (either the company name or the stock ticker symbol)
- From (optional keyword)
- Rating (optional previous rating)
- To
- Rating (new rating for the stock)

The training set is generated from the raw data by **tagging** the different components of the recommendation. The first (or initiate) rating for a stock does not have the fields 4 and 5 defined.

For example:

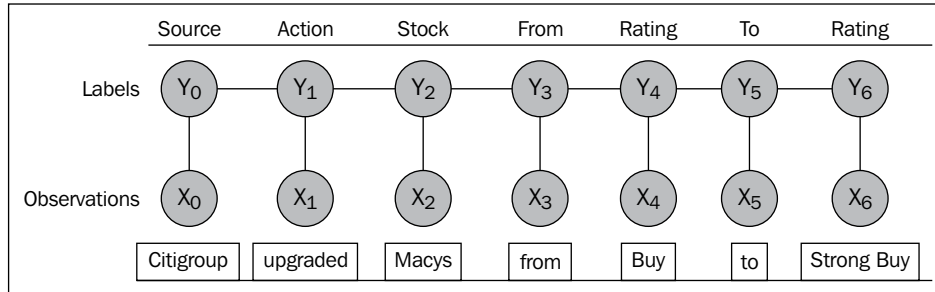
```
Citigroup // Y(0) = 1
upgraded // Y(1)
Macys // Y(2)
from // Y(3)
Buy // Y(4)
to // Y(5)
Strong Buy //Y(6) = 7
```



Tagging

Tagging a word may have a different meaning depending on the context. In **natural language processing (NLP)**, tagging refers to the process of assigning an attribute (adjective, pronoun, verb, proper name, and so on) to a word in a sentence [7:11].

A training sequence can be visualized with the following undirected graph:



An example of a recommendation as a CRF training sequence

You may wonder why we need to tag the "From" and "To" labels in the creation of the training set. The reason is that these keywords may not always be stated and/or their positions in the recommendation differ from one source to another.

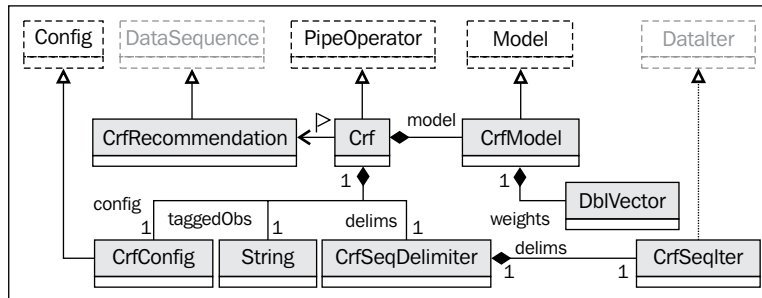
Software design

The implementation of the conditional random fields follows the design template for classifier, as explained in the *Design template for classifiers* section in *Appendix A, Basic Concepts*.

Its key components are as follows:

- A `CrfModel` model of the type `Model` is initialized through training during the instantiation of the classifier.
- The predictive or classification routine is implemented as a data transformation that implements the `PipeOperator` trait.
- The conditional random field classifier, `Crf`, has four parameters: the number of labels (or number of features), `nLabels`; configuration of type `CrfConfig`; the sequence of delimiters of the type `CrfSeqDelimiter`; and the labeled (or tagged) observations `taggedObs`.
- The `CrfRecommendation` class is required by the CRF library to implement the `DataSequence` interface. The class is used to recommend (or estimate) the next label.
- `CrfSeqIter` implements the `DataIter` iteration interface to traverse the labeled data sequence during training, as required by the CRF library.

The key software components of the conditional random fields are described in the following UML class diagram:



UML class diagram for the conditional random fields

The `DataSequence` and `DataIter` interfaces are grayed out to indicate that these are defined in the IITB's CRF Java library.

Implementation

The test case uses the IITB's CRF Java implementation from the Indian Institute of Technology at Bombay by Sunita Sarawagi. The JAR files can be downloaded from Source Forge (<http://sourceforge.net/projects/crf/>).

The library is available as JAR files and source code. Some of the functionality, such as the selection of a training algorithm, is not available through the API. The components (JAR files) of the library are as follows:

- CRF for the implementation of the CRF algorithm
- LBFGS for limited-memory Broyden-Fletcher-Goldfarb-Shanno nonlinear optimization of convex functions (used in training)
- CERN Colt library for manipulation of a matrix
- GNU generic hash container for indexing

The training of the conditional random field for sequences requires defining a few key interfaces:

- `DataSequence` to specify the mechanism to access observations and labels for training and test data
- `DataIter` to iterate through the sequence of data created using the `DataSequence` interface
- `FeatureGenerator` to aggregate all the features types

These interfaces have default implementations bundled in the CRF Java library [7:12].



The scope of the IITB CRF Java library evaluation

The CRF library has been evaluated with three simple text analytics test cases. Although the library is certainly robust enough to illustrate the internal workings of the CRF, I cannot vouch for its scalability or applicability in other fields of interest such as bioinformatics or process control.

Building the training set

The first step is to implement the structure of the training sequence, which implements the `DataIter` interface. The training file consists of a pair of files:

- Raw recommendations (such as *Raymond James upgrades Gentiva Health Services from Underperform to Market perform*)
- Tagged recommendations (such as Raymond James [1] upgrades [2] Gentiva Health Services [3], from [4] Underperform [5] to [6] Market perform [7])

Let's define the model for the CRF classifier. As mentioned earlier, the model for the CRF is similar to the logistic regression model and consists of the `weights` parameter:

```
class CrfModel(val weights: DblVector) extends Model
```

The tagged recommendations file requires a delimiter class, `CrfSeqDelimiter`. It delineates the sequence of observations using the following parameters:

- `obsDelim` is a regular expression to break down data input into a sequence of observations
- `labelsDelim` generates a sequence of labels from the data input
- `trainingDelim` generates a sequence of training tuples from the training set

The `CrfSeqDelimiter` class is defined as follows:

```
class CrfSeqDelimiter(val obsDelim: String, val labelsDelim: String,  
val trainingDelim:String)
```

The main purpose of the IITB CRF Java library's `DataIter` interface is to define the methods to iterate through a sequence of data, tags, or observations. The three methods are as follows:

- `hasNext` tests if the sequence has another entry
- `next` returns the next data or entry in the sequence and increments the iterator cursor
- `startScan` initializes the `DataIter` iterator

The `CrfSeqIter` sequence iterator uses the `iitb.segment.DataCruncher` class to read a training set from a file (a file with tagged words):

```
class CrfSeqIter(val nLabels: Int, val input: String, val delim:
SeqDelimiter) extends DataIter {
  lazy val trainData = DataCruncher.readTagged(nLabels, input, input,
delim.obsDelim, delim.labelsDelim, delim.trainingDelim, new labelMap)

  override def hasNext: Boolean = trainData.hasNext
  override def next: DataSequence = trainData.next
  override def startScan: Unit = trainData.startScan
}
```

The `trainData` training set is initialized only once when any of the `DataIter` overridden methods is invoked. The class is merely an adapter to the generation of the training set.

Generating tags

The second step consists of selecting the mechanism and class to generate the features observations. The extraction of the features from any data set requires implementation of the `FeatureGenerator` interface in order to access all the features observations from any kind of features.

Our problem is a simple linear tagging of data sequences (recommendations from analysts). Therefore, we can use the `iitb.Model.FeatureGenImpl` default implementation. Our tagging class, `TaggingGenerator` makes `FeatureGenImpl` as a subclass and specifies the model specification as a `CompleteModel`. The IITB CRF library supports both linear chain model of `CompleteModel` with a single edge iterator and the nested chain CRF model of the type `NestedModel` with a nested edge iterator. The complete model does not make any assumption regarding the independence between labels Y :

```
val addFeature = true
class TaggingGenerator (val nLabels: Int) extends FeatureGenImpl(new
CompleteModel (nLabels), nLabels, addFeature)
```

The class is defined within the scope of the `Crf` class and does not have to be exposed to the client code. The last parameter of `FeatureGenImpl`, `addFeature`, is set as `true` to allow the tags of dictionary to be built iteratively during the training.

Extracting data sequences

The `CrfTrainingSet` class implements the `DataSequence` interface. It is used to access all the raw analyst's recommendations and rating regarding stocks. The class needs to implement the following methods:

- `set_y` to assign a label index to a position `k`
- `y` to retrieve a label `y` at position `y`
- `x` to retrieve an observed feature vector at position `k`
- `length` to retrieve the number of entries in the sequence

The `CrfTrainingSet` class can be implemented as follows:

```
class CrfTrainingSet(val nLabels: Int, val entry: String, val delim:
String) extends DataSequence {
  val words = entry.split(delim)
  val map = new Array[Int](nLabels)

  override def set_y(k: Int, label: Int): Unit = map(k) = label
  override def y(k: Int): Int = map(k)
  override def length: Int = words.size
  override def x(k: Int): Object = words(k)
}
```

The class takes an analyst's recommendation regarding a stock, `entry`, as an input and breaks it down into words, using the delimiter or regular expression, `delim`.

CRF control parameters

The execution of the CRF algorithm is controlled by a wide variety of configuration parameters. For the sake of simplicity, we use the default configuration parameters, `CrfConfig`, to control the execution of the learning algorithm, with the exception of the following four variables:

- Initialization of the weights, w_ϕ , using either a predefined or a random value between 0 and 1 (default 0)
- Maximum number of iterations used in the computation of the weights during the learning phase `maxIters` (default 50)
- The scaling factor `lamdba` for the L_2 penalty function, used to reduce observations with a high value (default 1.0)
- Convergence criteria, `eps`, used in computing the optimum values for the weights w_j (default 1e-4)



Advanced configuration

The CRF model of the `itb` library is highly configurable. It allows developers to specify a state-label undirected graph with any combination of flat and nested dependencies between states. The source code includes several training algorithms such as the exponential gradient.

The test case does not assume any dependence between states:

```
class CrfConfig(w0: Double, maxIters: Int, lambda: Double, eps:
Double) extends Config
```

Putting it all together

The objective of the training is to compute the weights w_i that maximize the conditional log-likelihood without the L_2 penalty function.



Conditional log-likelihood for a linear chain CRF training set, $D = \{(x_i, y_i)\}_{0:n-1}$ is given as follows:

$$\mathcal{L}(w, D) = -\sum_{i=0}^{n-1} \log p(y_i | x_i, w)$$

Learning: Maximization of loss function and L_2 penalty is given as follows:

$$w^* = \arg \max_{\lambda} \left[\mathcal{L}(w, D) + \lambda \|w\|^2 \right] \quad \lambda = \frac{1}{2\sigma^2}$$

Maximizing the log-likelihood function \mathcal{L} is equivalent to minimizing the loss with L_2 penalty. The function is convex, and therefore, any variant gradient descent (greedy) algorithm can be applied iteratively.

The `Crf` class implements the learning, `train`, and classification methods. Like any other classifiers, `Crf` implements the `PipeOperator` trait; so, the classification can be included in a workflow. The class also implements the `Supervised` trait to force the developer to define a validation routine for the CRF:

```
class Crf(nLabels: Int, config: CrfConfig, delims: SeqDelimiter,
taggedObs: String) extends PipeOperator[String, Double] with
Supervised[String] {
  val features = new TaggingGenerator(nLabels) //1
  lazy val crf = new CRF(nLabels, features, config.params) //2
  val model: Option[CrfModel] = {
```



```
features.train(seqIter) //3
Some(new CrfModel(crf.train(seqIter))) //4
}
...
```

The computation of the CRF weights during training uses either methods defined in IITB's CRF library or methods described in the previous sections.

Once the features have been extracted from the data sequence input file (line 1), the CRF algorithm is instantiated (line 2) with the number of labels, extracted features, and the configuration. The model is trained using the iterator for features `seqIter` (line 3), and then returns a `CrfModel` instance (vector of weights) (line 4) if training succeeds, `None` otherwise.

The predictive method implements the data transformation operator, `|>`. It takes a new observation (analyst's recommendation on a stock) and returns the maximum likelihood, as shown here:

```
def |> : PartialFunction[String, Double] = {
  case obs: String if (obs.length > 1 && model != None) => {
    val dataSeq = new CrfTrainingSet(nLabels, obs, delims.obsDelim)
    crf.apply(dataSeq)
  }
}
```

The data transformation implements the Viterbi algorithm to extract the best sequence of labels for a newly observed recommendation, `obs`. It invokes the `apply` method of the `iitb.crf.CRF` class. The code to validate the arguments/parameters of the class and methods are omitted along with the exception handler for the sake of readability.

Tests

The client code to execute the test consists of defining the number of labels (tags for recommendation), the L_2 penalty factor, `LAMBDA`, and the delimiting string:

```
val LAMBDA = 0.5; val EPS = 1e-3
val NLABELS = 9; val MAX_ITERS = 100; val W0 = 0.7
val PATH = "resources/data/chap7/rating"

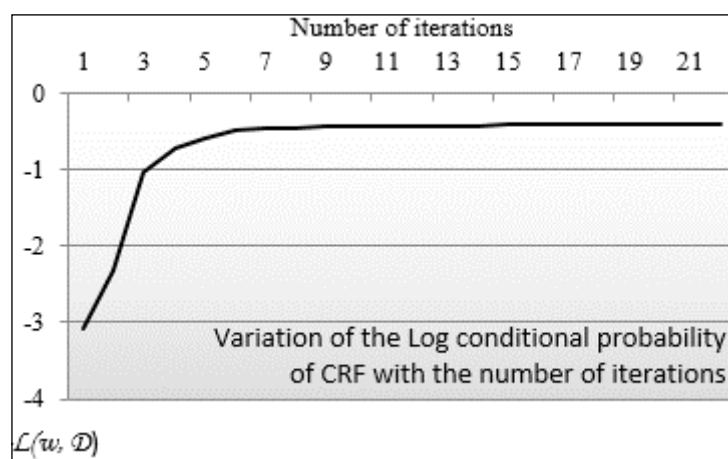
val config = CrfConfig(W0, MAX_ITERS, LAMBDA, EPS)
val delimiters = CrfSeqDelimiter(",\t/ -():.;' ?#`~&_", "//", "\n")

Crf(NLABELS, config, delimiters, PATH).weights match {
  case Some(weights) => weights
  case None => { ... }
}
```

For these tests, the initial value for the weights (with respect to the maximum number of iterations for the maximization of the log likelihood, and the convergence criteria) are set to 0.7 (with respect to 100 and 1e-3). The delimiters for labels sequence, observed features sequence, and the training set are customized for the format of input data files, `rating.raw` and `rating.tagged`.

The training convergence profile

The first training run discovered 136 features from 34 analyst's stock recommendations. The algorithm converged after 21 iterations. The value of the log of the likelihood for each of those iterations is plotted to illustrate the convergence toward a solution of optimum w :



Visualization of the log conditional probability of CRF during training

The training phase converges fairly quickly toward a solution. It can be explained by the fact that there is little variation in the six-field format of the analyst's recommendations. A loose or free-style format would have required a larger number of iterations during training to converge.

Impact of the size of the training set

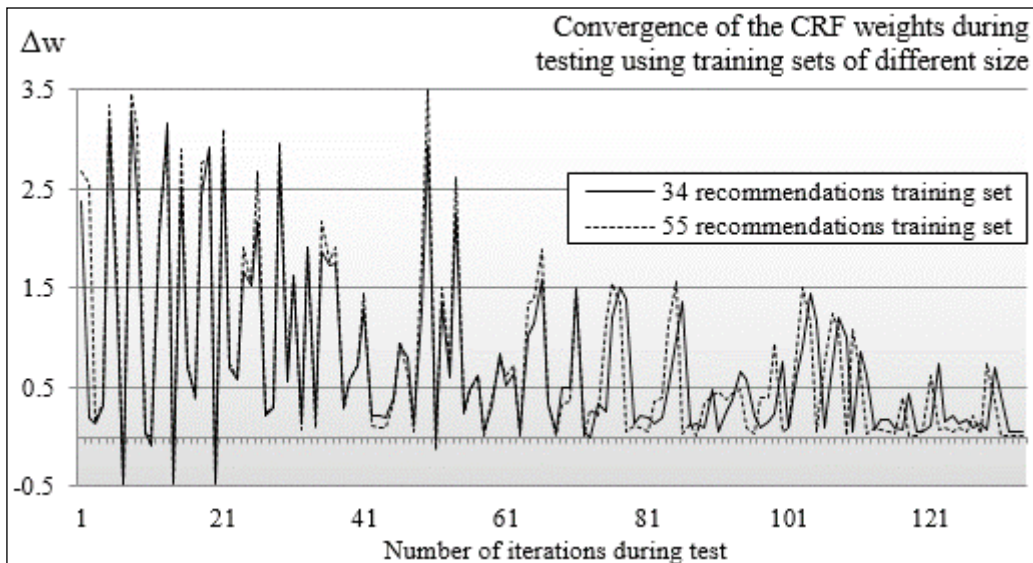
The second test evaluates the impact of the size of the training set on the convergence of the training algorithm. It consists of computing the difference Δw of the model parameters (weights) between two consecutive iterations $\{w_i^{t+1}$ and $\{w_i^t$:

$$\Delta w = \sum_{i=0}^{D-1} (w_i^{t+1} - w_i^t)$$

The test is run on 163 randomly chosen recommendations using the same model but with two different training sets:

- 34 analyst stock recommendations
- 55 stock recommendations

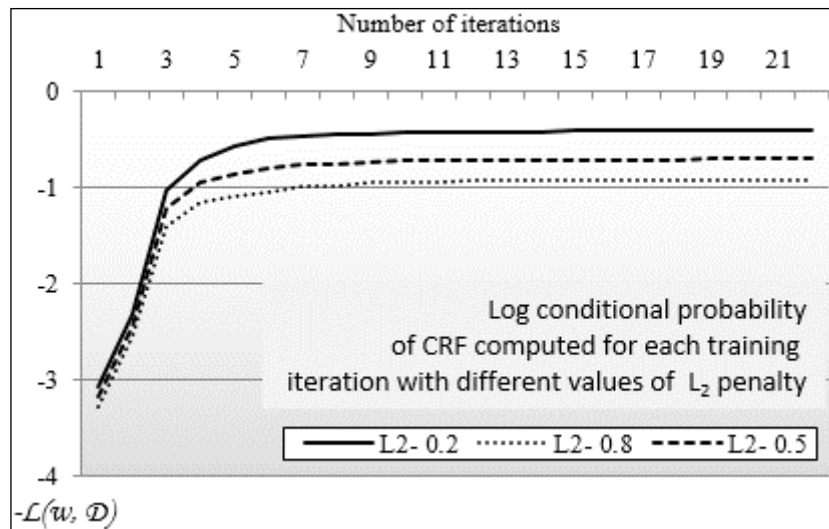
The larger training set is a super set of the 34 recommendations set. The following graph illustrates the comparison of features generated with 34 and 55 CRF training sequences:



The disparity between the test runs using two different size of training set is very small. This can be easily explained by the fact that there is a small variation in the format between the analyst's recommendations.

Impact of the L_2 regularization factor

The third test evaluates the impact of the L_2 regularization penalty on the convergence toward the optimum weights/features. The test is similar to the first test with different value of λ . The following charts plot $\log [p(Y|X, w)]$ for different values of $\lambda = 1/\sigma^2$ (0.2, 0.5, and 0.8):



Impact of the L_2 penalty on convergence of the CRF training algorithm

The log of the conditional probability decreases or the conditional probability increases with the number of iterations. The lower the L_2 regularization factor, the higher the conditional probability.

The variation of the analysts' recommendations within the training set is fairly small, which limits the risk of overfitting. A free-style recommendation format would have been more sensitive to overfitting.

Comparing CRF and HMM

The cost/benefit analysis of discriminative models relative to generative models applies to the comparison of the conditional random field with the hidden Markov model.

Contrary to the hidden Markov model, the conditional random field does not require the observations to be independent (conditional probability). The conditional random field can be regarded as a generalization of the HMM by extending the transition probabilities to arbitrary feature functions that can depend on the input sequence. HMM assumes the transition probabilities matrix to be constant.

HMM learns the transition probabilities a_{ij} on its own by providing more training data. The HMM can be regarded as a special case of CRF where the probabilities used in the state transition are constant.

Performance consideration

The time complexity for decoding and evaluating canonical forms of the hidden Markov model for N states and T observations is $O(N^2T)$. The training of HMM using the Baum-Welch algorithm is $O(N^2TM)$, where M is the number of iterations.

There are several options to improve the performance of HMM:

- Avoid multiplication by 0 in the emission probabilities matrix by using sparse matrices or keeping tab of the null entries
- Try to train HMM on a *relevant* subset of the training data, particularly in the case of tagging

The training of the linear chain conditional random fields is implemented using the same dynamic programming techniques as HMM implementation (Viterbi, forward-backward passes). Its time complexity for training T data sequence, N labels y , and M weights/features λ is $O(MTN^2)$. The time complexity of the training of a CRF can be reduced by distributing the computation of the log likelihood and gradient over multiple nodes [7:13].

Summary

In this chapter, we had a closer look at modeling sequences of observations with hidden states with the two most commonly used algorithms:

- Generative hidden Markov model (HMM) to maximize $p(X, Y)$
- Discriminative conditional random field (CRF) to maximize $\log p(Y | X)$

HMM is a special form of Bayes Network and requires the observations to be independent. Under these circumstances, the HMM is fairly easy to estimate, which is not the case for CRF.

You learned how to implement three dynamic programming techniques, Viterbi, Baum-Welch, and alpha/beta algorithms in Scala. These algorithms are routinely used to solve optimization problems and should be an essential component of your algorithmic toolbox.

8

Kernel Models and Support Vector Machines

This chapter introduces **kernel functions**, binary support vectors classifiers, one-class support vector machines for anomaly detection, and support vector regression.

In the *Binomial classification* section of *Chapter 6, Regression and Regularization*, you learned the concept of hyperplanes used to segregate observations from the training set and estimate the linear decision boundary. The logistic regression has at least one limitation: it requires that the datasets are linearly separated using a defined function (sigmoid). This limitation is especially an issue for high-dimension problems (large number of features that are highly nonlinearly dependent). **Support vector machines (SVMs)** overcome this limitation by estimating the optimal separating hyperplane using kernel functions.

In this chapter, you will discover the following topics:

- The impact of some of the SVM configuration parameters and the kernel method on the accuracy of the classification
- How to apply the binary support vector classifier to estimate the risk for a public company to curtail or eliminate its dividend
- How the support vector regression compares to the linear regression


Support vector machines are formulated as a convex optimization problem. Therefore, the mathematical foundation of these algorithms is described for reference.

Kernel functions

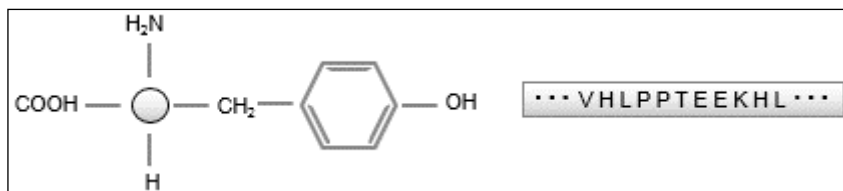
Every machine learning model introduced in this book so far assumes that observations are represented by a feature vector of a fixed size. However, some real-world applications such as text mining or genomics do not lend themselves to this restriction. The critical element of the process of classification is to define a similarity or a distance between two observations. Kernel functions allow developers to compute the similarity between observations without the need to encode them in feature vectors [8:1].

Overview

The concept of kernel methods may be a bit odd at first to a novice. It is usually better understood by using a concrete example. Let's consider the example of the classification of proteins. Proteins have different lengths and composition, but it does not prevent scientists from classifying them [8:2].

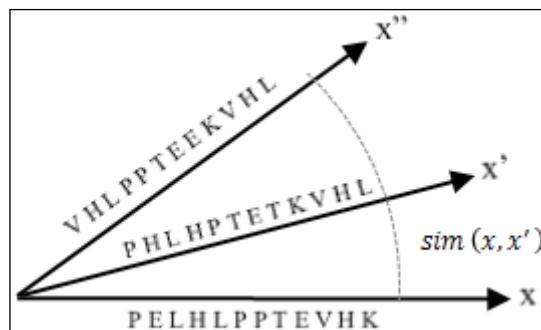
 **Proteins:** Proteins are polymers of amino acids joined together by peptide bonds. They are composed of a carbon atom bonded to a hydrogen atom, another amino acid, or a carboxyl group.

A protein is represented using a traditional molecular notation to which biochemists are familiar. Geneticists describe proteins in terms of a sequence of characters known as the **protein sequence annotation**. The sequence annotation encodes the structure and composition of the protein. The following picture illustrates the molecular (left) and encoded (right) representation of a protein:



Sequence annotation of a protein

The classification and the clustering of a set of proteins require the definition of a similarity factor or distance used to evaluate and compare the proteins. For example, the similarity between three proteins can be defined as a normalized dot product of their sequence annotation:



Similarity between the sequence annotations of three proteins

You do not have to represent the entire sequence annotation of the proteins as a feature vector in order to establish that they belong to the same class. You only need to compare each element of each sequence, one by one, and compute the similarity. For the same reason, the estimation of the similarity does not require the two proteins to have the same length.

In this example, we do not have to assign a numerical value to each element of the annotation. Let's represent an element of the protein annotation as its character c and position p (for example: K, 4). The dot product of the two protein annotations x and x' of the respective lengths n and n' can be defined as the number of identical elements (character and position) between the two annotations divided by the maximum length between the two annotations:

$$sim(x_{cp}, x'_{c'p'}) = \frac{1}{mx} \sum_{i=1}^{mx} (c = c') \cap (p = p') \quad mx = \max(n, n')$$

The computation of the similarity for the three proteins produces the result as $sim(x, x') = 6/12 = 0.50$, $sim(x, x'') = 3/13 = 0.23$, $sim(x', x'') = 4/13 = 0.31$.

Another similar aspect is that the similarity of two identical annotations is 1.0 and the similarity of two completely different annotations is 0.0.



Visualization of similarity:

It is usually more convenient to use a radial representation to visualize the similarity between features, as in the example of proteins' annotations. The distance $d(x, x') = 1/\text{sim}(x, x')$ is visualized as the angle or cosine between two features. The cosine metric is commonly used in text mining.

In this example, the similarity is known as a kernel function in the space of the sequence annotation of proteins.

Common discriminative kernels

Although the measure of similarity is very useful to understand the concept of a kernel function, kernels have a broader definition. A kernel $K(x, x')$ is a symmetric, non-negative real function that takes two real arguments (values of two features). There are many different types of kernel functions, among which the most common are:

- **The linear kernel** (dot product): This is useful in the case of very high-dimensional data where problems can be expressed as a linear combination of the original features
- **The polynomial kernel**: This extends the linear kernel for a combination of features that are not completely linear
- **The radial basis function (RBF)**: This is the most commonly applied kernel. It is appropriate where the labeled or target data is noisy and requires some level of regularization
- **The sigmoid kernel**: This is used in conjunction with neural networks
- **The laplacian kernel**: This is a variant of RBF with a higher regularization impact on training data
- **The log kernel**: This is used in image processing



RBF terminology

In this presentation and the library used in its implementation, the radial basis function is a synonym to the Gaussian kernel function. However, RBF also refers to the family of exponential kernel functions that encompasses Gaussian, Laplacian, and exponential functions.

The simple linear model for regression consists of the dot product of the regression parameters (weights) and the input data (refer to the *Ordinary least squares (OLS) regression* section of *Chapter 6, Regression and Regularization*).

The model is in fact the linear combination of weights and linear combination of inputs. The concept can be extended by defining a general regression model as the linear combination of nonlinear functions, known as basis functions:

$$f(x|w) = w_0 + \sum_{d=1}^D w_d \phi_d(x) \quad \phi_d: \mathbb{R} \rightarrow \mathbb{R}$$

The most commonly used basis functions are the power and Gaussian functions. The kernel function is described as the dot product of the two vectors of the basis function $\phi(x) \cdot \phi(x')$ of two features vector x and x' . A partial list of kernel methods is as follows:

The generic kernel:

$$K(x, x') = \phi(x) \cdot \phi(x') = \sum_{d=1}^D \phi_d(x) \phi_d(x')$$

The linear kernel:

$$K(x, x') = x^T x' = \sum_{d=1}^D x_d \cdot x'_d$$

The polynomial kernel with the slope γ , degree n , and constant c :

$$K(x, x') = (\gamma x^T x' + c)^n \quad \gamma > 0, c \leq 0$$



The sigmoid kernel with the slope γ and constant c :

$$K(x, x') = \tanh(\gamma x^T x' + c) \quad \gamma > 0, c \leq 0$$

The radial basis function kernel with the slope γ :

$$K(x, x') = e^{-\gamma \|x-x'\|^2} \quad \gamma > 0$$

The laplacian kernel with the slope γ :

$$K(x, x') = e^{-\gamma \|x-x'\|} \quad \gamma > 0$$

The log kernel with the degree n :

$$K(x, x') = -\log(1 + \|x-x'\|^n)$$

The list of discriminative kernel functions described earlier is just a subset of the kernel methods universe. Other types of kernels include:

- **Probabilistic kernels:** These are kernels derived from generative models. Probabilistic models such as Gaussian processes can be used as a kernel function [8:3].
- **Smoothing kernels:** This is the nonparametric formulation, averaging density with the nearest neighbor observations [8:4].
- **Reproducible Kernel Hilbert Spaces:** This is the dot product of finite or infinite basis functions [8:5].

The kernel functions play a very important role in support vector machines for nonlinear problems.

The support vector machine (SVM)

A **support vector machine (SVM)** is a linear discriminative classifier that attempts to maximize the margin between classes during training. This approach is similar to the definition of a hyperplane through the training of the logistic regression (refer to the *Binomial classification* section of *Chapter 6, Regularization and Regression*). The main difference is that the support vector machine computes the optimum separating hyperplane between groups or classes of observations. The hyperplane is indeed the equation that represents the model generated through training.

The quality of the SVM depends on the distance, known as margin, between the different classes of observations. The accuracy of the classifier increases as the margin increases.

The linear SVM

First, let's apply the support vector machine to extract a linear model (classifier or regression) for a labeled set of observations. There are two scenarios for defining a linear model. The labeled observations are as follows:

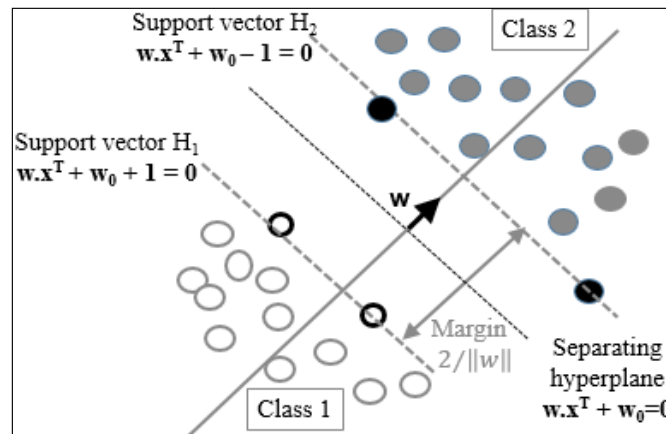
- Naturally segregated in the features space (the **separable** case)
- Intermingled with overlap (the **nonseparable** case)

It is easy to understand the concept of an optimal separating hyperplane in cases the observations are naturally segregated.

The separable case (hard margin)

The concept of separating a training set of observations with a hyperplane is better explained with a 2-dimensional (x, y) set of observations with two classes, C_1 and C_2 . The label y has the value -1 or +1.

The equation for the separating hyperplane is defined by the linear equation, $y = w \cdot x^T + w_0$, which sits in the midpoint between the boundary data points for class C_1 ($H_1: w \cdot x^T + w_0 + 1 = 0$) and class C_2 ($H_2: w \cdot x^T + w_0 - 1 = 0$). The planes H_1 and H_2 are the support vectors:



Support vector machine - separable case

In the separable case, the support vectors fully segregate the observations into two distinct classes. The margin between the two support vectors is the same for all the observations and is known as the **hard margin**.

Support vectors equation w is represented as:

$$y_i (w^T x + w_0) \geq 1 \quad \forall i$$

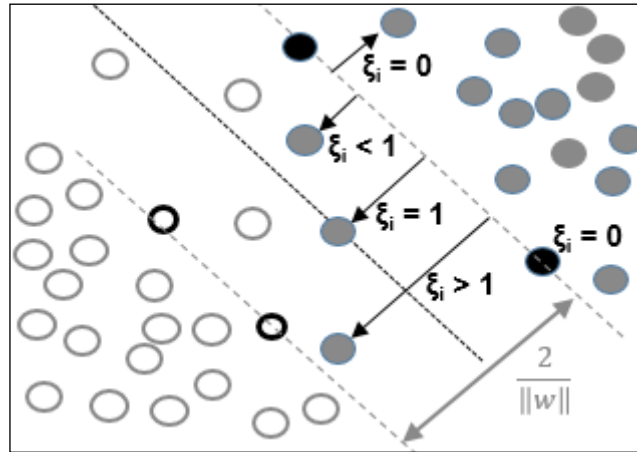


Hard margin optimization problem is given by:

$$\min_{w, w_0} \left\{ \frac{w^T w}{2} \right\} \text{ subject to } y_i (w^T x + w_0) \geq 1 \quad \forall i$$

The nonseparable case (soft margin)

In the nonseparable case, the support vectors cannot completely segregate observations through training. They merely become linear functions that penalize the few observations or outliers that are located outside (or beyond) their respective support vector, H_1 or H_2 . The penalty variable ξ , also known as the slack variable, increases if the outlier is further away from the support vector:



A support vector machine - the nonseparable case

The observations that belong to the appropriate (or own) class do not have to be penalized. The condition is similar to the hard margin, which means that the slack ξ is null. Observations that belong to the class but located beyond its support vector are penalized; the slack ξ increases as the observations get closer to the support vector of the other class and beyond. The margin is then known as a soft margin because the separating hyperplane is enforced through a slack variable.

Optimization of the soft-margin for a linear SVM with C formulation:

$$\min_{w, \xi} \left\{ \frac{w^T w}{2} + c \sum_{i=0}^{n-1} \xi_i \right\}$$


$$\xi_i \geq 0, \quad y_i (w^T x + w_0) \geq 1 - \xi \quad \forall i$$

C is the penalty (or inversed regularization) factor.

You may wonder how the minimization of the margin error is related to the loss function and the penalization factor introduced for the ridge regression (refer to the *Numerical optimization* section of *Chapter 6, Regularization and Regression*). The second factor in the formula corresponds to the ubiquitous loss function. You will certainly recognize the first term as the L_2 regularization penalty with $\lambda=1/2C$.

The problem can be reformulated as the minimization of a function known as the **primal problem** [8:6].

Primal problem formulation of the support vector classifier:




$$\min_{w, w_0} \left\{ \frac{w^T w}{2} + c \sum_{i=0}^{n-1} L_i \right\} \quad L_i = |1 - y_i (w^T x + w_0)|$$

The C penalty factor can be thought of as the inverse of the L_2 regularization factor. The loss function L is then known as the **hinge loss**. The formulation of the margin using the C penalty (or cost) parameter is known as the **C-SVM** formulation. C-SVM is sometimes called the C-Epsilon SVM formulation for the nonseparable case.

The **ν -SVM** (or Nu-SVM) is an alternative formulation to the C-SVM. The formulation is more descriptive than C-SVM; ν represents the upper bound of the training observations that are poorly classified and the lower bound of the observations on the support vectors [8:7].

ν -SVM formulation of a linear SVM:



$$\min_{w, p, \xi} \left\{ \frac{w^T w}{2} - p \frac{1}{n} \sum_{i=0}^{n-1} \xi_i \right\}$$

$$\xi_i \geq 0, \quad y_i (w^T x + w_0) \geq p - \xi_i \quad \forall i$$

Here, p is a margin factor used as a optimization variable.

The C-SVM formulation is used throughout the chapters for the binary, one class support vector classifier as well as the support vector regression.



Sequential Minimal Optimization

The optimization problem consists of the minimization of a quadratic objective function (w^2) subject to N linear constraints, N being the number of observations. The time complexity of the algorithm is $O(N^3)$. A more efficient algorithm, known as **Sequential Minimal Optimization (SMO)** has been introduced to reduce the time complexity to $O(N^2)$.

The nonlinear SVM

So far, it has been assumed that the separating hyperplane, and therefore, the support vectors, are linear functions. Unfortunately, such assumptions are not always correct in the real world.

Max-margin classification

Support vector machines are known as large or **maximum margin classifiers**. The objective is to maximize the margin between the support vectors with hard constraints for separable (similarly, soft constraints with slack variables for nonseparable) cases.

The model parameters $\{w_i\}$ are rescaled during optimization to guarantee that the margin is at least 1. Such algorithms are known as maximum (or large) margin classifiers.

The problem of fitting a nonlinear model into the labeled observations using support vectors is not an easy task. A better alternative consists of mapping the problem to a new, higher dimensional space using a nonlinear transformation. The nonlinear separating hyperplane becomes a linear plane in the new space, as illustrated in the following diagram:

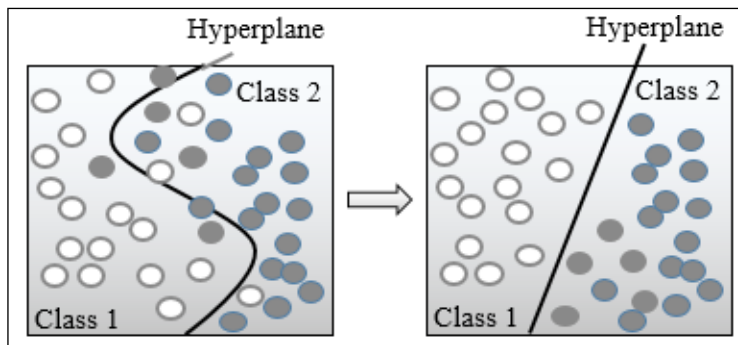


Illustration of the Kernel trick in an SVM

The nonlinear SVM is implemented using a basis function, $\phi(x)$. The formulation of the nonlinear C-SVM is very similar to the linear case. The only difference is the constraint along the support vector, using the basis function, ϕ :


$$y_i (w^T \phi(x) + w_0) \geq 1 - \xi_i \quad \xi_i \geq 0 \quad \forall i$$

The minimization of $w^T \cdot \phi(x)$ in the preceding equation requires the computation of the inner product $\phi(x)^T \cdot \phi(x)$. The inner product of the basis functions is implemented using one of the kernel functions introduced in the first section. The optimization of the preceding convex problem computes the optimal hyperplane w^* as the kernelized linear combination of the training samples, $y_i \cdot \phi(x_i)$, and **Lagrange multipliers**. This formulation of the optimization problem is known as the **SVM dual problem**. The description of the dual problem is mentioned as a reference and is well beyond the scope of this book [8:8].

Optimal hyperplane for the SVM dual problem:

$$w^* = \sum_{i=0}^{n-1} \alpha_i y_i \phi(x_i)$$

Hard margin formulation for the SVM dual problem:

 $y_i (w^T \cdot \phi(x) + w_0) = y_i \left(\sum_{i=0}^{n-1} \alpha_i y_i K(x_i, x) + w_0 \right) \geq 1$

$K(x_i, x) = \phi(x_i) \cdot \phi(x) \forall i$

The kernel trick

The transformation $(x, x') \Rightarrow K(x, x')$ maps a nonlinear problem into a linear problem in a higher dimensional space. It is known as the **kernel trick**.

Let's consider, for example, the polynomial kernel defined in the first section with a degree $d=2$ and coefficient of $C_0=1$ in a two-dimension space. The polynomial kernel function on two vectors, $x=[x_1, x_2]$ and $x'=[x'_1, x'_2]$, is decomposed into a linear function in a dimension 6 space:

$$\begin{aligned} K(x, x') &= (1 + x^T x')^2 \\ &= 1 + 2x_1 x'_1 + 2x_2 x'_2 + 2x_1 x'_1 x_2 x'_2 + (x_1 x'_1)^2 + (x_2 x'_2)^2 \\ &= \phi_1(x) \cdot \phi_1(x') + \phi_2(x) \cdot \phi_2(x') + \phi_3(x) \cdot \phi_3(x') + \dots \\ \phi_2(x) &= 1, \phi_2(x) = \sqrt{2}x_1, \phi_3(x) = \sqrt{2}x_2, \phi_4(x) = x_1^2 \dots \end{aligned}$$

Support vector classifier (SVC)

Support vector machines can be applied to classification, anomalies detection, and regression problems. Let's dive into the support vector classifiers first.

The binary SVC

The first classifier to be evaluated is the binary (2-class) support vector classifier. The implementation uses the LIBSVM library created by Chih-Chung Chang and Chih-Jen Lin from the National Taiwan University [8:9].

LIBSVM

The library was originally written in C and ported to Java. It can be downloaded from <http://www.csie.ntu.edu.tw/~cjlin/libsvm> as a .zip or tar.gz file. The library includes the following classifier modes:

- Support vector classifiers (C-SVC, ν -SVC, and one-class SVC)
- Support vector regression (ν -SVR and ϵ -SVR)
- RBF, linear, sigmoid, polynomial, and precomputed kernels

LIBSVM has the distinct advantage of using **Sequential Minimal Optimization (SMO)**, which reduces the time complexity of a training of n observations to $O(n^2)$. LIBSVM documentation covers both the theory and implementation of hard and soft margins and is available at <http://www.csie.ntu.edu.tw/~cjlin/papers/guide/guide.pdf>.

Why LIBSVM?



There are alternatives to the LIBSVM library for learning and experimenting with SVM. David Soergel from the University of Berkeley refactored and optimized the Java version [8:10]. Thorsten Joachims' **SVMLight** [8:11] **Spark/MLlib 1.0** includes two Scala implementations of SVM using resilient distributed datasets (refer to the *Apache Spark* section of *Chapter 12, Scalable Frameworks*). However, LIBSVM is the most commonly used SVM library.

The implementation of the different support vector classifiers and the support vector regression in LIBSVM is broken down into the following five Java classes:

- `svm_model`: This defines the parameters of the model created during training
- `svm_node`: This models the element of the sparse matrix Q , used in the maximization of the margins

- `svm_parameters`: This contains the different models for support vector classifiers and regressions, the five kernels supported in LIBSVM with their parameters, and the weights vectors used in cross-validation
- `svm_problem`: This configures the input to any of the SVM algorithm (number of observations, input vector data x as a matrix, and the vector of labels y)
- `svm`: This implements algorithms used in training, classification, and regression

The library also includes template programs for training, prediction, and normalization of datasets.



The LIBSVM Java code

The Java version of LIBSVM is a direct port of the original C code. It does not support generic types and is not easily configurable (the code uses switch statements instead of polymorphism). For all its limitations, LIBSVM is a fairly well-tested and robust Java library for SVM.

Let's create a Scala wrapper to the LIBSVM library to improve its flexibility and ease of use.

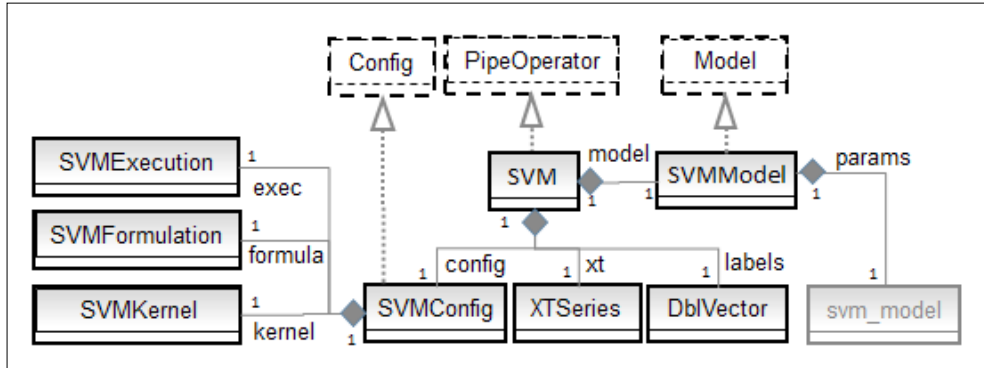
Software design

The implementation of the support vector machine algorithm uses the design template for classifiers (refer to the *Design template for classifier* section in *Appendix A, Basic Concepts*).

The key components of the implementation of an SVM are as follows:

- A model `SVMModel` of the type `Model`, which is initialized through training during the instantiation of the classifier. The model class is an adapter to the `svm_model` structure defined in LIBSVM.
- A predictive or classification routine is implemented as a data transformation extending the `PipeOperator` trait.
- The support vector machine class `SVM` has three parameters: the configuration wrapper of the type `SVMConfig`, the features/time series of the type `XTSeries`, and the target or labeled values `DblVector`.
- The configuration (the type `SVMConfig`) consists of three distinct elements: `SVMExecution` that defines the execution parameters such as maximum number of iterations or convergence criteria, `SVMKernel` that specifies the kernel function used during training, and `SVMFormulation` that defines the formula (C , ϵ , or ν) used to compute a nonseparable case for the support vector classifier and regression.

The key software components of the support vector machine are described in the following UML class diagram:



Configuration parameters

LIBSVM exposes a large number of parameters for the configuration and execution of any of the SVM algorithms. Any SVM algorithm is configured with three categories of parameters, which are as follows:

- Formulation (or type) of the SVM algorithms (multiclass classifier, one-class classifier, regression, and so on) using the `SVMFormulation` class
- The kernel function used in the algorithm (the RBF kernel, Sigmoid kernel, and so on) using the `SVMKernel` class
- Training and execution parameters (convergence criteria, number of folds for cross-validation, and so on) using the `SVMExecution` class

SVM Formulation

The instantiation of the configuration consists of initializing the LIBSVM parameter, `param`, by the SVM type, kernel, and the execution context selected by the user.

Each of the SVM parameters case class extends the generic trait, `SVMConfigItem`:

```
trait SVMConfigItem { def update(param: svm_parameter): Unit }
```

The classes inherited from `SVMConfigItem` are responsible for updating the list of the SVM parameters, `svm_parameter`, defined in LIBSVM. The update method encapsulates the configuration of the LIBSVM.

The formulation of the SVM algorithm is defined by classes implementing the `SVMFormulation` trait:

```
sealed trait SVMFormulation extends SVMConfigItem {
  def update(param: svm_parameter): Unit
}
```

The list of formulation for the SVM (C , ν , and ϵ for regression) is completely defined and known. Therefore, the hierarchy should not be altered and the `SVMFormulation` trait has to be declared sealed. Here is an example of the SVM formulation class, `CSVCFormulation`, which defines the C-SVM model:

```
class CSVCFormulation (c: Double) extends SVMFormulation {
  override def update(param: svm_parameter): Unit = {
    param.svm_type = svm_parameter.C_SVC
    param.C = c
  }
}
```

The other SVM formulation classes, `NuSVCFormulation`, `OneSVCFormulation`, and `SVRFormulation`, implement the ν -SVM, 1-SVM, and ϵ -SVM respectively for regression models.

The SVM kernel function

Next, you need to specify the kernel functions by defining and implementing the `SVMKernel` trait:

```
sealed trait SVMKernel extends SVMConfigItem {
  def update(param: svm_parameter): Unit
}
```

Once again, there are a limited number of kernel functions supported in LIBSVM. Therefore, the hierarchy of kernel functions is sealed. The following code snippet configures the radius basis function kernel, `RbfKernel`, as an example of definition of the kernel definition class:

```
class RbfKernel (gamma: Double) extends SVMKernel {
  override def update(param: svm_parameter): Unit = {
    param.kernel_type = svm_parameter.RBF
    param.gamma = gamma
  }
  ...
}
```

The fact that the LIBSVM Java byte code library is not very extensible does not prevent you from defining a new kernel function in the LIBSVM source code. For example, the Laplacian kernel can be added with the following steps:

1. Create a new kernel type in `svm_parameter`, such as `svm_parameter.LAPLACE = 5`.
2. Add the kernel function name to `kernel_type_table` in the `svm` class.
3. Add `kernel_type != svm_parameter.LAPLACE` to the `svm_check_parameter` method.
4. Add the implementation of the kernel function for two values in `svm.kernel_function` (java code):

```
case svm_parameter.LAPLACE:
    double sum = 0.0;
    for(int k = 0; k < x[i].length; k++) {
        final double diff = x[i][k].value - x[j][k].value;
        sum += diff*diff;
    }
    return Math.exp(-gamma*Math.sqrt(sum));
```
5. Add the implementation of the Laplace kernel function in the `svm.k_function` method by modifying the existing implementation of RBF (`distanceSqr`).
6. Rebuild the `libsvm.jar` file

SVM execution

The `SVMExecution` class defines the configuration parameters for the execution of the training of the model, namely, the convergence factor, `eps` for the optimizer, the size of the cache `cacheSize`, and the number of folds, `nFolds` used during cross-validation:

```
class SVMExecution(cacheSize: Int, eps: Double, nFolds: Int) extends SVMConfigItem {
    override def update(param: svm_parameter): Unit = {
        param.cache_size = cacheSize
        param.eps = eps
    }
}
```

The cross-validation is performed only if the `nFolds` value is greater than 1.

SVM implementation

We are finally ready to create the configuration class, `SVMConfig`, which hides and manages all of the different configuration parameters:

```
class SVMConfig(formula: SVMFormulation, kernel: SVMKernel, exec:
SVMExecution) {
    val param = new svm_parameter
    formula.update(param)
    kernel.update(param)
    exec.update(param)
}
```

The instantiation of `SVMConfig` initialized the internal LIBSVM list of configuration parameters through a sequence of update calls.

Next, let's implement the first support vector classifier for the two-class problems. As with any other data transformation, the parameterized class `SVM` implements the `PipeOperator`, as follows:

```
class SVM[T <% Double](config: SVMConfig, xt: XTSeries[Array[T]],
labels: DblVector) extends PipeOperator[Array[T], Double] {
    type Feature = Array[T]
    type SVMNodes = Array[Array[svm_node]]
}
```

This class has the same parameters as other classifiers presented in the previous chapters: a configuration, `config`, an input time series, `xt`, and labeled data, `labels`. The types are added for convenience. The internal types, `Feature` and `SVMNodes`, are added for convenience.

The LIBSVM type, `svm_node`, is the indexed value of an element of the feature vector in a particular observation:

```
public class svm_node implements java.io.Serializable {
    public int index;
    public double value;
}
```

The type `SVMNodes` defined in the scope of `SVM` class is the representation of a two-dimensional array of features vector elements by observations. The next step is to implement the training procedure. The training is executed during the instantiation of the `SVM` class. The SVM model, `svmModel`, is defined as a tuple or pair (`svmModel`, `accuracy`) with the following:

- The `svmModel` is the model defined in LIBSVM
- `accuracy` computed during an N-folds cross-validation if the number of folds, `nFolds`, has been set as one of the parameters of `SVMExecution`

Consider the following code:

```
class SVModel(val svmodel: svm_model, val accuracy: Double) extends Model
```

The instantiation of SVC is hidden from the client code. It is executed during the instantiation of the class, so a client code does not have to be aware of the LIBSVM types. Consider the following code:

```
val model: Option[SVModel] = {  
  val problem = new svm_problem //1  
  problem.l = xt.size;  
  problem.y = labels  
  problem.x = new SVNodes(xt.size)  
  
  val dim = dimension(xt)  
  xt.zipWithIndex.foreach( xt_i => { //2  
    val svm_col = new Array[svm_node](dim)  
    xt_i._1.zipWithIndex  
      .foreach(xi => {  
        val node = new svm_node  
        node.index= xi._2  
        node.value = xi._1  
        svm_col(xi._2) = node  
      })  
    problem.x(xt_i._2) = svm_col  
  })  
  Some(svm.svm_train(problem, config.param, accuracy(problem))//3  
}
```

The first step in the creation of the model is to define the SVM problem, `problem`, in the context of LIBSVM (line 1): length of the time series, labeled data, and input observations. The time series has to be converted into the LIBSVM internal class, `svm_nodes` (line 2), to complete the initialization of the problem. The Scala method, `zipWithIndex`, is used to access the index of each observation (time series entry). Finally, the model and the computed accuracy are returned as a tuple (line 3) after processing by the `svm_train` training method.

The accuracy is the ratio of true positive plus the true negative over the size of the test sample (refer to the *Key metrics* section of *Chapter 2, Hello World!*). It is computed through cross-validation only if the number of folds is initialized in the `SVMExecution` configuration class as greater than 1. Practically, the accuracy is computed by invoking the cross-validation method, `svm_cross_validation`, in the LIBSVM package, and then computing the ratio of the number of predicted values that match the labels over the total number of observations. Here is the essential part of the implementation of `accuracy(problem: svm_problem)`:

```
val target = new Array[Double](labels.size)
svm.svm_cross_validation(problem, config.param, config.exec.nFolds,
target)
val rawAccuracy = target.zip(labels)
                        .filter(z => Math.abs(z._1-z._2) < config.eps)
rawAccuracy.size.toDouble/labels.size
```

The Scala `filter` weeds out the observations that were poorly predicted. This minimalist implementation is good enough to start exploring the support vector classifier.

C-penalty and margin

The first evaluation consists of understanding the impact of the penalty factor `C` to the margin in the generation of the classes. Let's implement the computation of the margin. The margin is defined as $2/||w||$ and implemented as a method of the `SVC` class, as follows:

```
def margin: Option[Double] = model match {
  case Some(m) => {
    val wNorm = m.svmmodel.sv_coef(0)
                      .foldLeft(0.0)((s, r) => s + r*r) //1
    if(wNorm < config.eps) None
    else Some(2.0/Math.sqrt(wNorm)) //2
  }
  ...
}
```

The first instruction (line 1) computes the sum of the squares, `wNorm`, of the residuals $r = y - f(x|w)$. The margin (line 2) is ultimately computed if the sum of squares is significant enough to avoid rounding errors.

The margin is evaluated using an artificially generated time series and labeled data. First, we define the method to evaluate the margin for a specific value of the penalty (inversed regularization) factor C:

```
def evalMargin(observations: DblMatrix, labels: DblVector, c: Double):
  Unit = {
    val config = SVMConfig(CSVCFomulation(c), RbfKernel(GAMMA)) //3
    val xt = XTSeries[DblVector](observations)
    val svc = SVM[Double](config, xt, labels)
    svc.margin match {
    case Some(margin) => Display.show("Margin $margin", logger)
    ...
```

This test uses the default execution parameters, `cache_size= 25000` and `eps=1e-15`. Therefore, the 3rd value of `SVMConfig`, `exec`, is not specified in the `SVMConfig`. apply constructor (line 3). The method is invoked iteratively to evaluate the impact of the penalty factor on the margin extracted from the training of the model. The test uses a synthetic time series to highlight the relation between C and the margin. The synthetic time series consists of the following two training sets of an equal size, N:

- **First training set:** data points generated as $y = x(1 + r/5)$ for the label 1, r being a randomly generated number over the range [0,1]
- **Second training set:** randomly generated data point $y = r$ for the label of -1

Consider the following code:

```
def generate: (DblMatrix, DblVector) = {
  val z = Array.tabulate(N) (i =>
    Array[Double] (i, i*(1.0 + 0.2*Random.nextDouble))
  ) ++
  Array.tabulate(N) (i =>Array[Double] (i, i*Random.nextDouble))
  (z, Array.fill(N) (1.0) ++ Array.fill(N) (-1.0))
}
```

The `evalMargin` method is executed for a predefined value of gamma and the value C ranging from 0 to 5:

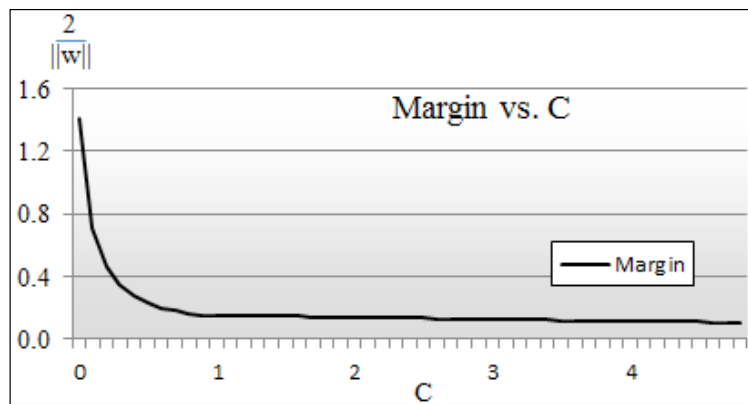
```
val gamma =0.8; val N = 100
val values = generate
Range(0, 50).foreach(i =>evalMargin(values._1, values._2, i*0.1))
```

val vs. final val

There is a difference between a val and a final val. A nonfinal value can be overridden in a subclass. Overriding a final value produces a compiler error, as follows:

```
class A {val x = 5; final val y = 8 }
class B extends A {
  override val x = 9 // OK
  override val y = 10 // Error
}
```

The following chart illustrates the relation between the penalty, or cost factor, C and the margin:



The margin value versus C-penalty for an SVC

As expected, the value of the margin decreases as the penalty term C increases. The C penalty factor is related to the L_2 regularization factor λ as $C \sim 1/\lambda$. A model with a large value of C has a high variance and a low bias, while a small value of C will produce lower variance and a higher bias.

**Optimizing C-penalty**

The optimal value for C is usually evaluated through cross-validation, by varying C in incremental powers of 2: $2^n, 2^{n+1} \dots$ [8:12].

Kernel evaluation

The next test consists of comparing the impact of the kernel function on the accuracy of the prediction. Once again, a synthetic time series is generated to highlight the contribution of each kernel.

First, the prediction method for the SVM class is implemented by overriding the pipe operator data transformation, `|>`:

```
def |> : PartialFunction[Feature, Double] = {
  case x: Feature if (x != null && x.size==dimension(xt) && model
    != None && model.get.accuracy >= 0.0) =>
    svm.svm_predict(model.get.svmmodel, toNodes(x))
}
```

The prediction model relies on the `svm_predict` LIBSVM to compute the output value. It takes two parameters: `svmmodel` and an array of `svm_nodes` (line 1). The conversion of a feature from the type `DblVector` to an array of the `svm_nodes` LIBSVM is performed by the `toNodes` method:

```
def toNodes(x: Feature): Array[svm_node] =
  x.zipWithIndex
    .foldLeft(new ArrayBuffer[svm_node])((xs, f) => { //2
      val node = new svm_node
      node.index = f._2
      node.value = f._1
      xs.append(node)
      xs
    }).toArray
```

A fold is used to construct the array of `svm_nodes` from the feature vector, `x`. The nodes (elements of the sparse matrix of the `svm_node` LIBSVM) are generated from the new observation `x` (line 1). The model extracted from the training of the model (instantiation of SVM) and the sparse matrix `nodes` are the input to the LIBSVM predictor, `svm_predict` (line 2).

The predictor is used by the test code for evaluating the different kernel functions. Let's create a method to evaluate and compare these kernel functions. All we need is the following:

- A training set, `observations`, by features of the type `DblMatrix`
- A test set, `test`, of the type `DblMatrix`
- A set of `labels` for the training set, taking the value 0 or 1
- A kernel function `kF`

Consider the following code:

```
def evalKernel(features: DblMatrix, test: DblMatrix, labels:
DblVector, kF: SVMKernel): Double = {
  val config = SVMConfig(new CSVCFomulation(C), kF) //3
  val xt = XTSeries[DblVector](features)
  val svc = SVM[Double](config, xt, labels) //4
  val successes = test.zip(labels)
    .count(t1 => {
      Try((svc |> t1._1) == t1._2)
      match { case Success(n) => true
              case Failure(e) => false }
    })
  successes.toDouble/test.size //6
}
```

The support vector classifier, `svc`, is configured with the default execution parameters and the C-formulation (line 3), and trained (instantiated) with the observed features, `xt` and the output, `labels` (line 4).

Once trained, `svc` is used to predict the value for a test sample extracted from the original dataset (line 5). Finally, the number of successful test observations is counted and the accuracy is computed as the ratio of the successful prediction over the size of the test sample (line 6).

In order to compare the different kernels, let's generate three datasets of the size $2N$ for a binomial classification using the following random generator, $y = \text{variance} * x - \text{mean}$:

```
def genData(variance: Double, mean: Double): DblMatrix =
  val adjVariance1 = variance*Random.nextDouble - mean
  val adjVariance2 = variance*Random.nextDouble - mean
  Array.fill(N)(Array[Double](adjVariance1, adjVariance2))
}
```

A training set is then created as the aggregate of two classes of data points:

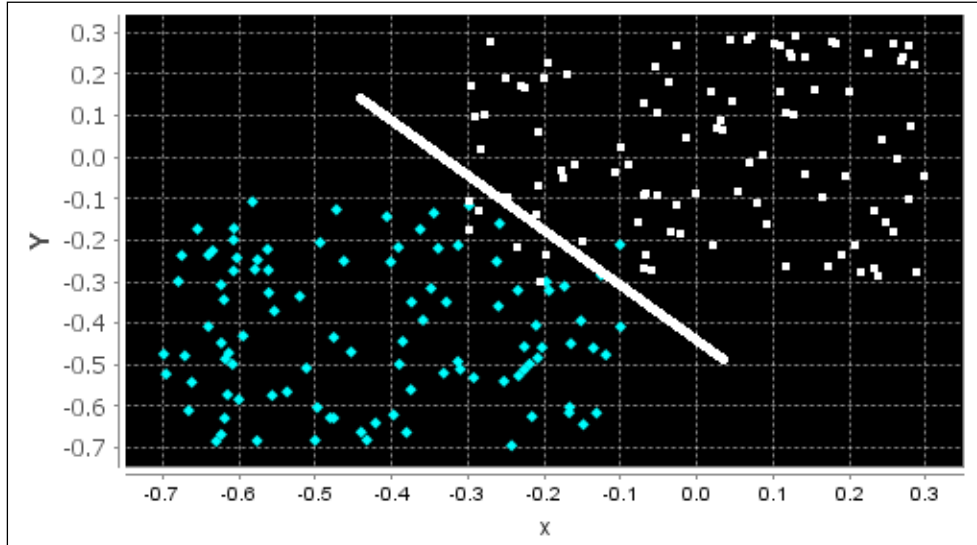
- Random data points (x,y) with variance a and mean $1-b$ with label 0.0
- Random data points with variance a and mean $b-1$ with label 1.0

Consider the following code

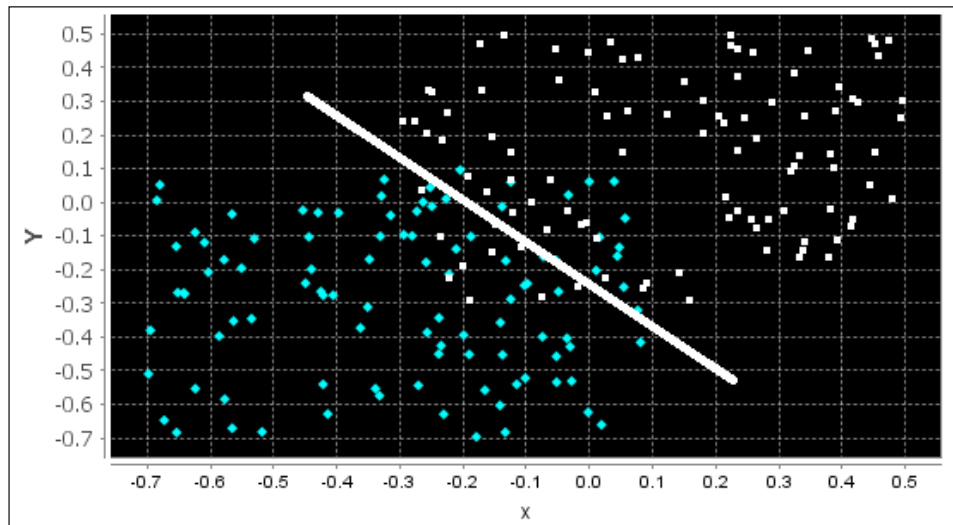
```
val trainingSet = genData(a,b) ++ genData(a,1-b)
val labels = Array.fill(N)(0.0) ++ Array.fill(N)(1.0)
```

The parameters a and b are selected from two groups of training data points with various degree of separation to illustrate the separating hyperplane.

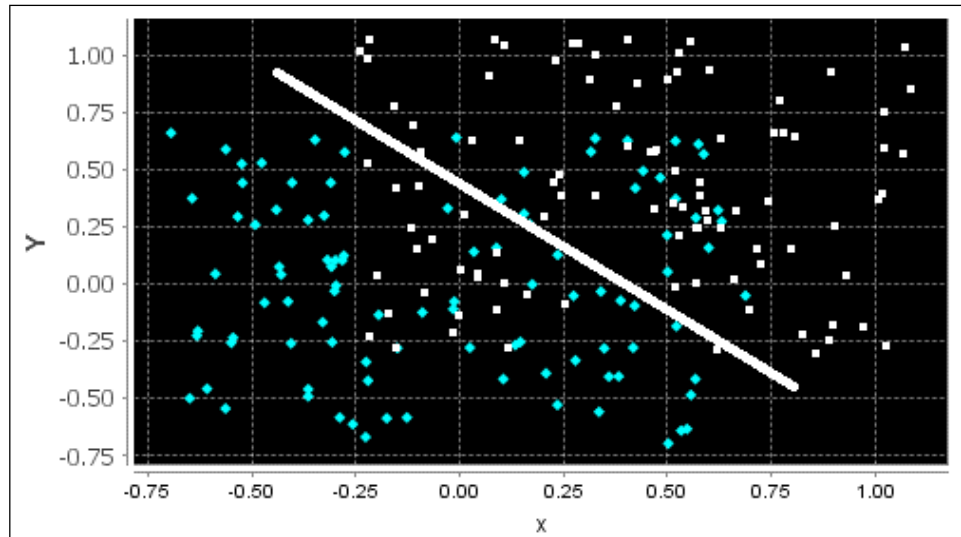
The following chart describes the high margin; the first training set generated with the parameters $a = 0.6$ and $b = 0.3$ illustrates the highly separable classes with a clean and distinct hyperplane:



The following chart describes the medium margin; the parameters $a = 0.8$ and $b = 0.3$ generate two groups of observations with some overlap:



The following chart describes the low margin; the two groups of observations in this last training are generated with $a = 1.4$ and $b = 0.3$ and show a significant overlap:



The test set is generated in a similar fashion as the training set, as they are extracted from the same data source:

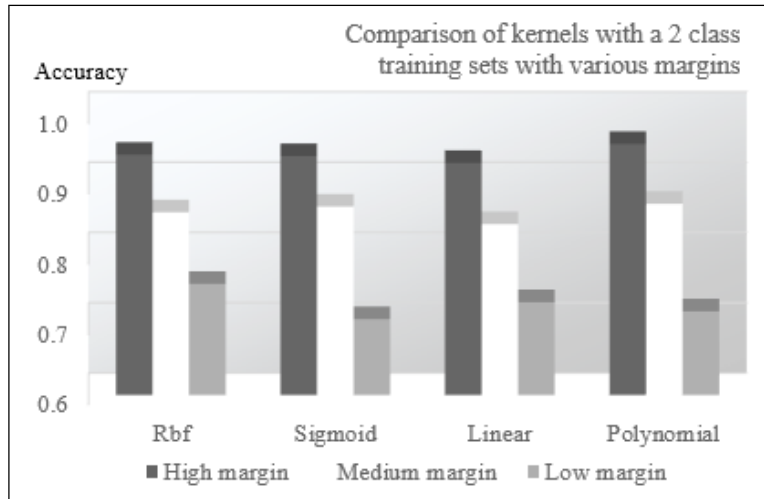
```
val EPS = 0.0001; val C = 1.0; val GAMMA = 0.8
val N = 100; val COEF0 = 0.5; val DEGREE = 2

val a = 1.4; val b = 0.3 //3 sets of values
val trainSet = genData(a, b) ++ genData(a, 1-b)
val testSet = genData(a, b) ++ genData(a, 1-b)
val labels = Array.fill(N)(0.0) ++ Array.fill(N)(1.0)

val result =
  evalKernel(trainSet, testSet, labels, RbfKernel(GAMMA)) ::
  evalKernel(trainSet, testSet, labels, SigmoidKernel(GAMMA)) ::
  evalKernel(trainSet, testSet, labels, LinearKernel) ::
  evalKernel(trainSet, testSet, labels, PolynomialKernel(GAMMA, COEF0,
  DEGREE)) :: List[Double]()
```

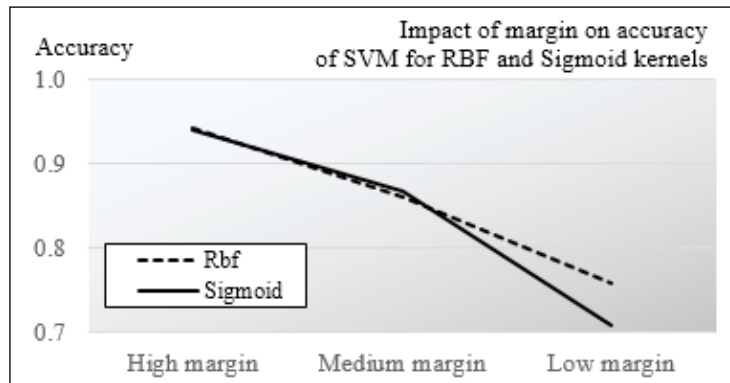
The value of the kernel function parameters are arbitrary selected from text books. The `evalKernel` method defined earlier is applied to the three training sets: high margin ($a = 1.4$), medium margin ($a = 0.8$), and low margin ($a = 0.6$) with each of the four kernels (RBF, sigmoid, linear, and polynomial).

The accuracy is assessed by counting the number of observations correctly classified for all of the classes for each invocation of the predictor, |>:



Comparative chart of kernel functions

Although the different kernel functions do not differ in terms of the impact on the accuracy of the classifier, you can observe that the RBF and polynomial kernels produce slightly more accurate results. As expected, the accuracy decreases as the margin decreases. A decreasing margin is a sign that the cases are not easily separable, affecting the accuracy of the classifier:





Test case design

The test to compare the different kernel methods is highly dependent on the distribution or mixture of data in the training and test sets. The synthetic generation of data in this test case is used for the purpose of illustrating the margin between classes of observations. Real-world datasets may produce different results.

In summary, there are four steps in creating a SVC-based model:

1. Select a features set.
2. Select the C-penalty (inverse regularization).
3. Select the kernel function.
4. Tune the kernel parameters.

As mentioned earlier, this test case relies on synthetic data to illustrate the concept of margin and compare kernel methods. Let's use the support vector classifier for a real-world financial application.

Application to risk analysis

The purpose of the test case is to evaluate the risk for a company to curtail or eliminate its quarterly or yearly dividend. The features selected are financial metrics relevant to a company's ability to generate cash flow and pay out its dividends over the long term.

Features and labels

We need to select any subset of the following financial technical analysis metrics (refer to the *Terminology* section in *Appendix A, Basic Concepts*):

- Relative change in stock prices over the last 12 months
- Long-term debt-equity ratio
- Dividend coverage ratio
- Annual dividend yield
- Operating profit margin
- Short interest (ratio of shares shorted over the float)
- Cash per share-share price ratio
- Earnings per share trend

The earnings trend has the following values:

- -2, if earnings per share decline by more than 15 percent over the last 12 months
- -1, if earnings per share decline between 5 percent and 15 percent
- 0, if earning per share is maintained within 5 percent
- +1, if earnings per share increase between 5 percent and 15 percent
- +2, if earnings per share increase by more than 15 percent

The features are normalized with values 0 and 1.

The labeled output, dividend changes, is categorized as follows:

- -1, if dividend is cut by more than 5 percent
- 0, if dividend is maintained within 5 percent
- +1, if dividend is increased by more than 5 percent

Let's combine two of these three labels $\{-1, 0, 1\}$ to generate two classes for the binary SVC:

- Class C_1 = stable or decreasing dividends and class C_2 = increasing dividends; represented by `dividendsA`
- Class C_1 = decreasing dividends and class C_2 = stable or increasing dividends; represented by `dividendsB`

The different tests are performed with a fixed set of configuration parameters `C` and `GAMMA` and a 2-fold validation configuration:

```
val path = "resources/data/chap8/dividendsA.csv"
val C = 1.0; val GAMMA = 0.5; val EPS = 1e-3; val NFOLDS = 2

val extractor = relPriceChange :: debtToEquity :: dividendCoverage
               :: cashPerShareToPrice :: epsTrend :: dividendTrend
               :: List[Array[String] =>Double] () //1
```

The components of the extractor are functions that convert a set of fields in the input .csv file into double floating point values:

```
val xs = DataSource(path, true, false, 1) |> extractor
val config = SVMConfig(new CSVCFomulation(C),
                        RbfKernel(GAMMA),
                        SVMExecution(EPS, NFOLDS))
val features = XTSeries.transpose(xs.take(xs.size-1))//2
val svc = SVM[Double](config, features, xs.last)

svc.accuracy match { //3
  case Some(acc) => Display.show(s"Accuracy: $acc", logger)
  case None => { ... }
}
```

The different fields are extracted from the `dividendsA.csv` file using the `DataSource` extractor with a filter (line 1). The purpose of the test A is to create a separating hyperplane (the predictive model) for `dividendsA`, that is, companies that cut or maintained their dividends and the companies that increased their dividends. The last field in the extractor is the labeled output. The observed features time series is created from all the fields extracted from the .csv file except the last. The time series has to be transposed to use the format required by LIBSVM (line 2). Once the support vector classifier is created, you can retrieve the accuracy of the cross-validation (line 3).

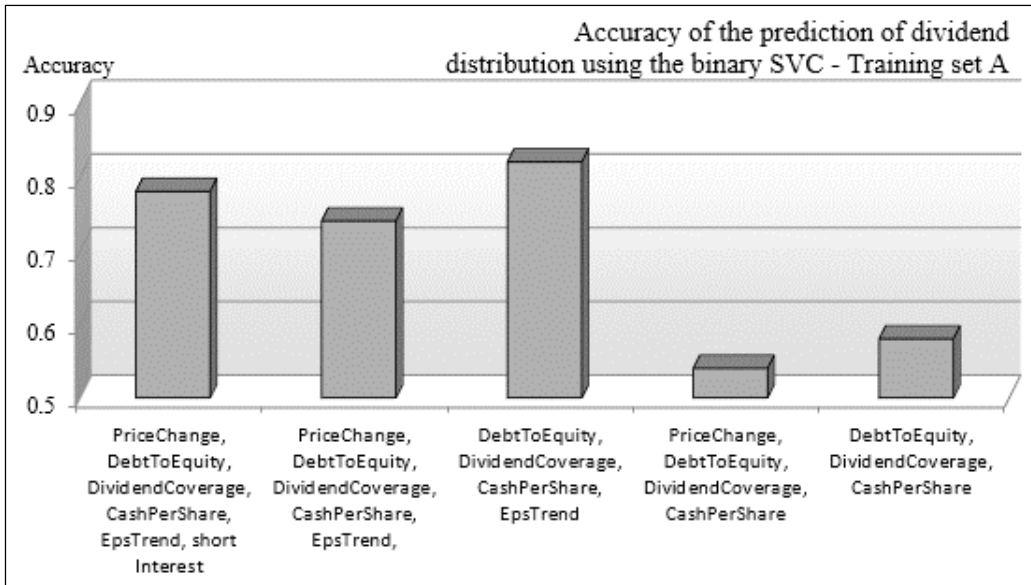
LIBSVM scaling




LIBSVM supports feature normalization known as scaling, prior to training. The main advantage of scaling is to avoid attributes in greater numeric ranges dominating those in smaller numeric ranges. Another advantage is to avoid numerical difficulties during the calculation. In our examples, we use the normalization of the time series, `XTSeries.normalize`. Therefore, the scaling flag in LIBSVM is disabled.

The test is repeated with a different set of features and consists of comparing the accuracy of the support vector classifier for different features sets. The features sets are selected from the content of the .csv file by assembling the extractor with different configurations, as follows:

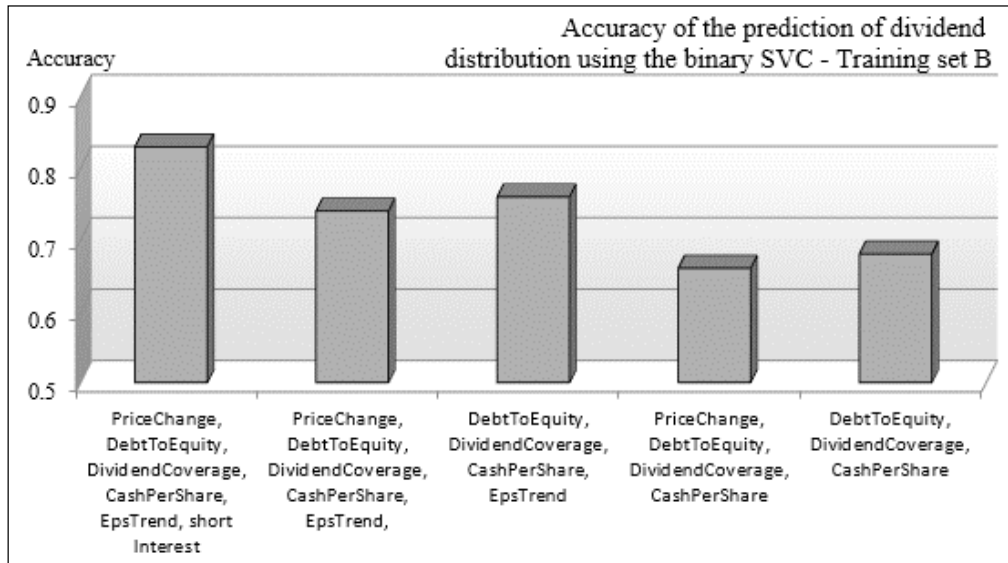
```
val extractor = ... :: dividendTrend :: List[Array[String] =>Double] ()
```



The test demonstrates that the selection of the proper features set is the most critical step in applying the support vector machine, and any other model for that matter, to classification problems. In this particular case, the accuracy is also affected by the small size of the training set. The increase in the number of features also reduces the contribution of each specific feature to the loss function.

 **N-fold cross-validation**
The cross-validation in this test example uses only 2 folds because the number of observations is small, and you want to make sure that any class contains at least a few observations.

The same process is repeated for the test B whose purpose is to classify companies with decreasing dividends and companies with stable or increasing dividends, as shown in the following graph:



The difference in terms of accuracy of prediction between the first three features set and the last two features set in the preceding graph is more pronounced in test A than test B. In both tests, the feature eps (earning per share) trend improves the accuracy of the classification. It is a particularly good predictor for companies with increasing dividends.

The problem of predicting the distribution (or not) dividends can be restated as evaluating the risk of a company to dramatically reduce its dividends.

What about the risk a company entails to eliminate its dividend altogether? Such a scenario is rare, and those cases are actually outliers. A one-class support vector classifier can be used to detect outliers or anomalies [8:13].

Anomaly detection with one-class SVC

The design of the one-class SVC is an extension of the binary SVC. The main difference is that a single class contains most of the baseline (or normal) observations and the other class is replaced by a reference point known as the **SVC origin**. The outliers (or abnormal) observations reside beyond (or outside) the support vector of the single class:

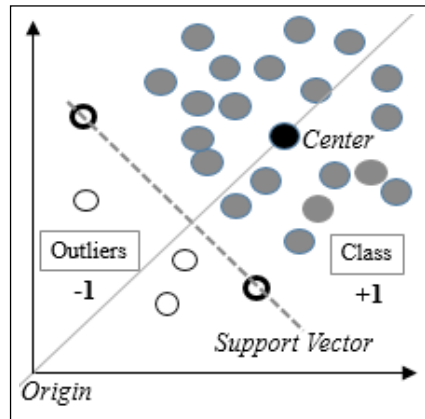


Illustration of the one-class SVC

The outlier observations have a labeled value of -1, while the remaining training sets are labeled +1. In order to create a relevant test, we add four more companies that have drastically cut their dividends (ticker symbols WLT, RGS, MDC, NOK, and GM). The dataset includes the stock prices and financial metrics recorded prior to the cut in dividends.

The implementation of this test case is very similar to the binary SVC driver code, except for the following:

- The classifier uses the Nu-SVM formulation, `OneSVFormulation`
- The labeled data is generated by assigning -1 to companies that have eliminated their dividend and +1 for all other companies

The test is executed against the dataset `resources/data/chap8/dividends2.csv`. First, we need to define the formulation for the one-class SVM:

```
class OneSVFormulation(nu: Double) extends SVMFormulation {  
  override def update(param: svm_parameter): Unit = {  
    param.svm_type = svm_parameter.ONE_CLASS  
    param.nu = nu  
  }  
}
```

The test code is similar to the execution code for the binary SVC. The only difference is the definition of the output labels; -1 for companies eliminating dividends and +1 for all other companies:

```
val NU = 0.2; val GAMMA = 0.5; val NFOLDS = 2
val path = "resources/data/chap8/dividends2.csv"

val xs = DataSource(path, true, false, 1) |> extractor
val config = SVMConfig(new OneSVCFormulation(NU),
                       RbfKernel(GAMMA),
                       SVMExecution(EPS, NFOLDS))
val features = XTSeries.transpose(xs.dropRight(1))
val svc = SVM[Double](config, features, xs.last.map( filter ( _ ) ))
svc.accuracy match {
  case Some(acc) => Display.show("Accuracy: $acc", logger)
  case None => { ... }
}
```

The test is executed with the following features: relPriceChange, debtToEquity, dividendCoverage, cashPerShareToPrice, and epsTrend.

The model is generated with the accuracy of 0.821. This level of accuracy should not be a surprise; the outliers (companies that completely eliminated their dividends) are added to the original dividend .csv file. These outliers differ significantly from the baseline observations (companies who have reduced, maintained, or increased their dividend) in the original input file.

Where the labeled observations are available, the one-class support vector machine is an excellent alternative to clustering techniques.



Definition of anomaly

The results generated by a one-class support vector classifier depend heavily on the subjective definition of an outlier. The test case assumes that the companies that eliminate their dividends have unique characteristics that set them apart, and are different even from companies who have cut, maintained, or increased their dividend. There is no guarantee that this assumption is indeed always valid.

Support vector regression (SVR)

Most of the applications using support vector machines are related to classification. However, the same technique can be applied to regression problems. Luckily, as with classification, LIBSVM supports two formulations for support vector regression:

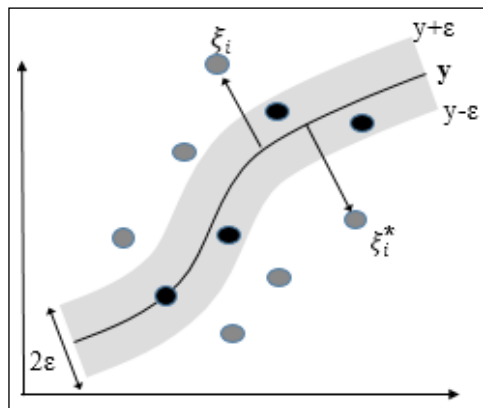
- ϵ -SVR (sometimes called C-SVR)
- ν -SVR

For the sake of consistency with the two previous cases, the following test uses the ϵ (or C) formulation of the support vector regression.

Overview

The SVR introduces the concept of **error insensitive zone** and insensitive error, ϵ . The insensitive zone defines a range of values around the predictive values, $y(x)$. The penalization component C does not affect the data point $\{x_i, y_i\}$ that belongs to the insensitive zone [8:14].

The following diagram illustrates the concept of an error insensitive zone, using a single variable feature x and an output y . In the case of a single variable feature, the error insensitive zone is a band of width 2ϵ . ϵ is known as the insensitive error. The insensitive error plays a similar role to the margin in the SVC.



For the mathematically inclined, the maximization of the margin for nonlinear models introduces a pair of slack variables. As you may remember, the C-support vector classifiers use a single slack variable. The preceding diagram illustrates the minimization formula.

$$\varepsilon \text{ SVR:}$$

$$\min_{w, \xi, \xi_i^*} \left\{ \frac{w^T w}{2} + c \sum_{i=0}^{n-1} (\xi_i + \xi_i^*) \right\}$$

$$- \varepsilon - \xi_i^* \leq w^T \phi(x_i) + w_0 - y_i \leq \varepsilon + \xi_i \quad \forall i$$

Here, ε is the insensitive error function.
The ε -SVR regression equation:

$$\hat{y}(x) = \sum_{i=0}^{n-1} \alpha_i K(x_i, x) + \hat{w}_0$$

Let's reuse the SVM class to evaluate the capability of the SVR, compared to the linear regression (refer to the *Ordinary least squares (OLS) regression* section of *Chapter 6, Regression and Regularization*).

SVR versus linear regression

This test consists of reusing the example on single-variate linear regression (refer to the *One-variate linear regression* section of *Chapter 6, Regression and Regularization*). The purpose is to compare the output of the linear regression with the output of the SVR for predicting the value of a stock price or an index. We select the S&P 500 exchange traded fund, SPY, which is a proxy for the S&P 500 index.

The model consists of the following:

- One labeled output: SPY-adjusted daily closing price
- One single variable feature set: the index of the trading session (or index of the values SPY)

The implementation follows a familiar pattern:

1. Define the configuration parameters for the SVR (the c cost/penalty function, GAMMA coefficient for the RBF kernel, EPS for the convergence criteria, and EPSILON for the regression insensitive error).
2. Extract the labeled data (the `SPY price`) from the data source (`DataSource`), which is the Yahoo financials CSV-formatted data file.

3. Create the linear Regression, `SingleLinearRegression`, with the index of the trading session as the single variable feature and the SPY-adjusted closing price as the labeled output.
4. Create the observations as a time series of indexes, `xt`
5. Instantiate the SVR with the index of trading session as features, and the SPY adjusted closing price as the labeled output
6. Run the prediction methods for both SVR and the linear regression and compare the results of the linear regression and SVR

```
val path = "resources/data/chap8/SPY.csv"
val C = 1; val GAMMA = 0.8; val EPS = 1e-3; val EPSILON = 0.1 //1

val price = DataSource(path, false, true, 1) |> adjClose //2
val priceIdx = price.zipWithIndex
                    .map(x => (x._1.toDouble, x._2.toDouble))
val linRg = SingleLinearRegression(priceIdx) //3
val config = SVMConfig(new SVRFormulation(C, EPSILON),
RbfKernel(GAMMA)) //3
val labels = price.toArray

val xt = XTSeries[DblVector](
    Array.tabulate(labels.size)(Array[Double](_))) //4
val svr = SVM[Double](config, xt, labels) //5
collect(svr, linRg, price) //6
```

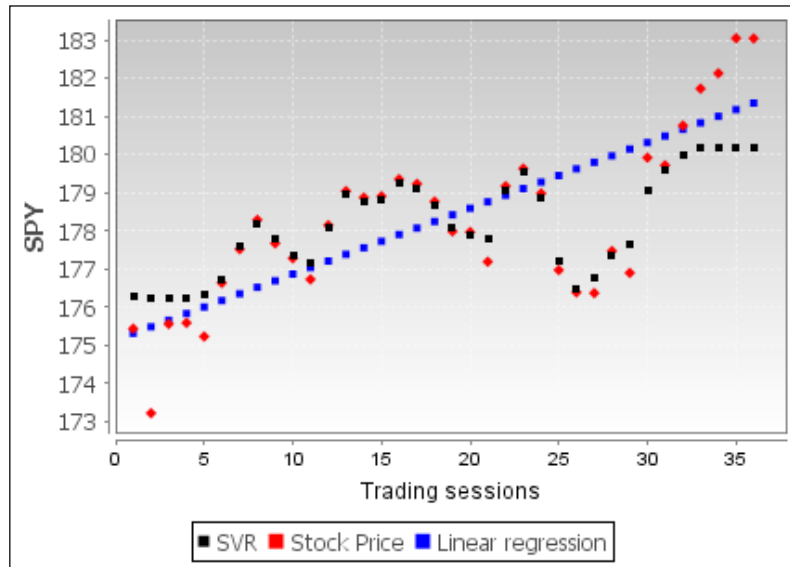
The `collect` method invokes the predictive method for the support vector regression (line 7) and the linear regression model (line 8), and then buffers the results along with the original observation, `price` (line 9).

```
def collect(svr: SVM_Double,
            lin: SingleLinearRegression[Double],
            price: DblVector): Array[XYTSeries] = {

    val collector = Array.fill(3)(new ArrayBuffer[XY]
Range(1, price.size-2).foldLeft(collector)( (xs, n) => {
    xs(0).append((n, (svr |> n.toDouble).get)) //7
    xs(1).append((n, (lin |> n).get)) //8
    xs(2).append((n, price(n))) //9
    xs
}).map( _.toArray)
}
```


The types `XY=(Double, Double)` and `XYTSeries=Array[(Double, Double)]` have already been defined in the *Primitive types* section of *Chapter 1, Getting Started*.

The results are displayed in the following graph, generated using the JFreeChart library. The code to plot the data is omitted because it is not essential to the understanding of the application.



Comparative plot linear regression and SVR

The support vector regression provides a more accurate prediction than the linear regression model. You can also observe that the L_2 regularization term of the SVR penalizes the data points (the SPY price) with a high deviation from the mean of the price. A lower value of C will increase the L_2 -norm penalty factor as $\lambda = 1/C$.



SVR and L_2 regularization

You are invited to run the use case with a different value of C to quantify the impact of the L_2 regularization on the predictive values of the SVR.

There is no need to compare SVR with the logistic regression as the logistic regression is a classifier. However, SVM is related to the logistic regression; the hinge loss in SVM is similar to the loss in the logistic regression [8:15].

Performance considerations

You may have already observed that the training of a support vector regression model on a large data set is time consuming. The performance of the support vector machine depends on the type of optimizer (for example, sequential minimal optimization) selected to maximize the margin during training.

- A linear model (SVM without kernel) has an asymptotic time complexity $O(N)$ for training N labeled observations.
- Nonlinear models rely on kernel methods formulated as a quadratic programming problem with an asymptotic time complexity of $O(N^3)$
- An algorithm that uses sequential minimal optimization techniques such as index caching or elimination of null values (as in LIBSVM), has an asymptotic time complexity of $O(N^2)$ with the worst case scenario (quadratic optimization) of $O(N^3)$
- Sparse problems for very large training sets ($N > 10,000$) also have an asymptotic time of $O(N^2)$

The time and space complexity of the kernelized support vector machine has been receiving a great deal of attention [8:16] [8:17].

Summary

This concludes our investigation of kernel and support vector machines. Support vector machines have become a robust alternative to logistic regression and neural networks for extracting discriminative models from large training sets.

Apart from the unavoidable references to the mathematical foundation of maximum margin classifiers such as SVM, you should have developed a basic understanding of the power and complexity of the tuning and configuration parameters of the different variants of SVM.

As with other discriminative models, the selection of the optimization method for SVMs has a critical impact not only on the quality of the model, but also on the performance (time complexity) of the training and cross-validation process.

The next chapter will describe the third most commonly used discriminative supervised model – artificial neural networks.

9

Artificial Neural Networks

The popularity of **neural networks** surged in the 90s. They were seen as the *silver bullet* to a vast number of problems. At its core, a neural network is a nonlinear statistical model that leverages the logistic regression to create a nonlinear distributed model. The concept of artificial neural networks is rooted in biology, with the desire to simulate key functions of the brain and replicate its structure in terms of neurons, activation, and synapses.

In this chapter, you will move beyond the hype and learn:

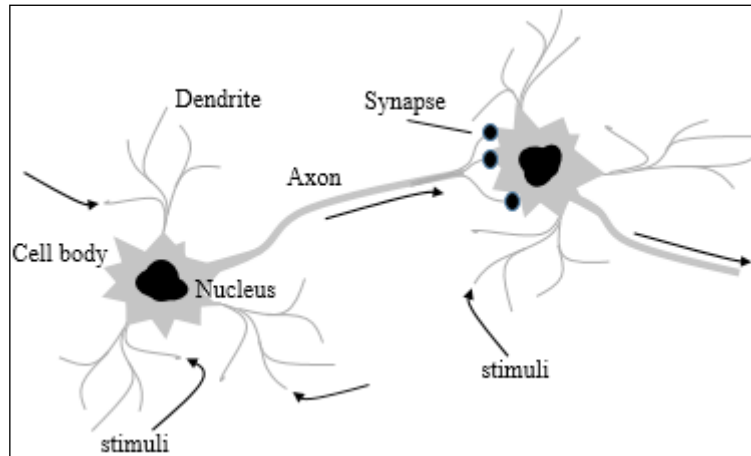
- The concept and elements of the **multilayer perceptron (MLP)**
- How to train a neural network using error backpropagation
- The evaluation and tuning of MLP configuration parameters
- Full Scala implementation of the MLP classifier
- How to apply MLP to extract correlation models for currency exchange rates

Feed-forward neural networks (FFNN)

The idea behind artificial neural networks was to build mathematical and computational models of the natural neural network in the brain. After all, the brain is a very powerful information processing engine that surpasses computers in domains such as learning, inductive reasoning, prediction and vision, and speech recognition.

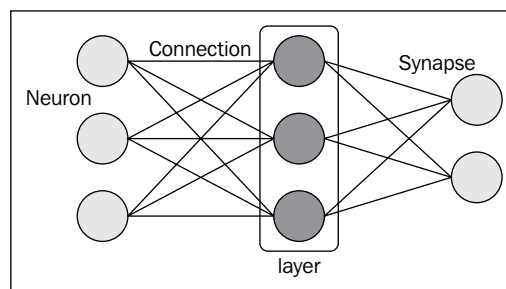
The Biological background

In biology, a neural network is composed of groups of neurons interconnected through synapses [9:1], as shown in the following image:



Neuroscientists have been especially interested in understanding how the billions of neurons in the brain can interact to provide human beings with parallel processing capabilities. The 60s saw a new field of study emerging, known as **connectionism**. Connectionism marries cognitive psychology, artificial intelligence, and neuroscience. The goal was to create a model for mental phenomena. Although there are many forms of connectionism, the neural network models have become the most popular and the most taught of all connectionism models [9:2].

Biological neurons communicate through electrical charges known as **stimuli**. This network of neurons can be represented as a simple schematic, as follows:



This representation categorizes groups of neurons as layers. The terminology used to describe the natural neural networks has a corresponding nomenclature for the artificial neural network.

The biological neural network	The artificial neuron network
Axon	Connection
Dendrite	Connection
Synapse	Weight
Potential	Weighted sum
Threshold	Bias weight
Signal, Stimulus	Activation
Group of neurons	Layer of neurons

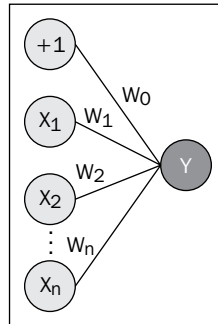
In the biological world, stimuli do not propagate in any specific direction between neurons. An artificial neural network can have the same degree of freedom. The artificial neural networks most commonly used by data scientists, have a predefined direction: from the input layer to output layers. These neural networks are known as FFNN.

The mathematical background

In the previous chapter, you learned that support vector machines have the ability to formulate the training of a model as a nonlinear optimization for which the objective function is convex. A convex objective function is fairly straightforward to implement. The drawback is that the kernelization of the SVM may result in a large number of basis functions (or model dimensions). Refer to the *The Kernel trick* section under *The support vector machine (SVM)* in *Chapter 8, Kernel Models and Support Vector Machines*.

One solution is to reduce the number of basis functions through parameterization, so these functions can adapt to different training sets. Such an approach can be modeled as a FFNN, known as the multilayer perceptron [9:3].

The linear regression can be visualized as a simple connectivity model using neurons and synapses, as follows:



A two-layer neural network

The feature $x_0 = +1$ is known as the **bias input** (or bias element), which corresponds to the intercept in the classic linear regression.

As with support vector machines, linear regression is appropriate for observations that can be linearly separable. The real world is usually driven by a nonlinear phenomena. Therefore, the logistic regression is naturally used to compute the output of the perceptron. For a set of input variable $x = \{x_i\}_{0,n}$ and the weights $w = \{w_i\}_{1,n}$, the output y is computed as:

$$y = \sigma(w_0 + w^T x) = \frac{1}{1 + e^{-(w_0 + w^T x)}}$$

An FFNN can be regarded as a stack of layers of logistic regression with the output layer as a linear regression.

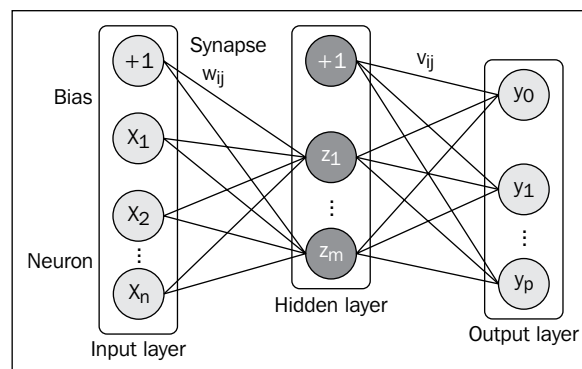
The value of the variables in each hidden layer is computed as the sigmoid of the dot product of the connection weights and the output of the previous layer. Although interesting, the theory behind artificial neural networks is beyond the scope of this book [9:4].

The multilayer perceptron (MLP)

The perceptron is a basic processing element that performs binary classification by mapping a scalar or vector to a binary (or **XOR**) value $\{true, false\}$ or $\{-1, +1\}$. The original perceptron algorithm was defined as a single layer of neurons for which each value x_i of the feature vector is processed in parallel and generates a single output y . The perceptron was later extended to encompass the concept of an activation function.

The single layer perceptrons are limited to process a single linear combination of weights and input values. Scientists found out that adding intermediate layers between the input and output layers enable them to solve more complex classification problems. These intermediate layers are known as **hidden layers** because they interface only with other perceptrons. Hidden nodes can be accessed only through the input layer.

From now on, we will use a three-layered perceptron to investigate and illustrate the properties of neural networks, as shown here:



A three-layered perceptron

The three-layered perceptron requires two sets of weights: w_{ij} to process the output of the input layer to the hidden layer and v_{ij} between the hidden layer and the output layer. The intercept value w_0 , in both linear and logistic regression, is represented with +1 in the visualization of the neural network ($w_0 \cdot 1 + w_1 \cdot x_1 + w_2 \cdot x_2 + \dots$).

FFNN with no hidden layer



A FFNN without a hidden layer is similar to a linear statistical model. The only transformation or connection between the input and output layer is actually a linear regression. A linear regression is a more efficient alternative to the FFNN without a hidden layer.

The description of the MLP components and their implementations rely on the following stages:

1. Overview of the software design.
2. Description of the MLP model components.
3. Implementation of the four-step training cycle.
4. Definition and implementation of the training strategy and the resulting classifier.

Terminology



Artificial neural networks encompass a large variety of learning algorithms, the multilayer perceptron being one of them. Perceptrons are indeed components of a neural network organized as input, output, and hidden layers. This chapter is dedicated to the multilayer perceptron with hidden layers. The terms "neural network" and "multilayer perceptron" are used interchangeably.

The activation function

The perceptron is represented as a linear combination of weights, w_j , and input values, x_j , processed by the **output unit activation** function h , as shown here:

$$\hat{y} = h\left(w_0 + \sum_{i=1}^n w_i x_i\right) = h\left(w_0 + w^T x\right)$$

The output activation function h has to be continuous and differentiable for a range of value of the weights. It takes different forms depending on the problems to be solved, as mentioned here:

- Identity for the output layer of the binary classification or regression problem
- Sigmoid, σ , for hidden layers

- Softmax for the multinomial classification
- Hyperbolic tangent, *tanh*, for classification using zero mean

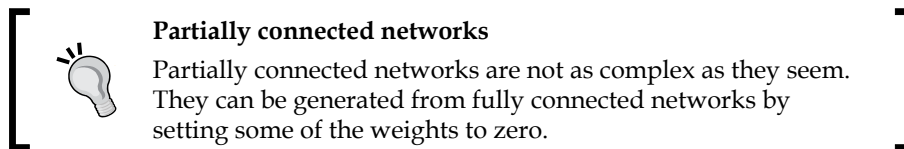
The Softmax formula is described in the next section.

The network architecture

The output layer and hidden layers have a computational capability (dot product of weights, inputs, and activation functions). The input layer does not transform data. An n -layer neural network is a network with n computational layers. Its architecture consists of the following components:

- 1 input layer
- $(n-1)$ hidden layer
- 1 output layer

A **fully connected neural network** has all its input nodes connected to hidden layer neurons. Networks are characterized as **partially connected neural networks** if one or more of their input variables are not processed. This chapter deals with a fully connected neural network.



The structure of the output layer is highly dependent on the type of problems (regression or classification) you need to solve, also known as the **objective of the neural network**. The type of problem at hand defines the number of output nodes [9:5], for example:

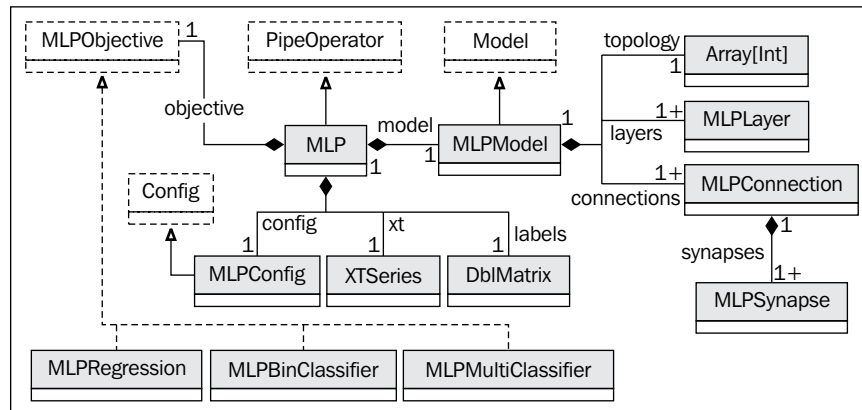
- A one-variate regression has one output node whose value is a real number $[0, 1]$
- A multivariate regression with n variables has n real output nodes
- A binary classification has one binary output node $\{0, 1\}$ or $\{-1, +1\}$
- A multinomial or K -class classification has K binary output nodes

Software design

The implementation of the MLP classifier follows the same pattern as previous classifiers (refer to the *Design template for classifiers* section in *Appendix A, Basic Concepts*):

- A model `MLPModel` of the type `Model` is initialized through training during the initialization of the classifier. The model is composed of a layer of neurons of the type `MLPLayer`, connected by synapses of the type `MLPSynapse` contained by a connector of the type `MLPConnection`.
- All of the configuration parameters are encapsulated into a single configuration class, `MLPConfig`.
- The predictive or classification routine is implemented as a data transformation, extending the `PipeOperator` trait.
- The multilayer perceptron class, `MLP`, takes three parameters: configuration instance, a features set or time series of the `XTSeries` class, and a labeled dataset of the type `DbIMatrix`.

The software components of the multilayer perceptron are described in the following UML class diagram:



A UML class diagram for the multilayer perceptron

The class diagram is a convenient navigation map to understand the role and relation of the Scala classes used to build an MLP. Let's start with the implementation of the MLP model and its components.

Model definition

The purpose of the model is to completely define the network architecture. It is implemented by the `MLPModel` parameterized class, which is responsible for creating and managing the different components of the network, layers, and connections as well as the topology.

Let's establish a simple naming convention for the layers of neurons as follows:

- The input layer, `inLayer`, consists of `nInputs` neurons
- A hidden layer, `hidLayer`, has `nHiddens` neurons
- The output layer, `outLayer`, has `nOutputs` neurons

The instantiation of the class requires a minimum set of three parameters:

```
class MLPModel[T <% Double](config: MLPConfig, nInputs: Int, nOutputs:
Int) extends Model {
  val layers: Array[MLPLayer]
  val connections: Array[MLPConnection]
  val topology: Array[Int]
}
```

Besides the `config` configuration, the model class has two parameters: the number of input features, $\{x\}$, `nInputs`; and the number of output values, $\{y\}$, `nOutputs`. These three parameters are all you need to initialize the topology of the network. A model has the following attributes:

- Multiple layers of the type `MLPLayers`
- Multiple connections of the type `MLPConnection`
- A `topology` array that wires these layers and connections

The topology is defined as an array of number of nodes per layer, starting with the input nodes. The array indices follow the forward path within the network. The size of the input layer is automatically generated from the observations as the size of the features vector. The size of the output layer is automatically extracted from the size of the output vector:

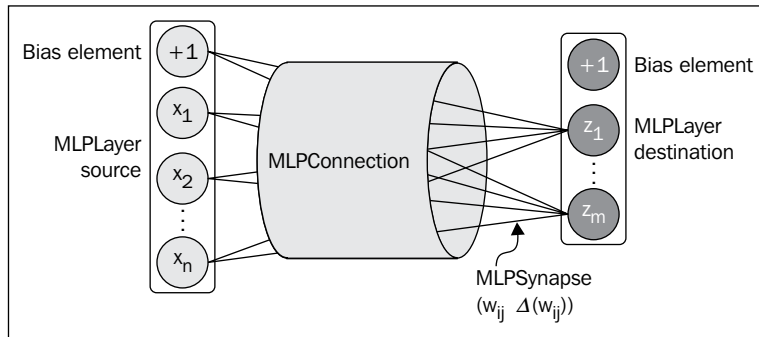
```
val topology = Array[Int](nInputs) ++ config.hidLayers ++
  Array[Int](nOutputs)
```

The sequence of hidden layers, `hidLayers`, is defined as an array of number of neurons (or nodes) per hidden layers:

```
val hidLayers: Array[Int]
```

This is an attribute of the `MLPConfiguration` class described in the next section. For instance, the topology of a neural network with three input variables, one output variable, and two hidden layers of three neurons each is specified as `Array[Int](4, 3, 3, 1)`.

The following diagram visualizes the interaction between the different components of a model: `MLPLayer`, `MLPConnection`, and `MLPSynapse`:



Components of the MLP model

Layers

First, let's start with the definition of the layer class, `MLPLayer`, which is completely specified by its position in the network and the number of nodes it contains:

```
class MLPLayer(val id: Int, val len: Int) {
  val output = new DblVector(len) //1
  val delta = new DblVector(len) //2
  ...output.update(0, 1.0) //3
```

The `id` parameter is the order of the layer (0 for input, 1 for the first hidden layer, ..., $n-1$ for the output layer) in the network. The `len` value is the number of elements or nodes, including the bias element, in this layer. The `output` vector for the layer (line 1) is an uninitialized vector of values updated during the forward propagation, except for the first value (bias element), which is set to 1 (line 3). The `delta` vector associated to the `output` vector (line 2) is updated through the error backpropagation algorithm, described in the next section.

The output values, except the bias element, is initialized using the `set` method:

```
def set(x: DblVector): Unit = x.copyToArray(output, 1)
```

Synapses

A synapse is defined as a pair of real values:

- The weight of the connection from the neuron i of the previous layer to the neuron j , w_{ij}
- The weights adjustment (or gradient of weights), Δw_{ij}

Its type is defined as `MLPSynapse`, as shown here:

```
type MLPSynapse = (Double, Double)
```

Connections

A connection between two consecutive layers implements the matrix of synapses, the $(w_{ij}, \Delta w_{ij})$ pairs. The `MLPConnection` instance is created with the following parameters:

- Configuration parameters, `config`
- The source layer, sometimes known as the ingress layer, `src`
- The destination (or egress) layer, `dst`

The `MLPConnection` class is defined as follows:

```
class MLPConnection(config: MLPConfig, src: MLPLayer, dst: MLPLayer)
```

The last step in the initialization of the MLP algorithm is the selection of the initial (usually random) values of the weights (synapse). The following code snippet initializes the weights for non-bias neurons as random values in the range $[0, \beta]$ with $\beta \leq 1.0$.

The weight for the bias is obviously defined as $w_0 = +1$, and its weight adjustment is initialized as $\Delta w_0 = 0$, as shown here:

```
Val beta = 0.1
val synapses = Array.tabulate(dst.len) (n =>
  if (n > 0) Array.fill(src.len) ((beta*Random.nextDouble, 0.0))
  else Array.fill(src.len) ((1.0, 0.0))
)
```

Random initialization of weights



The range $[0, \beta]$ of initial random values is domain specific. Some problems require a very small range, less than $1e-3$, while others use the probability space $[0, 1]$. The initial values impact the number of epochs required to converge toward an optimal set of weights. [9:6]

Once the topology, synapses, layers, and connections of the MLP algorithm are defined, the initialization of the `MLPModel` model is straightforward:

```
val layers = topology.zipWithIndex
                    .map(t => MLPLayer(t._2, t._1+1))
val connections = Range(0, layers.size-1).map(n =>
    new MLPConnection(config, layers(n), layers(n+1))).toArray
```

The layers are created by traversing the network topology and instantiating each layer with its proper index and number of elements. The connections are instantiated by selecting two consecutive layers of index n (with respect to $n+1$) as source (with respect to destination).



Encapsulation and the model factory

The model components: connections, layers, and synapses are implemented as top-level classes for clarity sake. However, there is no need for the model to expose its inner workings to the client code. These components should be declared as an inner class to the model.

Moreover, the model is responsible for creating its topology. A factory design pattern would be perfectly appropriate to instantiate an `MLPModel` instance dynamically [9:7].

Once initialized, the MLP model is ready to be trained using a combination of forward propagation, output error back propagation, and iterative adjustment of weights and gradients of weights.

Training cycle/epoch

The training of the model processes the training observations multiple times. A training cycle or iteration is known as an **epoch**. The five steps of the training cycle are as follows:

1. Forward propagation of the input value for a specific epoch.
2. Compute the sum of squared errors.
3. Backpropagation of the output error.
4. Recomputation of the synapse weight and gradient of weight.
5. Evaluate the convergence criteria and exit if criteria is met

The computation of the network weights during training could use the difference between labeled data and actual output for each layer. But this solution is not feasible, because the output of the hidden layers is unknown. The solution is to propagate the error on the output values backward through the hidden layers. This approach is not that different than the beta (or backward) pass in the hidden Markov model, covered in the *Beta class (the backward variable)* section in *Chapter 7, Sequential Data Models*.

The error at the output layer for p neurons can be computed in either of the following ways:

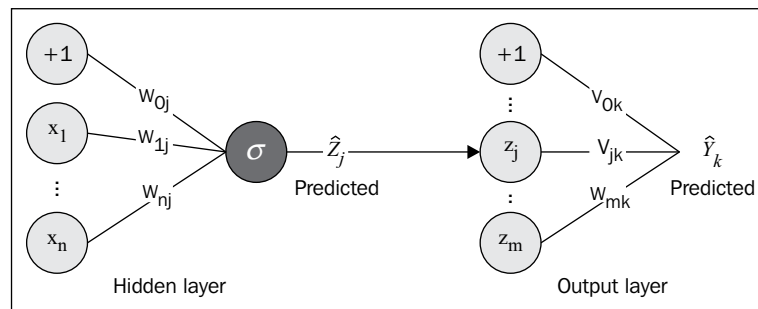
- **Sum of the squared of errors (SSE):** Calculated for each output, y_k
- **Mean squared error (MSE):** Calculated as $MSE = SSE/p$

We select the sum of the squared errors to initialize the error back-propagation algorithm.

Step 1 – input forward propagation

As mentioned earlier, the output values of a hidden layer are computed as a logistic function (the activation function) of the dot product of the weights w_{ij} and the input values x_i .

In the following diagram, the MLP algorithm computes the linear product of the weights w_{ij} and input x_i for the hidden layer. The product is then processed by the activation function σ (sigmoid or hyperbolic tangent). The output values z_j are then combined with the weights v_{ij} of the output layer. The output layer doesn't have an activation function.



The mathematical formulation of the output of a neuron j is defined as a composition of the activation function and the dot product of the weights w_{ij} and input values x_i .

Computation of the output y for the output layer:

$$\hat{y}_k = v_0 + \sum_{j=1}^m v_{kj} z_j$$

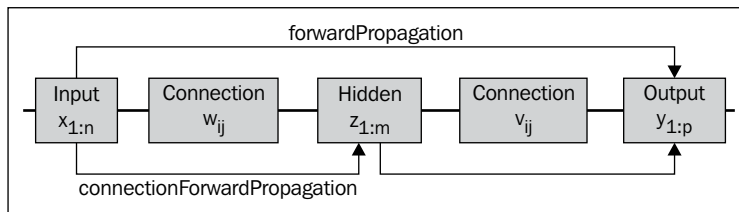
Estimation of the output values for binary classification with an activation function σ :

$$\hat{z}_j = \sigma \left(w_0 + \sum_{i=1}^n w_{ij} x_i \right) = \frac{1}{1 + e^{-w_0 - \sum_{i=1}^n w_{ij} x_i}}$$

As seen in the network architecture section, the output values for the multinomial (or multiclass) classification with more than two classes are normalized using an exponential function (softmax).

The computational model

The computation of the output values y from the input x is known as the input forward propagation. For the sake of simplicity, we represent the forward propagation between layers with the following block diagram. Such a representation will be quite convenient for the design and implementation of the MLP.



A computation model of input forward propagation

This diagram illustrates a computational model for the input forward propagation, as the programmatic relation between the source and destination layers and their connectivity. The input x is propagated forward through each connection.

The `connectionForwardPropagation` method computes the dot product of the weights and the input values, and applies the activation function in the case of hidden layers, for each connection. Therefore, it is a member of the `MLPConnection` class.

The forward propagation of input values across the entire network is managed by the `MLP` algorithm itself.

The forward propagation of the input value is used in the classification or prediction $y = f(x)$. It depends on the value weights w_{ij} and v_{ij} that need to be estimated through training. As you may have guessed, the weights define the model of a neural network similar to the regression models. Let's look at the `connectionForwardPropagation` method of the `MLPConnection` class:

```
def connectionForwardPropagation: Unit = {
  val synps= synapses.drop(1)
  val _output = synps.map(x => { //1
    val sum = x.zip(src.output)
      .foldLeft(0.0)((s, xy) => s + xy._1._1*xy._2)
    if(!isOutLayer) config.activation(sum) //2
    else sum
  })
  val out = if(isOutLayer) mlpObjective(_output) else _output //3
  out.copyToArray(dst.output, 1)
}
```

The first step is to compute the linear dot product of the `_output` output of the current source layer, `src`, for this connection, and the weights, `w` (line 1). The `activation` method, the implementation of which is described in the next paragraph, is applied to the dot product, `dot` (line 2). If the destination layer of the connection is the output layer, then the output values are processed according to the `mlpObjective` objective of the algorithm (line 3).

Objective

In the *The network architecture* section, you learned that the structure of the output layer depends on the type of problems that need to be resolved, or objective of the algorithm. Let's encapsulate the different objectives (binary, multiclass classifiers, and regression) into an `MLPObjective` hierarchy (nested in `MLP` companion object) and the transformation of the output values, `y`, using a simple `apply` method:

```
trait MLPObjective { def apply(y: DblVector): DblVector }
```

The output of the `apply` method is used to compute the sum of squared errors during training, after the forward propagation of features. The binary (2 class) classifier requires a single output without any transformation because the values are either 0 or 1.

```
class MLPBinClassifier extends MLPObjective {
  override def apply(y: DblVector): DblVector = output
}
```

The `MLPMultiClassifier` multiclass classifier objective class used the `softmax` method to boost the output with the highest value, as shown here:

```
class MLPMultiClassifier extends MLPObjective {
  override def apply(y:DblVector):DblVector = softmax(y.drop(1))
  def softmax(y: DblVector): DblVector = { ...}
}
```


The `softmax` method is applied to the actual output value, not the bias. Therefore, the first node $y(0)=+1$ has to be dropped before applying the `softmax` normalization.

Softmax

In case of a classification problem with K classes ($K > 2$), the output has to be converted into a probability $[0, 1]$. For problems that require a large number of classes, there is a need to boost the output y_k with the highest value (or probability). This process is known as the **exponential normalization** or softmax [9:8].

[

Softmax formula for multinomial ($K > 2$) classification is as follows:



$$\hat{y}_k = \frac{e^{-\hat{y}_k}}{\sum_i e^{-\hat{y}_i}}$$

]

Here is the simple implementation of the `softmax` method of the `MLPMultiClassifier` class:

```
def softmax(y: DblVector): DblVector = {
  val softmaxValues = new DblVector(y.size)
  val expY = y.map( Math.exp(_))//1
  val expYSum = expY.sum
  expY.map( _ /expYSum).copyToArray(softmaxValues, 1) //2
  softmaxValues
}
```

First, the output values are transformed to exponential, `expY` (line 1). The exponentially transformed outputs are then normalized by their sum, `expYSum`, to generate the array of `softmaxValues` output (line 2). Once again, you do not have to update the bias element $y(0)$.

The second step in the training phase is the back propagation of the output error.

Step 2 – sum of squared errors

Once the input features are propagated across the neural network, the sum of squared errors, `sse`, for the output layer of the `MPLayer` type is computed at each epoch, as follows:

```
def sse(labels: DblVector): Double = {
  var _sse = 0.0
  output.drop(1) //1
    .zipWithIndex
    .foreach(on => {
    val err = labels(on._2) - on._1 //2
    delta.update(on._2+1, on._1 * (1.0 - on._1) * err) //3
    _sse += err*err
  })
  _sse*0.5 //4
}
```

As expected, the computation of the sum of squared errors requires the labeled values, `labels`, and the `objective` method as arguments. The vector output values, `output`, stripped of the bias node (line 1) is used to compute the difference, `err`, between the label and the actual output (line 2). The `delta` value (line 3), described in the next section, is used in the back-propagation algorithm to adjust the weights of the output and hidden layers. Note that the sum of squares, `_sse`, is divided by 2 (line 4), so its derivative is `err`.

Step 3 – error backpropagation

The error backpropagation is an algorithm that estimates the error for the hidden layer in order to compute the change in weights of the network. It takes the sum of squared errors on the output as input.

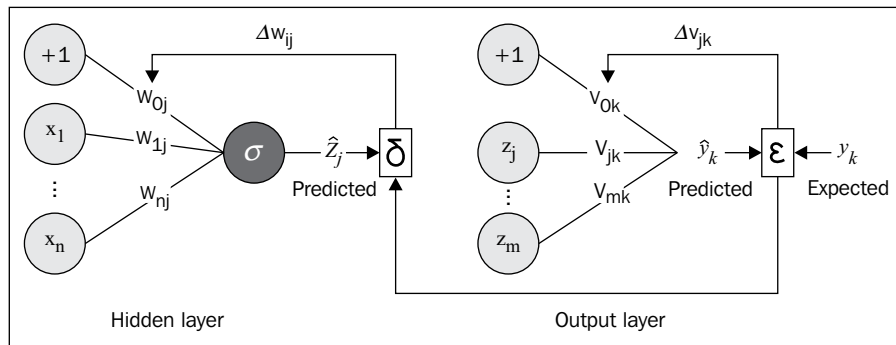


Terminology

Some authors refer to the backpropagation as a training methodology for an MLP, which applies the gradient descent to the output error defined as either the sum of squared errors, or the mean squared error. In this chapter, we keep the narrower definition of backpropagation as the backward computation of the sum of squared errors.

Error propagation

The objective of the training of a perceptron is to minimize the sum of squared errors at the output layer. The error ϵ_k for each output neuron, y_k , is computed as the difference between a predicted output value and label output value. This approach does not work for the hidden layers z_j because the label value is unknown.



The partial derivative of the sum of squared output error over each weight of the output layer is computed as the composition of the derivative of the square function, and the derivative of the dot product of weights and the input z .

Derivative of the output SSE over the weights of the output layer:


$$\epsilon_k = y_k - \hat{y}_k = y_k - v_0 - v^T z$$

$$\mathcal{E} = \frac{1}{2} \sum_{k=1}^p \epsilon_k^2$$

$$\frac{\partial \mathcal{E}}{\partial v_k} = - \sum_{j=1}^m \epsilon_k z_{jk}$$

As mentioned earlier, the computation of the partial derivative of the sum of squared error over the weights of the hidden layer is a bit tricky. Fortunately, the partial derivative can be broken down into the following three pieces using the output layer values and the output of the hidden layer:

- Derivative of sum of squared error \mathcal{E} over the output value y_k
- Derivative of the output value y_k over the hidden value z_j knowing that the derivative of a sigmoid σ is $\sigma(1 - \sigma)$
- Derivative of the output of the hidden layer z_j over the weights w_{ij}



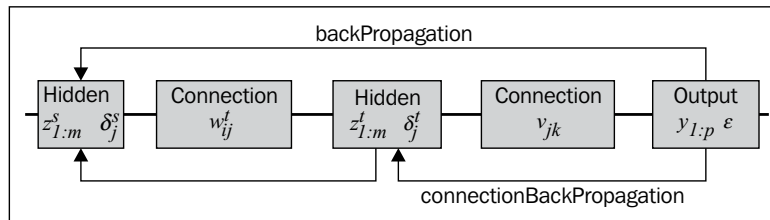
Derivative of error over the weights of the hidden layer:

$$\frac{\partial \varepsilon}{\partial w_{ij}} = \sum_{k=1}^p \frac{\partial \varepsilon}{\partial y_k} \frac{\partial y_k}{\partial z_j} \frac{\partial z_j}{\partial w_{ij}} = - \sum_{k=1}^p \delta_j x_j$$

$$\delta_j = \varepsilon_k z_j (1 - z_j)$$

The computational model

The computational model for the error backpropagation algorithm is very similar to the forward propagation of the input. The main difference is that the propagation of the derivative delta δ is performed from the output layer to the input layer. The following diagram illustrates the computational model of the backpropagation in the case of two hidden layers z_s and z_i :



The `connectionBackPropagation` method propagates the error back to the previous layer. It is a member of the `MLPConnection` class. The backpropagation of the output error across the entire network is managed by the `MLP` class.

It implements the two set of equations where `synapses(j)(i)._1` are the weights w_{ji} , `dst.delta` is the vector of error derivative in the destination or next layer, and `src.delta` is the error derivative on the outputs in the source (or antecedent) layer, as shown here:

```
def connectionBackpropagation: Unit =
  Range(1, src.len).foreach(i => {
    val dot = Range(1, dst.len).foldLeft(0.0)((s, j) =>
      s + synapses(j)(i)._1 * dst.delta(j)) //1
    src.delta(i) = src.output(i) * (1.0 - src.output(i)) * dot //2
  })
```

The dot product of the synapse weights and the errors of the destination layers (line 1) is used to compute the delta on the source (or previous layer) layers (line 2).

Step 4 – synapse/weights adjustment

The connection weights Δv and Δw are adjusted by computing the sum of the derivative of the error, over the weights scaled with a learning factor. The gradient of weights are then used to compute the error of the output of the source layer [9:9].

Momentum factor for gradient descent

The simplest algorithm to update the weights is the gradient descent [9:10].

The gradient descent is a very simple and robust algorithm. However, it is slower in converging toward a global minimum than the conjugate gradient or the quasi-Newton method (refer to the *Summary of optimization techniques* section in *Appendix A, Basic Concepts*).

There are several methods available to speed up the convergence of the gradient descent toward a minimum: momentum factor and adaptive learning coefficient [9:11].

Large variations of the weights (or large value of the gradient of weights) cause the gradient descent to require more training iteration in order to converge. This is particularly true for a training strategy known as online training. The training strategies are discussed in the next section. The momentum factor α is used for the remaining section of the chapter.

The computation of neural network weights using gradient descent is as follows:

$$w_{ij}^{(t+1)} = w_{ij}^{(t)} - \eta \frac{\partial \mathcal{E}_j^{(t)}}{\partial w_{ij}}$$



The computation of neural network weights using gradient descent method with momentum coefficient α is as follows:

$$w_{ij}^{(t+1)} = w_{ij}^{(t)} - \eta \frac{\partial \mathcal{E}_j^{(t)}}{\partial w_{ij}} + \alpha \Delta w_{ij}^{(t)}$$

The basic gradient descent algorithm is selected by setting the momentum factor α to zero.

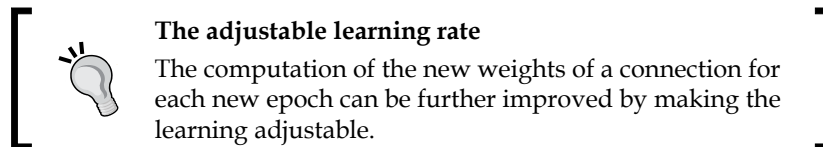
Implementation

The fourth step of the training phase is to adjust each connection's synapses ($w, \Delta w$). This task is performed by the `connectionUpdate` method of the `MLPConnection` class:

```
def connectionUpdate: Unit =
  Range(1, dst.len).foreach(i => {
    val delta = dst.delta(i) //1

    Range(0, src.len).foreach(j => {
      val _output = src.output(j) //2
      val oldSynapse = synapses(i)(j)
      val grad = config.eta*delta*_output //3
      val deltaWeight = grad + config.alpha* oldSynapse._2 //4
      synapses(i)(j) = (oldSynapse._1 + deltaWeight, grad) //5
    })
  })
```

The `connectionUpdate` method computes the error of each destination neuron (line 1). The `_output` output of each neuron source (line 2) is used in the computation of the grad gradient (line 3). The weight is then adjusted for a momentum (line 4) as per the mathematical formulation. Finally, the synapses for source and destination layers are updated (line 5).



Step 5 – convergence criteria

The convergence criterion consists of evaluating the sum of squared errors against a predetermined threshold `eps`. It is common to normalize the sum of squared errors by the number of observations.

Configuration

The `MLPConfig` configuration of the multilayer perceptron consists of the definition of the network configuration with hidden layers, the learning parameters, the training parameters, and the activation function:

```
Class MLPConfig(val alpha: Double, val eta: Double, val hidLayers:
  Array[Int], val numEpochs: Int, val eps: Double, val activation:
  Double=>Double) extends Config
```


For the sake of readability, the name of the configuration parameters matches the symbols defined in the mathematical formulation:

- `alpha`: This is the momentum factor.
- `eta`: This is the learning rate (fixed or adaptive).
- `hidLayers`: This is an array of size of hidden layers (for example, two hidden layers of two and four elements are specified as `Array[Int](2,4)`).
- `numEpochs`: This is the maximum number of epochs allowed for training the neural network.
- `eps`: This is the convergence criteria used as an exit condition for the training of the neural network, `error < eps`.
- `activation`: This is the activation function used for nonlinear regression applied to hidden layers. The default function is the sigmoid.

Putting all together

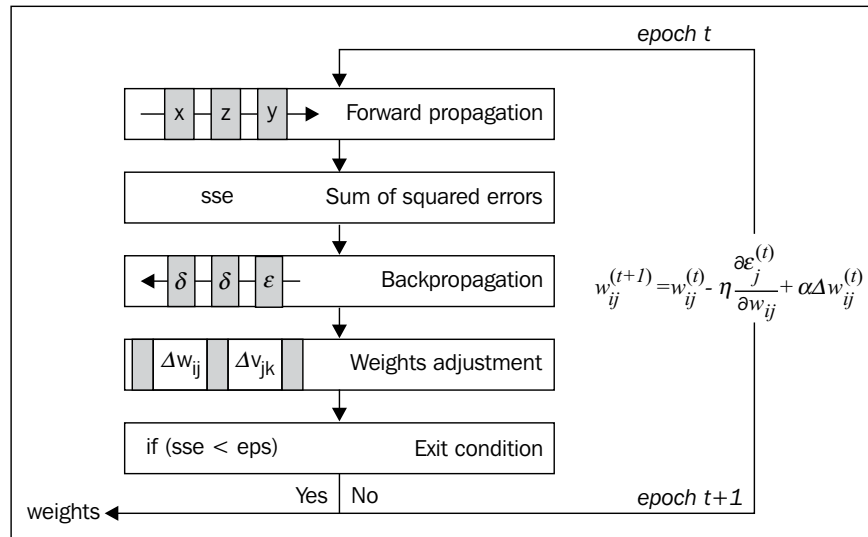
The five steps of the training cycle have been implemented for each connection or matrix of synapses (weights, gradient of weights). The management of the cycle is performed by the algorithm defined by the `MLP` class, as shown here:

```
class MLP[T <% Double](config: MLPConfig, xt: XTSeries[Array[T]],
  labels: DblMatrix)(implicit val mlpObjective: MLP.MLPObjective)
  extends PipeOperator[Array[T], DblVector] {
  val model: Option[MLPModel]
  def |> : PartialFunction[Array[T], DblVector]
}
```

The `MLP` algorithm takes the following parameters:

- `config`: The configuration of the algorithm
- `xt`: The time series of features used to train the model
- `labels`: The labeled output values for training purpose
- `mlpObjective`: The implicit objective of the algorithm (a type of problem)

The five steps of the training cycle or epoch is summarized in the following diagram:



Let's apply the five steps of a training epoch in a `trainEpoch` method of the `MLPModel` class using a simple the `foreach` Scala iterator, as shown here:

```

def trainEpoch(x: DblVector, y: DblVector): Double = {
  inLayer.set(x)

  connections.foreach(_.connectionForwardPropagation) //1
  val _sse = sse(y) //2
  val bckIterator = connections.reverseIterator
  bckIterator.foreach(_.connectionBackpropagation) //3
  connections.foreach(_.connectionUpdate) //4
  _sse
}
  
```

You can certainly recognize the first four stages of the training cycle: forward propagation of the input, `x` (line 1), computation of the sum of squared errors, `_sse` (line 2), the back propagation of the error (line 3), and the recomputation of the weight and gradient of weight associated with each synapse (line 4).

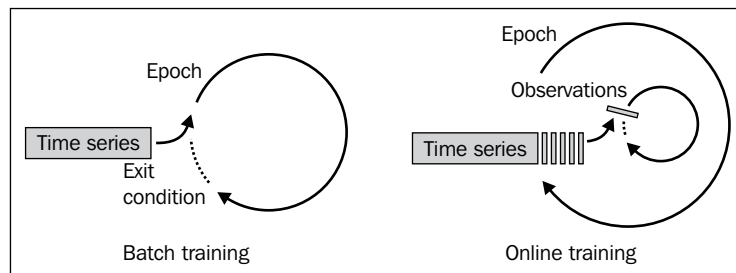
Training strategies and classification

Once the training cycle or epoch is defined, it is merely a matter of defining and implementing a strategy to create a model using a sequence of data or time series.

Online versus batch training

One important remaining issue is finding a strategy to conduct the training of time series, as ordered sequences of data. There are two strategies to create an MLP model for time series:

- **Batch training:** The entire time series is processed at once as a single input to the neural network. The weights (synapses) are updated at each epoch using the sum of squared errors on the output of the time series. The training exits once the sum of the squared errors meets the convergence criteria.
- **Online training:** The observations are fed to the neural network one at a time. Once the time series has been processed, the total of the sum of the squared error (sse) for the time series for all the observations are computed. If the exit condition is not met, the observations are reprocessed by the network.



An illustration on online and batch training

An online training is faster than batch training because the convergence criterion has to be met for each data point, possibly resulting in a smaller number of epochs [9:12]. Techniques such as the momentum factor, which is described earlier, or any adaptive learning scheme improve the performance of the online training process further.

The online training strategy is applied to a financial time series for the remainder of this chapter.

Regularization

There are two approaches to find the most appropriate network architecture for a given classification or regression problem; they are:

- **Destructive tuning:** Starting with a large network, then removing nodes, synapses, and hidden layers that have no impact on the sum of squared errors
- **Constructive tuning:** Starting with a small network, then incrementally adding the nodes, synapses, and hidden layers that reduce the output error

The destructive tuning strategy removes the synapses by zeroing out their weights. This is commonly accomplished by using regularization.

You have seen that regularization is a powerful technique to address overfitting in the case of the linear and logistic regression in the *The ridge regression* section in *Chapter 6, Regression and Regularization*. Neural networks can benefit from adding a regularization term to the sum of squared errors. The larger the regularization factor is, the more likely some weights will be reduced to zero, thus reducing the scale of the network [9:13].

Model instantiation

The `model` instance is created (trained) during the instantiation of the multilayer perceptron. The model is created by iterating the training cycle over all the data points of the time series `xt`, and through multiple epochs until the total sum of squared errors is smaller than the threshold `eps`, as in the following code:

```
var converged = false
val model: Option[MLPModel] = {
  val _model = new MLPModel(config, xt(0).size, labels(0).size)
  (mlpObjective) //1
  val errScale = 1.0/(labels(0).size*xt.size) //4

  converged = Range(0, config.numEpochs).find( _ => {
    xt.toArray.zip(labels)
      .foldLeft(0.0)((s, xtlbl) =>
        s + _model.trainEpoch(xtlbl._1, xtlbl._2) //2
      )*errScale < config.eps //3
  }) != None
  _model
}
```

The model is first initialized (line 1). The first four stages of the MLP training cycle are executed by the `MLPModel.trainEpoch` method described in the previous section (line 2). The method returns the sum of squared errors for each observation in the time series. The sum of squared errors for the observations are summed, then evaluated against the convergence criterion, `eps` (line 3). The sum of squared errors is normalized for the size of the time series and the size of the output vector (line 5). The implementation uses the Scala method, `find`, to exit from the iterative loop before the maximum number of epochs, `config.numEpochs`, is reached.



The exit condition

In this implementation a flag, `converged`, is set to indicate that the execution of the training has not converged before the maximum number of epochs has been reached; however, the model is still instantiated nevertheless. It allows the client code to evaluate the pattern of the sum of squared errors in regard to a local minimum.

Once the model is created during the instantiation of the multilayer perceptron, it is available to predict the class of a new observation.

Prediction

The prediction method of the `MLPModel` class, `getOutput`, takes a new observation (feature vector) as argument and returns the output by using the forward propagation algorithm:

```
def getOutput(x: DblVector): DblVector = {
  inLayer.set(x)
  connections.foreach( _.connectionForwardPropagation)
  outLayer.output
}
```

The classification method is implemented as the data transformation `|>`. It returns the predicted value, normalized as a probability if the model was successfully trained; `None`, otherwise:

```
def |> : PartialFunction[Array[T], DblVector] = {
  case x: Array[T] if(model!=None && x.size == dimension(xt)) =>
    model.get.getOutput(x)
}
```

Our MLP class is now ready to tackle some classification challenges.

Evaluation

Before applying our multilayer perceptron to understand fluctuations in the currency market exchanges, let's get acquainted with some of the key learning parameters introduced in the first section.

Impact of learning rate

The purpose of the first exercise is to evaluate the impact of the learning rate, η , on the convergence of the training epoch, as measured by the sum of the squared errors of all output variables. The observations x (with respect to the labeled output, y) are synthetically generated using several noisy patterns: functions f_1 , f_2 , and noise , as follows:

```
val noise = () => NOISE_RATIO*Random.nextDouble
val f1 = (x: Double) => x*(1.0 + noise())
val f2 = (x: Double) => x*x*(1.0 + noise())

def vec1(x: Double): DblVector = Array[Double](f1(x), noise(), f2(x),
noise())
def vec2(x: Double): DblVector = Array[Double](noise(), noise())
val x = XTSeries[DblVector](Array.tabulate(TEST_SIZE)(vec1(_)))
val y = XTSeries[DblVector](Array.tabulate(TEST_SIZE)(vec2(_)))
```

The x and y values are normalized $[0, 1]$. The test is run with a sample of size `TEST_SIZE` data points over a maximum of 250 epochs, a single hidden layer of five neurons with no softmax transformation and the following MLP parameters:

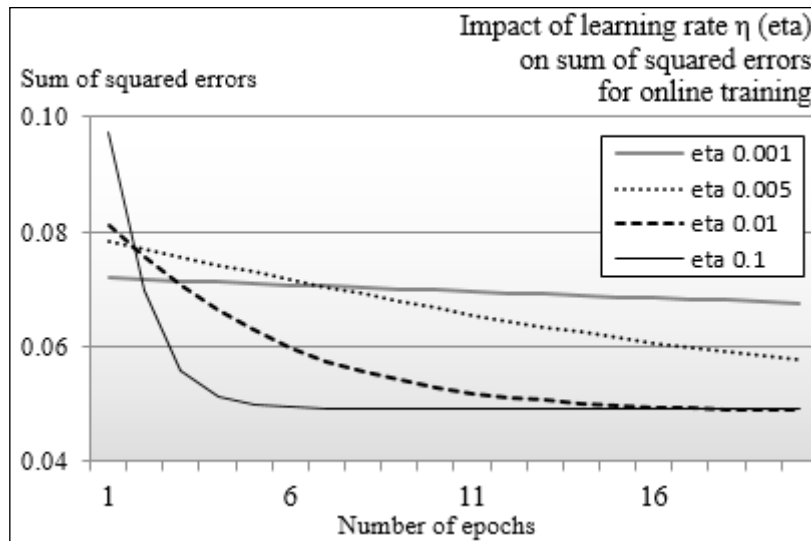
```
val NUM_EPOCHS = 250; val EPS = 1.0e-4
val HIDDENLAYER = Array[Int](5)
val ALPHA = 0.9; val TEST_SIZE = 40

val features = XTSeries.normalize(x).get
val labels = XTSeries.normalize(y).get.toArray
val config = MLPConfig(ALPHA, _eta, SIZE_HIDDEN_LAYER, NUM_EPOCHS,
EPS)

implicit val mlpObjective = new MLP.MLPBinClassifier
val mlp = MLP[Double](config, features, labels)
```

The objective of the algorithm, `m1pObjective`, has to be implicitly defined prior to the instantiation of the `MLP` class.

The test is performed with a different learning rate, `eta`. For clarity's sake, the graph displays the sum of squared errors for the first 22 epochs.

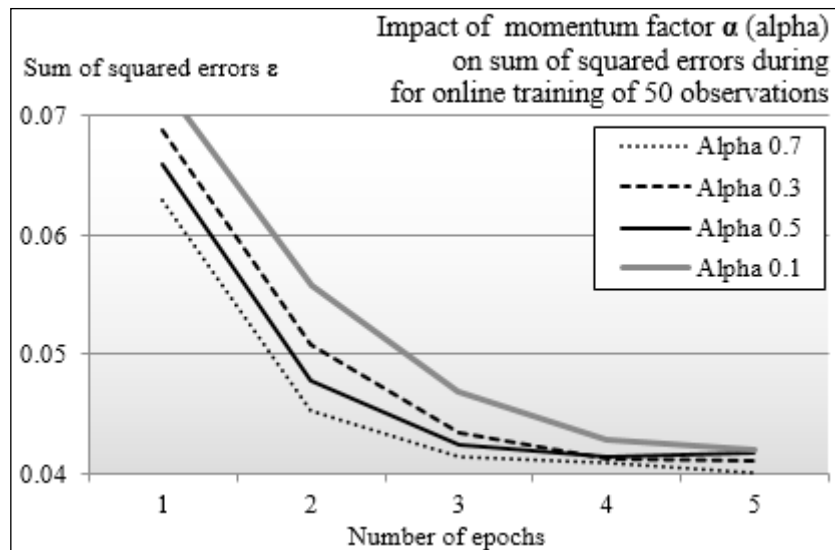


Impact of the learning rate on the MLP training

The chart illustrates that the MLP model training converges a lot faster with a larger value of learning rate. You need to keep in mind, however, that a very steep learning rate may lock the training process into a local minimum for the sum of squared errors generating weights with lesser accuracy. The same configuration parameters are used to evaluate the impact of the momentum factor on the convergence of the gradient descent algorithm.

Impact of the momentum factor

Let's quantify the impact of the momentum factor, α , on the convergence of the training process toward an optimal model (synapse weights). The total sum of squared errors for the entire time series is plotted for the first five epochs in the following graph:



Impact of the momentum factor on the MLP training

The graph shows that the rate the sum of squared errors declines as the momentum factor increases. In other words, the momentum factor has a positive although limited impact on the convergence of the gradient descent.

Let's apply our newfound knowledge regarding neural networks and the classification of variables, that impact the exchange rate of certain currency.

Test case

Neural networks have been used in financial applications from risk management in mortgage applications and hedging strategies for commodities pricing, to predictive modeling of the financial markets [9:14].

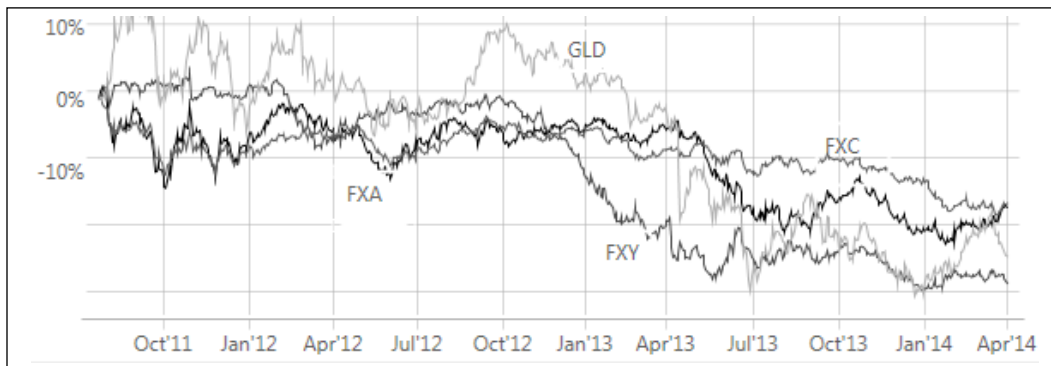
The objective of the test case is to understand the correlation factors between the exchange rate of some currencies, the spot price of gold and the S&P 500 index. For this exercise, we will use the following **exchange-traded funds (ETFs)** as proxies for exchange rate of currencies:

- **FXA**: Rate of an Australian dollar in US dollar
- **FXB**: Rate of a British pound in US dollar
- **FXE**: Rate of an Euro in US dollar

- **FXC**: Rate of a Canadian dollar in US dollar
- **FXF**: Rate of a Swiss franc in US dollar
- **FXY**: Rate of a Japanese yen in US dollar
- **CYB**: Rate of a Chinese yuan in US dollar
- **SPY**: S&P 500 index
- **GLD**: The price of gold in US dollar

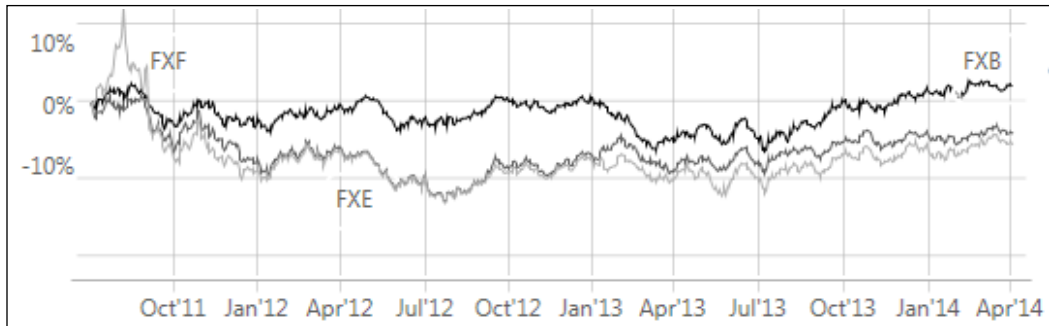
Practically, the problem to solve is to extract one or more regressive models that link one ETFs y with a basket of other ETFs $\{x_i\} y=f(x_i)$. For example, is there a relation between the exchange rate of the Japanese yen (FXY) and a combination of the spot price for gold (GLD), exchange rate of the Euro in US dollar (FXE) and the exchange rate of the Australian dollar in US dollar (FXA), and so on? If so, the regression f will be defined as $FXY = f(GLD, FXE, FXA)$.

The following two charts visualize the fluctuation between currencies over a period of two and a half years. The first chart displays an initial group of potentially correlated ETFs:



An example of correlated currency-based ETFs

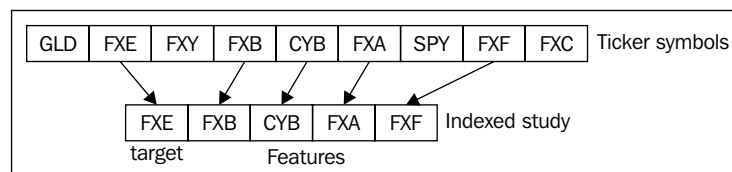
The second chart displays another group of currency-related ETFs that shares a similar price action behavior. Neural networks do not provide any analytical representation of their internal reasoning; therefore, a *visual* correlation can be extremely useful to novice engineers in validating their models.



An example of correlated currency-based ETFs

A very simple approach for finding any correlation between the movement of the currency exchange rates and the gold spot price, is to select one ticker symbol as the target and a subset of other currency-based ETFs as features.

Let's consider the following problem: finding the correlation between the price of FXE and a range of currencies FXB, CYB, FXA, and FXC, as illustrated in the following diagram:



The mechanism to generate features from ticker symbols

Implementation

The first step is to define the configuration parameter for the MLP classifier, is as follows:

```
val path = "resources/data/chap9/"
val ALPHA = 0.5; val ETA = 0.03
val NUM_EPOCHS = 250; val EPS = 1.0e-6
var hidLayers = Array[Int](7, 7) //1

var config = MLPConfig(ALPHA, ETA, hidLayers, NUM_EPOCHS, EPS)
```

Besides the learning parameters, the network is initialized with two configurations:

- One hidden layer with four nodes
- Two hidden layers of four neurons each (line 1)

Next, let's create the search space of the prices of all the ETFs used in the analysis:

```
val symbols = Array[String] ("FXE", "FXA", "SPY", "GLD", "FXB", "FXF",  
"FXC", "FXY", "CYB") //2
```

The closing prices of all the ETFs over a period of three years are extracted from the Google Financial tables, using the `GoogleFinancials` extractor (line 3) for a basket of ETFs (line 2):

```
val prices = symbols.map(s =>DataSource(s"$path$s.csv", true))  
                .map( _ |> GoogleFinancials.close) //3  
                .map( _.toArray)
```

The next step consists of implementing the mechanism to extract the target and the features from a basket of ETFs, or studies introduced in the previous paragraph. Let's consider the following `study` as the list of ETF ticker symbols (line 4):

```
val study = Array[String] ("FXE", "FXF", "FXB", "CYB") //4
```

The first element of the `study`, `FXE`, is the labeled output; the remaining three elements are observed features. For this study, the network architecture has three input variables {`FXF`, `FXB`, `CYB`} and one output variable `FXE`:

```
val obs = study.map(s =>index.get(s).get).map( prices( _ )) //5  
val features = obs.drop(1).transpose //6  
val target = Array[DoubleVector](obs(0)).transpose //7
```

The set of observations is built using an index (line 5). By convention, the first observation is selected as the label data and the remaining studies as the features for training. As the observations are loaded as an array of time series, the time features of series is computed through `transpose` (line 6). The single output variable, `target`, has to be converted into a matrix before transposition (line 7).

Ultimately, the model is built through instantiation of the `MLP` class:

```
val THRESHOLD = 0.08  
implicit val mlpObjective = new MLP.MLPBinClassifier  
val mlp = MLP[Double](config, features, target)  
mlp.accuracy(THRESHOLD)
```

The objective type, `mLpObjective`, is implicitly defined as an MLP binary classifier, `MLPBinClassifier`. The square root of the sum of squares of the difference between the predicted output generated by the MLP and the target value is computed and compared to a predefined threshold. The accuracy value is computed as the percentage of data points, whose prediction matches the target value within a range `< THRESHOLD`:

```

val nCorrects = xt.toArray.zip(labels).foldLeft(0)((s, xtl) => {
  val output = model.get.getOutput(xtl._1) //8
  val _sse = xtl._2.zip(output.drop(1))
    .foldLeft(0.0)((err, tp) => {
      val diff= tp._1 - tp._2
      err + diff*diff
    }) //9
  val error = Math.sqrt(_sse)/(output.size-1) //10
  if(error < threshold) s + 1
  else s
})
nCorrects.toDouble/xt.size

```

The implementation of the computation of the accuracy, as in the previous code snippet, retrieves the values of the output layer (line 8). The `error` value (line 10) is computed as the square root of the sum of squared errors, `_sse` (line 9). Finally, a prediction is considered correct if it is equal to the labeled output, within the margin error, `threshold`.

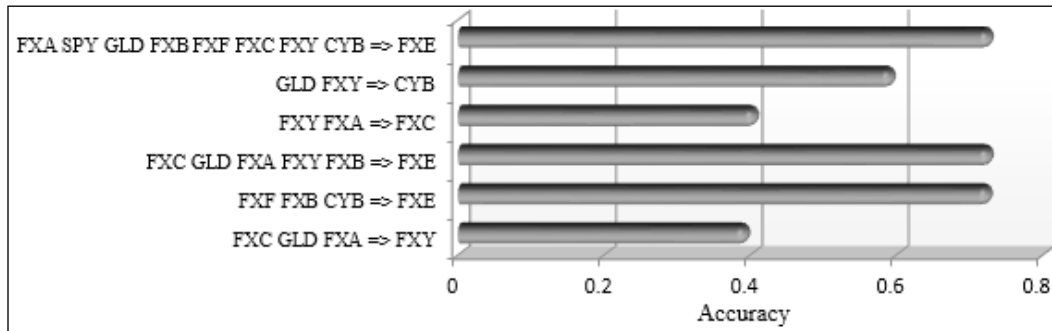
Models evaluation

The test consists of evaluating six different models to determine which ones provide the most reliable correlation. It is critical to ensure that the result is somewhat independent of the architecture of the neural network. Different architectures are evaluated as part of the test.

The following charts compare the models for two architectures:

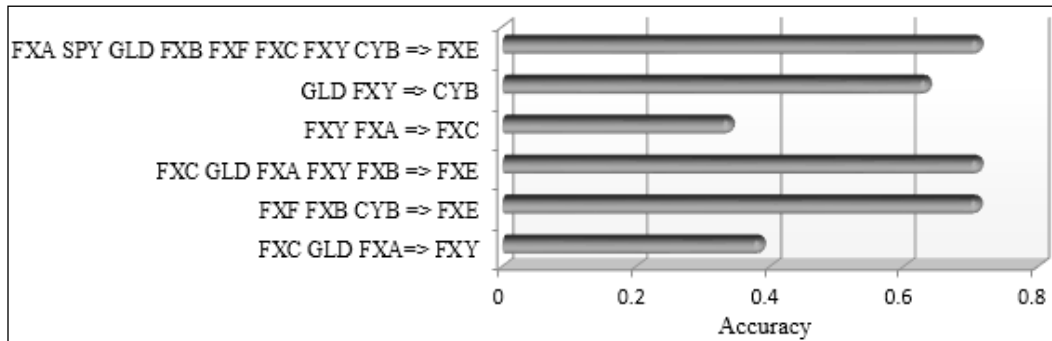
- Two hidden layers with four nodes each
- Three hidden layers with eight (with respect to five and six) nodes

This first chart visualizes the accuracy of the six regression models with an architecture consisting of a variable number of inputs [2, 7], one output variable, and two hidden layers of four nodes each. The features (ETF symbols) are listed on the left-hand side of the arrow => along the y-axis. The symbol on the right-hand side of the arrow is the expected output value:



Accuracy of MLP with two hidden layers of four nodes each

The next chart displays the accuracy of the six regression models for an architecture with three hidden layers of eight, five, and six nodes, respectively:



Accuracy of MLP with three hidden layers with 8, 5, and 6 nodes, respectively

The two network architectures shared a lot of similarity: in both cases, the most accurate regression models are as follows:

- $FXE = f(FXA, SPY, GLD, FXB, FXF, FXD, FXY, CYB)$
- $FXE = g(FXC, GLD, FXA, FXY, FXB)$
- $FXE = h(FXF, FXB, CYB)$

On the other hand, the prediction the Canadian dollar to US dollar's exchange rate (FXC) using the exchange rate for the Japanese yen (FXY) and the Australian dollar (FXA) is poor with both configuration.



The empirical evaluation

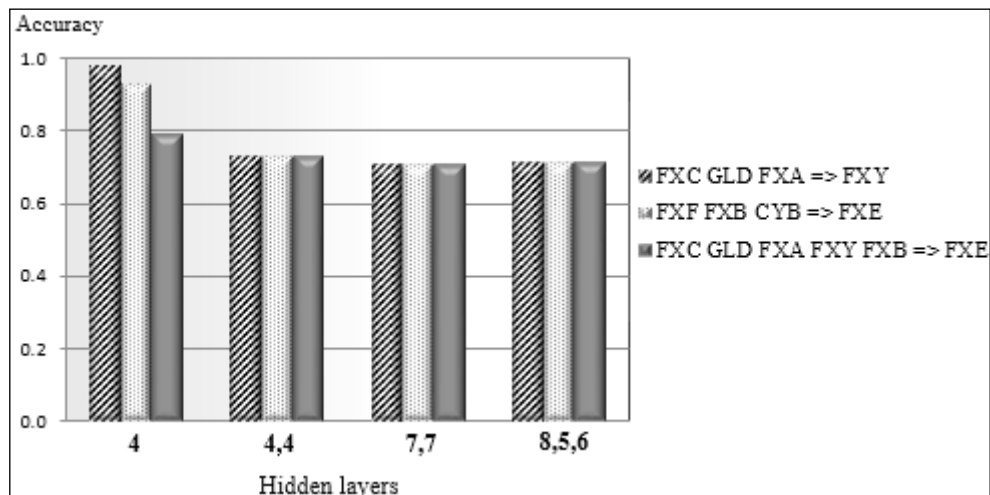
These empirical tests use a simple accuracy metric. A formal comparison of the regression models would systematically analyze every combination of input and output variables. The evaluation would also compute the precision, the recall, and the F1 score for each of those models (refer to the *Key metrics* section under *Validation* in the *Assessing a model* section in *Chapter 2, Hello World!*).

Impact of hidden layers architecture

The next test consists of evaluating the impact of the hidden layer(s) of configuration on the accuracy of three models: $(FXF, FXB, CYB \Rightarrow FXE)$, $(FCX, GLD, FXA \Rightarrow FXY)$, and $(FXC, GLD, FXA, FXY, FXB \Rightarrow FXE)$. For this test, the accuracy is computed by selecting a subset of the training data as a test sample, for the sake of convenience. The objective of the test is to compare different network architectures using some metrics, not to estimate the absolute accuracy of each model.

The four network configurations are as follows:

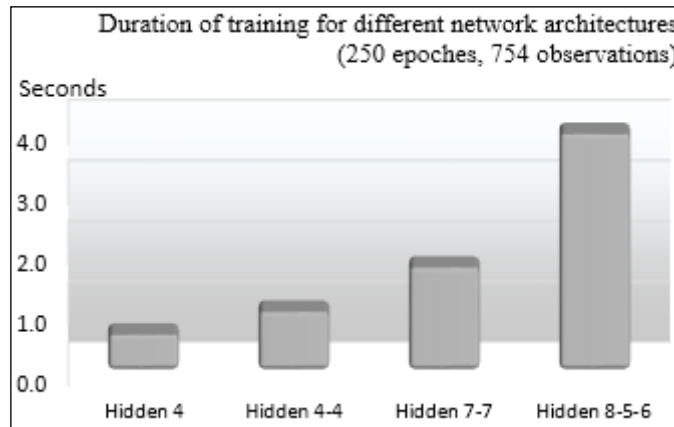
- A single hidden layer with four nodes
- Two hidden layers with four nodes each
- Two hidden layers with seven nodes each
- Three hidden layer with eight, five, and six nodes



Impact of hidden layers architecture on the MLP accuracy

The complex neural network architecture with two or more hidden layers generates weights with similar accuracy. The four-node single hidden layer architecture generates the highest accuracy. The computation of the accuracy using a formal cross-validation technique would generate a lower accuracy number.

Finally, we look at the impact of the complexity of the network on the duration of the training, as in the following graph:



Impact of hidden layers architecture on duration of training

Not surprisingly, the time complexity increases significantly with the number of hidden layers and number of nodes.

Benefits and limitations

The advantages and disadvantages of neural networks depend on which other machine learning methods they are compared to. However, neural-network-based classifiers, particularly the multilayer perceptron using error backpropagation, have some obvious advantages, such as:

- The mathematical foundation of a neural network does not require expertise in dynamic programming or linear algebra, beyond the basic gradient descent algorithm.
- A neural network can perform tasks that a linear algorithm cannot.

- MLP is usually reliable for highly dynamic and nonlinear processes. Contrary to the support vector machines, they do not require us to increase the problem dimension through kernelization.
- MLP does not make any assumption on linearity, variable independence, or normality.
- The execution of training of the MLP lends itself to concurrent processing quite well for online training. In most architecture, the algorithm can continue even if a node in the network fails.

However, as with any machine learning algorithm, neural networks have their detractors. Among the most documented limitations are as follows:

- MLP models are black boxes for which the association between features and classes may not be easily described.
- MLP requires a lengthy training process, especially using the batch strategy. For example, a two-layer network has a time complexity (number of multiplications) of $O(n.m.p.N.e)$ for n input variables, m hidden neurons, p output values, N observations, and e epochs. It is not uncommon that a solution emerges after thousands of epochs. The online training strategy using momentum factor tends to converge faster and require a smaller number of epochs than the batch process.
- Tuning the configuration parameters, such as learning rate, selection of the activation method, application of softmax transformation, or momentum factor, can turn into a lengthy process.
- Estimating the minimum size of the training set to get accurate results is not obvious.
- A neural network cannot be incrementally retrained. Any new labeled data requires an entirely new training cycle.

Summary

This concludes not only the journey inside the multilayer perceptron, but also the introduction of the supervised learning algorithms. In this chapter, you learned:

- The components and architecture of a neural networks
- The stages of the training cycle of a backpropagation multilayer perceptron
- How to implement an MLP from the ground up in Scala
- The numerous configuration parameters and options to use MLP as a classifier and regression
- To evaluate the impact of the learning rate and the gradient descent momentum factor on the convergence of the sum of squared errors during training
- How to apply a multilayer perceptron to the financial analysis of the fluctuation of currencies

The next chapter will introduce the concept of genetic algorithms with a full implementation in Scala. Although, strictly speaking, genetic algorithms do not belong to the family of machine learning algorithms, they play a crucial role in the optimization of nonlinear, nondifferentiable problems and the selection of strong classifiers within ensembles.

10

Genetic Algorithms

This chapter introduces the concept of **evolutionary computing**. Algorithms derived from the theory of evolution are particularly efficient in solving large combinatorial or **NP problems**. Evolutionary computing has been pioneered by **John Holland** [10:1] and **David Goldberg** [10:2]. Their findings should be of interest to anyone eager to learn about the foundation of **genetic algorithms (GA)** and **artificial life**.

This chapter covers the following topics:

- The origin of evolutionary computing
- The theoretical foundation of genetic algorithms
- Advantages and limitations of genetic algorithms

From a practical perspective, you will learn how to:

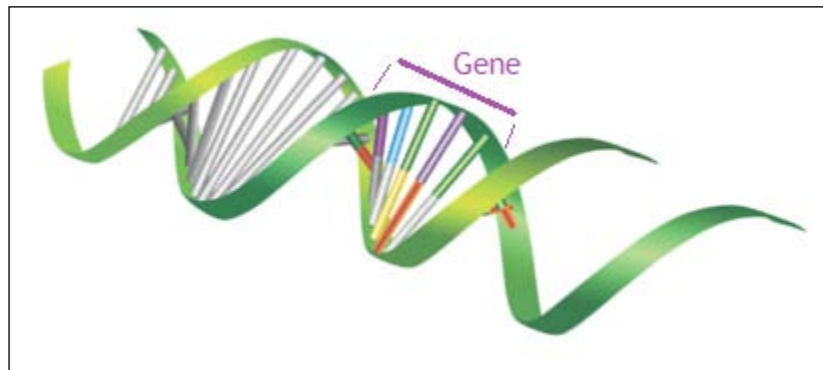
- Apply genetic algorithms to leverage technical analysis of market price and volume movement to predict future returns
- Evaluate or estimate the search space
- Encode solutions in the binary format using either hierarchical or flat addressing
- Tune some of the genetic operators
- Create and evaluate fitness functions

Evolution

The **theory of evolution**, enunciated by Charles Darwin, describes the morphological adaptation of living organisms [10:3].

The origin

The **Darwinian** process consists of optimizing the morphology of organisms to adapt to the harshest environments – hydrodynamic optimization for fishes, aerodynamic for birds, or stealth skills for predators. The following diagram shows a gene:



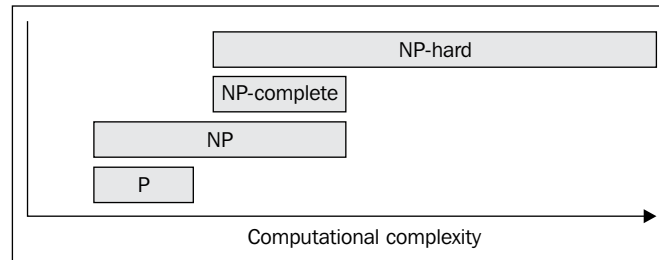
The **population** of organisms varies over time. The number of individuals within a population changes, sometimes dramatically. These variations are usually associated with the abundance or lack of predators and prey as well as the changing environment. Only the fittest organisms within the population can survive over time by adapting quickly to sudden changes in living environments and new constraints.

NP problems

NP stands for nondeterministic polynomial time. The NP problems concept relates to the theory of computation and more precisely, time and space complexity. The categories of NP problems are as follows:

- **P-problems** (or P decision problems): For these problems, the resolution on a deterministic Turing machine (computer) takes a deterministic polynomial time.
- **NP problems**: These problems can be resolved in a polynomial time on nondeterministic machines.
- **NP-complete problems**: These are NP-hard problems that are reduced to NP problems for which the solution takes a deterministic polynomial time. These types of problems may be difficult to solve but their solution can be validated.

- **NP-hard problems:** These problems have solutions that may not be found in polynomial time.



Problems such as the traveling salesman, floor shop scheduling, the computation of a graph K-minimum spanning tree, map coloring, or cyclic ordering have a search execution time that is a nondeterministic polynomial, ranging from $n!$ to 2^n for a population of n elements [10:4].

NP problems cannot always be solved using analytical methods because of the computation overhead – even in the case of a model, it relies on differentiable functions. Genetic algorithms were invented by John Holland in the 1970s, and they derived their properties from the Theory of Evolution of Darwin to tackle NP and NP-complete problems.

Evolutionary computing

A living organism consists of cells that contain identical chromosomes. **Chromosomes** are strands of **DNA** and serve as a model for the whole organism. A chromosome consists of **genes** that are blocks of DNA and encode a specific protein.

Recombination (or crossover) is the first stage of reproduction. Genes from parents generate the whole new chromosome (**offspring**) that can be mutated. During mutation, one or more elements, also known as individual bases of the DNA strand or chromosomes, are changed. These changes are mainly caused by errors that occur when the genes from parents are being passed on to their offspring. The success of an organism in its life measures its fitness [10:5].

Genetic algorithms use reproduction to evolve a solution for a problem that is similar to unsupervised learning, for which a class or clusters are identified through an iterative or optimization methodology.

Genetic algorithms and machine learning

The practical purpose of a genetic algorithm as an optimization technique is to solve problems by finding the most relevant or fittest solution among a set or group of solutions. Genetic algorithms have many applications in machine learning, as follows:

- **Discrete model parameters:** Genetic algorithms are particularly effective in finding the set of discrete parameters that maximizes the log likelihood. For example, the colorization of a black and white movie relies on a large but finite set of transformations from shades of grey to the RGB color scheme. The search space is composed of the different transformations and the objective function is the quality of the colorized version of the movie.
- **Reinforcement learning:** Systems that select the most appropriate rules or policies to match a given data set rely on genetic algorithms to evolve the set of rules over time. The search space or population is the set of candidate rules, and the objective function is the credit or reward for an action triggered by these rules (refer to the *Introduction* section of *Chapter 11, Reinforcement Learning*).
- **Neural network architecture:** A genetic algorithm drives the evaluation of different configurations of networks. The search space consists of different combinations of hidden layers and the size of those layers. The fitness or objective function is the sum of the squared errors.
- **Ensemble learning [10:6]:** A genetic algorithm can weed out the weak learners among a set of classifiers in order to improve the quality of the prediction.

Genetic algorithm components

Genetic algorithms have the following three components:

- **Genetic encoding (and decoding):** This is the conversion of a solution candidate and its components into the binary format (an array of bits or a string of 0 and 1 characters)
- **Genetic operations:** This is the application of a set of operators to extract the best (most genetically fit) candidates (chromosomes)
- **Genetic fitness function:** This is the evaluation of the fittest candidate using an objective function

Encodings and the fitness function are problem dependent. Genetic operators are not.

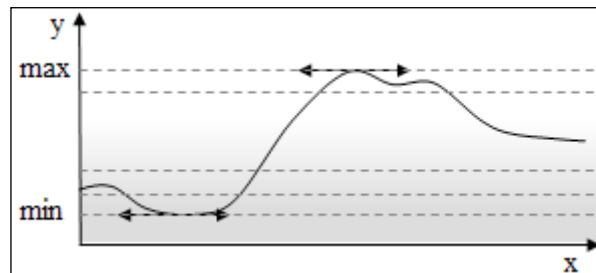
Encodings

Let's consider the optimization problem in machine learning that consists of maximizing the log likelihood or minimizing the loss function. The goal is to compute the parameters or weights, $w=\{w_i\}$, that minimize or maximize a function $f(w)$. In the case of a nonlinear model, variables may depend on other variables, which make the optimization problem particularly challenging.

Value encoding

The genetic algorithm manipulates variables as bits or bit strings. The conversion of a variable into a bit string is known as encoding. In the case where the variable is continuous, the conversion is known as **discretization**. Each type of variable has a unique encoding scheme, as follows:

- Boolean values are easily encoded with 1 bit: 0 for false and 1 for true.
- Continuous variables are discretized in a fashion similar to the conversion of an analog to a digital signal. Let's consider the function with a maximum **max** (similarly **min** for minimum) over a range of values, encoded with $n=16$ bits:

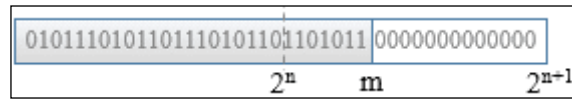


The step size of the discretization is computed as:

$$step = \frac{max-min}{2^n}$$

The step size of the discretization of the sine $y = \sin(x)$ in 16 bits is 1.524e-5.

- Discrete or categorical variables are a bit more challenging to encode to bits. At a minimum, all the discrete values have to be accounted for. However, there is no guarantee that the number of variables will coincide with the bits boundary:



In this case, the next exponent, $n+1$, defined the minimum number of bits required to represent the set of values: $n = \log_2(m).toInt + 1$. A discrete variable with 19 values requires 5 bits. The remaining bits are set to an arbitrary value (0, NaN,...) depending on the problem. This procedure is known as **padding**.

Encoding is as much art as it is science. For each encoding function, you need a decoding function to convert the bits representation back to actual values.

Predicate encoding

A predicate for a variable x is a relation defined as $x \text{ operator } [target]$, for instance, $unit \text{ cost} < [9\$]$, $temperature = [82F]$, or $Movie \text{ rating is } [3 \text{ stars}]$.

The simplest encoding scheme for predicates is as follows:

- Variables are encoded as category or type (for example, temperature, barometric pressure, and so on) because there is a finite number of variables in any model
- Operators are encoded as discrete type
- Values are encoded as either discrete or continuous values



Encoding format for predicates

There are many approaches for encoding a predicate in a bits string. For instance, the format $\{operator, left\text{-operand}, right\text{-operand}\}$ is useful because it allows you to encode a binary tree. The entire rule, $IF \text{ predicate } THEN \text{ action}$, can be encoded with the action being represented as a discrete or categorical value.

Solution encoding

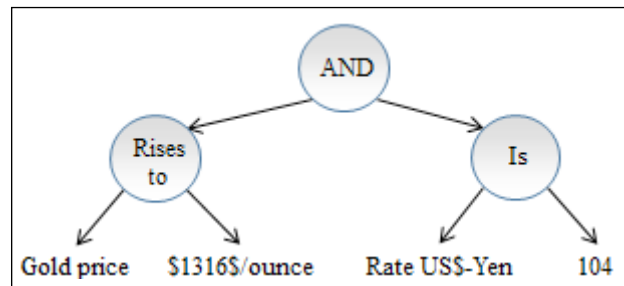
The solution encoding approach describes the solution to a problem as an unordered sequence of predicates. Let's consider the following rule:

```
IF {Gold price rises to [1316$/ounce]} AND
   {US$/Yen rate is [104]}.
THEN {S&P 500 index is [UP]}
```

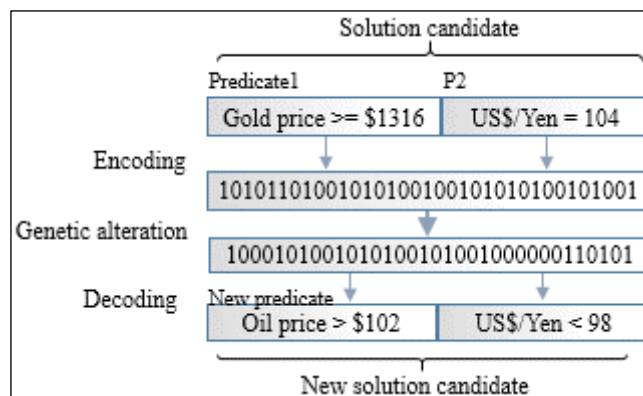
In this example, the search space is defined by two levels:

- Boolean operators (for example, AND) and predicates
- Each predicate is defined as a tuple $\{variable, operator, target\}$ value}

The tree representation for the search space is shown in the following diagram:



The bits string representation is decoded back to its original format for further computation:



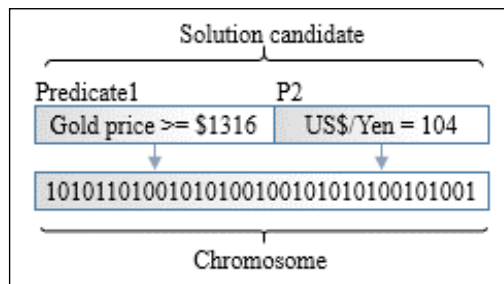
The encoding scheme

There are two approaches to encode such a candidate solution or chain of predicates:

- Flat coding of a chromosome
- Hierarchical coding of a chromosome as a composition of genes

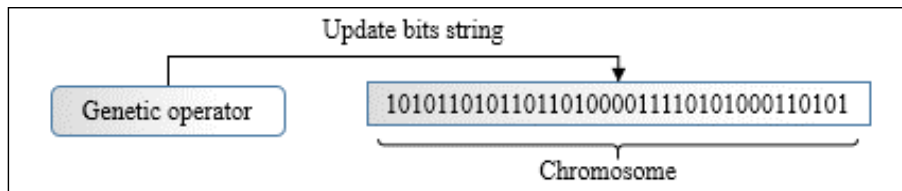
Flat encoding

The flat encoding approach consists of encoding the set of predicates into a single chromosome (bits string) representing a specific solution candidate to the optimization problem. The identity of the predicates is not preserved:



An overview of flat addressing

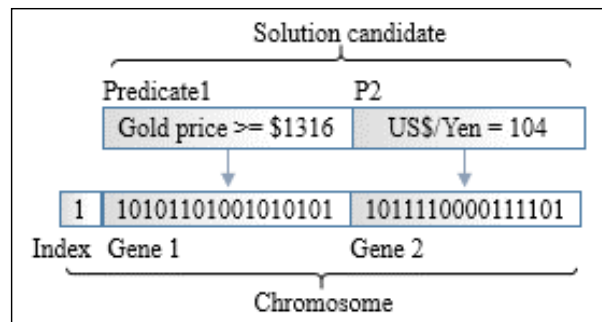
A genetic operator manipulates the bits of the chromosome regardless of whether the bits refer to a particular predicate:



Chromosome encoding with flat addressing

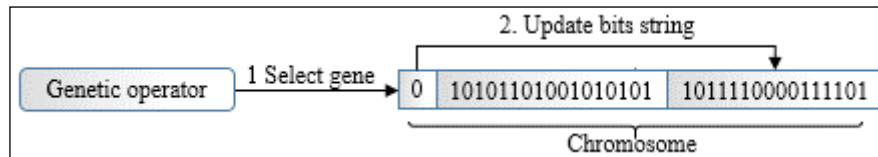
Hierarchical encoding

In this configuration, the characteristic of each predicate is preserved during the encoding process. Each predicate is converted into a gene represented by a bit string. The genes are aggregated to form the chromosome. An extra field is added to the bits string or chromosome for the selection of the gene. This extra field consists of the index or the address of the gene:



An overview of hierarchical addressing

A generic operator selects the predicate it needs to manipulate first. Once the target gene is selected, the operator updates the bits string associated to the gene, as follows:



A chromosome with hierarchical addressing

The next step is to define the genetic operators that manipulate or update the bits string representing either a chromosome or individual genes.

Genetic operators

The implementation of the reproduction cycle attempts to replicate the natural reproduction process [10:7]. The reproduction cycle that controls the population of chromosomes consists of three genetic operators:

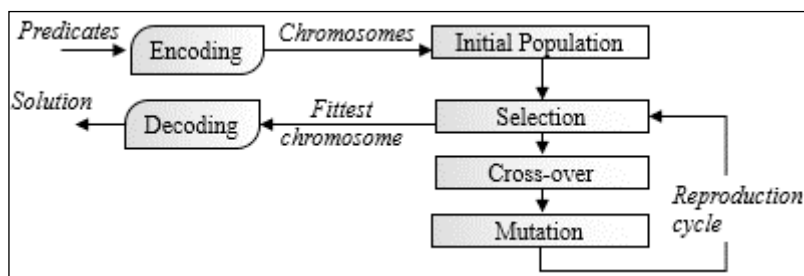
- **Selection:** This operator ranks chromosomes according to a fitness function or criteria. It eliminates the weakest or less-fit chromosomes and controls the population growth.
- **Crossover:** This operator pairs chromosomes to generate offspring chromosomes. These offspring chromosomes are added to the population along with their parent chromosomes.
- **Mutation:** This operator introduces minor alteration in the genetic code (bits string representation) to prevent the successive reproduction cycles from electing the same fittest chromosome. In optimization terms, this operator reduces the risk of the genetic algorithm converging quickly towards a local maximum or minimum.



Transposition operator

Some implementations of genetic algorithms use a fourth operator, genetic transposition, in case the fitness function cannot be very well defined and the initial population is very large. Although additional genetic operators could potentially reduce the odds of finding a local maximum or minimum, the inability to describe the fitness criteria or the search space is a sure sign that a genetic algorithm may not be the most suitable tool.

The following diagram gives an overview of the genetic algorithm workflow:



Initialization

The initialization of the search space (a set of potential solutions to a problem) in any optimization procedure is challenging, and genetic algorithms are no exception. In the absence of bias or heuristics, the reproduction initializes the population with randomly generated chromosomes. However, it is worth the effort to extract the characteristics of a population. Any well-founded bias introduced during initialization facilitates the convergence of the reproduction process.

Each of these genetic operators has at least one configurable parameter that has to be estimated and/or tuned. Moreover, you will likely need to experiment with different fitness functions and encoding schemes in order to increase your odds of finding a fittest solution (or chromosome).

Selection

The purpose of the genetic selection phase is to evaluate, rank, and weed out the chromosomes (that is, the solution candidates) that are not a good fit for the problem. The selection procedure relies on a fitness function to score and rank candidate solutions through their chromosomal representation. It is a common practice to constrain the growth of the population of chromosomes by setting a limit to the size of the population.

There are several methodologies to implement the selection process from scaled relative fitness, Holland roulette wheel, and tournament selection to rank-based selection [10:8].

Relative fitness degradation



As the initial population of chromosomes evolves, the chromosomes tend to get more and more similar to each other. This phenomenon is a healthy sign that the population is actually converging. However, for some problems, you may need to scale or magnify the relative fitness to preserve a meaningful difference in the fitness score between the chromosomes [10:9].

The following implementation relies on rank-based selection using either a fitness or unfitness function to score chromosomes.

The selection process consists of the following steps:

1. Apply the fitness/unfitness function to each chromosome j in the population, f_j
2. Compute the total fitness/unfitness score for the entire population, $\sum f_j$
3. Normalize the fitness/unfitness score of each chromosome by the sum of the fitness/unfitness scores of all the chromosomes, $f_j = f_j / \sum f_j$
4. Sort the chromosomes by their descending fitness score or ascending unfitness score
5. Compute the cumulative fitness/unfitness score for each chromosome, $j f_j = f_j + \sum_k$
6. Generate the selection probability (for the rank-based formula) as a random value, $p \in [0,1]$
7. Eliminate the chromosome, k , having a low fitness score $f_k < p$ or high unfitness cost, $f_k > p$
8. Reduce the size of the population further if it exceeds the maximum allowed number of chromosomes.

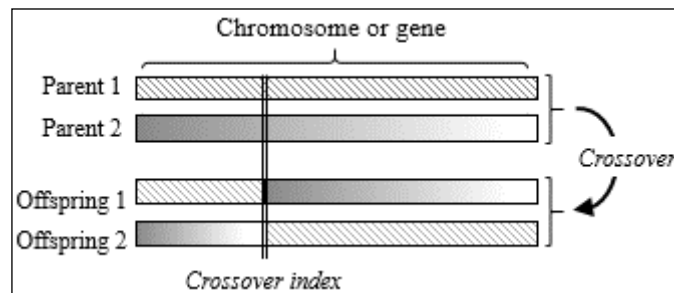
Natural selection



You should not be surprised by the need to control the size of population of chromosomes. After all, nature does not allow any species to grow beyond a certain point in order to avoid depleting natural resources. The predator-prey process modeled by the **Lotka-Volterra equation** [10:10] keeps the population of each species in check.

Crossover

The purpose of the genetic crossover is to expand the current population of chromosomes in order to intensify the competition among the solution candidates. The crossover phase consists of reprogramming chromosomes from one generation to the next. There are many different variations of crossover techniques. The algorithm for the evolution of the population of chromosomes is independent of the crossover technique. Therefore, the case study uses the simpler one-point crossover. The crossover swaps sections of the two-parent chromosomes to produce two offspring chromosomes, as illustrated in the following diagram:



A chromosome's crossover

An important element in the crossover phase is the selection and pairing of parent chromosomes. There are different approaches for selecting and pairing the parent chromosomes that are the most suitable for reproduction:


- Selecting only the n fittest chromosomes for reproduction
- Pairing chromosomes ordered by their fitness (or unfitness) value
- Pairing the fittest chromosome with the least-fit chromosome, the second fittest chromosome with the second least-fit chromosome, and so on

It is a common practice to rely on a specific optimization problem to select the most appropriate selection method as it is highly domain dependent.

The crossover phase that uses hierarchical addressing as the encoding scheme consists of the following steps:

1. Extract pairs of chromosomes from the population.
2. Generate a random probability $p \in [0,1]$.
3. Compute the index ri of the gene for which the crossover is applied as $ri = p \cdot num_genes$, where num_genes are the number of genes in a chromosome.

4. Compute the index of the bit in the selected gene for which the crossover is applied as $xi=p.gene_length$, where $gene_length$ is the number of bits in the gene.
5. Generate two offspring chromosomes by interchanging strands between parents.
6. Add the two offspring chromosomes to the population.

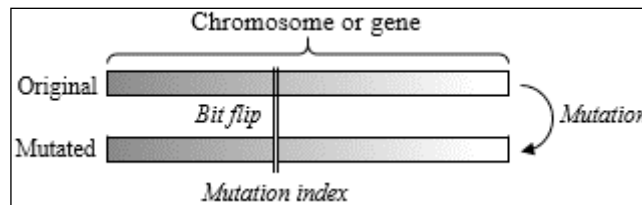


Preserving parent chromosomes

You may wonder why the parents are not removed from the population once the offspring chromosomes are created. This is because there is no guarantee that any of the offspring chromosomes are a better fit.

Mutation


The objective of genetic mutation is preventing the reproduction cycle from converging towards a local optimum by introducing a pseudo-random alteration to the genetic material. The mutation procedure inserts a small variation in a chromosome to maintain some level of diversity between generations. The methodology consists of flipping one bit in the bits string representation of the chromosome, as illustrated in the following diagram:



The chromosome mutation

The mutation is the simplest of the three phases in the reproduction process. In the case of hierarchical addressing, the steps are as follows:

1. Select the chromosome to be mutated.
2. Generate a random probability $p \in [0,1]$.
3. Compute the index mi of the gene to be mutated using the formula $mi = p.num_genes$.
4. Compute the index of the bit in the gene to be mutated $xi=p.genes_length$.
5. Perform a flip XOR operation on the selected bit.

 **The tuning issue**
The tuning of a genetic algorithm can be a daunting task. A plan including a systematic design experiment for measuring the impact of the encoding, fitness function, crossover, and mutation ratio is necessary to avoid lengthy evaluation and self-doubt.

Fitness score

The fitness function is the centerpiece of the selection process. There are three categories of fitness functions:

- **The fixed fitness function:** In this function, the computation of the fitness value does not vary during the reproduction process
- **The evolutionary fitness function:** In this function, the computation of the fitness value morphs between each selection according to predefined criteria
- **An approximate fitness function:** In this function, the fitness value cannot be computed directly using an analytical formula [10:11]

Our implementation of the genetic algorithm uses a fixed fitness function.

Implementation

As mentioned earlier, the genetic operators are independent of the problem to be solved. Let's implement all the components of the reproduction cycle. The fitness function and the encoding scheme are highly domain specific.

In accordance with the principles of object-oriented programming, the software architecture defines the genetic operators using a top-down approach: starting with the population, then each chromosome, down to each gene.

Software design

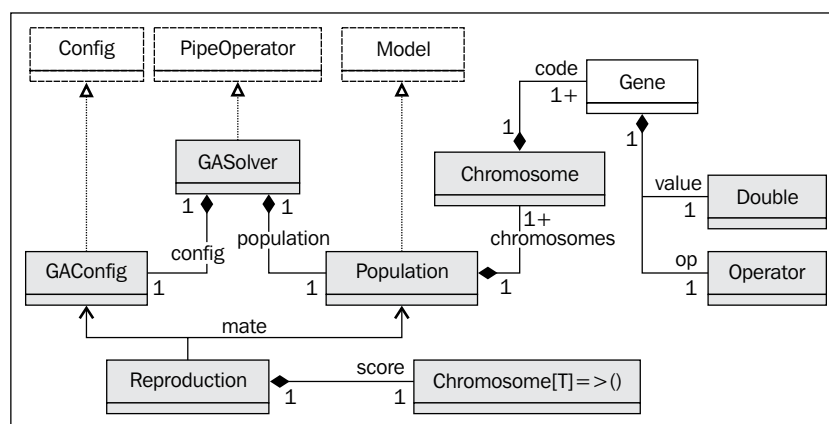
The implementation of the genetic algorithm uses a design that is similar to the template for classifiers (refer to the *Design template for classifier* section in *Appendix A, Basic Concepts*).

The key components of the implementation of the genetic algorithm are as follows:

- The `Population` class defines the current set of solution candidates or chromosomes.

- The `Gasolver` class implements the GA solver and has two components: a configuration object of the type `GAConfig` and the initial population. This class defines a data transformation by implementing the `PipeOperator` trait.
- The configuration class `GAConfig` consists of the GA execution and reproduction configuration parameters.
- The reproduction (of the type `Reproduction`) controls the reproduction cycle between consecutive generations of chromosomes through the `mate` method.

The following UML class diagram describes the relation between the different components of the genetic algorithm:



UML class diagram of genetic algorithm components

Let's start by defining the key classes that control the genetic algorithm.

Key components

The parameterized class `Population` (with the subtype `Gene`) contains the set or pool of chromosomes. A population contains chromosomes that are a sequence or list of element of the type inherited from `Gene`. A `Pool` is a mutable array in order to avoid excessive duplication of the `Chromosome` instances associated with immutable collections.

A case for mutability

It is a good Scala programming practice to stay away from mutable collections. However, in this case, the number of chromosomes can be very large. Most implementations of genetic algorithms update the population potentially three times per reproduction cycle, generating a large number of objects and taxing the Java garbage collector.

The `Population` class takes two parameters:

- `limit`: This is the maximum size of the population
- `chromosomes`: This is the pool of chromosomes defining the current population

A reproduction cycle executes the following sequence of three genetic operators on a population: `select` for selection across all the chromosomes of the population, `+-` for crossover of all the chromosomes, and `^` for the mutation of each chromosome. Consider the following code:


```
type Pool[T <: Gene] = ArrayBuffer[Chromosome[T]]
class Population[T <: Gene](limit: Int, val chromosomes: Pool[T]) {
  def select(score: Chromosome[T] => Unit, cutOff: Double)
  def +- (xOver: Double)
  def ^ (mu: Double)
  ...
}
```

The `limit` value specifies the maximum size of the population during optimization. It defines the hard limit or constraints on the population growth.

The chromosome is the second level of containment in the genotype hierarchy. The `Chromosome` class takes a list of genes as parameter (`code`). The signature of the crossover and mutation methods, `+-` and `^`, are similar to their implementation in the `Population` class except for the fact that the crossover and mutable parameters are passed as indices relative to the list of genes and each gene. The section dedicated to the genetic crossover describes the `GeneticIndices` class:

```
class Chromosome[T <: Gene](val code: List[T]) {
  var unfitness: Double = 1e+5*(1 + Random.nextDouble)
  def +- (that: Chromosome[T], idx: GeneticIndices):
  (Chromosome[T], Chromosome[T])
  def ^ (idx: GeneticIndices): Chromosome[T]
  ...
}
```

The algorithm assigns the fitting score an `unfitness` value in this implementation to enable the ranking of the population and ultimately the selection of the fittest chromosomes.

	<p>Fitness vs. unfitness</p> <p>The machine learning algorithms used the loss function or its variant as an objective function to be minimized. This implementation of the GA uses unfitness scores to be consistent with the concept of minimization of cost, loss, or penalty function.</p>	
---	--	--

Finally, the reproduction process executes the genetic operators on each gene:

```
class Gene(val id: String, val target: Double, op: Operator)(implicit
  discr: Discretization) {
  val bits: BitSet
  ...
  def +- (index: Int, that: Gene): Gene
  def ^ (index: Int): Unit
}
```

The Gene class takes four parameters:

- `id`: This is the identifier of the gene. It is usually the name of the variable represented by the gene.
- `target`: This is the target value or threshold to be converted or discretized into a bit string.
- `op`: This is the operator that is applied to the target value.
- `discr`: This is the discretization class that converts a double value to an integer to be converted into bits and vice versa.

The discretization is implemented as a case class:

```
case class Discretization(toInt: Double => Int, toDouble: Int =>
  Double) {
  def this(R: Int) =
    this((x: Double) => (x*R).floor.toInt, (n: Int) => n/R)
}
```

The first function, `toInt`, converts a real value to an integer and `toDouble` converts the integer back to a real value. The discretization and inverse functions are encapsulated into a class to reduce the risk of inconsistency between the two opposite conversion functions.

The instantiation of a gene converts the predicate representation into a bit string (bits of the type `java.util.BitSet`) using the discretization function `Discretization.toInt`. The bit string is decoded by the `decode` method of the `Gene` companion object.

The `Operator` trait defines the signature of any operator. Each domain-specific problem requires a unique set of operations: Boolean, numeric, or string manipulation:

```
trait Operator {
  def id: Int
  def apply(id: Int): Operator
}
```

The preceding operator has two methods: an identifier `id` and an `apply` method that converts an index to an operator.


Selection

The first genetic operator of the reproduction cycle is the selection process. The `select` method of the `Population` class implements the steps of the selection phase to the population of chromosomes in the most efficient manner, as follows:

```
def select(score: Chromosome[T] => Unit, cutOff: Double) = {
  val cumul = chromosomes.foldLeft(0.0)((s,x) =>{
    score(xy); s + xy.unfitness}) //1
  chromosomes foreach( _ /= cumul) //2
  val newChromosomes = chromosomes.sortWith(_.unfitness < _.unfitness)
  //3

  val cutOffSize = (cutOff*newChromosomes.size).floor.toInt //4
  val newPopSize = if(limit<cutOffSize) limit else cutOffSize //5
  chromosomes.clear //6
  chromosomes += newChromosomes.take(newPopSize) //7
}
```

The `select` method computes the cumulative sum of an unfitness value, `cumul`, for the entire population (line 1). It normalizes the unfitness of each chromosome (line 2), orders the population by decreasing value (line 3), and applies a soft limit function on population growth, `cutOff` (line 4). The next step reduces the size of the population to the lowest of the two limits: the hard limit, `limit`, or the soft limit, `cutOffSize` (line 5). Finally, the current population is cleared (line 6) and updated with the next generation (line 7).

 **Even population size**
The next phase in the reproduction cycle is the crossover, which requires the pairing of parent chromosomes. It makes sense to pad the population so that its size is an even integer.

The scoring function `score` takes a chromosome as parameter and updates its unfitness value for this chromosome.

Controlling population growth

The natural selection process controls or manages the growth of the population of species. The genetic algorithm uses two mechanisms:

- The absolute maximum size of the population (hard limit).
- The incentive to reduce the population as the optimization progresses (soft limit). This incentive (or penalty) on the population growth is defined by the `cutOff` value used during selection (the `select` method).

The `cutOff` value is computed through a user-defined function, `softLimit`, of the type `Int => Double`, provided as a configuration parameter (`softLimit(cycle: Int) => a.cycle + b`).

GA configuration

The four configurations and tuning parameters required by the genetic algorithm are:

- `xover`: This is the crossover ratio (or probability) and has a value in the interval $[0, 1]$.
- `mu`: This is the mutation ratio with a value in the interval $[0, 1]$.
- `maxCycles`: This is the maximum number of reproduction cycles.
- `softLimit`: This is the soft constraint on the population growth. The constraint function takes the number of iterations as argument and returns the maximum number of chromosomes allowed in the population.

Consider the following code:

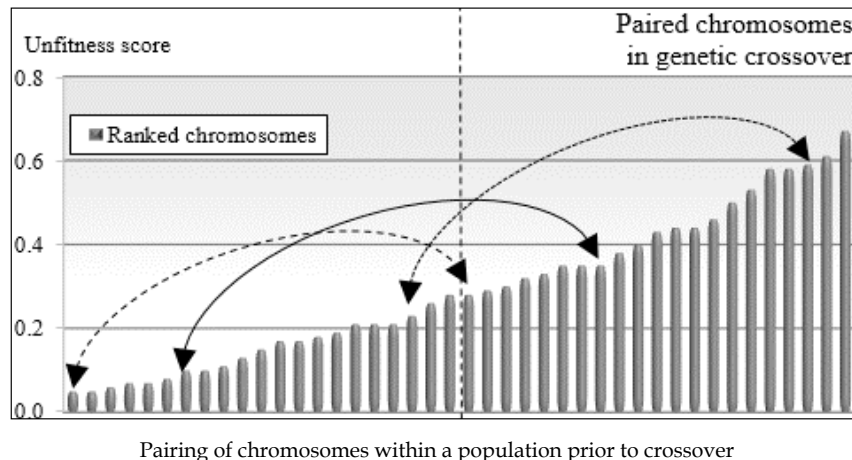
```
class GAConfig(val xover: Double, val mu: Double, val maxCycles: Int, val softLimit: Int => Double) extends Config
```

Crossover

As mentioned earlier, the genetic crossover operator couples two chromosomes to generate two offspring chromosomes that compete with all the other chromosomes in the population, including their own parents, in the selection phase of the next reproduction cycle.

Population

We use the notation `+-` as the implementation of the crossover operator in Scala. There are several options to select pairs of chromosomes for crossover. This implementation ranks the chromosomes by their fitness value and then divides the population into two halves. Finally, it pairs the chromosomes of identical rank from each half as illustrated in the following diagram:



The crossover implementation, `+-`, selects the parent chromosome candidates for crossover using the pairing scheme described earlier. Consider the following code:

```
def +- (xOver: Double): Unit = {
  if( size > 1) {
    val mid = size>>1
    val bottom = chromosomes.slice(mid, size) //1
    val gIdx = geneticIndices(xOver) //5
    val offSprings = chromosomes.take(mid)
      .zip(bottom) //2
      .map(p => p._1 +- (p._2, gIdx))
      .unzip //3
    chromosomes +=+ offSprings._1 ++ offSprings._2 //4
  }
}
```

This method splits the population into two subpopulations of equal size (line 1) and applies the Scala `zip` method (line 2) to generate the set of pairs of offspring chromosomes (line 3). The crossover operator, `+-`, is applied to each chromosome pair to produce an array of `offspring`. Finally, the crossover method adds offspring chromosomes to the existing population (line 4). The crossover value, `xOver`, is a probability randomly generated over the interval `[config.xOver, 1]`.

The `geneticIndices` method (line 5) computes the relative indices of the crossover bit in the chromosomes and genes:

```
case class GeneticIndices(val chOpIdx: Int, val geneOpIdx: Int)
def geneticIndices(prob: Double): GeneticIndices = {
  var idx = (prob*chromosomeSize).floor.toInt
  val chIdx = if(idx==0) 1
    else if(idx == chromosomeSize) chromosomeSize-1 else idx

  idx = (prob*geneSize).floor.toInt
  val gIdx = if(idx == 0) 1
    else if(idx == geneSize) geneSize-1 else idx
  GeneticIndices(chIdx, gIdx)
}
```

The `GeneticIndices` case class defines two indices of the bit whenever a crossover or a mutation occurs. The first index, `chOpIdx`, is the absolute index of the bit affected by the genetic operation in the chromosome. The second index, `geneOpIdx`, is the index of the bit within the gene subjected to crossover or mutation. The `geneticIndices` method of the `Population` class computes the two indices from a randomly generated value, `prob`, selected over the interval `[config.xover, 1]` for crossover and `[config.mu, 1]` for mutation.

Chromosomes

First, we need to define the `Chromosome` class, which takes a list of genes, code (for genetic code), as the parameter:

```
class Chromosome[T <: Gene](val code: List[T])
```

The implementation of the crossover for a pair of chromosomes using hierarchical encoding follows two steps:

- Find the gene on each chromosome that corresponds to the crossover index, `gIdx.chOpIdx`, and then swap the remaining genes
- Split and splice the gene crossover at `xoverIdx`

Consider the following code:

```
def +- (that: Chromosome[T], gIdx: GeneticIndices): (Chromosome[T],
Chromosome[T]) = {
  val xoverIdx = gIdx.chOpIdx //6
  val xGenes = spliceGene(gIdx, that.code(xoverIdx) ) //7

  val offSprng1 = code.slice(0, xoverIdx) ::: xGenes._1 :: that.code.
drop(xoverIdx+1) //8
```

```
    val offSprng2 = that.code.slice(0, xoverIdx) ::: xGenes._2 :: code.  
    drop(xoverIdx+1)  
    (Chromosome [T] (offSprng1), Chromosome [T] (offSprng2)) //9  
  }
```

The crossover method computes the index of the bit that defines the crossover (`xoverIdx`) in each parent chromosome (line 6). The genes `this.code(xoverIdx)` and `that.code(xoverIdx)` are swapped and spliced by the `spliceGene` method to generate a spliced gene (line 7).

```
  def spliceGene(gIdx: GeneticIndices, thatCode: T): (T, T) = {  
    ((this.code(gIdx.chOpIdx) +- (thatCode, gIdx)),  
     (thatCode +- (code(gIdx.chOpIdx), gIdx)) )  
  }
```

The offspring chromosomes are gathered by collating the first `xOverIdx` genes of the parent chromosome, the crossover gene, and the remaining genes of the other parent (line 8). The method returns the pair of offspring chromosomes (line 9).

Genes

The crossover is applied to a gene through the `+-` method of the `Gene` class. The exchange of bits between the two genes `this` and `that` uses the `BitSet` Java class to rearrange the bits after the permutation:

```
  def +- (that: Gene, idx: GeneticIndices): Gene = {  
    val clonedBits = cloneBits(bits) //10  
  
    Range(gIdx.geneOpIdx, bits.size).foreach(n =>  
      if( that.bits.get(n) ) clonedBits.set(n)  
      else clonedBits.clear(n)  
    ) //11  
  
    val valOp = decode(clonedBits) //12  
    Gene(id, valOp._1, valOp._2)  
  }
```

The bits of the gene are cloned (line 10) and then spliced by exchanging their bits along the crossover point `xOverIdx` (line 11). The `cloneBits` function duplicates a bit string, which is then converted into a (target value, operator) tuple using the `decode` method (line 12). We omit these two methods because they are not critical to the understanding of the algorithm.

Mutation

The mutation of the population uses the same algorithmic approach as the crossover operation.

Population

The mutation operator `^` invokes the same operator for all the chromosomes in the population and then adds the mutated chromosomes to the existing population, so that they can compete with the original chromosomes. We use the notation `^` to define the mutation operator to remind the reader that the mutation is implemented by flipping one bit:

```
def ^ (mu: Double): Unit =
  chromosomes += chromosomes.map(_ ^ geneticIndices(mu))
```

The mutation parameter `mu` is used to compute the absolute index of the mutating gene, `geneticIndices(mu)`.

Chromosomes

The implementation of the mutation operator `^` on a chromosome consists of mutating the gene of the index `gIdx.chOpIdx` (line 1) and then updating the list of genes in the chromosome (line 2). The method returns a new chromosome (line 3) that will compete with the original chromosome:

```
def ^ (gIdx: GeneticIndices): Chromosome[T] = { //1
  val mutated = code(gIdx.chOpIdx) ^ gIdx
  val xs = Range(0, code.size).map(i =>
    if(i==gIdx.chOpIdx) mutated else code(i)).toList //2
  Chromosome[T](xs) //3
}
```

Genes

Finally, the mutation operator flips (XOR) the bit at the index `gIdx.geneOpIdx`:

```
def ^ (gIdx: GeneticIndices): Gene = {
  val clonedBits = cloneBits(bits) //4
  clonedBits.flip(idx.geneOpIdx) //5

  val valOp = decode(clonedBits) //6
  Gene(id, valOp._1, valOp._2) //7
}
```


The `^` method mutates the cloned bit string, `clonedBits` (line 4) by flipping the bit at the index `gIdx.geneOpIdx` (line 5). It decodes and converts the mutated bit string by converting it into a (target value, operator) tuple (line 6). The last step creates a new gene from the target-operator tuple (line 7).

The reproduction cycle

Let's wrap the reproduction cycle into a `Reproduction` class that uses the scoring function `score`:

```
class Reproduction[T <: Gene](score: Chromosome[T] => Unit)
```

The reproduction function, `mate`, implements the sequence or workflow of the three genetic operators: `select` for the selection, `+-` (`xover`) for the crossover, and `^` (`mu`) for the mutation:

```
def mate(population: Population[T], config: GAConfig, cycle: Int): Boolean = population.size match {  
  case 0 | 1 | 2 => false  
  case _ => {  
    population.select(score, config.softLimit(cycle))  
    population +- (1.0 - Random.nextDouble*config.xover)  
    population ^ (1.0 - Random.nextDouble*config.mu)  
    true  
  }  
}
```

This method returns `true` if the size of the population is larger than 2. The last element of the puzzle is the exit condition. There are two options for estimating that the reproducing cycle is converging:

- **Greedy:** In this approach, the objective is to evaluate whether the n fittest chromosomes have not changed in the last m reproduction cycles
- **Loss function:** This approach is similar to the convergence criteria for the training of supervised learning

A simple exit condition describes the state, of the type `GAState`, of the genetic algorithm at each reproduction cycle:

```
def converge(population: Population[T], cycle: Int): GAState = {  
  if(population == null) GA_FAILED  
  else if(iters >= config.cycles)  
    GA_NO_CONVERGENCE(s"failed after $cycle cycles")  
  ...  
}
```

Let's define the state of the genetic algorithm as a case class of the super type `GASState`:

```
sealed abstract class GASState(val description: String)
case class GA_FAILED(val _description: String) extends GASState(_
description)
object GA_RUNNING extends GASState("Running")
case class GA_NO_CONVERGENCE(val _desc: String) extends GASState(_desc)
...
```

The last class `GASolver` manages the reproduction cycle and evaluates the exit condition or the convergence criteria:

```
class GASolver[T <: Gene](config: GAConfig, score: Chromosome[T]
=>Unit) extends PipeOperator[Population[T], Population[T]] {
  var state: GASState = GA_NOT_RUNNING
```

This class implements the data transformation `|>`, which transforms a population to another one, given a configuration, `config` and a scoring method, `score`, as follows:

```
def |> : PartialFunction[Population[T], Population[T]] = {
  case population: Population[T] if (population.size > 1) => {
    val reproduction = Reproduction[T](score)
    state = GA_RUNNING

    Range(0, config.maxCycles).find(n => { //1
      reproduction.mate(population, config, n) match { //2
        case true => converge(population, n) != GA_RUNNING //3
        case false => { ... }
      }
    }) match {
      case Some(n) => population
    }
  }
  ...
```

The reproduction cycle is controlled by the `find` function (line 1) that tests whether an error occurs during the reproduction, `mate` (line 2), before the convergence criteria (line 3) are applied.

GA for trading strategies


Let's apply our fresh expertise in genetic algorithms to evaluate different strategies to trade securities using trading signals. Knowledge in trading strategies is not required to understand the implementation of a GA. However, you may want to get familiar with the foundation and terminology of technical analysis of securities and financial markets, described briefly in the *Technical analysis* section in *Appendix A, Basic Concepts*.

The problem is to find the best trading strategy to predict the increase or decrease of the price of a security given a set of trading signals. A trading strategy is defined as a set of trading signals ts_j that are triggered or fired when a variable $x = \{x_j\}$, derived from financial metrics such as the price of the security or the daily or weekly trading volume, either exceeds or equals or is below a predefined target value, a_j (refer to the *Trading signals and strategy* section in *Appendix A, Basic Concepts*).

The number of variables that can be derived from price and volume can be very large. Even the most seasoned financial professionals face two challenges:

- Selecting a minimal set of trading signals that are relevant to a given data set (minimize a cost or unfitness function)
- Tuning those trading signals with heuristics derived from personal experience and expertise

Alternative to GA



The problem described earlier can certainly be solved using one of the machine learning algorithms introduced in the previous chapters. It is just a matter of defining a training set and formulating the problem as minimizing the loss function between the predictor and the training score.

The following table lists the trading classes with their counter part in the 'genetic world':

Generic classes	Corresponding securities trading classes
Operator	SOperator
Gene	Signal
Chromosome	Strategy
Population	StrategiesFactory

Definition of trading strategies

A chromosome is the genetic encoding of a trading strategy. A factory class, `StrategyFactory`, assembles the components of a trading strategy: operators, unfitness function and signals.

Trading operators

Let's extend the `Operator` trait with the `SOperator` class to define the operations we need to trigger the signals. The `SOperator` instance has a single parameter: its identifier, `_id`. The class overrides the `id()` method to retrieve the ID (similarly, the class overrides the `apply` method to convert an ID into an `SOperator` instance):

```
class SOperator(val _id: Int) extends Operator {
  override def id: Int = _id
  override def apply(idx: Int): SOperator = new SOperator(idx)
}
```

The operators used by trading signals are the logical operators: `<`, `>`, and `=`, as follows:

```
object LESS_THAN extends SOperator(1)
object GREATER_THAN extends SOperator(2)
...
```

Each operator is associated with a scoring function by the map `operatorFuncMap`. The function computes the unfitness of the signal against a real value or a time series:

```
val operatorFuncMap = Map[Operator, (Double, Double) => Double](
  LESS_THAN -> ((x: Double, target: Double) => target - x),
  GREATER_THAN -> ((x: Double, target: Double) => x - target),
  ... )
```

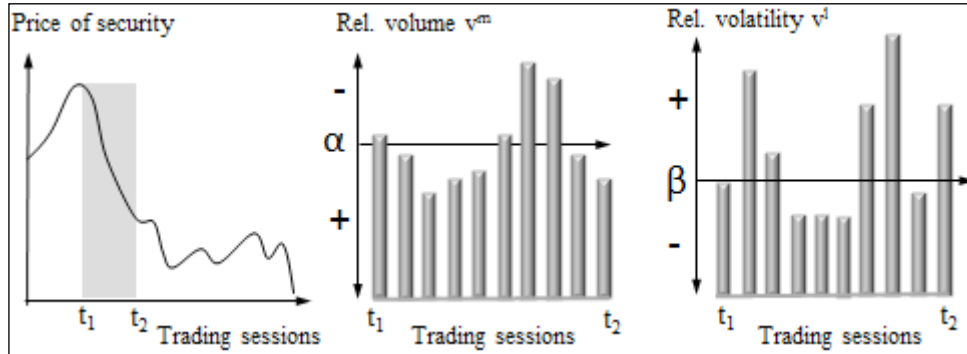
The `select` method of `Population` computes the unfitness value of a signal by quantifying the truthfulness of the predicate. For instance, the unfitness value for a trading signal, $x > 10$, is penalized as $5 - 10 = -5$ for $x = 5$ and credited as $14 - 10 = 4$ if $x = 14$. In this regard, the unfitness value is similar to the cost or loss in a discriminative machine learning algorithm.

The cost/unfitness function

Let's consider the following trading strategy defined as a set of two signals to predict the sudden relative decrease Δp of the price of a security:

- Relative volume v^m with a condition $v^m < a$
- Relative volatility v^l with the condition $v^l > \beta$

Have a look at the following graphs:



As the goal is to model a sudden crash in stock price, we should reward the trading strategies that predict the steep decrease in the stock price and penalize the strategies that work well only with a small decrease or increase in stock price. For the case of the trading strategy with two signals, relative volume v^m and relative volatility v^l , n trading sessions, the cost or unfitness function C , and given a relative variation of stock price and a penalization $w = -\Delta p$:

$$w_i = -\Delta p_i$$

$$C(p, v^m, v^l | \alpha, \beta) = \sum_{i=0}^{n-1} (\alpha - v_i^m) w_i + (v_i^l - \beta) w_i$$

Trading signals

Let's subclass the `Gene` class to define the trading signal:

```
class Signal(_id: String, _target: Double, _op: Operator, xt:
  DblVector, weights: DblVector)(implicit discr: Discretization) extends
  Gene(_id, _target, _op)
```

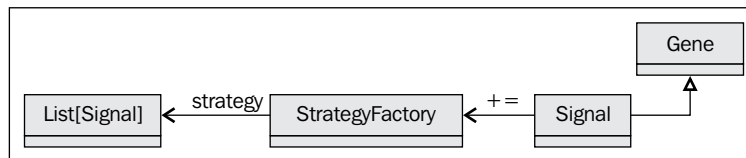
The `Signal` class takes the identifier for the feature, the target value, an operator `op`, the time series `xt` of the type `DblVector`, and the weights associated to each data point of the time series `xt`. The main purpose of the `Signal` class is to compute its score. The chromosome updates its unfitness by summing the score or weighted score of the signals it contains.

The score of the trading signal is simply the summation of the penalty or truthfulness of the signal for each entry of the time series, t_s :

```
def score: Double = sumScore(operatorFuncMap.get(op).get)
def sumScore(f: (Double, Double) => Double): Double = xt.foldLeft(0.0)
  ((s, x) => s + f(x, target))
```

Trading strategies

A trading strategy is an unordered list of trading signals. It makes sense to create a factory class to generate the trading strategies. The `StrategyFactory` class creates strategies of the type `List[Signal]` from an existing pool of signals of the subtype `Gene`:



The `StrategyFactory` class has two arguments: the number of signals, `nSignals`, in a trading strategy and the implicit discretization instance:

```

class StrategyFactory(nSignals: Int)(implicit discr: Discretization){
  val signals = new ListBuffer[Signal]
  lazy val strategies: Pool[Signal]
  ...
}
  
```

The `+=` method adds the trading signals to the factor. The `StrategyFactory` class generates all possible sequences of signals as trading strategies. The `+=` method takes five arguments: the identifier (`id`), `target`, operation (`op`) to qualify the class as a `Gene`, the times series `xt` for scoring the signals, and the `weights` associated to the overall cost function:

```

def += (id: String, target: Double, op: Operator, xt:
  XTSeries[Double], weights: DblVector): Unit =
  signals.append(Signal(id, target, op, xt.toArray, weights) )
  
```

The `StrategyFactory` class defines strategies as lazy values to avoid unnecessary regeneration of the pool on demand:

```

lazy val strategies: Pool[Signal] = {
  implicit val ordered = Signal.orderedSignals //7

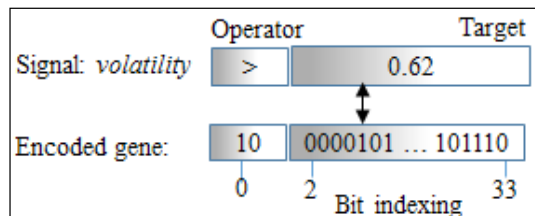
  val xss = new Pool[Signal] //1
  val treeSet = new TreeSet[Signal] += signals.toList //2
  val subsetsIterator = treeSet.subsets(nSignals) //3
  while( subsetsIterator.hasNext) { //4
    val subset = subsetsIterator.next
    val signalList: List[Signal] = subset.toList //5
    xss.append(Chromosome[Signal](signalList)) //6
  } xss
}
  
```

The implementation of the `strategies` value creates `Pool` (line 1) by converting the list of signals to a `treeSet` (line 2). It breaks down the tree set into unique subtrees of `nSignals` nodes each (line 3). It instantiates a `subsetsIterator` iterator (line 3) to traverse the sequence of subtrees (line 4) and converts them into a list (line 5) as arguments of the new chromosome (trading strategy) (line 6). The procedure to order the signals, `orderedSignals`, in the tree set has to be implicitly defined (line 7):

```
val orderedSignals = Ordering.by((signal: Signal) => signal.id)
```

Signal encoding

The encoding of trading predicates is the most critical element of the genetic algorithm. In our example, we encode a predicate as a tuple (target value, operator). Let's consider the simple predicate `volatility > 0.62`. The discretization converts the value 0.62 into 32 bits for the instance and a 2-bit representation for the operator:



Encoding price volatility as a gene

IEEE-732 encoding

The threshold value for predicates is converted into an integer (the type `Int` or `Long`). The IEEE-732 binary representation of floating point values makes the bit addressing required to apply genetic operators quite challenging. A simple conversion consists of the following:

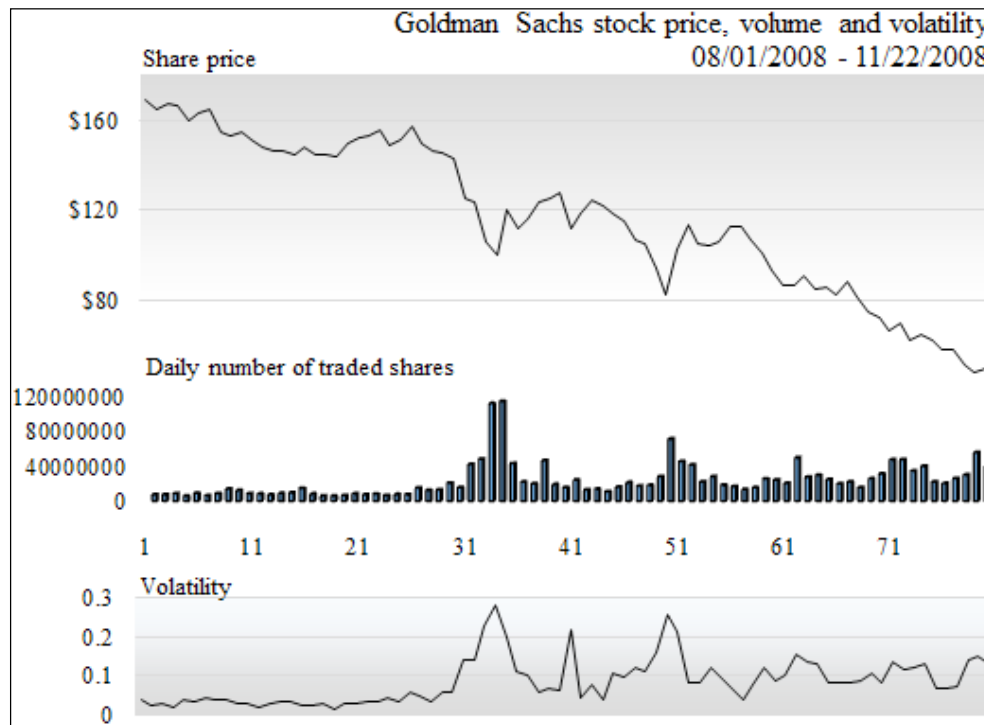
```
encoding e: (x: Double) => (x*100000).toInt
decoding d: (x: Int) => x*1e-5
```

All values are normalized; so, there is no risk of overflowing the 32-bit representation.



Test case

The goal is to evaluate which trading strategy was the most relevant (fittest) during the crash of the stock market in fall 2008. Let's consider the stock price of one of the financial institutions, Goldman Sachs, as a proxy of the sudden market decline:



Goldman-Sachs fall 2008

Besides the variation of the price of the stock between two consecutive trading sessions ($\Delta Price$), the model uses the following parameters:

- $\Delta Volume$: This is the relative variation of the volume between two consecutive trading sessions
- $\Delta Volatility$: This is the relative variation of volatility between two consecutive trading sessions
- $relVolatility$: This is the relative volatility within a trading session
- $relCloseOpen$: This is the relative difference of the stock opening and closing price

The execution of the genetic algorithm requires the following steps:

1. Extraction of model parameters or variables.
2. Generation of the initial population of trading strategies.
3. Setting up the GA configuration parameters with the maximum number of reproduction cycles allowed, the crossover and mutation ratio, and the soft limit function for population growth.
4. Instantiating the GA algorithm with the scoring/unfitness function.
5. Extracting the fittest trading strategy that can best explain the sharp decline in the price of Goldman Sachs stocks.

Data extraction

The first step is to extract the model parameters as illustrated for the variation of the stock price between two consecutive trading sessions:

```
val path = "resources/data/chap10/GS.csv"
val src = DataSource(path, false, true, 1)
val price = src |> YahooFinancials.adjClose
val deltaPrice = price.drop(1)
                    .zip(price.dropRight(1))
                    .map(p => (1.0 - p._2/p._1))
```

The extraction of relative variation in volume and volatility is similar to the extraction of the relative variation of the stock price.

Initial population

The next step consists of generating the initial population of strategies that compete to become relevant to the decline of the price of stocks of Goldman Sachs. The factory is initialized with a set of signals:

```
val NUM_SIGNALS_PER_STRATEGY = 3
val factory = new StrategyFactory(NUM_SIGNALS_PER_STRATEGY)
factory += ("Delta_volume", 1.1, GREATER_THAN, deltaVolume,
deltaPrice)
factory += ("Rel_volatility", 1.3, GREATER_THAN, relVolatility.
drop(1), deltaPrice)
...
```

The test code generates population by retrieving the pool of strategies:

```
val limit = factory.strategies.size // 1 <<4
val population = Population[Signal](limit, factory.strategies)
```

The maximum size of the population (hard limit) is arbitrarily set as 16 times the number of the initial trading strategies (line 1).

At this stage, we need to instantiate a `Discretization` instance:

```
val R=1024.0
implicit val digitize = new Discretization(R)
```

Configuration

The four configuration parameters for the GA are the maximum number of reproduction cycles (`MAX_CYCLES`) allowed in the execution, the crossover (`XOVER`), the mutation ratio (`MU`), and the soft limit function (`softLimit`) to control the population growth:

```
val XOVER = 0.2; val MU = 0.6; val MAX_CYCLES = 250
val CUTOFF_SLOPE = -0.003; val CUTOFF_INTERCEPT = 1.003

val softLimit = (n: Int) => CUTOFF_SLOPE*n + CUTOFF_INTERCEPT
val config = GAConfig(XOVER, MUTATE, MAX_NUM_ITERS, softLimit)
```

The soft limit is implemented as a linearly decreasing function of the number of cycles (`n`) to restrain the growth of the population as the execution of the genetic algorithm progresses.

GA instantiation

Let's implement the chromosome `scoring` function using the formula introduced in the cost/unfitness section. The trading strategy/chromosome scoring function sums up the score for each gene and updates it:

```
val scoring = (chr: Chromosome[Signal]) => {
  val signals: List[Gene] = chr.code
  chr.unfitness = signals.foldLeft(0.0)((s, x) => s + x.score)
}
```

The configuration `config` and the scoring function, `scoring`, are all you need to create and execute the solver `gaSolver`:

```
val gaSolver = GASolver[Signal](config, scoring)
```

GA execution

The execution of the genetic algorithm transforms an initial population to a very small group of the NFITS fittest trading strategies:

```
val NFITS = 2
val best = gaSolver |> population
best.fittest(NFITS)
  .getOrElse(ArrayBuffer.empty)
  .foreach(ch => Display.show(s"Best: ${ch.toString(" ")}", logger))
...
```

Tests

The cost function C and the unfitness score of each trading strategy are weighted for the rate of decline of the price of the Goldman Sachs stock. Let's run two tests:

- Evaluation of the genetic algorithm with an unweighted score function
- Evaluation of the configuration of the genetic algorithm with the weighted score

The unweighted score

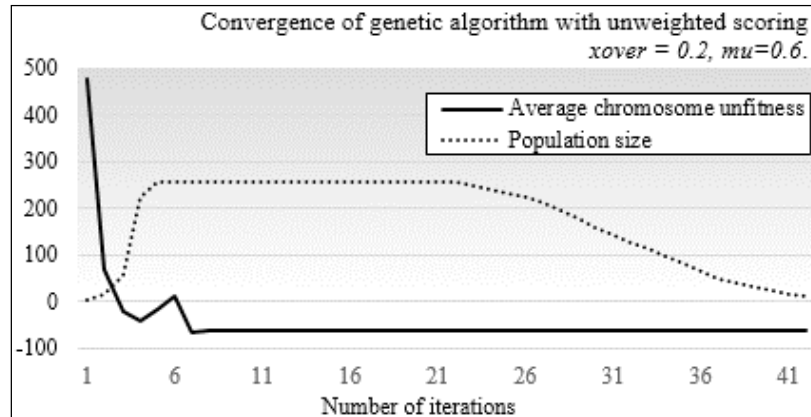
The test uses three different sets of crossover and mutation ratios: (0.6, 0.2), (0.3, 0.1), and (0.2, 0.6). The best trading strategy for each scenario are as follows:

- **0.6-0.2:** For this, $\Delta_{\text{volume}} > 1.10$, $\text{Rel_close-Open} > 0.75$, and $\text{Rel_volatility} > 0.97$ with average chromosome unfitness = 0.025
- **0.3-0.1:** For this, $\Delta_{\text{volatility}} > 0.9$, $\text{Rel_close-Open} < 0.8$, and $\text{Rel_volatility} > 1.77$ with unfitness = 0.100
- **0.2-0.6:** For this, $\Delta_{\text{volatility}} > 0.9$, $\Delta_{\text{volume}} > 33.09$, and $\text{Rel_volatility} > 1.09$ with unfitness = 0.099

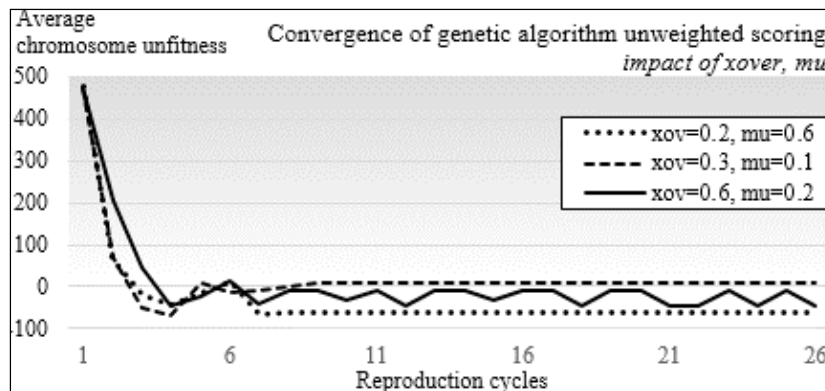
The fittest trading strategy for each case does not differ much from the initial population for one or several of the following reasons:

- The initial guess for the trading signals was good
- The size of the initial population is too small to generate genetic diversity
- The test does not take into account the rate of decline of the stock price

Let's examine the behavior of the genetic algorithm during execution. We are particularly interested in the convergence of the average chromosome unfitness score. The average chromosome unfitness is the ratio of the total unfitness score for the population over the size of the population: Have a look at the following graph:



The GA converges quite quickly and then stabilizes. The size of the population increases through crossover and mutation operations until it reaches the maximum of 256 trading strategies. The soft limit or constraint on the population size kicks in after 23 trading cycles. The test is run again with a different values of crossover and mutation ratio, as shown in the following graph:

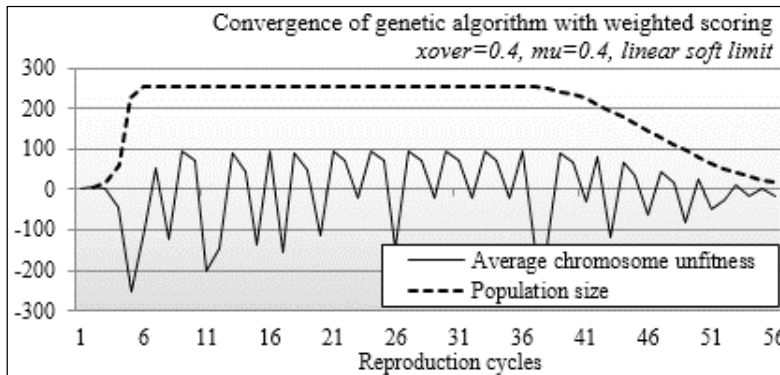


The profile of the execution of the genetic algorithm is not overly affected by the different values of crossover and mutation ratios. The chromosome unfitness score for the high crossover ratio, 0.6, oscillates as the execution progresses. In some cases, the unfitness score between chromosomes is so small that the GA recycles the same few trading strategies.

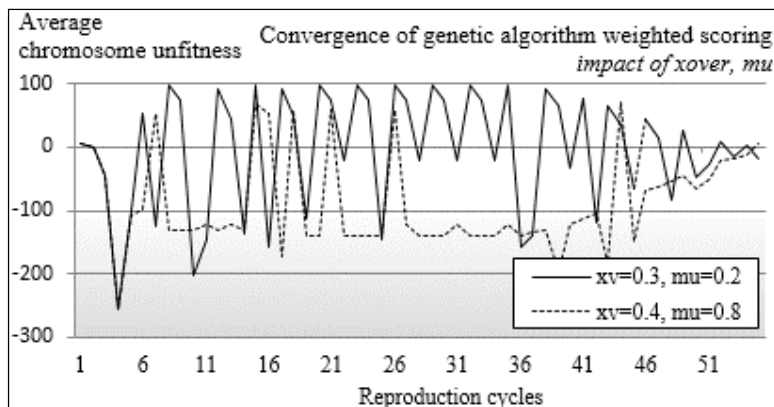
The quick decline in the unfitness of the chromosomes is consistent with the fact that some of the fittest strategies were part of the initial population. It should, however, raise some concerns that the GA locked on a local minimum early on.

The weighted score

The execution of a test that is similar to the previous one with the weighted unfitness scoring formula produces some interesting results, as shown in the following graph:



The profile for the size of the population is similar to the test using unweighted unfitness. However, the average chromosome unfitness does not stabilize as the optimization goes on until the size of the population is reduced by the soft limit function. This phenomenon is confirmed by running the test using different configurations, as shown in the following graph:



The weighting function adds the rate of decline of the stock price into the scoring of the unfitness. The formula to compute the cost/unfitness of a trading strategy is not a linear function; its complexity increases the odds of the genetic algorithm not converging properly, which is confirmed with extra runs with different values of the crossover and mutation ratios.

The possible solutions to the convergence problem are as follows:

- Make the weighting function additive (less complex)
- Increase the size and diversity of the initial population

Advantages and risks of genetic algorithms

It should be clear by now that genetic algorithms provide scientists with a powerful toolbox with which to optimize problems that:

- Are poorly understood.
- May have more than one good enough solutions.
- Have discrete, discontinuous, and non-differentiable functions.
- Can be easily integrated with the rules engine and knowledge bases (for example, learning classifiers systems).
- Do not require deep domain knowledge. The genetic algorithm generates new solution candidates through genetic operators. The initial population does not have to contain the fittest solution.
- Do not require knowledge of numerical methods such as the Newton-Raphson, conjugate gradient, or BFGS as optimization techniques, which frighten those with little inclination for mathematics.

However, evolutionary computation is not suitable for problems for which:

- A fitness function cannot be clearly defined
- Finding the global minimum or maximum is essential to the problem
- The execution time has to be predictable
- The solution has to be provided in real time or pseudo-real time

Summary

Are you hooked on evolutionary computation, genetic algorithms in particular, and their benefits, limitations as well as some of the common pitfalls? If the answer is yes, then you may find learning classifier systems, introduced in the next chapter, fascinating. This chapter dealt with the following topics:

- Key concepts in evolutionary computing
- The key components and operators of genetic operators
- The pitfalls in defining a fitness or unfitness score using a financial trading strategy as a backdrop
- The challenge of encoding predicates in the case of trading strategies
- Advantages and risks of genetic algorithms
- The process for building a genetic algorithm forecasting tool from the bottom up

The genetic algorithm is an important element of a special class of reinforcement learning introduced in the *Learning classifier systems* section of the next chapter.

11

Reinforcement Learning

This chapter presents the concept of **reinforcement learning**, which is widely used in gaming and robotics. The second part of this chapter is dedicated to **learning classifier systems**, which combine reinforcement learning techniques with evolutionary computing introduced in the previous chapter. Learning classifiers are an interesting breed of algorithms that are not commonly included in literature dedicated to machine learning. I highly recommend you to read the seminal book on reinforcement learning by R. Sutton and A. Barto [11:1] if you are interested to know about the origin, purpose, and scientific foundation of reinforcement learning.

In this chapter, you will learn the following:

- Basic concepts behind reinforcement learning
- Detailed implementation of the Q-learning algorithm
- A simple approach to manage and balance an investment portfolio using reinforcement learning
- An introduction to learning classifier systems
- A simple implementation of extended learning classifiers

The section on **learning classifier systems (LCS)** is mainly informative and does not include a test case.

Introduction

The need of an alternative to traditional learning techniques arose with the design of the first autonomous systems.

The problem

Autonomous systems are semi-independent systems that perform tasks with a high degree of autonomy. Autonomous systems touch every facet of our life, from robots and self-driving cars to drones. Autonomous devices react to the environment in which they operate. The reaction or action requires the knowledge of not only the current state of the environment but also the previous state(s).

Autonomous systems have specific characteristics that challenge traditional methodologies of machine learning, as listed here:

- Autonomous systems have poorly defined domain knowledge because of the sheer number of possible combinations of states.
- Traditional non-sequential supervised learning is not a practical option because of the following:
 - Training consumes significant computational resources, which are not always available on small autonomous devices
 - Some learning algorithms are not suitable for real-time prediction
 - The models do not capture the sequential nature of the data feed
- Sequential data models such as hidden Markov models require training sets to compute the emission and state transition matrices (as explained in the *The hidden Markov model (HMM)* section in *Chapter 7, Sequential Data Models*), which are not always available. However, a reinforcement learning algorithm benefits from a hidden Markov model in case some of the states are unknown. These algorithms are known as **behavioral hidden Markov models** [11:2].
- Genetic algorithms are an option if the search space can be constrained heuristically. However, genetic algorithms have unpredictable response time, which makes them impractical for real-time processing.

A solution – Q-learning

Reinforcement learning is an algorithmic approach to understanding and ultimately automating goal-based decision-making. Reinforcement learning is also known as control learning. It differs from both supervised and unsupervised learning techniques from the knowledge acquisition standpoint: **autonomous**, automated systems or devices learn from direct, real-time interaction with their environment. There are numerous practical applications of reinforcement learning from robotics, navigation agents, drones, adaptive process control, game playing, and online learning, to schedule and routing problems.

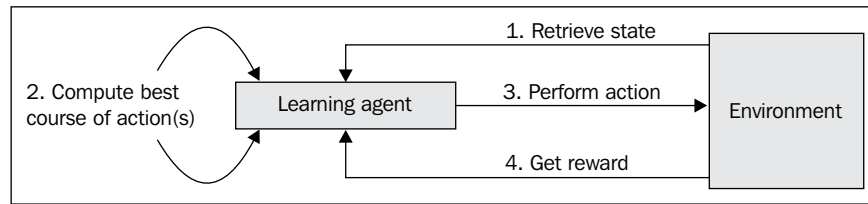
Terminology

Reinforcement learning introduces a new terminology as listed here, quite different from that of older machine learning techniques:

- **Environment:** The environment is any system that has states and mechanisms to transition between states. For example, the environment for a robot is the landscape or facility it operates in.
- **Agent:** The agent is an automated system that interacts with the environment.
- **State:** The state of the environment or system is the set of variables or features that fully describe the environment.
- **Goal or absorbing state or terminal state:** A goal state is the state that provides a higher discounted cumulative rewards than any other state. It is a constraint on the training process that prevents the best policy from being dependent on the initial state.
- **Action:** An action defines the transition between states. The agent is responsible for performing or at least recommending an action. Upon execution of the action, the agent collects a reward or punishment from the environment.
- **Policy:** The policy defines the action to be selected and executed for any state of the environment.
- **Best policy.** This is the policy generated through training. It defines the model in Q-learning and is constantly updated with any new episode.
- **Reward:** A reward quantifies the positive or negative interaction of the agent with the environment. Rewards are essentially the training set for the learning engine.
- **Episode:** This defines the number of steps necessary to reach the goal state from an initial state. Episodes are also known as trials.
- **Horizon:** The horizon is the number of future steps or actions used in the maximization of the reward. The horizon can be infinite, in which case the future rewards are discounted in order for the value of the policy to converge.

Concept


The key component in reinforcement learning is a **decision-making agent** that reacts to its environment by selecting and executing the best course of actions and being rewarded or penalized for it [11:3]. You can visualize these agents as robots navigating through an unfamiliar terrain or a maze. Robots use reinforcement learning as part of their reasoning process after all. The following diagram gives the overview architecture of the reinforcement learning agent:



The agent collects the state of the environment, selects, and then executes the most appropriate action. The environment responds to the action by changing its state and rewarding or punishing the agent for the action.

The four steps of an episode or learning cycle are as follows:

1. The learning agent either retrieves or is notified of a new state of the environment.
2. The agent evaluates and selects the action that may provide the highest reward.
3. The agent executes the action.
4. The agent collects the reward or penalty and applies it to calibrate the learning algorithm.

 **Reinforcement versus supervision**
The training process in reinforcement learning rewards features that maximize a value or return. Supervised learning rewards features that meet a predefined labeled value. Supervised learning can be regarded as forced learning.

The action of the agent modifies the state of the system, which in turn notifies the agent of the new operational condition. Although not every action will trigger a change in the state of the environment, the agent collects the reward or penalty nevertheless. At its core, the agent has to design and execute a sequence of actions to reach its goal. This sequence of actions is modeled using the ubiquitous Markov decision process (refer to the *Markov decision processes* section in *Chapter 7, Sequential Data Models*.)

Dummy actions



It is important to design the agent so that actions may not automatically trigger a new state of the environment. It is easy to think about a scenario in which the agent triggers an action just to evaluate its reward without affecting the environment significantly. A good metaphor for such a scenario is the *rollback* of the action. However, not all environments support such a *dummy* action, and the agent may have to run Monte-Carlo simulations to try out an action.

Value of policy

Reinforcement learning is particularly suited to problems for which long-term rewards can be balanced against short-term rewards. A policy enforces the trade-off between short-term and long-term rewards. It guides the behavior of the agent by mapping the state of the environment to its actions. Each policy is evaluated through a variable known as the **value of policy**.

Intuitively, the value of a policy is the sum of all the rewards collected as a result of the sequence of actions taken by the agent. In practice, an action over the policy farther in the future obviously has a lesser impact than the next action from state S_t to state S_{t+1} . In other words, the impact of future actions on the current state has to be discounted by a factor, known as the **discount coefficient for future rewards** < 1 .



State transition matrix

The state transition matrix has been introduced in the *The hidden Markov model* section in *Chapter 7, Sequential Data Models*.


The optimum policy, π^* , is the agent's sequence of actions that maximizes the future reward discounted to the current time.

The following table introduces the mathematical notation of each component of reinforcement learning:

Notation	Description
$S = \{s_i\}$	States of the environment
$A = \{a_i\}$	Actions on the environment
$\Pi_t = p(a_t s_t)$	Policy (or strategy) of the agent
$V^\pi(s_t)$	Value of the policy at the state
$p_t = p(s_{t+1} s_t a_t)$	State transition probabilities from state s_t to state s_{t+1}

Notation	Description
$r_t = p(r_{t+1} s_t, s_{t+1}, a_t)$	Reward of an action a_t for a state s_t
R_t	Expected discounted long term return
γ	Coefficient to discount the future rewards

The purpose is to compute the maximum expected reward, R_t , from any starting state, s_t , as the sum of all discounted rewards to reach the current state, s_t . The value V^π of a policy π at state s_t is the maximum expected reward R_t given the state s_t .




The value of a policy π at state s_t with reward r_j in previous state s_j :

$$R_t = \sum_{k=0}^{+\infty} \gamma^k r_{t+1+k}$$

$$V^\pi(s_t) = E\{R_t | s_t\}$$

Bellman optimality equations

The problem of finding the optimal policies is indeed a nonlinear optimization problem whose solution is iterative (dynamic programming). The expression of the value function V^π of a policy π can be formulated using the Markovian state transition probabilities p_t .



Value of state s_t using the transition probability

$$V^\pi(s_t) = \sum_{a \in A} \pi_t \sum_k \{p_k (r_k + \gamma \cdot V^\pi(s_k))\}$$

$$V^*(s_t) = \max_{\pi} V^\pi(s_t)$$

$V^*(s_t)$ is the optimal value of state s_t across all the policies. The equations are known as the Bellman optimality equations.



The curse of dimensionality

The number of states for a high-dimension problem (large-feature vector) becomes quickly insolvable. A workaround is to approximate the value function and reduce the number of states by sampling. The application test case introduces a very simple approximation function.

If the environment model, state, action, and rewards, as well as transition between states, are completely defined, the reinforcement learning technique is known as model-based learning. In this case, there is no need to explore a new sequence of actions or state transitions. Model-based learning is similar to playing a board game in which all combinations of steps necessary to win are completely known.

However, most practical applications using sequential data do not have a complete, definitive model. Learning techniques that do not depend on a fully defined and available model are known as model-free techniques. These techniques require exploration to find the best policy for any given state. The remaining sections in this chapter deal with model-free learning techniques, and more specifically the temporal difference algorithm.

Temporal difference for model-free learning

Temporal difference is a model-free learning technique that samples the environment. It is a commonly used approach to solve the Bellman equations iteratively. The absence of a model requires a discovery or **exploration** of the environment. The simplest form of exploration is to use the value of the next state and the reward defined from the action to update the value of the current state, as described in the following diagram:

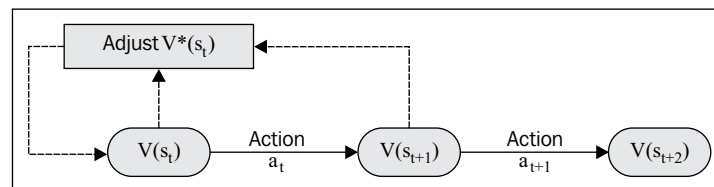



Illustration of the temporal difference algorithm

The iterative feedback loop used to adjust the value action on the state plays a role similar to back propagation of errors in artificial neural networks or minimization of the loss function in supervised learning. The adjustment algorithm has to:

- Discount the estimate value of the next state using the discount rate γ
- Strike a balance between the impacts of the current state and the next state on updating the value at time t using the learning rate α

The iterative formulation of the first Bellman equation predicts $V^\pi(s_t)$, the value function of state s_t from the value function of the next state s_{t+1} . The difference between the predicted value and the actual value is known as the temporal difference error abbreviated as δ_t .

[



Formula for tabular temporal difference:


$$\delta_t = r_{t+1} + \gamma V(s_{t+1}) - V(s_t)$$

$$\hat{V}^\pi(s_t) = V^\pi(s_t) + \alpha \delta_t$$

]

An alternative to evaluating a policy using the value of the state, $V^\pi(s_t)$, is to use the value of taking an action on a state s_t known as the value of action (or action-value) $Q^\pi(s_t, a_t)$.

[



Value of action at state s_t

$$Q_t^\pi = Q^\pi(s_t, a_t) = E(R_t | s_t, a_t)$$

]

There are two methods to implement the temporal difference algorithm:

- **On-policy:** This is the value for the next best action that uses the policy
- **Off-policy:** This is the value for the next best action that does not use the policy


Let's consider the temporal difference algorithm using an off-policy method and its most commonly used implementation: Q-learning.

Action-value iterative update

Q-learning is a model-free learning technique using an off-policy method. It optimizes the action-selection policy by learning an action-value function. Like any machine learning technique that relies on convex optimization, the Q-learning algorithm iterates through actions and states using the quality function, as described in the following mathematical formulation.

The algorithm predicts and discounts the optimum value of action, $\max\{Q_t\}$, for the current state s_t and action a_t on the environment to transition to state s_{t+1} .

Similar to genetic algorithms that reuse the population of chromosomes in the previous reproduction cycle to produce offspring, the Q-learning technique strikes a balance between the new value of the quality function Q_{t+1} and the old value Q_t using the learning rate, α . Q-learning applies temporal difference techniques to the Bellman equation for an off-policy methodology.




Q-learning action-value updating formula:

$$\hat{Q}_t^\pi = Q_t^\pi + \alpha \left[r_{t+1} + \gamma \max_{a_{t+1}} Q^\pi(s_{t+1}, a_{t+1}) \right] - Q_t^\pi$$

A value 1 for the learning rate α discards the previous state, while a value 0 discards learning. A value 1 for the discount rate γ uses long-term rewards only, while a value 0 uses the short-term reward only.

Q-learning estimates the cumulative reward discounted for future actions.



Q-learning as reinforcement learning

Q-learning qualifies as a reinforcement learning technique because it does not strictly require labeled data and training. Moreover, the Q-value does not have to be a continuous, differentiable function.

Let's apply our hard-earned knowledge of reinforcement learning to management and optimization of a portfolio of exchange-traded funds.

Implementation

Let us implement the Q-learning algorithm in Scala.

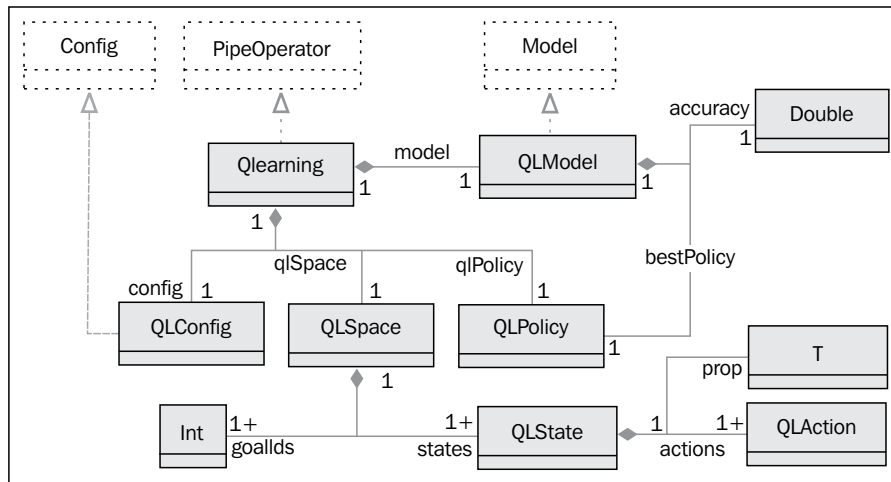
Software design

The key components of the implementation of the Q-learning algorithm are as follows:

- The `QLearning` class implements training and prediction methods. It defines a data transformation by implementing the `PipeOperator` trait. The constructor has three arguments: a configuration of type `QLConfig`, a search space of type `QLSpace`, and a mutable policy of type `QLPolicy`.

- The `QLSpace` class has two components: a sequence of states of type `QLState` and the ID of one or more goal states within the sequence.
- A state, `QLState`, contains a sequence of `QLAction` instances used in its transition to another state.
- The model of type `QLModel` is generated through training. It contains the best policy and the accuracy for a model.

The following diagram shows the flow of the Q-learning algorithm:



States and actions

The `QLAction` class specifies the transition of one state with ID `from` to another state with ID `to`, as shown here:

```
class QLAction[T <% Double] (val from: Int, val to: Int)
```

Actions have a Q value (or action-value), a reward, and a probability. The implementation defines these three values in three separate matrices: *Q* for the action values, *R* for rewards, and *P* for probabilities, in order to stay consistent with the mathematical formulation.

A state of type `QLState` is fully defined by its ID, the list of actions to transition to some other states, and a property `prop` of parameterized type, as shown in the following code:

```
class QLState [T] (val id: Int, val actions: List [QLAction [T] = List . empty, val prop: T])
```

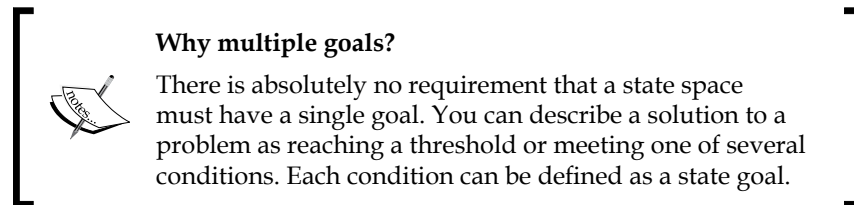
The state might not have any actions. This is usually the case of the goal or absorbing state. In this case, the list is empty. The parameterized `prop` property is a placeholder for any information, heuristic about the state, or any action performed by the state.

The next step consists of creating the graph or search space.

Search space

The search space is the container responsible for any sequence of states. The `QLSpace` class takes the following parameters:

- The sequence of all the possible `states`
- The ID of one or several states that have been selected as `goals`



The `QLSpace` class can be implemented as follows:

```
class QLSpace[T] (states: Seq[QLState[T]], goals: Array[Int]) {
  val statesMap = states.map(st => (st.id, st)).toMap //1
  val goalStates = new HashSet[Int]() ++ goals //2

  def maxQ(state: QLState[T], policy: QLPolicy[T]): Double //3
  def init(r: Random) = states(r.nextInt(states.size-1)) //4
  def nextStates(st: QLState[T]): List[QLState[T]] //5
  ...
}
```

The instantiation of the `QLSpace` class generates a map, `statesMap`, to retrieve the state using its `id` (line 1) and the set of goals, `goalStates` (line 2). Furthermore, the `maxQ` method computes the maximum action-value, `maxQ`, for a state given a policy (line 3), the `init` method selects an initial state for training episodes (line 4), and finally, the `nextStates` method retrieves the list of states resulting from the execution of all the actions associated to the `st` state (line 5).


The search space is actually created by the instance factory defined in the `QLSpace` companion object, as shown here:

```
def apply[T](numStates: Int, goals: Array[Int], features: Set[T],
neighbors: (Int, Int) => List[Int]): QLSpace[T] = {
  val states = features
    .zipWithIndex
    .map(x => {
      val actions = neighbors(x._2, numStates)
        .map(j => QLAction[T](x._2, j))
        .filter(x._2 != _.to)
      QLState[T](x._2, actions, x._1)
    })
  new QLSpace[T](states.toArray, goals)
}
```

The `apply` method creates a list of states using the `features` set as input. Each state creates its list of actions. The user-defined function, `neighbors`, constrains the number of actions assigned to each state. The test case describes a very simple implementation of the `neighbors` function, which is defined in the configuration.

Policy and action-value

Each action has an action-value, a reward, and a potentially probability. The probability variable is introduced to model simply the hindrance or adverse condition for an action to be executed. If the action does not have any external constraint, the probability is 1. If the action is not allowed, the probability is 0.



Dissociating policy from states

The action and states are the edges and vertices of the search space or search graph. The policy defined by the action-value, rewards, and probabilities is completely dissociated from the graph. The Q-learning algorithm initializes the reward matrix and updates the action-value matrix independently of the structure of the graph.

The `QLData` class is a container for three variables: reward, probability, and value for the Q-value, as shown here:

```
class QLData(var reward: Double = 1.0, var probability: Double = 1.0
var value: Double = 0.0) {
  def estimate: Double = value*probability
}
```

The `estimate` method adjusts the Q-value, `value`, with the probability to reflect any external condition that can impede the action.



Mutable data

You might wonder why the `QLData` class uses variables instead of values as recommended by the best Scala coding practices [11:4]. An instance of an immutable class would be created for each action or state transition. The training of the Q-learning model entails iterating across several episodes, each episode being defined as a multiple iteration. For instance, the training of a model with 400 states for 10 episodes of 100 iterations can potentially create 160 million instances of `QLData`. Although not quite elegant, mutability reduces the load on the JVM garbage collector.

Next, let us create a simple schema or class, `QLInput`, to initialize the reward and probability associated with each action as follows:

```
class QLInput(val from: Int, val to: Int, val reward: Double =1.0, val
probability: Double =1.0)
```

The first two arguments are the identifiers for the source state, `from`, and target state, `to`, for this specific action. The last two arguments are the `reward`, collected at the completion of the action, and its `probability`. There is no need to provide an entire matrix. Actions have a reward of 1 and a probability of 1 by default. You only need to create an input for actions that have either a higher reward or a lower probability.

The number of states and a sequence of input define the policy of type `QLPolicy`. It is merely a data container, as shown here:

```
class QLPolicy[T](numStates: Int, input: Array[QLInput]) {
  val qlData = {
    val data = Array.tabulate(numStates)(v =>
      Array.fill(numStates)(new QLData[T]))
    input.foreach(i => {
      data(i.from)(i.to).reward = i.reward //1
      data(i.from)(i.to).probability = i.probability //2
    })
    data
  }
  ...
}
```

The constructor initializes the `qlData` matrix of type `QLData` with the input data, reward (line 1) and probability (line 2). The `QLPolicy` class defines the methods of the element in the reward (line 3), probability, and Q-learning action-value (line 4) matrices as follows:

```
def R(from: Int, to: Int): Double = qlData(from)(to).reward //3
def Q(from: Int, to: Int): Double = qlData(from)(to).value //4
```

The Q-learning training

The `QLearning` class encapsulates the Q-learning algorithm, and more specifically the action-value updating equation. It implements `PipeOperator` to the prediction used as a transformation between states, as shown here:

```
class QLearning[T](config: QLConfig, qlSpace: QLSpace[T], qlPolicy:
  QLPolicy[T]) extends PipeOperator[QLState[T], QLState[T]]
```

The constructor takes the following parameters:

- Configuration of the algorithm, `config`
- Search space, `qlSpace`
- Policy, `qlPolicy`

The model is generated or trained during the instantiation of the class (refer to the *Design template for classifier* section in *Appendix A, Basic Concepts*.)

The configuration defines the learning rate, `alpha`; the discount rate, `gamma` the maximum number of states (or length) of an episode, `episodeLength`; the number of episodes used in training, `numEpisodes`; the minimum coverage of the state transition/actions during training to select the best policy, `minCoverage`; and the search constraint function, `neighbors`, as shown here:

```
class QLConfig(val alpha: Double, val gamma: Double, val
  episodeLength: Int, val numEpisodes: Int, val minCoverage: Double, val
  neighbors: (Int, Int) => List[Int]) extends Config
```

Let us look at the computation of the best policy during training. First, we need to define a model class, `QLModel`, with the best policy and its state-transition coverage of training as parameters:


```
class QLModel[T](val bestPolicy: QLPolicy[T], val coverage: Double)
```

The creation of `model` consists of executing multiple episodes to extract the best policy. Each episode starts with a randomly selected state, as shown in the following code:

```
val model: Option[QLModel[T]] = {
  val r = new Random(System.currentTimeMillis) //1
  val rg = Range(0, config.numEpisodes)
  val cnt =rg.foldLeft(0)((s, _) => s+(if(train(r)) 1 else 0))//2

  val accuracy = cnt.toDouble/config.numEpisodes
  if( accuracy > config.minCoverage )
    Some(new QLModel[T](qlPolicy, coverage)) //3
  else None
}
```

The model initialization code creates a random number generator (line 1), and iterates the generation of the best policy starting from a randomly selected state `config.numEpisodes` times (line 2). The transition coverage is computed as the percentage of times the search ends with the goal state (line 3). The initialization succeeds only if the accuracy exceeds a threshold value, `config.minCoverage`, specified in the configuration.



Quality of the model

The implementation uses the coverage to measure the quality of the model or best policy. The F1 measure (refer to the *Assessing a model* section in *Chapter 2, Hello World!*), is not appropriate because there are no false positives.

The `train` method does the heavy lifting at each episode. It triggers the search by selecting the initial state using a random generator `r` with a new seed, as shown in the following code:

```
def train(r: Random): Boolean = {
  r.setSeed(System.currentTimeMillis*Random.nextInt)
  qlSpace.isGoal(search((qlSpace.init(r), 0))._1)
}
```

The implementation of `search` for the goal state(s) from any random states is a textbook implementation of the Scala tail recursion.

Tail recursion to the rescue

Tail recursion is a very effective construct to apply an operation to every item of a collection [11:5]. It optimizes the management of the function stack frame during the recursion. The annotation triggers a validation of the condition necessary for the compiler to optimize the function calls, as shown here:

```
@scala.annotation.tailrec
def search(st: (QLState[T], Int)): (QLState[T], Int) = {
  val states = qlSpace.nextStates(st._1) //1

  if( states.isEmpty || st._2 >= config.episodeLength ) st //2
  else {
    val state = states.maxBy(s => qlPolicy.R(st._1.id,s.id ))//3

    if( qlSpace.isGoal(state) ) (state, st._2) //4
    else {
      val r = qlPolicy.R(st._1.id, state.id)
      val q = qlPolicy.Q(st._1.id, state) //5
      val nq = q + config.alpha*(r + config.gamma *
        qlSpace.maxQ(state, qlPolicy) - q)//6
      qlPolicy.setQ(st._1.id, state.id, nq) //7
      search((state, st._2))
    }
  }
}
```

Let us dive into the implementation for the Q action-value updating equation. The recursion uses the tuple (state, iteration number in the episode) as argument. First, the recursion invokes the `nextStates` method of `QLSpace` to retrieve all the states associated with the current state, `st`, through its `actions`, as shown here:

```
def nextStates(st: QLState[T]): List[QLState[T]] =
  st.actions.map(ac => statesMap.get(ac.to).get )
```

The search completes and returns the current state if either the length of the episode (maximum number of states visited) is reached or the goal is reached or there is no further state to transition to (line 2). Otherwise the recursion computes the state to which the transition generates the higher reward R from the current policy (line 3). The recursion returns the state with the highest reward if it is one of the goal states (line 4). The method retrieves the current q action value and r reward matrices from the policy, and then applies the equation to update the action-value (line 6). The method updates the action-value Q with the new value nq (line 7).

The action-value updating equation requires the computation of the maximum action-value associated with the current state, which is performed by the `maxQ` method of the `QLSpace` class:

```
def maxQ(state: QLState[T], policy: QLPolicy[T]): Double = {
  val best = states.filter(_ != state)
    .maxBy(st => policy.EQ(state.id, st.id))
  policy.EQ(state.id, best.id)
}
```

Reachable goal



The algorithm does not require the goal state to be reached for every episode. After all, there is no guarantee that the goal will be reached from any randomly selected state. It is a constraint on the algorithm to follow a positive gradient of the rewards when transitioning between states within an episode. The goal of the training is to compute the best possible policy or sequence of states from any given initial state. You are responsible for validating the model or best policy extracted from the training set, independent from the fact that the goal state is reached for every episode.

Prediction

The last functionality of the `QLearning` class is the prediction using the model created during training. The method predicts a state from an existing state.

```
def |> : PartialFunction[QLState[T], QLState[T]] = {
  case state: QLState[T] if (state != null && model != None)
    => nextState(state, 0)._1
}
```

The data transformation `|>` computes the best outcome, `nextState`, given a state using another tail recursion, as follows:

```
@scala.annotation.tailrec
def nextState(st: (QLState[T], Int)): (QLState[T], Int) = {
  val states = qlSpace.nextStates(st._1)

  if (states.isEmpty || st._2 >= config.episodeLength) st
  else nextState( (states.maxBy(s =>
    model.get.bestPolicy.R(st._1.id, s.id)), st._2+1))
}
```

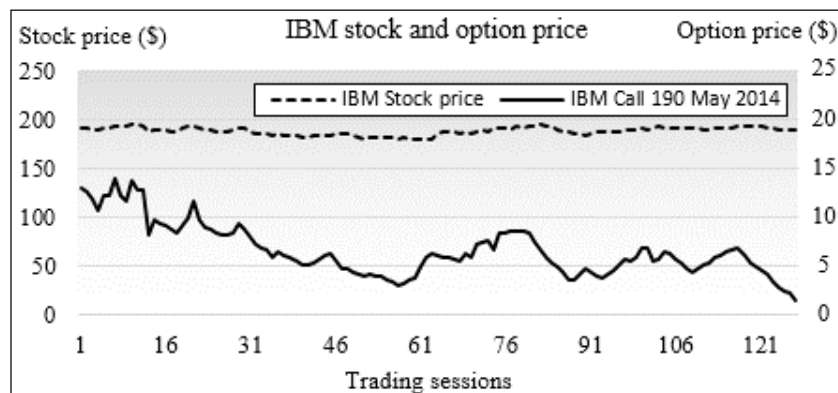

The prediction ends when no more states are available or the maximum number of iterations within the episode is exceeded. You can define a more sophisticated exit condition. The challenge is that there is no explicit error or loss variable/function that can be used except the temporal difference error. The prediction returns either the best possible state, or `None` if the model cannot be created during training.

Option trading using Q-learning

The Q-learning algorithm is used in many financial and market trading applications [11:6]. Let us consider the problem of computing the best strategy to trade certain types of options given some market conditions and trading data.

The **Chicago Board Options Exchange (CBOE)** offers an excellent online tutorial on options [11:7]. An option is a contract giving the buyer the right but not the obligation to buy or sell an underlying asset at a specific price on or before a certain date (refer to the *Options trading* section under *Finances 101* in *Appendix A, Basic Concepts*.) There are several option pricing models, the Black-Scholes stochastic partial differential equations being the most recognized [11:8].

The purpose of the exercise is to predict the price of an option on a security for N days in the future according to the current set of observed features derived from the time to expiration, price of the security, and volatility. Let's focus on the call options of a given security, IBM. The following chart plots the daily price of IBM stock and its derivative call option for May 2014 with a strike price of \$190:



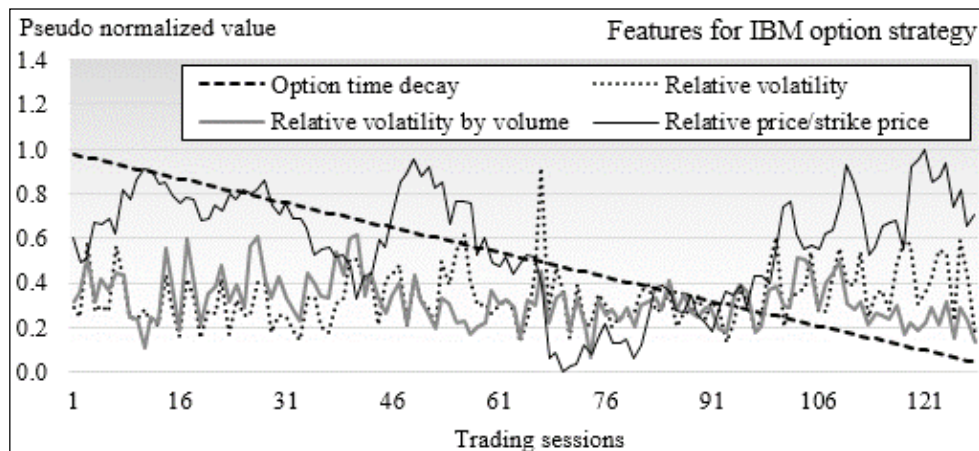
The price of an option depends on the following parameters:

- Time to expiration of the option (time decay)
- The price of the underlying security
- The volatility of returns of the underlying asset

Pricing model usually does not take into account the variation in trading volume of the underlying security. So it would be quite interesting to include it in our model. Let us define the state of an option using the following four normalized features:

- **Time decay:** This is the time to expiration once normalized over $[0, 1]$.
- **Relative volatility:** This is the relative variation of the price of the underlying security within a trading session. It is different from the more complex volatility of returns defined in the Black-Scholes model, for example.
- **Volatility relative to volume:** This is the relative volatility of the price of the security adjusted for its trading volume.
- **Relative difference between the current price and strike price:** This measures the ratio of the difference between price and strike price to the strike price.

The following graph shows the four normalized features for IBM option strategy:



The implementation of the option trading strategy using Q-learning consists of the following steps:

1. Describing the property of an option
2. Defining the function approximation
3. Specifying the constraints on the state transition

Option property

Let us select $N=2$ as the number of days in the future for our prediction. Any longer-term prediction is quite unreliable because it falls outside the constraint of the discrete Markov model. Therefore, the price of the option two days in the future is the value of the reward – profit or loss.

The `OptionProperty` class encapsulates the four attributes of an option as follows:

```
class OptionProperty(timeToExp: Double, relVolatility: Double,
  volatilityByVol: Double, relPriceToStrike: Double) {
  val toArray = Array[Double](timeToExp, relVolatility,
    volatilityByVol, relPriceToStrike)
}
```



Modular design

The implementation avoids subclassing the `QLState` class to define the features of our option pricing model. The state of the option is a parameterized `prop` parameter for the state class.

Option model

The `OptionModel` class is a container and a factory for the properties of the option. It creates the list of option properties, `propsList`, by accessing the data source of the four features introduced earlier. It takes the following parameters:

- The symbol of the security.
- The strike price for the option, `strikePrice`.
- The source of data, `src`.
- The minimum time decay or time to expiration, `minTDecay`. Out-of-the-money options expire worthless and in-the-money options have very different price behavior as they get closer to the expiration date (refer to the *Options trading* section in *Appendix A, Basic Concepts*). Therefore, the last `minTDecay` trading sessions prior to the expiration date are not used in the training of the model.
- The number of steps (or buckets), `nSteps`, used in approximating the values of each feature. For instance, an approximation of four steps creates four buckets `[0, 25]`, `[25, 50]`, `[50, 75]`, and `[75, 100]`.

The implementation of the `OptionModel` class is as follows:

```
class OptionModel(symbol: String, strikePrice: Double, src:
  DataSource, minExpT: Int, nSteps: Int) {

  val propsList = {
    val volatility = normalize((src |> relVolatility).get.toArray
    val rVolByVol = normalize((src |> volatilityByVol).get.toArray
    val priceToStrike = normalize(price.map(p => 1.0-strikePrice/p)

    volatility.zipWithIndex //1
      .foldLeft(List[OptionProperty]())((xs, e) => {
```

```

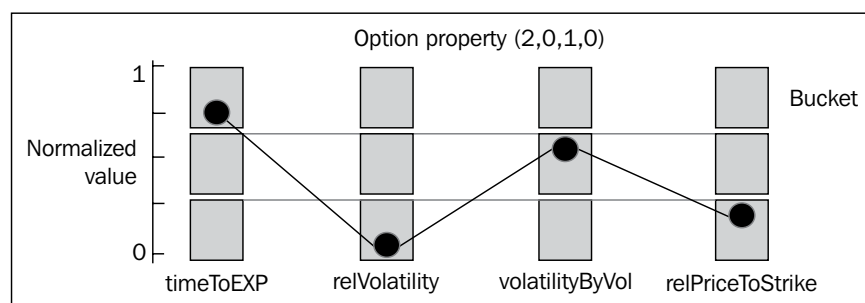
    val normDecay = (e._2+minExpT).toDouble/(price.size+minExpT) //2
    new OptionProperty(normDecay, e._1, volByVol(e._2),priceToStrik
e(e._2)) :: xs
  }).drop(2).reverse
}

```

The factory uses the `zipWithIndex` Scala method to model the index of the trading sessions (line 1). All feature values are normalized over the interval $[0, 1]$, including the time decay (or time to expiration) of the `normDecay` option (line 2).

Function approximation

The four properties of the option are continuous values, normalized as a probability $[0, 1]$. The states in the Q-learning algorithm are discrete and require a discretization or categorization known as a **function approximation**, although a function approximation scheme can be quite elaborate [11:9]. Let us settle for a simple linear categorization as illustrated in the following diagram:



The function approximation defines the number of states. In this example, a function approximation that converts a normalized value into three intervals or buckets generates $3^4 = 81$ states or potentially $3^8 - 3^4 = 6480$ actions! The maximum number of states for l buckets function approximation and n features is l^n with a maximum number of $l^{2n} - l^n$ actions.

Function approximation guidelines

The design of the function to approximate the state of options has to address the following two conflicting requirements:

- Accuracy demands a fine-grained approximation
- Limited computation resources restrict the number of states, and therefore, level of approximation

The `approximate` method of the `OptionModel` class converts the normalized value of each option property of features into an array of bucket indices. It returns a map of profit and loss for each bucket keyed on the array of bucket indices, as shown in the following code:

```
def approximate(y: DblVector): Map[Array[Int], Double] = {
  val mapper = new HashMap[Int, Array[Int]] //1

  val acc = new NumericAccumulator //2
  propsList.map( _.toArray)
    .map( toArrayInt( _ )) //3
    .map(ar => {
      val enc = encode(ar) //4
      mapper.put(enc, ar)
      enc })
    .zip(y)
    .foldLeft(acc)((acc,t) => {acc += (t._1,t._2);acc})//5
  acc.map(kv => (kv._1, kv._2._2/kv._2._1)) //6
    .map(kv => (mapper(kv._1), kv._2)).toMap
}
```

The method creates a `mapper` instance to index the array of buckets (line 1). An accumulator, `acc`, of type `NumericAccumulator` extends `Map[Int, (Int, Double)]` and computes the tuple (number of occurrences of features on each buckets, the sum of increase or decrease of the option price) (line 2). The `toArrayInt` method converts the value of each option property (`timeToExp`, `relVolatility`, and so on) into the index of the appropriate bucket (line 3). The array of indices is then encoded (line 4) to generate the `id` or index of a state. The method updates the accumulator with the number of occurrences and the total profit and loss for a trading session for the option (line 5). It finally computes the reward on each action by averaging the profit and loss on each bucket (line 6).

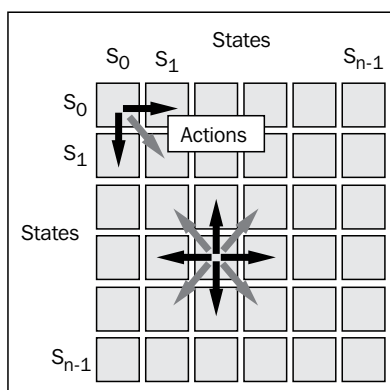
```
def toArrayInt(feature: DblVector): Array[Int] =
  feature.map(x => (nSteps*x).floor.toInt)
```

Constrained state-transition

Each state is potentially connected to any other state through actions. There are two methodologies to reduce search space or number of actions/transitions:

- Static constraint defines the actions/transition when the model is instantiated. The state transition map is fixed for the entire life cycle of the model.

- Dynamic constraint relies on the probability of an action to prevent or hinder state transitions.



The implementation of the static constraint avoids the unnecessary creation of a large number of `QLAction` object at the expense of the inability to modify the search space during training. The test case uses the static constraint as defined in the `neighbors` function passed as a parameter of the `QLSpace` class:

```
val RADIUS = 4
val neighbors = (idx: Int, numStates: Int) => {

  def getProximity(idx: Int, radius: Int): List[Int] = {
    val idx_max = if(idx + radius >= numStates) numStates-1 else idx+
radius
    val idx_min = if(idx < radius) 0 else idx - radius
    Range(idx_min, idx_max+1).filter(_ != idx)
      .foldLeft(List[Int]())((xs, n) => n :: xs)
  }
  getProximity(idx, RADIUS).toList
}
```

The `neighbors` function restrains the number of actions to up to `RADIUS*2` states, depending on the ID, `idx`, of the state. The function is implemented as a closure: it requires the value `numStates` to be defined within the function or in its outer scope.

Putting it all together

The final piece of the puzzle is the code that configures and executes the Q-learning algorithm on one or several options on a security, IBM:

```
val stockPricePath = "resources/data/chap11/IBM.csv"
val optionPricePath = "resources/data/chap11/IBM_O.csv"
```

```
val MIN_TIME_EXP = 6; val APPROX_STEP = 3; val NUM_FEATURES = 4
val ALPHA = 0.4; val DISCOUNT = 0.6; val NUM_EPISODES = 202520

val src = DataSource(stockPricePath, false, false, 1) //1
val ibmOption = new OptionModel("IBM", 190.0, src, MIN_TIME_EXP,
APPROX_STEP) //2

DataSource(optionPricePath, false, false, 1) extract match {
case Some(v) => initializeModel (ibmOption, v)
...
}
```

The client code instantiates the option model, `ibmOption`, for the IBM stock (line 1). It invokes the `initializeModel` method once the historical price of the option is downloaded through the appropriate data source (line 2). The `initializeModel` method does all the work as shown in the following code:

```
def initializeModel(ibmOption: OptionModel, oPrice: DblVector):
QLearning[Array[Int]] {
  val fMap = ibmOption.approximate(oPrice) //3
  val input = new ArrayBuffer[QLInput]

  val profits = fMap.values.zipWithIndex
  profits.foreach(v1 =>
    profits.foreach( v2 =>
      input.append(new QLInput(v1._2, v2._2, v2._1-v1._1))))//4

  val goal = input.maxBy( _.reward).to
  val config = new QLConfig(ALPHA, DISCOUNT, EPISODE_LEN, NUM_
EPISODES, MIN_ACCURACY, getNeighbors)
  QLearning[Array[Int]](config, fMap , goal, input.toArray, fMap.
keySet)
}
```

The `initializeModel` method generates the approximation map, `fMap` (line 3), which contains the profit and loss for each state. Next, the method initializes the input to the policy by computing the reward as the difference of the profit/loss of the source `v1` and the destination `v2` of each action (line 4). The goal is initialized as the action with the highest reward (line 5). The last step is the instantiation of the `QLearning` class that executes the training.



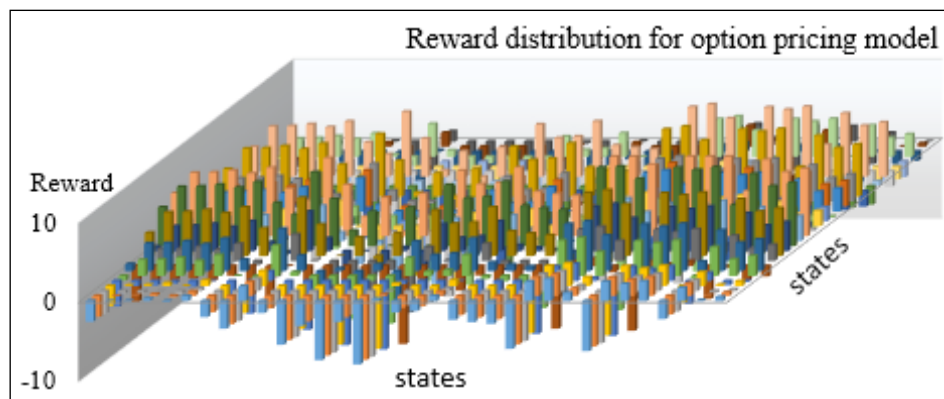
The anti-goal state

The goal state is the state with the highest assigned reward. It is a heuristic to reward a strategy for good performance. However, it is conceivable and possible to define an anti-goal state with the highest assigned penalty or the lowest assigned reward to guide the search away from some condition.

Evaluation

Besides the function approximation, the size of the training set has an impact on the number of states. A well-distributed or large training set provides at least one value for each bucket created by the approximation. In this case, the training set is quite small and only 34 out of 81 buckets have actual values. As result, the number of states is 34.

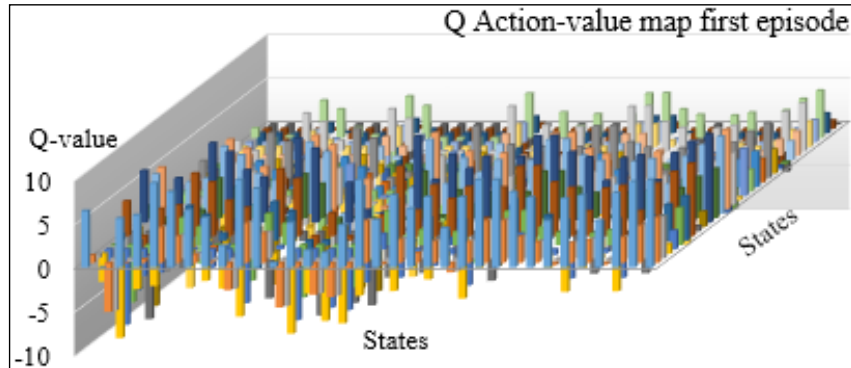
The initialization of the Q-learning model generates the following reward matrix:



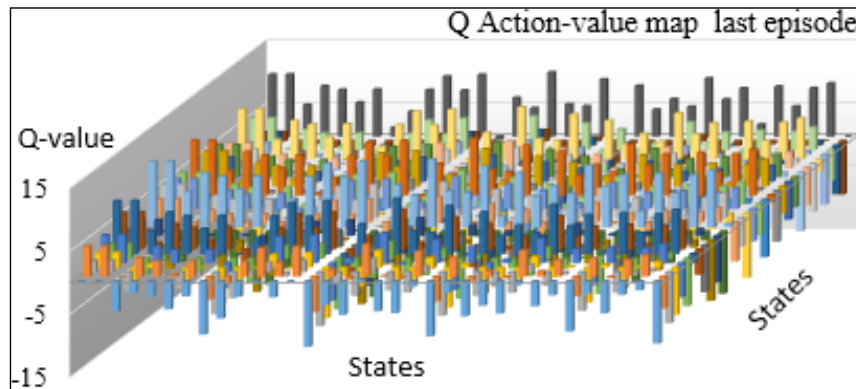
The graph visualizes the distribution of the rewards computed from the profit and loss of the option. The xy plane represents the actions between states. The states' IDs are listed on x and y axes. The z -axis measures the actual value of the reward associated with each action.

The reward reflects the fluctuation in the price of the option. The price of an option has a higher volatility than the price of the underlying security.

The xy reward matrix R is rather highly distributed. Therefore, we select a small value for the learning rate, 0.4, to reduce the impact of the previous state on the new state. The value for the discount rate, 0.6, accommodates the fact that the number of states is limited. There is no reason to compute the future discounted reward using a long sequence of states. The training of the policies generates the following action-value matrix Q of 34 states by 34 states after the first episode:



The distribution of the action-values between states at the end of the first episode reflects the distribution of the reward across state-to-state action. The first episode consists of a sequence of nine states from an initial randomly selected state to the goal state. The action-value map is compared with the map generated after 20 episodes in the following graph:



The action-value map at the end of the last episode shows some clear patterns. Most of the rewarding actions transition from a large number of states (X-axis) to a smaller number of states (Y-axis). The chart illustrates the following issues with the small training sample:

- The small size of the training set forces us to use an approximate representation of each feature. The purpose is to increase the odds that most buckets have at least one data point.
- However, a loose function approximation tends to group quite different states into the same bucket.
- The bucket with a very low number can potentially mischaracterize one property or feature of a state.

Pros and cons of reinforcement learning

Reinforcement learning algorithms are ideal for the following problems:

- Online learning
- The training data is small or non-existent
- A model is non-existent or poorly defined
- Computation resources are limited

However, these techniques perform poorly in the following cases:

- The search space (number of possible actions) is large causing the maintenance of the states, action graph, and rewards matrix become challenging
- The execution is not always predictable in terms of scalability and performance

Learning classifier systems

J. Holland introduced the concept of **learning classifier systems** (LCS) more than 30 years ago as an extension to evolutionary computing [11:10]:

Learning classifier systems are a kind of rule-based system with general mechanisms for processing rules in parallel, for adaptive generation of new rules, and for testing the effectiveness of new rules.

However, the concept started to get the attention of computer scientists only a few years ago, with the introduction of several variants of the original concept, including **extended learning classifier systems** (XCS). Learning classifier systems are interesting because they combine rules, reinforcement learning, and genetic algorithms.



Disclaimer

The implementation of the extended learning classifier is presented for informational purposes only. Validating XCS against a known and labeled population of rules is a very significant endeavor. The source code snippet is presented only to illustrate the different components of the XCS algorithm.

Introduction to LCS

Learning classifier systems merge the concepts of reinforcement learning, rule-based policies, and evolutionary computing. This unique class of learning algorithms represents the merger of the following research fields [11:11]:

- Reinforcement learning
- Genetic algorithms and evolutionary computing
- Supervised learning
- Rule-based knowledge encoding

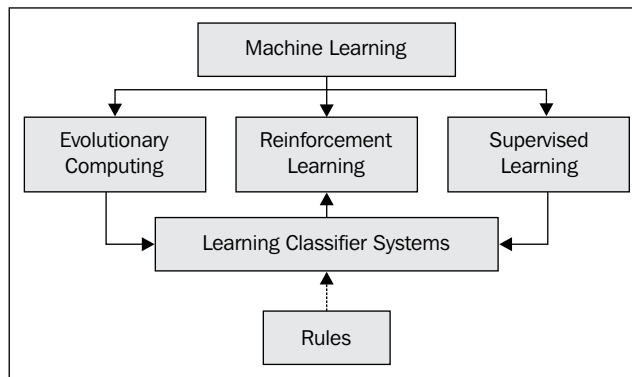


Diagram of the scientific disciplines required for learning classifier systems

Learning classifier systems are an example of **complex adaptive systems**. A learning classifier system has the following four components:

- A population of classifiers or rules that evolves over time. In some cases, a domain expert creates a primitive set of rules (core knowledge). In other cases, the rules are randomly generated prior to the execution of the learning classifier system.

- A genetic algorithm-based discovery engine that generates new classifiers or rules from the existing population. This component is also known as the **rules discovery module**. The rules rely on the same pattern of evolution of organisms introduced in the previous chapter. The rules are encoded as strings or bit strings to represent a condition (predicate) and action.
- A performance or evaluation function that measures the positive or negative impact of the actions from the fittest classifiers or policies.
- A reinforcement learning component that rewards or punishes the classifiers that contribute to the action, as seen in the previous section. The rules that contribute to an action that improves the performance of the system are rewarded, while those that degrade the performance of the system are punished. This component is also known as the credit assignment module.

Why LCS

Learning classifier systems are particularly appropriate to problems in which the environment is constantly changing, and are the combination of learning strategy and an evolutionary approach to build and maintain a knowledge base [11:12].

Supervised learning methods alone can be effective on large datasets, but they require either a significant amount of labeled data or a reduced set of features to avoid overfitting. Such constraints may not be practical in the case of ever-changing environments.

The last 20 years have seen the introduction of many variants of learning classifier systems that belong to the following two categories:

- Systems for which accuracy is computed from the correct predictions and that apply the discovery to a subset of those correct classes. They incorporate elements of supervised learning to constrain the population of classifiers. These systems are known to follow the **Pittsburgh approach**.
- Systems that explore all the classifiers and apply rule accuracy in the genetic selection of the rules. Each individual classifier is a rule. These systems are known to follow the **Michigan approach**.

The rest of this section is dedicated to the second type of learning classifiers – more specifically extended learning classifier systems. In a context of LCS, the term **classifier** refers to the predicate or rule generated by the system. From this point on, the term "rule" replaces the term classifier to avoid confusion with the more common definition of classification.

Terminology

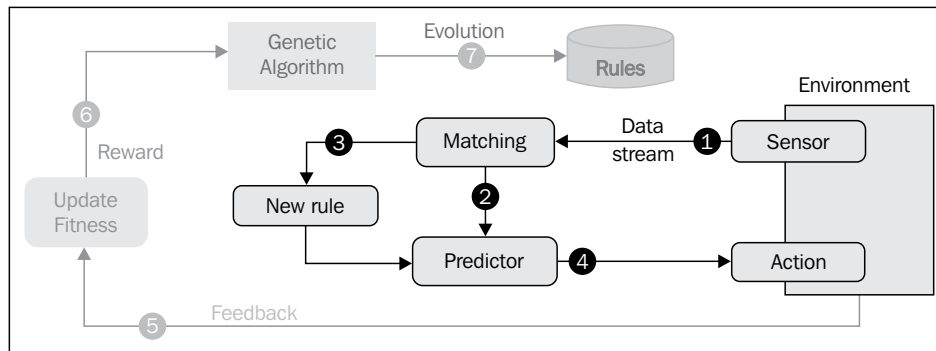
Each domain of research has its own terminology and LCS is no exception.

The terminology of LCS consists of the following terms:

- **Environment:** Environment variables in the context of reinforcement learning.
- **Agent:** An agent used in reinforcement learning.
- **Predicate:** A clause or fact using the format: *variable- operator- value*, and usually implemented as (operator, variable value); for example, *Temperature- exceeds - 87F* or (*'Temperature', 87F*), *Hard drive - failed* or (*'Status hard drive', FAILED*), and so on. It is encoded as a gene in order to be processed by the genetic algorithm.
- **Compound predicate:** Composition of several predicates and Boolean logic operators, which is usually implemented as a logical tree (for example, *((predicate1 AND predicate2) OR predicate3* is implemented as *OR (AND (predicated 1, predicate 2), predicate3)*). It uses a chromosome representation.
- **Action:** A mechanism that alters the environment by modifying the value of one or several of its parameters using a format (type of action, target), for example, *change thermostat settings, replace hard drive, and so on.*
- **Rule:** A formal first-order logic formula using the format *IF compound predicate THEN sequence of action*, for example, *IF gold price < \$1140 THEN sell stock of oil and gas producing companies.*
- **Classifier:** A rule in the context of an LCS.
- **Rule fitness or score:** This is identical to the definition of the fitness or score in the genetic algorithm. In the context of an LCS, it is the probability of a rule to be invoked and fired in response of change in environment.
- **Sensors:** Environment variables monitored by agent, for example, *temperature and hard drive status.*
- **Input data stream:** Flow of data generated by sensors. It is usually associated with online training.
- **Rule matching:** Mechanism to match a predicate or compound predicate with a sensor.
- **Covering:** The process of creating new rules to match a new condition (sensor) in the environment. It generates the rules by either using a random generator or mutating existing rules.
- **Predictor:** An algorithm to find the action with the maximum number of occurrences within a set of matching rules.

Extended learning classifier systems (XCS)

Similar to reinforcement learning, the XCS algorithm has an **exploration** phase and an **exploitation** phase. The exploitation process consists of leveraging the existing rules to influence the target environment in a profitable or rewarding manner.

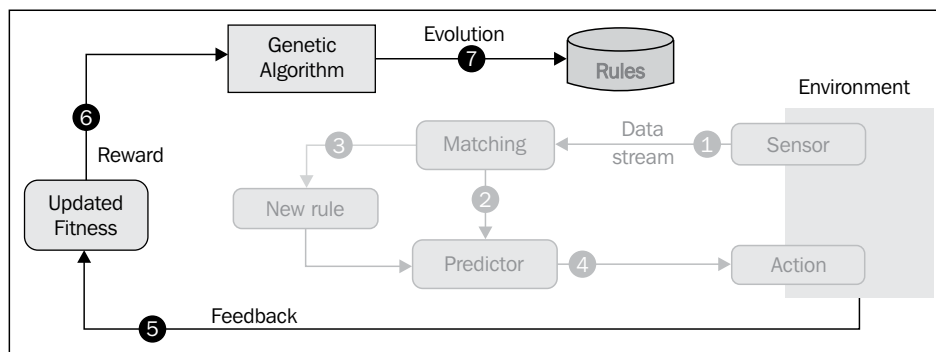


Exploitation component of the XCS algorithm

The following list describes each numbered block:

- **1:** Sensors acquire new data or events from the system.
- **2:** Rules for which the condition matches the input event are searched and extracted from the current population.
- **3:** A new rule is created if no match is found in the existing population. This process is known as covering.
- **4:** The chosen rules are ranked by their fitness values, and the rules with the highest predicted outcome are used to trigger the action.

The purpose of exploration components is to increase the rule base as a population of the chromosomes that encode these rules.



Exploration components of the XCS algorithm

The following list describes each numbered block of the block diagram:

- **5:** Once the action is performed, the system rewards the rules for which the action has been executed. The reinforcement learning module assigns credit to these rules.
- **6:** Rewards are used to update the rule fitness, applying evolutionary constraints to the existing population.
- **7:** The genetic algorithm updates the existing population of classifiers/rules using operators such as crossover and mutation.

XCS components

This section describes the key classes of the XCS. The implementation leverages the existing design of the genetic algorithm and the reinforcement learning. It is easier to understand the inner workings of the XCS algorithm with a concrete application.

Application to portfolio management

Portfolio management and trading have benefited from the application of extended learning classifiers [11:13]. The use case is the management of a portfolio of **exchange-traded funds (ETFs)** in an ever-changing financial environment. Contrary to stocks, exchange traded funds are representative of an industry-specific group of stocks or the financial market at large. Therefore, the price of these ETFs is affected by the following macroeconomic changes:

- Gross domestic product
- Inflation
- Geopolitical events
- Interest rates

Let's select the value of the 10-year Treasury yield as a proxy for the macroeconomic conditions, for the sake of simplicity.

The portfolio has to be constantly adjusted in response to any specific change in the environment or market condition that affects the total value of the portfolio, and can be done referring to the following table:

XCS component	Portfolio management
Environment	Portfolio of securities defined by its composition, total value, and the yield of the 10-year Treasury bond
Action	Change in the composition of the portfolio
Reward	Profit and loss of the total value of the portfolio
Input data stream	Feed of stock and bond price quotation
Sensor	Trading information regarding securities in the portfolio such as price, volume, volatility, or yield, and the yield on the-10 year Treasury bond
Predicate	Change in composition of the portfolio
Action	Rebalancing a portfolio by buying and selling securities
Rule	Association of trading data with the rebalancing of a portfolio

The first step is to create an initial set of rules regarding the portfolio. This initial set can be created randomly, much like the initial population of a genetic algorithm, or be defined by a domain expert.

The XCS initial population

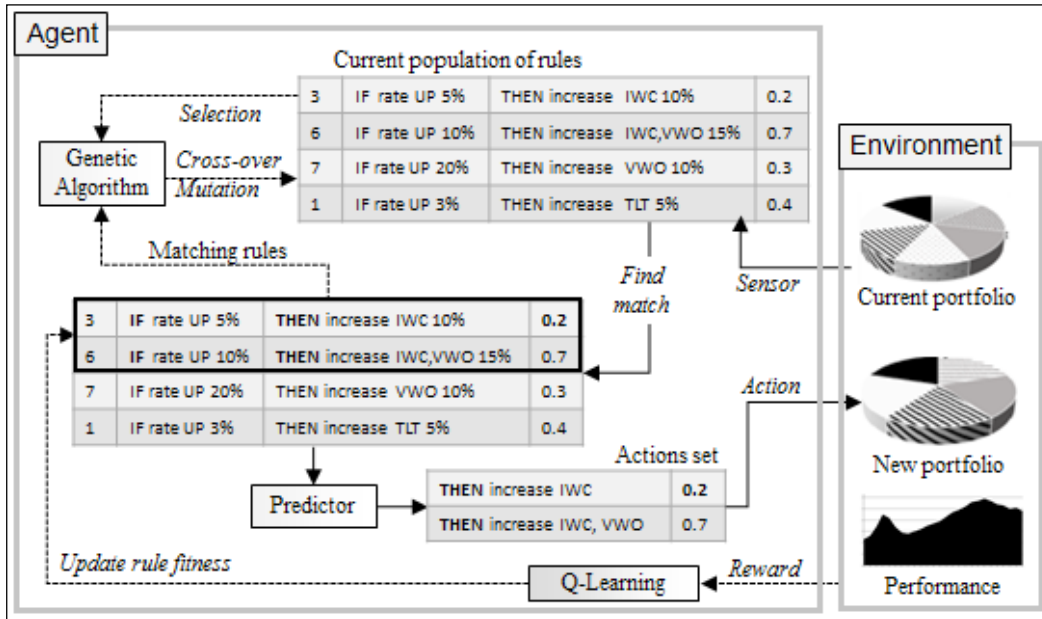


Rules or classifiers are defined and/or refined through evolution. Therefore, there is no absolute requirement for the domain expert to set up a comprehensive knowledge base. In fact, rules can be randomly generated at the start of the training phase. However, seeding the XCS initial population with a few relevant rules improves the odds of having the algorithm converge quickly.

The reader is invited to initialize the population of rules with as many relevant and financially sound trading rules as possible. Over time, the execution of the XCS algorithm will confirm whether or not the initial rules are indeed appropriate. The following diagram describes the application of the XCS algorithm to the composition of a portfolio of ETFs, such as VWO, TLT, IWC, and so on, with the following components:

- The population of trading rules
- An algorithm to match rules and compute the prediction
- An algorithm to extract the actions sets

- The Q-learning module to assign credit or reward to the selected rules
- The genetic algorithm to evolve the population of rules



Overview of XCS algorithm to optimize portfolio allocation

The agent responds to the change in the allocation of ETFs in the portfolio by matching one of the existing rules.

Let's build the XCS agent from the ground.

XCS core data

There are three types of data that are manipulated by the XCS agent:

- `Signal`: This is the trading signal
- `xcsAction`: This is the action on the environment
- `xcsSensor`: This is the sensor or data from the environment

The `xcsAction` class was introduced for the evaluation of the genetic algorithm in the *Trading signals* section in *Chapter 10, Genetic Algorithms*. The agent creates, modifies, and deletes actions. It makes sense to define these actions as mutable genes, as follows:

```
class XcsAction(val sensorid: String, val target: Double)(implicit val
  discr: Discretization) extends Gene(sensorid, target, EQUAL)
```

The `XcsAction` class has the identifier of the sensor, `sensorId`, and the target value as parameters. For example, the action to increase the number of shares of ETF, VWO in the portfolio to 80 is defined as follows:


```
Val vwoTo80 = new XcsAction("VWO", 80.0)
```

The only type of action allowed in this scheme is setting a value using the `EQUAL` operator. You can create actions that support other operators, such as `+=` used to increase an existing value. These operators need to implement the operator trait, explained in the *Trading operators* section in *Chapter 10, Genetic Algorithms*.

A discretization instance has to be implicitly defined in order to encode the target value.

Finally, the `XcsSensor` class encapsulates the `sensorId` identifier for the variable and value of the sensor, as shown here:

```
case class XcsSensor(val sensorId: String, val value: Double)
val new10ytb = new XcsSensor("10yTBYield", 2.76)
```



Setters and getters

In this simplistic scenario, the sensors retrieve a new value from an environment variable. The action sets a new value to an environment variable. You can think of a sensor as a get method of an environment class and an action as a set method with variable/sensor ID and value as arguments.

XCS rules

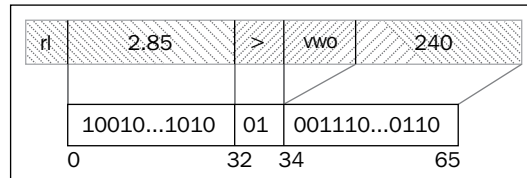
The next step consists of defining a rule as a pair of two genes: a signal and an action, as shown in the following code:

```
class XcsRule(val signal: Signal, val action: XcsAction)
```


The rule: *r1: IF(yield 10-year TB > 2.84%) THEN reduce VWO shares to 240* is implemented as follows:

```
val signal = new Signal("10ytb", 2.84, GREATER_THAN)
val action = new XcsAction("vwo", 240)
val r1 = new XcsRule(signal, action)
```

The agent encodes the rule as a chromosome using 2 bits to represent the operator and 32 bits for values, as shown in the following diagram:



In this implementation, there is no need to encode the type of action as the agent uses only one type of action – set. A complex action requires encoding of its type.



Knowledge encoding

This example uses very simple rules with a single predicate as the condition. Real-world domain knowledge is usually encoded using complex rules with multiple clauses. It is highly recommended that you break down complex rules into multiple basic rules of classifiers.

Matching a rule to a new sensor consists of matching the sensor to the signal. The algorithm matches the new `new10ytb` sensor against the signal in the current population of `s10ytb1` and `s10ytb2` rules that uses the same sensor or variable `10ytb`, as follows:

```

val new10ytb = new XcsSensor("10ytb", 2.76)

val s10ytb1 = Signal("10ytb", 2.5, GREATER_THAN)
val s10ytb2 = Signal("10ytb", 2.2, LESS_THAN)

val r23: XcsRule(s10ytb1, act12)
val r34: XcsRule(s10ytb2, act17)
...

```

In this case, the agent selects the rule `r23` but not `r34` in the existing population. The agent then adds the `act12` action to the list of possible actions. The agent lists all the rules that match the sensor: `r23`, `r11`, and `r46`, as shown in the following code:

```

val r23: XcsRule(s10yTB1, act12)
val r11: XcsRule(s10yTB6, act6)
val r46: XcsRule(s10yTB7, act12)

```

The action with the most references, `act12`, is executed. The Q-learning algorithm computes the reward from the profit or loss incurred by the portfolio following the execution of the selected rules `r23` and `r46`. The agent uses the reward to adjust the fitness of `r23` and `r46`, before the genetic selection in the next reproduction cycle. These two rules will reach and stay in the top tier of the rules in the population, until either a new genetic rule modified through crossover and mutation or a rule created through covering, triggers a more rewarding action on the environment.

Covering

The purpose of the covering phase is to generate new rules if no rule matches the input or sensor. The `cover` method of an `XcsCover` singleton generates a new `XcsRule` instance given a sensor and an existing set of actions, as shown here:

```
def cover(sensor: XcsSensor, actions: List[XcsAction]) (implicit
  discr: Discretization): List[XcsRule] = {
  actions.foldLeft(List[XcsRule]()) ((xs, act) => {
    val rIdx = Random.nextInt(Signal.numOperators)
    val signal = new Signal(sensor.id, sensor.value, new
      SOperator(rIdx))
    new XcsRule(signal, XcsAction(act, Random)) :: xs
  })
}
```

You might wonder why the `cover` method uses a set of actions as arguments knowing that covering consists of creating new actions. The method mutates (`operator ^`) an existing action to create a new one instead of using a random generator. This is one of the advantages of defining an action as a gene. The mutation is executed by one of the constructors of `XcsAction`, as follows:

```
def apply(action: XcsAction, r: Random): XcsAction =
  (action ^ r.nextInt(XCSACTION_SIZE))
```

The index of the operator type, `rIdx`, is a random value in the interval `[0, 3]` because a signal uses four types of operators: `None`, `>`, `<`, and `=`.

Example of implementation

The `Xcs` class has the following purposes:

- `gaSolver`: This is the selection and generation of genetically modified rules
- `qlLearner`: This is the rewarding and scoring the rules

- `xcs`: These are the rules for matching, covering, and generation of action
- ```
class Xcs(config: XcsConfig, population: Population[Signal],
score: Chromosome[Signal]=> Unit, input: Array[QLInput]) extends
PipeOperator[XcsSensor, List[XcsAction]] {

 val gaSolver = GASolver[Signal](config.gaConfig, score)
 val featuresSet: Set[Chromosome[Signal]] = population.
chromosomes.toSet
 val qLearner = QLearning[Chromosome[Signal]](config.qlConfig,
computeNumStates(input), extractGoals(input), input, featuresSet)
 ...
}
```

The XCS algorithm is initialized with a configuration, `config`, an initial set of rules, `population`, a fitness function, `score`, and an input to the Q-learning policy generate reward matrix for `qLearner`. The goals and number of states are extracted from the input to the policy of the Q-learning algorithm.

In this implementation, the generic algorithm, `gaSolver`, is mutable. It is instantiated along with the `xcs` container class. The Q-learning algorithm uses the same design, as any classifier, as immutable. The model of Q-learning is the best possible policy to reward rules. Any changes in the number of states or the rewarding scheme require a new instance of the learner.

## Benefits and limitation of learning classifier systems

Learning classifier systems and XCS in particular, hold many promises, which are as follows:

- They allow non-scientists and domain experts to describe the knowledge using familiar Boolean constructs and inferences such as predicates and rules
- They provide analysts with an overview of the knowledge base and its coverage by distinguishing between the need for exploration and exploitation of the knowledge base

However, the scientific community has been slow to recognize the merits of these techniques. The wider adoption of learning classifier systems is hindered by the following factors:

- Sheer complexity of the configuration of the algorithm because of the large number of parameters for exploration and exploitation.
- Lack of a unified theory to validate the concept of evolutionary policies or rules. After all, these algorithms are the merger of standalone techniques. The accuracy and performance of the execution of LCSes depend on each component as well as the interaction between components.
- An execution that is not always predictable in terms of scalability and performance.
- Too many variants of LCS.

## Summary

Reinforcement learning algorithms are sometimes overlooked by the software engineering community. Let's hope that this chapter provides adequate answers to the following questions:

- What is reinforcement learning?
- What are the different types of algorithms that qualify as reinforcement learning?
- How can we implement the Q-learning algorithm in Scala?
- How can we apply Q-learning to the optimization of option trading?
- What are the pros and cons of using reinforcement learning?
- What are learning classifier systems?
- What are the key components of the XCS algorithm?
- What are the potentials and limitations of learning classifier systems?

This concludes the introduction of the last category of learning techniques. The ever-increasing amount of data that surrounds us requires data processing and machine learning algorithms to be highly scalable. This is the subject of the next and the final chapter.



# 12

## Scalable Frameworks

The advent of social networking, interactive media, and deep analysis has caused the amount of data processed daily to skyrocket. For data scientists, it's no longer just a matter of finding the most appropriate and accurate algorithm to mine data; it is also about leveraging multi-core CPU architectures and distributed computing frameworks to solve problems in a timely fashion. After all, how valuable is a data mining application if the model does not scale?

There are many options available to Scala developers to build classification and regression applications for very large datasets. This chapter covers the Scala parallel collections, Actor model, Akka framework, and Apache Spark in-memory clusters. The following are the topics addressed in this chapter:

- Introduction to Scala parallel collections
- Evaluation of performance of a parallel collection on multicore CPU
- The actor model and reactive systems.
- Clustered and reliable distributed computing using Akka
- Design of computational workflow using Akka routers
- Introduction to Apache Spark clustering and its design principles
- Using Spark MLlib for clustering
- Relative performance tuning and evaluation of Spark
- Benefits and limitations of the Apache Spark framework



## Overview

The support for distributing and concurrent processing is provided by different stacked frameworks and libraries. Scala concurrent and parallel collections classes leverage the threading capabilities of the Java virtual machine. Akka.io implements a reliable action model originally introduced as part of the Scala standard library. The Akka framework supports remote actors, routing, and load balancing protocol; dispatchers, clusters, events, and configurable mailboxes management; and support for different transport modes, supervisory strategies and typed actors. Apache Spark's resilient distributed datasets with advanced serialization, caching, and partitioning capabilities leverage Scala and Akka libraries.

The following stack representation illustrates the interdependencies between frameworks:

|              |                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|--------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Spark</b> | <b>Partitioner, Accumulator:</b> <i>org.apache.spark</i><br><b>Broadcast:</b> <i>org.apache.spark.broadcast</i><br><b>Resilient datasets:</b> <i>org.apache.spark.rdd</i><br><b>Caching:</b> <i>org.apache.spark</i><br><b>Listeners:</b> <i>org.apache.spark.scheduler._</i><br><b>Serialization:</b> <i>org.apache.spark.serializer</i>                                                                                              |
| <b>Akka</b>  | <b>Actors, Supervisors:</b> <i>akka.actors._</i><br><b>Remote actors:</b> <i>akka.remote</i><br><b>Type actors:</b> <i>akka.actors._</i><br><b>Mailbox management:</b> <i>akka.mailbox._</i><br><b>Clusters:</b> <i>akka.cluster._</i><br><b>Dispatchers:</b> <i>akka.dispatch</i><br><b>Events management:</b> <i>akka.event._</i><br><b>Routing, Broadcast:</b> <i>akka.routing</i><br><b>Persistence:</b> <i>akka.persistence._</i> |
| <b>Scala</b> | <b>Scheduler:</b> <i>scala.actors.scheduler</i><br><b>Concurrency:</b> <i>scala.concurrent</i><br><b>Parallel collections:</b> <i>scala.collection.parallel</i>                                                                                                                                                                                                                                                                        |
|              | <b>Threads, executors:</b> <i>java.util.concurrent*</i>                                                                                                                                                                                                                                                                                                                                                                                |

Stack representation of Scalable frameworks using Scala

Each layer adds a new functionality to the previous one to increase scalability. The Java virtual machine runs as a process within a single host. Scala concurrent classes support effective deployment of an application by leveraging multicore CPU capabilities without the need to write multithreaded applications. Akka extends the Actor paradigm to clusters with advanced messaging and routing options. Finally, Apache Spark leverages Scala higher-order collection methods and the Akka implementation of the Actor model to provide large-scale data processing systems with better performance and reliability, through its resilient distributed datasets and in-memory persistency.

---

## Scala

The Scala standard library offers a rich set of tools, such as parallel collections and concurrent classes to scale number-crunching applications. Although these tools are very effective in processing medium-sized datasets, they are unfortunately quite often discarded by developers in favor of more elaborate frameworks.

### Controlling object creation

Although code optimization and memory management is beyond the scope of this chapter, it is worthwhile to remember that a few simple steps can be taken to improve the scalability of an application. One of the most frustrating challenges in using Scala to process large datasets is the creation of a large number of objects and the load on the garbage collector.

A partial list of remedial actions is as follows:

- Limiting unnecessary duplication of objects in an iterated function by using a mutable instance
- Using lazy values and **Stream** classes to create objects as needed
- Leveraging efficient collections such as **bloom filters** or **skip lists**
- Running `javap` to decipher the generation of byte code by the JVM

### Parallel collections

The Scala standard library includes parallelized collections, whose purpose is to shield developers from the intricacies of concurrent thread execution and race condition. Parallel collections are a very convenient approach to encapsulate concurrency constructs to a higher level of abstraction [12:1].

There are two ways to create parallel collections in Scala:

- Converting an existing collection into a parallel collection of the same semantic using the `par` method, for example, `List [T] .par : ParSeq [T]`, `Array [T] .par : ParArray [T]`, `Map [K, V] .par : ParMap [K, V]`, and so on
- Using the collections classes from the `collection.parallel`, `parallel.immutable`, or `parallel.mutable` packages, for example, `ParArray`, `ParMap`, `ParSeq`, `ParVector`, and so on

## Processing a parallel collection

A parallel collection does lend itself to concurrent processing until a pool of threads and a tasks scheduler are assigned to it. Fortunately, Scala parallel and concurrent packages provide developers with a powerful toolbox to map partitions or segments of collection to tasks running on different CPU cores. The components are as follows:

- `TaskSupport`: This trait inherits the generic `Tasks` trait. It is responsible for scheduling the operation on the parallel collection. There are three concrete implementations of `TaskSupport`.
- `ThreadPoolTaskSupport`: This uses the threads pool in an older version of the JVM.
- `ExecutionContextTaskSupport`: This uses `ExecutorService`, which delegates the management of tasks to either a thread pool or the `ForkJoinTasks` pool.
- `ForkJoinTaskSupport`: This uses the fork-join pools of type `java.util.concurrent.ForkJoinPool` introduced in Java SDK 1.6. In Java, a **fork-join pool** is an instance of `ExecutorService` that attempts to run not only the current task but also any of its subtasks. It executes the `ForkJoinTask` instances that are lightweight threads.

The following example implements the generation of random exponential value using a parallel vector and `ForkJoinTaskSupport`:

```
val rand = new ParVector[Float]
Range(0, MAX).foreach(n =>rand.updated(n, n*Random.nextFloat()))//1
rand.taskSupport = new ForkJoinTaskSupport(new ForkJoinPool(16))
val randExp = vec.map(Math.exp(_))//2
```

The parallel vector of random probabilities, `rand`, is created and initialized by the main task (line 1), but the conversion to a vector of exponential value, `randExp`, is executed by a pool of 16 concurrent tasks (line 2).



### Preserving order of elements

Operations that traverse a parallel collection using an iterator preserve the original order of the element of the collection. Iterator-less methods such as `foreach` or `map` do not guarantee that the order of the elements that are processed will be preserved.



## Benchmark framework



### Scala library benchmark

The Scala standard library has a trait, `testing.Benchmark`, for testing using the command line [12:2]. All you need to do is to insert your function or code in the `run` method:

```
object test with Benchmark { def run { /* fill
the blank /* }
```

The main purpose of parallel collections is to improve the performance of execution through concurrency. First, let us create a parameterized class, `Benchmark`, to evaluate the performance of operations on a parallel array, `v`, relative to an array, `u`, as follows:

```
class ParArrayBenchmark[U](u: Array[U], v: ParArray[U], times: Int)
```

Next, you need to create a method, `timing`, that computes the ratio of the duration of a given operation on a parallel collection over the duration of the same operation on a single threaded collection, as shown here:

```
def timing(g: Int => Unit): Long = {
 var startTime = System.currentTimeMillis
 Range(0, times).foreach(g)
 System.currentTimeMillis - startTime
}
```

This method measures the time it takes to process a user-defined function, `g`, `times` times.

Let's compare the parallelized and default array on the `map` and `reduce` methods of `Benchmark` as follows

```
def map(f: U => U)(nTasks: Int): Unit = {
 val pool = new ForkJoinPool(nTasks)
 v.taskSupport = new ForkJoinTaskSupport(pool)
 val duration = timing(_ => u.map(f)).toDouble //3
 val ratio = timing(_ => v.map(f))/duration //4
 Display.show(s"$nTasks, $ratio", logger)
}
```

The user has to define the mapping function,  $f$ , and the number of concurrent tasks,  $nTasks$ , available to execute a map transformation on the array  $u$  (line 3) and its parallelized counterpart  $v$  (line 4). The `reduce` method follows the same design as shown in the following code:

```
def reduce(f: (U,U) => U) (nTasks: Int): Unit = {
 val pool = new ForkJoinPool(nTasks)
 v.tasksupport = new ForkJoinTaskSupport(pool)
 val duration = timing(_ => u.reduceLeft(f)).toDouble
 val ratio = timing(_ => v.reduceLeft(f))/duration
 Display.show(s"$nTasks, $ratio", logger)
}
```

The same template can be used for other higher Scala methods, such as `filter`. The absolute timing of each operation is completely dependent on the environment. It is far more useful to record the ratio of the duration of execution of operation on the parallelized array, over the single thread array.

The benchmark class, `ParMapBenchmark`, used to evaluate `ParHashMap` is similar to the benchmark for `ParArray`, as shown in the following code:

```
class ParMapBenchmark[U](val u: Map[Int, U], val v: ParMap[Int, U],
 times: Int)
```

For example, the `filter` method of `ParMapBenchmark` evaluates the performance of the parallel map  $v$  relative to single threaded map  $u$ . It applies the filtering condition to the values of each map as follows:

```
def filter(f: U => Boolean) (nTasks: Int): Unit = {
 val pool = new ForkJoinPool(nTasks)
 v.tasksupport = new ForkJoinTaskSupport(pool)
 val duration = timing(_ => u.filter(e => f(e._2))).toDouble
 val ratio = timing(_ => v.filter(e => f(e._2)))/duration
 Display.show(s"$nTasks, $ratio", logger)
}
```

## Performance evaluation

The first performance test consists of creating a single-threaded and a parallel array of random values and executing the evaluation methods, `map` and `reduce`, on using an increasing number of tasks, as follows:

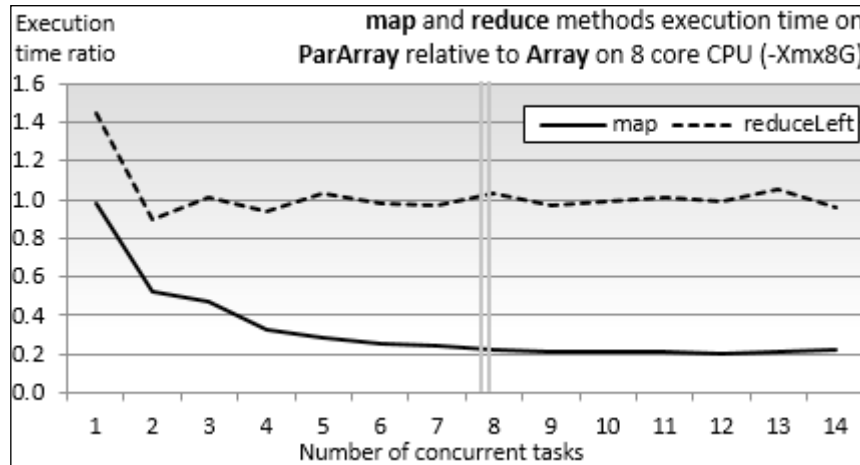
```
val sz = 1000000
val data = Array.fill(sz)(Random.nextDouble)
val pData = ParArray.fill(sz)(Random.nextDouble)
val times: Int = 50
```

```

val bench1 = new ParArrayBenchmark[Double](data, pData, times)
val mapper = (x: Double) => Math.sin(x*0.01) + Math.exp(-x)
Range(1, 16).foreach(n => bench1.map(mapper)(n))
val reducer = (x: Double, y: Double) => x+y
Range(1, 16).foreach(n => bench1.reduce(reducer)(n))

```

The following graph shows the output of the performance test:



The test executes the mapper and reducer functions 1 million times on an 8-core CPU with 8 GB of available memory on JVM.

The results are not surprising in the following respects:

- The reducer doesn't take advantage of the parallelism of the array. The reduction of `ParArray` has a small overhead in the single-task scenario and then matches the performance of `Array`.
- The performance of the `map` function benefits from the parallelization of the array. The performance levels off when the number of tasks allocated equals or exceeds the number of CPU core.

The second test consists of comparing the behavior of two parallel collections, `ParArray` and `ParHashMap`, on two methods, `map` and `filter`, using a configuration identical to the first test as follows:

```

val sz = 1000000
val mData = new HashMap[Int, Double]
Range(0, sz).foreach(n => mData.put(n, Random.nextDouble)) //1
val mParData = new ParHashMap[Int, Double]
Range(0, sz).foreach(n => mParData.put(n, Random.nextDouble))

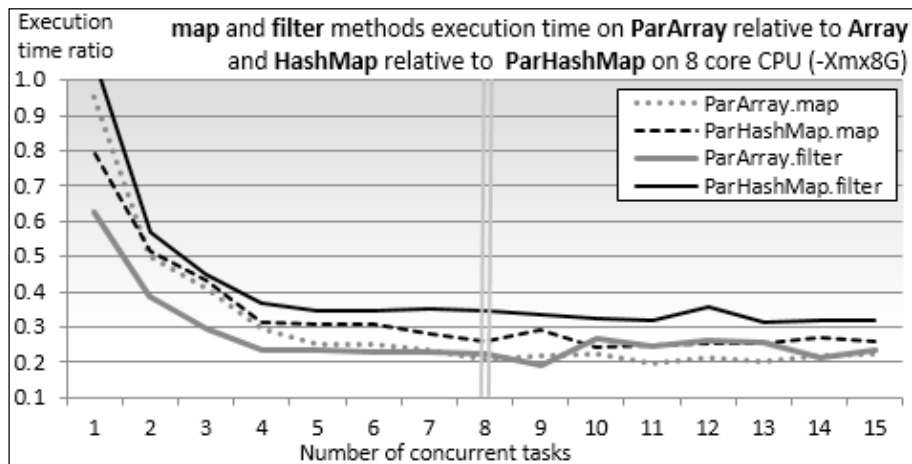
```

```

val bench2 = new ParMapBenchmark[Double](mData, mParData, times)
Range(1, 16).foreach(n => bench2.map(mapper)(n)) //2
val filterer = (x: Double) => (x > 0.8)
Range(1, 16).foreach(n => bench2.filter(filterer)(n)) //3

```

The test initializes a `HashMap` instance and its parallel counter `ParHashMap` with 1 million random values (line 1). The benchmark, `bench2`, processes all the elements of these hash maps with the `mapper` instance introduced in the first test (line 2) and a filtering function, `filterer` (line 3), with 16 tasks. The output is as shown here:



The impact of the parallelization of collections is very similar across methods and across collections. It's important to notice that the performance of the parallel collections levels off at around four times the single thread collections for five concurrent tasks and above. **Core parking** is partially responsible for this behavior. Core parking disables a few CPU cores in an effort to conserve power, and in the case of single application, consumes almost all CPU cycles.

#### Further performance evaluation



The purpose of the performance test was to highlight the benefits of using Scala parallel collections. You should experiment further with collections other than `ParArray` and `ParHashMap` and other higher-order methods to confirm the pattern.

Clearly, a four-times increase in performance is nothing to complain about. That being said, parallel collections are limited to single host deployment. If you cannot live with such a restriction and still need a scalable solution, the Actor model provides a blueprint for highly distributed applications.

## Scalability with Actors

Traditional multithreaded applications rely on accessing data located in shared memory. The mechanism relies on synchronization monitors such as locks, mutexes, or semaphores to avoid deadlocks and inconsistent mutable states. Even for the most experienced software engineer, debugging multithreaded applications is not a simple endeavor.

The second problem with shared memory threads in Java is the high computation overhead caused by continuous context switches. Context switching consists of saving the current stack frame delimited by the base and stack pointers into the heap memory and loading another stack frame.

These restrictions and complexities can be avoided by using a concurrency model that relies on the following key principles:

- Immutable data structures
- Asynchronous communication

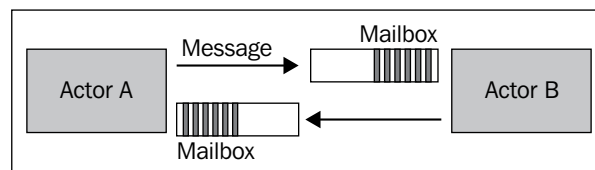
## The Actor model

The Actor model, originally introduced in the **Erlang** programming language, addresses these issues [12:3]. The purpose of using the Actor model is twofold:

- It distributes the computation over as many cores and servers as possible
- It reduces or eliminates race conditions and deadlocks which are very prevalent in Java development

The model consists of the following components:

- Independent processing units known as Actors. Actors communicate by exchanging messages asynchronously instead of sharing states.
- Immutable messages are sent to queues, known as mailboxes, before being processed by each actor one at a time.



Representation of messaging between actors



There are two message-passing mechanisms:

- **Fire-and-forget or tell:** Sends the immutable message asynchronously to the target or receiving actor, and returns immediately without blocking. The syntax is as follows:

```
targetActorRef ! message
```

- **Send-and-receive or ask:** Sends a message asynchronously, but returns a `Future` instance that defines the expected reply from the target actor

```
val future = targetActorRef ? message
```

The generic construct for the Actor message handler is somewhat similar to the `Runnable.run()` method in Java, as shown in the following code:

```
while(true){
 receive { case msg1: MsgType => handler }
}
```

The `receive` keyword is in fact a partial function of type `PartialFunction[Any, Unit]` [12:4]. The purpose is to avoid forcing developers to handle all possible message types. The Actor consuming messages may very well run on a separate component or even application, than the Actor producing these messages. It not always easy to anticipate the type of messages an Actor has to process in a future version of an application.

A message whose type is not matched is merely ignored. There is no need to throw an exception from within the Actor's routine. Implementations of the Actor model strive to avoid the overhead of context switching and creation of threads [12:5].

#### I/O blocking operations



Although it is highly recommended not to use Actors for blocking operations such as I/O, there are circumstances that require the sender to wait for a response. The reader needs to be mindful that blocking an underlying thread inside the Actor might starve other Actors from CPU cycles. It is recommended to either configure the runtime system to use a large thread pool, or to allow the thread pool to be resized by setting the `actors.enableForkJoin` property as `false`.

## Partitioning

A dataset is defined as a Scala collection, for example, `List`, `Map`, and so on.

Concurrent processing requires the following steps:

1. Breaking down a dataset into multiple subdatasets.
2. Processing each dataset independently and concurrently.
3. Aggregating all the resulting datasets.

These steps are defined through a monad associated with a collection in the *Abstraction* section under *Why Scala?* in *Chapter 1, Getting Started*.

1. The `apply` method creates the subcollection or partitions for the first step, for example, `def apply[T](a: T): List[T]`.
2. A map-like operation defines the second stage. The last step relies on the monoidal associativity of the Scala collection, for example, `def ++ (a: List[T], b: List[T]): List[T] = a ++ b`.
3. The aggregation, such as `reduce`, `fold`, `sum`, and so on, consists of flattening all the subresults into a single output, for example, `val xs: List(...) = List(List(..), List(..)).flatten`.

The methods that can be parallelized are `map`, `flatMap`, `filter`, `find`, and `filterNot`. The methods that cannot be completely parallelized are `reduce`, `fold`, `sum`, `combine`, `aggregate`, `groupBy`, and `sortWith`.

## Beyond actors – reactive programming

The Actor model is an example of the reactive programming paradigm. The concept is that functions and methods are executed in response to events or exceptions. Reactive programming combines concurrency with event-based systems [12:6].

Advanced functional reactive programming constructs rely on composable futures and **continuation-passing style (CPS)**. An example of a Scala reactive library can be found at <https://github.com/ingoem/scala-react>.

## Akka

The Akka framework extends the original Actor model in Scala by adding extraction capabilities such as support for typed Actor, message dispatching, routing, load balancing, and partitioning, as well as supervision and configurability [12:7].

The Akka framework can be downloaded from the [www.akka.io](http://www.akka.io) website, or through the Typesafe Activator at <http://www.typesafe.com/platform>.

Akka simplifies the implementation of Actor by encapsulating some of the details of Scala Actor in the `akka.actor.Actor` and `akka.actor.ActorSystem` classes.

The three methods you want to override are as follows:

- `preStart`: This is an optional method, invoked to initialize all the necessary resources such as file or database connection before the Actor is executed
- `receive`: This method defines the Actor's behavior and returns a partial function of type `PartialFunction[Any, Unit]`
- `postStop`: This is an optional method to clean up resources such as releasing memory, closing database connections, and socket or file handles

#### Typed versus untyped actors



**Untyped actors** can process messages of any type. If the type of the message is not matched by the receiving actor, it is discarded. Untyped actors can be regarded as contract-less actors. They are the default actors in Scala.

**Typed actors** are similar to Java remote interfaces. They respond to a method invocation. The invocation is declared publicly, but the execution is delegated asynchronously to the private instance of the target actor [12:8].

Akka offers a variety of functionalities to deploy concurrent applications. Let us create a generic template for a master Actor and worker Actors to transform a dataset using any preprocessing or classification algorithm inherited from the `PipeOperator` trait, as explained in the *The pipe operator* section under *Designing a workflow* in *Chapter 2, Hello World!*. The master Actor manages the worker actors in one of the following ways:

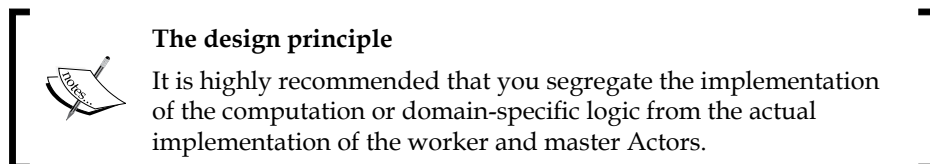
- Individual actors
- Clusters through a **router** or a **dispatcher**

The router is a very simple example of Actor supervision. Supervision strategies in Akka are an essential component to make the application fault-tolerant [12:9]. A supervisor Actor manages the operations, availability, and life cycle of its children, known as **subordinates**. The supervision among actors is organized as a hierarchy. Supervision strategies are categorized as follows:

- **One-for-one strategy**: This is the default strategy. In case of a failure of one of the subordinates, the supervisor executes a recovery, restart, or resume action for that subordinate only.
- **All-for-one strategy**: The supervisor executes a recovery or remedial action on all its subordinates in case one of the Actors fails.

## Master-workers

The first model to evaluate is the traditional **master-slaves** or **master-workers** design for computation workflow. In this design, the worker Actors are initialized and managed by the master Actor which is responsible for controlling the iterative process, state, and termination condition of the algorithm. The orchestration of the distributed tasks is performed through message passing.



## Messages exchange

The first step in implementing the master-worker design is to define the different classes of messages exchanged between the master and each worker, to control the execution of the iterative procedure. The implementation of the master-worker design is as follows:

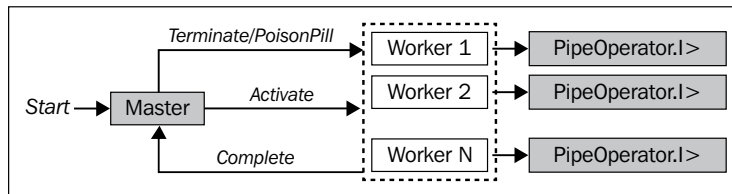
```
type DblSeries = XTSeries[Double]

sealed abstract class Message(val id: Int)
case class Start(i: Int = 0) extends Message(i) //1
case class Activate(i: Int, xt: DblSeries) extends Message(i) //2
case class Completed(i: Int, xt: DblSeries) extends Message(i) //3
```

Let's define the messages that control the execution of the algorithm. We need at least the following message types or case classes:

1. `Start` is sent by the client code to the master to start the computation.
2. `Activate` is sent by the master to the workers to activate the computation. This message contains the time series, `xt`, to be processed by the worker Actors.
3. `Completed` is sent by each worker back to `sender`. It contains the variance of the data in the group.
4. The master stops a worker using a `PoisonPill` message. The different approaches to terminate an actor are described in the *The Master actor* section.

The hierarchy of the `Message` class is sealed to prevent third-party developers from adding another message type. The worker responds to the `activate` message by executing a data transformation of type inherited from `PipeOperator`. The messages exchanged between master and worker actors are shown in the following diagram:



### Messages as case classes



The actor retrieves the messages queued in its mailbox by managing each message instance (copy, matching, and so on). Therefore, the message type has to be defined as a case class. Otherwise, the developer will have to override the `equals` and `hashCode` methods.

## Worker actors

The worker actors are responsible for transforming each partition created by the master Actor, as follows:

```

class Worker(id: Int, fct: PipeOperator[DblSeries, DblSeries]) extends
 Actor { //1
 override def receive = {
 case msg: Activate => {
 msg.sender ! Completed(msg.id+id, transform(msg.xt)) //2
 context.stop(self)
 }
 case _ => Display.show("Unknown message", logger)
 }
 def transform(xt: DblSeries): DblSeries = fct |>
}

```

The `Worker` class constructor takes the `fct` data transformation as an argument (line 1). The worker launches the processing or transformation of the `msg.xt` data upon arrival of the `Activate` message (line 2). It returns the `Completed` message to the master once the data transformation, `transform`, is completed.



### The design principle

It is highly recommended that you segregate the implementation of the computation or domain-specific logic from the actual implementation of the worker and master Actors.

## The workflow controller

In the *Scalability* section in *Chapter 1, Getting Started*, we introduced the concepts of workflow and controller, to manage the training and classification process as a sequence of transformation on time series. Let's define an abstract class for all controller actors, `Controller`, with the following three key parameters:

- A time series, `xt`, to be a process
- A data transformation, `fct`, of type `PipeOperator`
- A partitioning method, `partitioner`, to break down a time series for concurrent processing

The `Controller` class can be defined as follows:

```
abstract class Controller(val xt: DblSeries, val fct:
 PipeOperator[DblSeries, DblSeries], val partitioner: Partitioner)
 extends Actor
```

The workflow controller is responsible for splitting the time series into several partitions and assigning each partition to a dedicated worker Actor. A helper class, `Partitioner`, implements the partitioning of the dataset as follows:

```
class Partitioner(val numPartitions: Int) {
 def split(xt: DblSeries): Array[Int] = {
 val sz = (xt.size.toDouble/numPartitions).floor.toInt
 val indices = Array.tabulate(numPartitions)(i=>(i+1)*sz)
 indices.update(numPartitions - 1, xt.size)
 indices
 }
}
```

The `split` method breaks down a time series, `xt`, into `numPartitions` partitions, and returns the index of each partition relative to the original time series.

## The master Actor

Let's define a master Actor class, `Master`. The three methods to override are as follows:

- `preStart` is a method invoked to initialize all the necessary resources such as file or database connection before the actor executes
- `receive` is a partial function that dequeues and processes the messages from the mail box
- `postStop` cleans up resources such as releasing memory and closing database connections, sockets, or file handles

The Master class can be defined as follows:

```
abstract class Master(xt: DblSeries, fct: PipeOperator[DblSeries,
DblSeries], partitioner: Partitioner) extends Controller(xt, fct,
partitioner) {
 val workers = List.tabulate(partitioner.numPartitions)(n =>
 context.actorOf(Props(new Worker(n, fct)))) //4
 val aggregator = new ListBuffer[DblVector] //5

 override def preStart: Unit = {} //6
 override def postStop: Unit = {} //7
 override def receive
```

The Master class has the following parameters:

- `xt`: This is the time series to transform
- `fct`: This is the transformation function
- `partitioner`: This is the instance of time series partitioning

The worker actors are created through the `actorOf` factory method of the `ActorSystem` context (line 4). A list buffer, `aggregator`, collects and reduces the results from each worker (line 5). The `preStart` method implements any initialization required to process the messages (line 6). The `postStop` method releases all the resources allocated to process the messages (line 7).

The `receive` message handler processes only two types of messages: `Start` from the client code and `Completed` from the workers, as shown in the following code:

```
override def receive = {
 case Start => split //8
 case msg: Completed => { //10
 if(aggregator.size >= partitioner.numPartitions-1) { //12
 aggregate //14
 //13 workers.foreach(_ ! PoisonPill)
 context.stop(self) //15
 }
 aggregator.append(msg.xt.toArray) //11
 }
}

def aggregate: Seq[Double]

def split: Unit = {
 val partIdx = partitioner.split(xt)
```

```

workers.zip(partIdx).foreach(w =>
 w._1 ! Activate(0, xt.slice(w._2-partIdx(0), w._2)) //9
}

```

The `Start` message triggers the split of the input time series into partitions (line 8), which are then dispatched to each worker with the `Activate` message (line 9). Each worker sends a `Completed` message back to master upon the completion of their task (line 10). The master aggregates the results from the each worker (line 11). Once every worker has completed its task (line 12), the master terminates all the workers, through a `PoisonPill` message in case the worker actors do not terminate themselves (line 13). The master aggregate the results (line 14) before it terminates itself through a request to its context to stop it (line 15).

The aggregate method can be defined as a parameter either of the `Master` class or of one of its subclasses.

The previous code snippet uses two different approaches to terminate an actor. There are four different methods of shutting down an actor, as mentioned here:

- `actorSystem.shutdown`: This method is used by the client to shut down the parent actor system
- `actor ! PoisonPill`: This method is used by the client to send a poison pill message to the actor
- `context.stop(self)`: This method is used by the Actor to shut itself down within its context
- `context.stop(childActorRef)`: This method is used by the Actor to shut itself down through its reference

## Master with routing

The previous design makes sense only if each worker has a unique characteristic that requires direct communication with the master. This is not the case in most applications. The communication and internal management of the worker can be delegated to a router. The implementation of the master routing capabilities is very similar to the previous design, as shown in the following code:

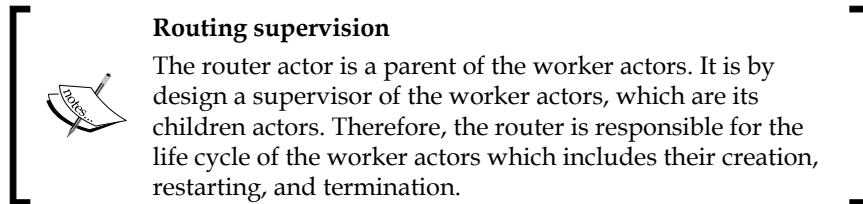
```

abstract class MasterWithRouter(xt: DblSeries, fct:
PipeOperator[DblSeries, DblSeries], partitioner: Partitioner) extends
Controller(xt, fct, partitioner) {
 val router = context.actorOf(Props(new Worker(0, fct))
 .withRouter(RoundRobinPool(partitioner.numPartitions,
 supervisorStrategy = this.supervisorStrategy)))
 ...
}

```



The only difference is that the `context.actorOf` factory creates an extra actor, `router`, along with the workers. This particular implementation relies on round-robin assignment of the message by the router to each worker. Akka supports several routing mechanisms that select a random actor, or the actor with the smallest mailbox, or the first to respond to a broadcast, and so on.



The implementation of the `receive` message handler is almost identical to the message handler in the master without routing capabilities, except that the partitioning (line 1) is delegated to the router instead of being applied to each individual worker, as follows:

```
override def receive = {
 case msg: Start => split
 case msg: Completed => {
 if (aggregator.size >= partitioner.numPartitions-1) {
 aggregate
 context.stop(self) //2
 }
 aggregator.append(msg.xt.toArray)
 }
}
def split: Unit = {
 val indices = partitioner.split(xt)
 indices.foreach(n =>
 router ! Activate(xt.slice(n - indices(0), n)) //1
)
}
```

The supervising router terminates itself automatically once all its child actors are terminated (line 2).

## Distributed discrete Fourier transform

Let's select the **discrete Fourier transform (DFT)** on a time series, `xt`, as our data transformation. We discussed it in the *Discrete Fourier transform (DFT)* section in *Chapter 3, Data Preprocessing*. The testing code is exactly the same, whether the master has routing capabilities or not.

First, let's define a master controller, `DFTMaster`, dedicated to the execution of the distributed discrete Fourier transform, as follows:

```
class DFTMaster(xt: XTSeries[Double], partitioner: Partitioner)
 extends Master(xt, DFT[Double], partitioner) {
 override def aggregate: Seq[Double] =
 aggregator.transpose.map(_.sum).toSeq
}
```

The `aggregate` method aggregates or reduces the results of the discrete Fourier transform (frequencies distribution) from each worker. In the case of the discrete Fourier transform, the `aggregate` method transposes the list of frequencies distribution then summed the amplitude for each frequency, as shown here:

```
val NUM_WORKERS = 4
val NUM_DATAPOINTS = 1000000
val h = (x:Double) =>2.0*Math.cos(Math.PI*0.005*x) +
 Math.cos(Math.PI*0.05*x) +
 0.5*Math.cos(Math.PI*0.2*x) +
 0.3* Random.nextDouble //1
val xt = XTSeries[Double](Array.tabulate(NUM_DATAPOINTS)(h(_)))
val partitioner = new Partitioner(NUM_WORKERS) //2

implicit val actorSystem = ActorSystem("system") //3
val master = actorSystem.actorOf(Props(new DFTMaster(xt,
partitioner)), "DFTMaster") //4
master ! Start //5
Thread.sleep(15000)
actorSystem.shutdown //6
```

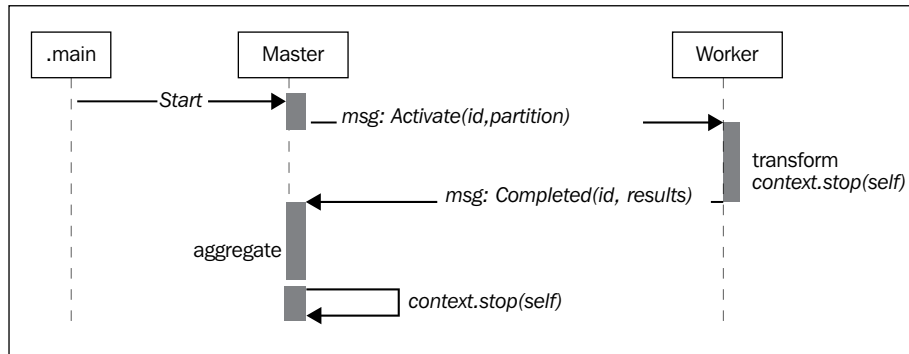
The input time series is synthetically generated by the noisy function, `h` (line 1). The function `h` has three distinct harmonics, 0.005, 0.05, and 0.2, so the results of the transformation can be easily validated. A `partitioner` instance is created for `NUM_WORKERS` worker Actors (line 2). The Actor system, `ActorSystem`, is instantiated (line 3) and the `master` Actor is generated through the Akka `ActorSystem.actorOf` factory. The main program sends a `Start` message to the master to trigger the distributed computation of the discrete Fourier transform. The main program has to sleep for a period of time long enough to allow the master to complete its task. Finally, the main program shuts down the actor system (line 6).

**Actor instantiation**



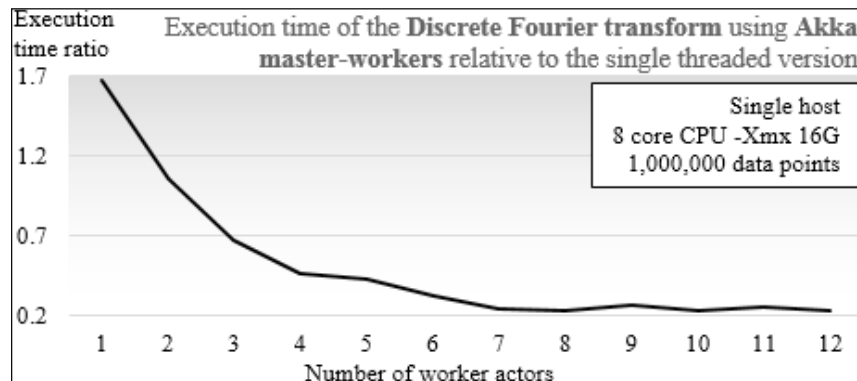
Although the `scala.actor.Actor` class can be instantiated using the constructor, `akka.actor.Actor` is instantiated using a context, `ActorSystem`; a factory, `actorOf`; and a configuration object, `Props`. This second approach has several benefits, including decoupling the deployment of the actor from its functionality and enforcing a default supervisor or parent for the Actor, in this case `ActorSystem`.

The following sequential diagram illustrates the message exchange between the main program, master, and worker Actors:



Sequential diagram for the normalization of cross-validation groups

The purpose of the test is to evaluate the performance of the computation of the discrete Fourier transform using the Akka framework relative to the original implementation, without actors. As with the Scala parallel collections, the absolute timing for the transformation depends on the host and the configuration, as shown in the following graph:



The single-threaded version of the discrete Fourier transform is significantly faster than the implementation using the Akka master-worker model with a single worker actor. The cost of partitioning and the aggregating (or reducing) the results adds a significant overhead to execution of the Fourier transform. However, the master-worker model is far more efficient with three or more worker actors.

## Limitations

The master-worker implementation has a few problems:

- In the message handler of the master Actor, there is no guarantee that the poison pill will be consumed by all the workers before the master stops.
- The main program has to sleep for a period of time long enough to allow the master and workers to complete their tasks. There is no guarantee that the computation will be completed when the main program awakes.
- There is no mechanism to handle failure in delivering or processing messages.

The culprit is the exclusive use of the fire-and-forget mechanism to exchange data between master and workers. The send-and-recv protocol and futures are remedies to these problems.

## Futures

A future is an object, more specifically a monad, used to retrieve the results of concurrent operations, in a non-blocking fashion. The concept is very similar to a callback supplied to a worker, which invokes it when the task is completed. Futures hold a value that might or might not become available in the future when a task is completed, successful or not [12:10].

There are two options to retrieve results from futures:

- Blocking execution using `scala.concurrent.Await`
- Callback functions, `onComplete`, `onSuccess`, and `onFailure`

### Which future?



A Scala environment provides developers with two different Future classes: `scala.actor.Future` and `scala.concurrent.Future`. The `actor.Future` class is used to write continuation-passing style workflows in which the current actor is blocked until the value of the future is available. Instances of type `scala.concurrent.Future` used in this chapter are the equivalent of `java.concurrent.Future` in Scala.

## The Actor life cycle

Let's reimplement the normalization of cross-validation groups by their variance, which we introduced in the previous section, using futures to support concurrency. The first step is to import the appropriate classes for execution of the main actor and futures, as follows:

```
import akka.actor.{Actor, ActorSystem, ActorRef, Props}
import akka.util.Timeout
import scala.concurrent.{Await, Future}
```

The Actor classes are provided by the package `akka.actor`, instead of the `scala.actor._` package because of Akka's extended actor model. The future-related classes, `Future` and `Await`, are imported from the `scala.concurrent` package, which is similar to the `java.concurrent` package. The `akka.util.Timeout` class is used to specify the maximum duration the actor has to wait for the completion of the futures.

There are two options for a parent actor or the main program to manage the futures it creates:

- **Blocking:** The parent actor or main program stops execution until all futures have completed their tasks.
- **Callback:** The parent actor or the main program initiates the futures during execution. The future tasks are performed concurrently with the parent actor, that is then notified when each future task is completed.

## Blocking on futures

The following design consists of blocking the actor that launches the futures until all the futures have been completed, either returning with a result or throwing an exception. Let's modify the master Actor into a class, `TransformFutures`, that manages futures instead of workers or routing actors, as follows:

```
abstract class TransformFutures(xt: DblSeries,
 fct: PipeOperator[DblSeries, DblSeries],
 partitioner: Partitioner)(implicit timeout: Timeout)
 extends Controller(xt, fct, partitioner) { //1

 override def receive = {
 case Start => compute(transform) //2
 case _ => Display.error("Message not recognized", logger)
 }
 def aggregate(results: Array[DblSeries]): Seq[Double]
 ...
}
```

The `TransformFutures` class requires the same parameters as the `Master` actor: a time series, `xt`; a data transformation, `fct`; and `partitioner`. The timeout parameter is an implicit argument of the `Await.result` method, and therefore, needs to be declared as an argument (line 1). The only message, `Start`, triggers the computation of the data transformation of each future, and then the aggregation of the results (line 2). The `transform` and `compute` methods have the same semantics as those in the master-workers design.

### The generic message handler



You may have read or even written examples of actors that have generic case `_ =>` handlers in the message loop for debugging purposes. The message loop takes a partial function as argument. Therefore, no error or exception is thrown in case the message type is not recognized. There is no need for such a handler aside from one for debugging purposes. Message types should inherit from a sealed abstract class or a sealed trait in order to prevent a new message type from being added by mistake.

Let's have a look at the `transform` method. Its main purpose is to instantiate, launch, and return an array of futures responsible for the transformation of the partitions, as shown in the following code:

```
def transform: Array[Future[DblSeries]] = {
 val partIdx = partitioner.split(xt)
 val partitions = partIdx.map(n =>
 XTSeries[Double](xt.slice(n - partIdx(0), n).toArray)) //3

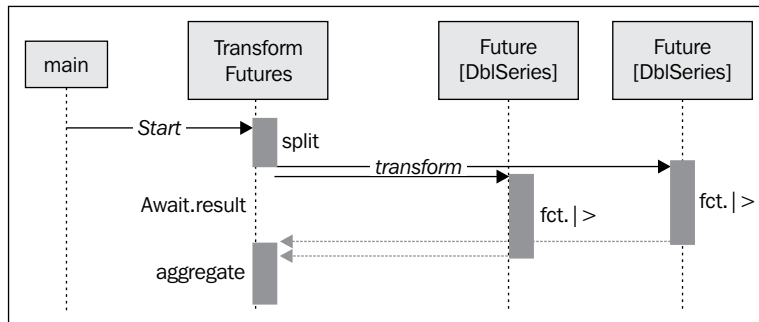
 val futures = new Array[Future[DblSeries]](partIdx.size) //4
 partitions.zipWithIndex.foreach(pi => {
 futures(pi._2) = Future[DblSeries] { fct |> pi._1 }
 })
 futures
}
```

First, the `transform` method splits the input time series into several partitions (line 3), similar to the master Actor in the previous section. An array of futures (one future per partition) is created (line 4). Each future executes the data transformation, `fct`, to the partition assigned to the future (line 5) as the worker Actor did in the previous section.

The `compute` method has the same purpose as the `aggregate` method in the master-workers design. The execution of the Actor is blocked until the `Await` class method (line 6) `scala.concurrentAwait.result` returns the result of each future computation. In the case of the discrete Fourier transform, the list of frequencies is transposed before the amplitude of each frequency is summed (7), as follows:

```
def compute(futures: Array[Future[DblSeries]]): Seq[Double] = {
 val results = futures.map(Await.result(_, timeout.duration))
 aggregate(results)
}
```

The following sequential diagram illustrates the blocking design and the activities performed by the Actor and the futures:



Sequential diagram for actor blocking on future results

## Handling future callbacks

Callbacks are an excellent alternative to having the actor blocks on futures, as they can simultaneously execute other functions concurrently with the future execution.

There are two simple ways to implement the callback function:

- `Future.onComplete`
- `Future.onSuccess` and `Future.onFailure`

The `onComplete` callback function takes a function of type `Try[T] => U` as argument with an implicit reference to the execution context, as shown in the following code:

```
val f: Future[T] = future { executeSomeTask }
f onComplete {
 case Success(s) => { ... }
 case Failure(e) => { ... }
}
```

You can surely recognize the `{Try, Success, Failure}` monad.

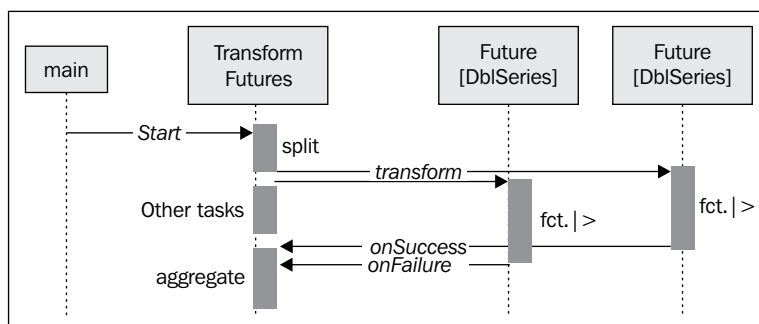
An alternative implementation is to invoke the `onSuccess` and `onFailure` methods that use partial functions as arguments to implement the callbacks, as follows:

```
f onFailure { case e: Exception => { ... } }
f onSuccess { case t => { ... } }
```

The only difference between blocking one future data transformation and handling callbacks is the implementation of the `compute` method or reducer. The class definition, message handler, and initialization of futures are identical, as shown in the following code:

```
def compute(futures: Array[Future[DbfSeries]]): Seq[Double] = {
 val aggregation = new ArrayBuffer[DbfSeries]
 futures.foreach(f => {
 f onSuccess { //1
 case data: DbfSeries => aggregation.append(data)
 }
 f onFailure { //2
 case e: Exception => aggregation.append(XTSeries.empty)
 }
 })
 if(aggregation.find(_.isEmpty) == None) //3
 aggregate(aggregation.toArray) //4
 else Seq.empty
}
```

Each future calls the master Actor back with either the result of the data transformation, the `onSuccess` message (line 1), or an exception, the `onFailure` message (line 2). If every future succeeds (line 3), the values of every frequency for all the partitions are summed (line 4). The following sequential diagram illustrates the handling of the callback in the master Actor:



Sequential diagram for actor handling future result with Callbacks



**Execution context**

The Futures method requires that the execution context be implicitly provided by the developer. There are three different ways to define the execution context:



- Import the context:  
`import ExecutionContext.Implicits.global`
- Create an instance of the context within the actor (or actor context):  
`implicit val ec = ExecutionContext.fromExecutorService( ... )`
- Define the context when instantiating the future:  
`val f= Future[T] = { } (ec)`

**Putting all together**

Let's reuse the discrete Fourier transform. The client code uses the same synthetically created time series as with the master-worker test model.

The first step is to create a transform future for the discrete Fourier transform, `DFTTransformFuture`, as follows:

```
class DFTTransformFutures(xt: DblSeries, partitioner: Partitioner)
 (implicit timeout: Timeout)
 extends TransformFutures(xt, DFT[Double], partitioner) {

 override def aggregate(xt: Array[DblSeries]): Seq[Double] =
 xt.map(_.toArray).transpose.map(_.sum).toSeq
}
```

The only purpose of the `DFTTransformFuture` class is to define the aggregation method, `aggregate`, for the discrete Fourier transform, as follows:

```
import akka.pattern.ask
val duration = Duration(10000, "millis")
implicit val timeout = new Timeout(duration)
implicit val actorSystem = ActorSystem("system")

val xt = XTSeries[Double](Array.tabulate(NUM_DATAPOINTS)(h(_)))
val partitioner = new Partitioner(NUM_WORKERS)

val master = actorSystem.actorOf(Props(new DFTTransformFutures(xt,
partitioner)), "DFTTransform") //1
```

```

val future = master ? Start //2
Await.result(future, timeout.duration) //3
actorSystem.shutdown //4

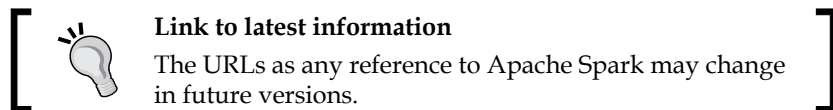
```

The master Actor is initialized as of the `TransformFutures` type with the input time series, `xt`; discrete Fourier transform, `DFT`; and `partitioner` as arguments (line 1). The program creates a `future` instance, by sending (`ask`) the `Start` message to `master`. The program blocks until the completion of the future (line 3), and then shuts down the Akka actor system (line 4).

## Apache Spark

Apache Spark is a fast and general-purpose cluster computing system, initially developed as **AMPLab / UC Berkeley** as part of the **Berkeley Data Analytics Stack (BDAS)**, [http://en.wikipedia.org/wiki/UC\\_Berkeley](http://en.wikipedia.org/wiki/UC_Berkeley). It provides high-level APIs for the following programming languages that make large, concurrent parallel jobs easy to write and deploy [12:11]:

- **Scala:** <http://spark.apache.org/docs/latest/api/scala/index.html>
- **Java:** <http://spark.apache.org/docs/latest/api/java/index.html>
- **Python:** <http://spark.apache.org/docs/latest/api/python/index.html>



The core element of Spark is **Resilient Distributed Dataset (RDD)**, which is a collection of elements partitioned across the nodes of a cluster and/or CPU cores of servers. An RDD can be created from a local data structure such as list, array, or hash table, from the local file system or the **Hadoop Distributed File System (HDFS)**.

The operations on an RDD in Spark are very similar to the Scala higher-order methods. These operations are performed concurrently over each partition. Operations on RDD can be classified as follows:

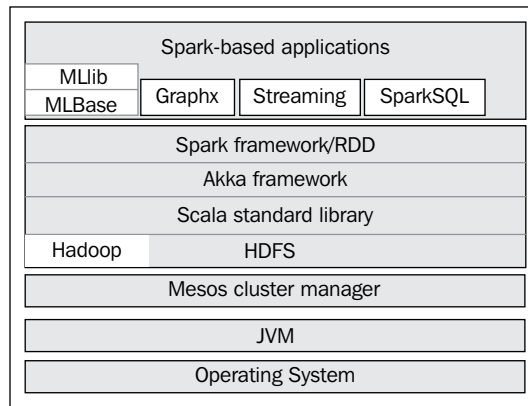
- **Transformation:** This operation converts, manipulates, and filters the elements of an RDD on each partition
- **Action:** This operation aggregates, collects, or reduces the elements of the RDD from all partitions

An RDD can persist, be serialized, and be cached for future computation.

Spark is written in Scala and built on top of Akka libraries. Spark relies on the following mechanisms to distribute and partition RDDs:

- Hadoop/HDFS for the distributed and replicated files system
- Mesos for management of cluster and shared pool of data nodes

The Spark ecosystem can be represented as stacks of technology and framework, as seen in the following diagram:



Spark framework ecosystem

The Spark ecosystem has grown to support some machine-learning algorithms out of the box, **MLlib**; a SQL-like interface to manipulate datasets with relational operators, **SparkSQL**; a library for distributed graphs, **GraphX**; and a streaming library [12:12].

## Why Spark

The authors of Spark attempt to address the limitations of Hadoop in terms of performance and real-time processing by implementing in-memory iterative computing, which is critical to most discriminative machine-learning algorithms. Numerous benchmark tests have been performed and published to evaluate the performance improvement of Spark relative to Hadoop. In the case of iterative algorithms, the time per iteration can be reduced by a ratio of 1:10 or more.

Spark provides a large array of prebuilt transforms and actions that go well beyond the basic map-reduce paradigm. Those methods on RDDs are a natural extension of the Scala collections, making code migration seamless for Scala developers.

Finally, Apache Spark supports fault-tolerant operations by allowing RDDs to persist both in memory and in the filesystems. Persistency enables automatic recovery from node failures. The resiliency of Spark relies on the supervisory strategy of the underlying Akka actors, the persistency of their mailboxes, and the replication schemes of HDFS.

## Design principles


The performance of Spark relies on four core design principles [12:13]:

- In-memory persistency
- Laziness in scheduling tasks
- Transform and actions applied to RDDs
- Implementation of shared variables

## In-memory persistency

The developer can decide to persist and/or cache an RDD for future usage. An RDD may persist in memory only or on disk only – in memory if available, or on disk otherwise as deserialized or serialized Java objects. For instance, an RDD, `rdd`, can be cached through serialization through a simple statement, as shown in the following code:

```
rdd.persist(StorageLevel.MEMORY_ONLY_SER).cache
```



**Kryo serialization**

Java serialization through the `Serializable` interface is notoriously slow. Fortunately, the Spark framework allows the developer to specify a more efficient serialization mechanism such as the **Kryo** library.

## Laziness

Scala supports lazy values natively. The left side of the assignment, which can either be a value, object reference, or method, is performed once, that is, the first time it is invoked, as shown in the following code:

```
class Pipeline {
 lazy val x = { println("x"); 1.5 }
 lazy val m = { println("m"); 3 }
 val n = { println("n"); 6 }
 def f = (m <<1)
```

```
def g(j: Int) = Math.pow(x, j)
}
val pipeline = new Pipeline //1
...
pipeline.g(pipeline.f) //2
```

The order of the variables printed is  $n$ ,  $m$ , and then  $x$ . The instantiation of the `Pipeline` class initializes  $n$  but not  $m$  or  $x$ . At a later stage, the `g` method is called, which in turn invokes the `f` method. The `f` method initializes the value  $m$  it needs, then `g` initializes  $x$  to compute its power to  $m < 1$ .

Spark applies the same principle to RDDs by executing the transformation only when an action is performed. In other words, Spark postpones memory allocation, parallelization, and computation until the driver code gets the result through the execution of an action. The cascading effect of invoking all these transformations backwards is performed by the direct acyclic graph scheduler.

## Transforms and Actions

Spark is implemented in Scala, so you should not be too surprised that the most relevant Scala higher methods on collections are supported in Spark. The first table describes the transformation methods using Spark, as well as their counterparts in the Scala standard library. We use the  $(K, V)$  notation for (key, value) pairs.

| Spark                         | Scala                   | Description                                                                                    |
|-------------------------------|-------------------------|------------------------------------------------------------------------------------------------|
| <code>map(f)</code>           | <code>map(f)</code>     | Transforms an RDD by executing the <code>f</code> function on each element of the collection.  |
| <code>filter(f)</code>        | <code>filter(f)</code>  | Transforms an RDD by selecting the element for which the <code>f</code> function returns true. |
| <code>flatMap(f)</code>       | <code>flatMap(f)</code> | Transforms an RDD by mapping each element to a sequence of output items.                       |
| <code>mapPartitions(f)</code> |                         | Executes the <code>map</code> method separately on each partition.                             |
| <code>sample</code>           |                         | Samples a fraction of the data with or without a replacement using a random generator.         |
| <code>groupByKey</code>       | <code>groupBy</code>    | Called on $(K, V)$ to generate a new $(K, Seq(V))$ RDD.                                        |
| <code>union</code>            | <code>union</code>      | Creates a new RDD as union of this RDD and the argument.                                       |
| <code>distinct</code>         | <code>distinct</code>   | Eliminates duplicate elements from this RDD.                                                   |
| <code>reduceByKey(f)</code>   | <code>reduce</code>     | Aggregates or reduces the value corresponding to each key using the <code>f</code> function.   |

| Spark     | Scala    | Description                                                                                                  |
|-----------|----------|--------------------------------------------------------------------------------------------------------------|
| sortByKey | sortWith | Reorganizes $(K, V)$ in an RDD by the ascending, descending, or otherwise specified order of the keys, $K$ . |
| join      |          | Joins an RDD $(K, V)$ with an RDD $(K, W)$ to generate a new RDD $(K, (V, W))$ .                             |
| coGroup   |          | Implements a join operation but generates an RDD $(K, Seq(V), Seq(W))$ .                                     |

Action methods trigger the collection or the reduction of the datasets from all partitions back to the driver, as listed here:

| Spark          | Scala     | Description                                                                                                |
|----------------|-----------|------------------------------------------------------------------------------------------------------------|
| reduce(f)      | reduce(f) | Aggregates all the elements of the RDD across all the partitions and returns a Scala object to the driver. |
| collect        | collect   | Collects and returns all the elements of the RDD across all the partitions as a list in the driver.        |
| count          | count     | Returns the number of elements in the RDD to the driver.                                                   |
| first          | head      | Returns the first element of the RDD to the driver.                                                        |
| take(n)        | take(n)   | Returns the first $n$ elements of the RDD to the driver.                                                   |
| takeSample     |           | Returns an array of random elements from the RDD back to the driver.                                       |
| saveAsTextFile |           | Writes the elements of the RDD as a text file in either the local files system or HDFS.                    |
| countByKey     |           | Generates a $(K, Int)$ RDD with the original keys, $K$ , and the count of values for each key.             |
| foreach        | foreach   | Executes a $T \Rightarrow Unit$ function on each elements of the RDD.                                      |

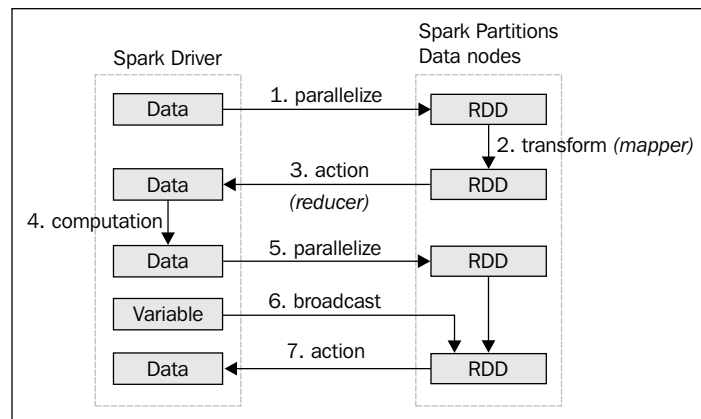
Scala methods such as `fold`, `find`, `drop`, `flatten`, `min`, `max`, and `sum` are not currently implemented in Spark. Other Scala methods such as `zip` have to be used carefully, as there is no guarantee that the order of the two collections in `zip` is maintained between partitions.

## Shared variables

In a perfect world, variables are immutable and local to each partition to avoid race conditions. However, there are circumstances where variables have to be shared without breaking the immutability provided by Spark. To this extent, Spark duplicates shared variables and copies them to each partition of the dataset. Spark supports the following types of shared variables:

- **Broadcast values:** These values encapsulate and forward data to all the partitions
- **Accumulator variables:** These variables act as summations or reference counters

The four design principles can be summarized in the following diagram:



Interaction between Spark driver and RDDs

The preceding diagram illustrates the most common interaction between the Spark driver and its workers, as listed in the following steps:

1. The input data, residing in either memory as a Scala collection or HDFS as a text file, is parallelized and partitioned into an RDD
2. A transformation function is applied on each element of the dataset across all the partitions
3. An action is performed to reduce and collect the data back to the driver
4. The data is processed locally within the driver
5. A second parallelization is performed to distribute computation through the RDDs
6. A variable is broadcast to all the partitions as an external parameter of the last RDD transformation


7. Finally, the last action aggregates and collects the final result back in the driver

If you look closely, the management of datasets and RDDs by the Spark driver is not very different from that by Akka master and worker actors of futures.

## Experimenting with Spark

Spark's in-memory computation for iterative computing makes it an excellent candidate to distribute the training of machine learning models, implemented with dynamic programming or optimization algorithms. Spark runs on Windows, Linux, and Mac OS operating systems. It can be deployed either in local mode for a single host, or master mode for a distributed environment. The version of the Spark framework used is 1.1.

[



**Scala- and Java SE-compatible versions**

At the time of writing, the version of Spark 1.0.0 required Java 1.7+ and Scala 2.10.2 or 2.10.3. Spark 1.1 is compatible with both Java 1.7 and 1.8 and Scala 2.10.4 and 2.11.1.

]

## Deploying Spark

The easiest way to learn Spark is to deploy a localhost in standalone mode. You can either deploy a precompiled version of Spark from the website, or build the JAR files using the **simple build tool (sbt)** or maven [12:14] as follows:

1. Go to the download page at <http://spark.apache.org/downloads.html>.
2. Choose a package type (Hadoop distribution). The Spark framework relies on HDFS to run in cluster mode; therefore, you need to select a distribution of Hadoop, or an open source distribution, MapR or Cloudera.
3. Download and decompress the package.
4. If you are interested in the latest functionality added to the framework, check out the newest source code at <https://github.com/apache/spark.git>.
5. Next, you need to build, or assemble, the Apache Spark libraries from the top-level directory using either Maven or sbt:

- **Maven:** Set the following maven options to support build, deployment, and execution:

```
MAVEN_OPTS="-Xmx4g -XX:MaxPermSize=512M
-XX:ReservedCodeCacheSize=512m"
mvn -DskipTests clean package
```



- **Simple build tool:** Use the following command:

```
sbt/sbt assembly
```



#### Installation instructions

The directory and name of artifacts used in Spark will undoubtedly change over time. Please refer to the documentation and installation guide for the latest version of Spark.

## Using Spark shell

Use any of the following methods to use the Spark shell:

- The shell is an easy way to get your feet wet with Spark-resilient distributed datasets (RDD). To launch the shell locally, execute `./bin/spark-shell -master local[8]` to execute the shell on an 8-core localhost.
- To launch a Spark application locally, connect with the shell and execute the following command line:

```
./bin/spark-submit --class application_class --master local[4]
--executor-memory 12G --jars myApplication.jar -class myApp.class
```

The command launches the application, `myApplication`, with the main method, `myApp.main`, on a 4-core CPU local host, and 12 GB of memory.

- To launch the same Spark application remotely, connect with the shell execute the following command line:

```
./bin/spark-submit --class application_class --master
spark://162.198.11.201:7077 -total-executor-cores 80 --executor-
memory 12G --jars myApplication.jar -class myApp.class
```

```
Using Spark's default log4j profile: org/apache/spark/log4j-defaults.properties
14/10/13 14:12:36 INFO SecurityManager: SecurityManager: authentication disabled;
14/10/13 14:12:36 INFO HttpServer: Starting HTTP Server
14/10/13 14:12:36 INFO Utils: Successfully started service 'HTTP class server'
Welcome to

 SPARK version 1.1.0

Using Scala version 2.10.4 (Java HotSpot(TM) 64-Bit Server VM, Java 1.7.0_45)
Type in expressions to have them evaluated.
Type :help for more information.

14/10/13 14:12:40 INFO SparkILoop: Created spark context..
Spark context available as sc.
```

Partial screenshot of Spark shell



### Potential pitfalls with Spark shell

Depending on your environment, you might need to disable logging information into the console by reconfiguring `conf/log4j.properties`. The Spark shell might also conflict with the declaration of classpath in the profile or the environment variables list. In this case, it has to be replaced by `ADD_JARS` as environment variable as `ADD_JARS = path1/jar1, path2/jar2`.

## MLlib

MLlib is a scalable machine learning library built on top of Spark. As of version 1.0, the library is a work in progress.

The main components of the library are as follows:

- Classification algorithms, including logistic regression, Naïve Bayes, and support vector machines
- Clustering limited to K-means in version 1.0
- L1 and L1 regularization
- Optimization techniques such as gradient descent, logistic gradient and stochastic gradient descent, and L-BFGS.
- Linear algebra such as singular value decomposition
- Data generator for K-means, logistic regression, and support vector machines

The machine learning bytecode is conveniently included in the Spark assembly JAR file built with the simple build tool.

## RDD generation

The transformation and actions are performed on RDDs. Therefore, the first step is to create a mechanism to facilitate the generation of RDDs from a time series. Let's create an `RDDSource` singleton with a `convert` method that transforms a time series, `xt`, into an RDD, as shown here:

```
def convert(xt: XTSeries[DblVector], rddConfig: RDDConfig)(implicit
 sc: SparkContext): RDD[DblVector] = {
 val rdd: = sc.parallelize(xt.toArray
 .map(new DenseVector(_))) //1
 rdd.persist(rddConfig.persist) //2
 if(rddConfig.cache) rdd.cache //3
 rdd
}
```


The last parameter, `rddConfig`, specifies the configuration for the RDD. In this example, the configuration of the RDD consists of enabling/disabling cache and selecting the persistency model, as follows:

```
case class RDDConfig(val cache: Boolean, val persist: StorageLevel)
```

It is fair to assume that `SparkContext` has already been implicitly defined in a manner quite similar to `ActorSystem` in the Akka framework.

The generation of the RDD is performed in the following steps:

1. Create an RDD by using the `parallelize` method of the context and converting into a vector (`SparseVector` or `DenseVector`) (line 1)
2. Specify the persistency model or the storage level if the default level needs to be overridden for the RDD (line 2)
3. Specify whether the RDD has to persist in memory (line 3)

 **Alternative for the creation of an RDD**  
An RDD can be generated from data loaded from either the local filesystems or HDFS using the `SparkContext.textFile` method that returns an RDD of string.

Once the RDD is created, it can be used as an input for any algorithm defined as a sequence of transformation and actions. Let's experiment with the implementation of the K-means algorithm in Spark/MLlib.

## K-means using Spark

The first step is to create a `SparkKMeansConfig` class to define the configuration of the Apache Spark K-means algorithm, as follows:

```
class SparkKMeansConfig(K: Int, maxIters: Int, numRuns: Int =1) {
 val kmeans: KMeans = {
 val kmeans = new KMeans
 kmeans.setK(K) //4
 kmeans.setMaxIterations(maxIters) //5
 kmeans.setRuns(numRuns) //6
 kmeans
 }
}
```

The minimum set of initialization parameters for MLlib K-means algorithm is as follows:

- Number of clusters,  $\kappa$  (line 4)
- Maximum number iterations for the reconstruction of the total error, `maxIters` (line 5)
- The number of training runs, `numRuns` (line 6)

The `SparkKMeans` class wraps the Spark `KMeans` into a data transformation of type `PipeOperator` so that it can be used in a computation workflow. The class follows the design template for classifier as explained in the *Design template for classifiers* section in *Appendix A, Basic Concepts*.

```
class SparkKMeans(config: SparkKMeansConfig, rddConfig: RDDConfig, xt:
 XTSeries[DblVector])(implicit sc: SparkContext)
 extends PipeOperator[DblVector, Int] {
 val model = config.kmeans.run(RDDSource.convert(xt, rddConfig))
 ...
}
```

The constructor takes three arguments: the Apache Spark `KMeans` configuration, `config`; the RDD configuration, `rddConfig`; and the input time series to clustering, `xt`. The generation of `model` merely consists of converting the time series `xt` into an RDD using `rddConfig` and invoking MLlib `KMeans.run`. Once created, the clusters (`KMeansModel`) are available for predicting new observation, `obs`, as follows:

```
def |> : PartialFunction[DblVector, Int] = {
 case x: DblVector if(x!= null && x.size>0 && model != null) =>
 model.predict(new DenseVector(x))
}
```

The prediction method, `|>`, returns the index of the cluster of observations.

Finally, let's write a simple client program to exercise the `SparkKMeans` model using the trading volume of each trading session, and the volatility of the price of the stock during the session:

```
val K = 8; val MAXITERS = 100; val NRUNS = 16
val PATH = "resources/data/chap12/CSCO.csv"
val CACHE = true
val extractors = List[Array[String] => Double](
 YahooFinancials.volatility, YahooFinancials.volume) //7
)
val input = DataSource(PATH, true) |> extractors //8

val volatilityVol = input(0).zip(input(1)) //9
```

```

 .map(x => Array[Double](x._1, x._2))

 implicit val sc = new SparkContext("Local","SparkKMeans") //10
 val config = new SparkKMeansConfig(K, MAXITERS, NRUNS)
 val rddConfig = RDDConfig(CACHE , StorageLevel.MEMORY_ONLY)
 val xt = XTSeries[DblVector](volatilityVol)


 val sparkKMeans = SparkKMeans(config, rddConfig, xt) //11
 val obs = Array[Double](0.23, 0.67)
 val clusterId = sparkKMeans |> obs//12
 Display.show(s"cluster = $clusterId", logger)

```

The first step is to define the variable to be extracted from the CSV file (line 7). The spark context is created (line 10) once the volatility and volume are extracted (line 8) and zipped (line 9). The K-means wrapper, `sparkKMeans`, is initialized (line 11). The final step consists of correctly predicting the cluster for a new observation (line 12).

## Performance evaluation

Let's execute the normalization of the cross-validation group on an 8-core CPU machine with 32 GB of RAM. The data is partitioned with a ratio of two partitions per CPU core.



**Meaningful performance test**  
 The scalability test should be performed with a large number of data points (normalized volatility, normalized volume), in excess of 1 million in order to be meaningful.

The actual values of the data points have no bearing on the overall performance of the Spark cluster.

## Tuning parameters

The performance of a Spark application depends greatly on the configuration parameters. Selecting the appropriate value for those configuration parameters in Spark can be overwhelming – there are 54 configuration parameters as of the last count. Fortunately, the majority of those parameters have relevant default values. However, there are few parameters that deserve your attention, including:

- Number of cores available to execute transformation and actions on RDDs: `config.cores.max`.

- Memory available for the execution of the transformation and actions `spark.executor.memory`. Setting the value as 60 percent of the maximum JVM heap is a generally a good compromise.
- Number of concurrent tasks to use across all the partitions for shuffle-related operations, they use key such as `reduceByKey: spark.default.parallelism`. The recommended formula is *parallelism = total number of cores x 2*. The value of the parameter can be overridden with the `spark.reduceby.partitions` parameter for specific RDD reducers.
- Flag to compress serialized RDD partition for `MEMORY_ONLY_SER: spark.rdd.compress`. The purpose is to reduce memory footprints at the cost of extra CPU cycles.
- Maximum size of message containing the results of an action sent to the `spark.akka.frameSize` driver. This value has to be increased if a collection may potentially generate a large size array.
- Flag to compress large size broadcasted `spark.broadcast.compress` variables. It is usually recommended.

## Tests

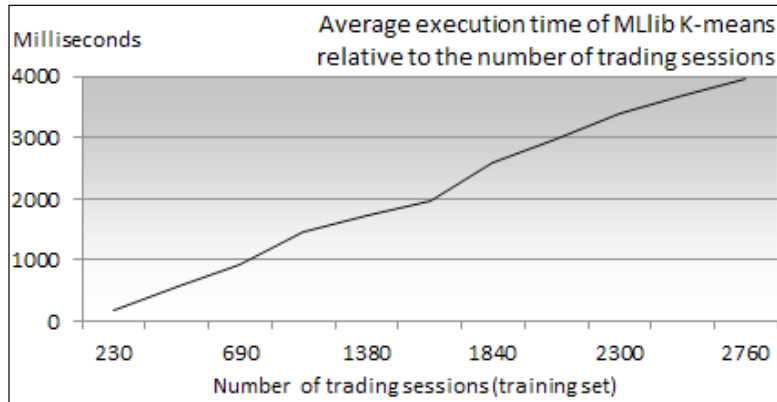
The purpose of the test is to evaluate how the execution time is related to the size of the training set. The test executes K-means from MLlib library on the volatility and trading session volume on **Bank of America (BAC)** stock over the following periods: 3 months, 6 months, 12 months, 24 months, 48 months, 60 month, 72 month, 96 months, and 120 months.

The following configuration is used to perform the training of the K-means: 10 clusters, 30 maximum iterations, and 3 runs. The test is run on a single host with 8-CPU cores and 32 GB RAM.

The test was conducted with the following values of parameters:

- `StorageLevel = MEMORY_ONLY`
- `spark.executor.memory=12G`
- `spark.default.parallelism = 48`
- `spark.akka.frameSize = 20`
- `spark.broadcast.compress=true`
- No serialization


The first step after executing a test for a specific dataset is to log in to the Spark monitoring console at `http://host_name:4040/stages`:



Average duration of K-means clustering versus size of trading data in months

Obviously, each environment produces somewhat different performance results, but confirms that the time complexity of the Spark K-means is a linear function of the training set.

**Evaluation in distributed environment**

 A Spark deployment on multiple hosts would add latency of the TCP communication to the overall execution time. The latency is related to the collection of the results of the clustering back to the Spark driver, which is negligible and independent of the size of the training set.

## Performance considerations

This test barely scratches the surface of the capabilities of Apache Spark. The following are the lessons learned from personal experience in order to avoid the most common performance pitfalls when deploying Spark 1.1:

- Get acquainted with the most common Spark configuration parameters regarding partitioning, storage level, and serialization.
- Avoid serializing complex or nested objects unless you use an effective Java serialization library such as Kryo.
- Look into defining your own partitioning function to reduce large key-value pair datasets. The convenience of `reduceByKey` has its price. The ratio of number of partitions to number of cores has an impact on the performance of a reducer using key.

- Avoid unnecessary actions such as `collect`, `count`, or `lookup`. An action reduces the data residing in the RDD partitions, and then forwards it to the Spark driver. The Spark driver (or master) program runs on a single JVM with limited resources.
- Relies on shared or broadcast variables whenever necessary. Broadcast variables, for instance, improve the performance of operations on multiple datasets with very different sizes. Let us consider the common case of joining two datasets of very different sizes. Broadcasting the smaller dataset to each partition of the RDD of the larger dataset is far more efficient than converting the smaller dataset into an RDD and executing a join operation between the two datasets.
- Use an accumulator variable for summation as it is faster than using a reduce action on an RDD.

## Pros and cons

An increasing number of organizations are adopting Spark as their distributed data processing platform for real-time, or pseudo real-time operations. There are several reasons for the fast adoption of Spark:

- Supported by a large and dedicated community of developers [12:15]
- In-memory persistency is ideal for iterative computation found in machine learning and statistical inference algorithms
- Excellent performance and scalability that can be extended with the Streaming module
- Apache Spark leverages Scala functional capabilities and a large number of open source Java libraries
- Spark can leverage the Mesos cluster manager, which reduces the complexity of defining fault-tolerance and load balancing between worker nodes
- Spark is to be integrated with commercial Hadoop vendors such as Cloudera

However, no platform is perfect and Spark is no exception. The most common complaints or concerns regarding Spark are:

- Creating a Spark application can be intimidating for a developer with no prior knowledge of functional programming.
- The integration with the database has been somewhat lagging, relying heavily on Hive. The Spark development team has started to address these limitations with the introduction of SparkSQL.



## Oxdata Sparkling Water

Sparkling water is an initiative to integrate **Oxdata H2O** with Spark and complement MLlib [12:16]. H2O from Oxdata is a very fast, open source, in-memory platform for machine learning for very large datasets, <http://0xdata.com/product/>. The framework is worth mentioning for the following reasons:

- It has a Scala API
- It is fully dedicated to machine learning and predictive analytics
- It leverages both the frame data representation of H2O and in-memory clustering of Spark

H2O has an extensive implementation of the generalized linear model and gradient boosted classification, among other goodies. Its data representation consists of hierarchical **data frames**. A data frame is a container of vectors potentially shared with other frames. Each vector is composed of **data chunks**, which themselves are containers of **data elements** [12:17]. At the time of writing, Sparkling Water is in beta version.

## Summary

This completes the introduction of the most common scalable frameworks built using Scala. It is quite challenging to describe frameworks such as Akka and Spark, as well as new computing models such as Actors, Futures, and RDDs, in a few pages. This chapter should be regarded as an invitation to further explore the capabilities of those frameworks in both a single host and a large deployment environment.

In this last chapter, we learned:

- The benefits of asynchronous concurrency
- The essentials of the actor model, composing futures with blocking or callback modes
- How to implement a simple Akka cluster to squeeze performance of distributed applications
- The ease and blazing performance of Spark's resilient distributed datasets and the in-memory persistency approach



# Basic Concepts

Machine learning algorithms make significant use of linear algebra and optimization techniques. Describing the concepts and the implementation of linear algebra, calculus, and optimization algorithms in detail would have added significant complexity to the book and distracted the reader from the essence of machine learning.

This appendix lists a set of basic elements of linear algebra and optimization mentioned throughout the book. It also summarizes the coding practices that have been covered, and acquaints the reader with basic knowledge of financial analysis.

## Scala programming

The following is a partial list of coding practices and design techniques used throughout the book.

## List of libraries

The `libraries` directory contains the JAR files related to the third-party libraries or frameworks used in this book. Not all libraries are needed for every chapter. The list is as follows:

- Apache Commons Math 3.3 in *Chapter 3, Data Preprocessing*; *Chapter 4, Unsupervised Learning*; and *Chapter 6, Regression and Regularization*
- JFChart 1.0.1 in *Chapter 1, Getting Started*; *Chapter 2, Hello World!*; *Chapter 5, Naïve Bayes Classifiers*; and *Chapter 9, Artificial Neural Networks*
- Itib CRF 0.2 (including L-BFGS and Colt libraries) in *Chapter 7, Sequential Data Models*
- LIBSVM 0.1.6 in *Chapter 8, Kernel Models and Support Vector Machines*
- Akka framework 2.2.4 in *Chapter 12, Scalable Frameworks*
- Apache Spark/MLlib 1.1 in *Chapter 12, Scalable Frameworks*



### Note for Spark developers

The Scala library and compiler JAR files bundled with the assembly JAR file of Apache Spark contain a version of the Scala standard library and compiler JAR file that may conflict with an existing Scala library (for example, Eclipse default ScalaIDE library).

## Format of code snippets

For the sake of readability of the implementation of algorithms, all non-essential pieces of code such as error checking, comments, exceptions, or imports have been omitted. *The following code elements have been discarded in the code snippets presented in the book:*

- Comments:

```
// The MathRuntime exception has to be caught here!
```

- Validation of class parameters and method arguments:

```
class BaumWelchEM(val lambda: HMMLambda ...) {
 require(lambda != null, "Lambda model is undefined")
}
```

- Class qualifiers such as final, private, and so on:

```
final protected class MLP[T <% Double] ...
```

- Method qualifiers and access controls (final, private, and so on):

```
final def inputLayer: MLPLayer
private def recurse: Unit =
```

- Java-style exceptions:

```
try { ... }
catch { case e: ArrayIndexOutOfBoundsException => ... }
if (y < EPS)
 throw new IllegalStateException(...)
```

- Scala-style exceptions:

```
Try(process(args)) match {
 case Success(results) => ...
 case Failure(e) => ...
}
```

- Non-essential annotations:

```
@inline def mean = { ... }
```

- Logging and debugging code:
 

```
m_logger.debug(...)
Console.println(...)
```
- Auxiliary methods not essential to the understanding of an algorithm

## Encapsulation

One important objective while creating an API is reducing access to supporting or helper classes. There are two options to encapsulate helper classes, as follows:

- **Package scope:** In this, the supporting classes are first-level classes with protected access
- **Class or object scope:** In this, the supported classes are nested in the main class

The algorithms presented in this book follow the first encapsulation pattern.

## Class constructor template

The constructors of a class are defined in the companion object using `apply` and the class has package scope (protected):

```
protected class MyClass[T](val x: X, val y: Y,...) { ... }
object MyClass {
 def apply[T](x: X, y:Y, ..): MyClass[T] = new MyClass(x,y,..)
 final val y0 = ..
 def apply[T](x: , ..): MyClass[T] = new MyClass(x, y0, ...)
}
```

For example, the configuration of the support vector machine classifier is defined as follows:

```
protected class SVMConfig(val formulation: SVMFormulation, val kernel:
SVMKernel, val svmExec: SVMExecution) extends Config
```

Its constructors are defined as follows:

```
object SVMConfig {
 val DEFAULT_CACHE = 25000
 val DEFAULT_EPS = 1e-15
 ...
 def apply(svmType: SVMFormulation, kernel: SVMKernel, svmExec:
SVMExecution): SVMConfig = new SVMConfig(svmType, kernel, svmExec)
```

```
def apply(svmType: SVMFormulation, kernel: SVMKernel): SVMConfig
= new SVMConfig(svmType, kernel, new SVMExecution(DEFAULT_CACHE,
DEFAULT_EPS, -1))
}
```

## Companion objects versus case classes

In the preceding example, the constructors are explicitly defined in the companion object. Although the invocation of the constructor is very similar to the instantiation of case classes, there is a major difference—the Scala compiler generates several methods to manipulate an instance as regular data (equals, copy, hash, and so on).

Case classes should be reserved for single-state data objects, that is, objects with no methods.

## Enumerations versus case classes

It is not uncommon to read or hear discussions regarding the relative merit of enumerations and pattern matching with case classes in Scala [A:1]. As a very general guideline, enumeration values can be regarded as lightweight case classes or case classes can be considered as heavyweight enumeration values.

Let's take an example of a Scala enumeration that consists of evaluating the uniform distribution of `scala.util.Random`:

```
object MyEnum extends Enumeration {
 type TMyEnum = Value
 val A, B, C = Value
}

import MyEnum._
val counters = Array.fill(MyEnum.maxId+1)(0)
Range(0, 1000).foreach(_ => Random.nextInt(10) match {
 case 3 => counters(A.id) += 1
 ...
 case _ => { }
})
```

The previous pattern matching is very similar to the `switch` statement of Java.

Let's consider the following example of pattern matching using case classes that selects a mathematical formula according to the input:

```
package MyPackage {
 sealed abstract class MyEnum(val level: Int)
 case class A extends MyEnum(3) { def f =(x:Double) => 23*x}
 ...
}

import MyPackage._
def compute(myEnum: MyEnum, x: Double): Double = myEnum match {
 case a: A => a.f(x)
 ...
}
```

The previous pattern matching is performed using the default equals method, whose byte code is automatically set for each case class. This approach is far more flexible than simple enumeration, at the cost of extra computation cycles.

The advantages of using enumerations over case classes are as follows:

- Enumerations involve less code for a single attribute comparison
- Enumerations are more readable, especially for Java developers

The advantages of using case classes are as follows:

- Case classes are data objects and support more attributes than enumeration IDs
- Pattern matching is optimized for sealed classes as the Scala compiler is aware of the number of cases

In a nutshell, you should use enumeration for single value constants and case classes to match data objects.

## Overloading

Contrary to C++, Scala does not actually overload operators. Here is the meaning of the operators used in code snippets:

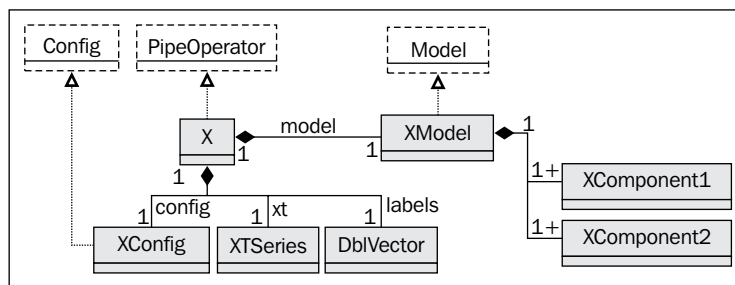
- +=: This adds an element to a collection or container.
- +: This sums two elements of the same type.
- |>: This transforms a collection of data. It is also known as pipe operator. The type of output collections and elements can be different from that of the input.

## Design template for classifiers

The machine learning algorithms described in this book use the following design pattern:

- A model instance that implements the `Model` trait is created through training during the initialization of the classifier
- All configuration parameters are encapsulated into a single configuration class inheriting the `Config` trait
- The predictive or classification routine is implemented as a data transformation extending the `PipeOperator` trait
- The classifier takes at least three parameters: configuration instance, a features set or time series, and a labeled dataset

Have a look at the following diagram:



A generic UML class diagram for classifiers

For example, the key components of the support vector machine package are as follows:

```

final protected class SVM[T <% Double](val config: SVMConfig, val xt:
XTSeries[Array[T]], val labels: DblVector)
 extends PipeOperator[Array[T], Double] {
 val model: Option[SVModel] = { ... }
 override def |> (x: Feature): Option[Double] = { prediction }
 ...
}

```


```

final protected class SVMConfig(val formulation: SVMFormulation, val
kernel: SVMKernel, val svmExec: SVMExecution) extends Config
protected class SVModel(val params: (svm_model, Double)) extends
Model

```

The two data inputs required to train a model are the configuration of the classifier (`config`) and the training set (`xt` and `labels`). Once trained and validated, the model is available for prediction or classification.

This design has the main advantage of reducing the life cycle of the classifier; a model is either defined, available for classification, or is not created.

 **Implementation considerations**  
The validation phase is omitted in most of the practical examples throughout this book for the sake of readability.

## Data extraction

A CSV file is the most common format used to store historical financial data. It is the default format used to import data throughout this book:

```
type Fields = Array[String]
class DataSource(pathName: String,
 normalize: Boolean,
 reverseOrder: Boolean,
 headerLines: Int = 1,
 srcFilter: Option[Fields=>Boolean])
 extends PipeOperator[List[Fields =>Double], List[DblVector]]
```

The parameters for the `DataSource` class are as follows:

- `pathName`: This is the relative pathname of a data file to be loaded if the argument is a file, or the directory containing multiple input data files. Most of the files are CSV files.
- `normalize`: This is a flag to specify if the data has to be normalized over  $[0, 1]$ .
- `reverseOrder`: This is a flag to specify whether the order of the data in the file has to be reversed—for example, time series—if its value is `true`.
- `headerLines`: This specifies the number of lines for column headers and comments.
- `srcFilter`: This is a filter or condition for some of the row fields to skip the data set, for example, missing data or incorrect format.



The most important method of `DataSource` is the following data transformation from a file to a typed time series (`XTSeries [T]`) implemented as the pipe operator method. The method takes the extractor from a row of literal values to `Double` floating-point values:

```
def |> : PartialFunction[List[Fields=>Double], List[DblVector]] = {
 case extr: List[Fields=>Double] if (extr != null && extr.size > 0) =>
 load match { //1
 case Some(data) => {
 if (normalize) // 2
 extr.map(t => Stats[Double](data._2.map(t(_))) //3
 .normalize) //4
 else extr.map(t => data._2.map(t(_)))
 }
 }
 ...
}
```

The data is loaded from the file and converted into a list of vectors using the extractor, `extr` (line 1). The data is normalized if required (line 2) by converting each literal to a floating point value and a `Stats` object is created (line 3). Finally, the `Stats` instance normalizes the sequence of floating-point values (line 4).

A second data transformation consists of transforming a single literal per row to create a time series of single variables:

```
def |> (extr: Fields => Double): Option[XTSeries[Double]]
```

## Data sources

The examples in this book rely on three different sources of financial data using CSV format:

- `YahooFinancials` for Yahoo schema for historical stock and ETF price
- `GoogleFinancials` for Google schema for historical stock and ETF price
- `Fundamentals` for fundamental financial analysis ratio (CSV file)

Let's illustrate the extraction from a data source using `YahooFinancials` as an example:

```
object YahooFinancials extends Enumeration {
 type YahooFinancials = Value
 val DATE, OPEN, HIGH, LOW, CLOSE, VOLUME, ADJ_CLOSE = Value
 val adjClose = ((s: Fields) => s(ADJ_CLOSE.id).toDouble)
 ...
}
```

```

def toDouble(v: Value): Fields => Double =
 (s: Fields) => s(v.id).toDouble

def vol: Fields => Double = (s: Fields) => {
 s(HIGH.id).toDouble/s(LOW.id).toDouble -1.0) * s(VOLUME.id).
toDouble)
}
...
}

```

Let's look at an example of application of a `DataSource` transformation: loading historical stock data from the Google finance website. The data is downloaded as a CSV-formatted file. The first step is to specify the column name using an enumeration singleton, `YahooFinancials`:

```

object GoogleFinancials extends Enumeration {
 type GoogleFinancials = Value
 val DATE, OPEN, HIGH, LOW, CLOSE, VOLUME = Value
 val close = ((s: Fields) => s(CLOSE.id).toDouble)//5
 ...
}

```

Each column is associated with an extractor function (line 5). Consider the following code:

```

val symbols = Array[String] ("CSCO", ...) //6
val prices = symbols
 .map(s => DataSource(path+s+".csv", true, true, 1))//7
 .map(_ |> YahooFinancials.close) //8

```

The list of stocks for which the historical data has to be downloaded is defined as an array of symbols (line 6). Each symbol is associated with a CSV file (for example, CSCO is associated with `resources/CSCO.csv`) (line 7). Finally, the `YahooFinancials` extractor for the close price is invoked (line 8).

## Extraction of documents

The `DocumentsSource` class is responsible for extracting the date, title, and content of a list of text documents or text files. This class does not support HTML documents:

```

class DocumentsSource(val pathName: String)

```

The extraction of terms is performed by the data transformation `|>`, as follows:

```
def |> : Corpus = {
 filesList.map(fName => {
 val src = Source.fromFile(pathName + fName) //1
 val fieldIter = src.getLines //2

 val date = nextField(fieldIter)
 val title = nextField (fieldIter)
 val content = fieldIter.foldLeft(new StringBuilder)((b, str)
 => b.append(str.trim)) //3

 src.close //4
 if(date == None || title == None)
 throw new IllegalStateException(...) //6
 (date.get, title.get, content.toString) //5
 })
}
```

This method loads the text files for each filename in the list, `filesList` (line 1). It gets a reference to the document lines iterator, `fieldIter` (line 2). The iterator is used to extract (line 3) and return the tuple (document date, document title, document content) (line 5) once the file handle is closed (line 4). An `IllegalStateException` is thrown and caught if the text file is malformed. The `nextField` method moves the iterator forward to the next non-null line:

```
def nextField(iter: Iterator[String]): Option[String] =
 iter.find(s=> (s != null && s.length > 1))
```

## Matrix class

Some discriminative learning models require operations performed on rows and columns of the matrix. The parameterized `Matrix` class facilitates the read/write operations on columns and rows:

```
class Matrix[@specialized(Double, Int) T: ClassTag](val nRows: Int,
 val nCols: Int, val data:Array[T])(implicit f: T => Double){
 def apply(i: Int, j: Int): T = data(i*nCols+j)
 def cols(i: Int): Array[T] = {
 (i until data.size by nCols)
 .map(data(_)).toArray
 }
 ...
 def += (i: Int, j : Int, t: T): Unit = data(i*nCols +j) = t
 def += (iRow: Int, t: T): Unit = {
 val i = iRow*nCols
```

```

 Range(0, nCols).foreach(k => data(i + k) =t)
 }
 def /= (iRow: Int, t: T)(implicit g: Double => T): Unit = {
 val i = iRow*nCols
 Range(0, nCols).foreach(k => data(i + k) /= t)
 }
}

```

The `apply` method returns an element. Similarly, the `cols` method returns a column. The write methods consist of updating an element or a column of elements (`+=`) with a value and dividing the elements of a column by a value (`/=`). The matrix is specialized with the type `Double` in order to generate a dedicated byte code for this type.

The generation of the transpose matrix is performed by the `transpose` method. It is an alternative to the Scala methods `Array.transpose` and `List.transpose`:

```

def transpose: Matrix[T] = {
 val m = Matrix[T](nCols, nRows)
 Range(0, nRows).foreach(i => {
 val col = i*nCols
 Range(0, nCols).foreach(j => m += (j, i, data(col+j)))
 })
 m
}

```

The constructors of the `Matrix` class are defined by its companion object:

```

def apply[T: ClassTag](nR: Int, nC: Int, data: Array[T])
 (implicit f: T => Double): Matrix[T] =
 new Matrix(nRows, nCols, data)

```

## Mathematics

This section describes very briefly some of the mathematical concepts used in this book.

### Linear algebra

Many algorithms used in machine learning such as minimization of a convex loss function, principal component analysis, or least squares regression invariably involve manipulation and transformation of matrices. There are many good books on the subject, from the inexpensive [A:2] to the sophisticated [A:3].

## QR Decomposition

QR decomposition (or QR factorization) is the decomposition of a matrix  $A$  into a product of an orthogonal matrix  $Q$  and upper triangular matrix  $R$ . So,  $A=QR$  and  $Q^TQ=I$  [A:4].

The decomposition is unique if  $A$  is a real, square, and invertible matrix. In the case of a rectangle matrix  $A$ ,  $m$  by  $n$  with  $m > n$ , the decomposition is implemented as the dot product of two vectors of matrix  $A = [Q_1, Q_2] \cdot [R_1, R_2]^T$ , where  $Q_1$  is an  $m$  by  $n$  matrix,  $Q_2$  is an  $m$  by  $n$  matrix,  $R_1$  is an  $n$  by  $n$  upper triangular matrix, and  $R_2$  is an  $m$  by  $n$  null matrix.

QR decomposition is a reliable method of solving a large system of linear equations in which the number of equations (rows) exceeds the number of variables (columns). Its asymptotic computational time complexity for a training set of  $m$  dimensions and  $n$  observations is  $O(mn^2-n^3/3)$ .

It is used to minimize the loss function for ordinary least squares regression (refer to the *Ordinary least squares (OLS) regression* section of *Chapter 6, Regression and Regularization*).

## LU factorization

**LU factorization** is a technique used to solve a matrix equation  $A \cdot x = b$  where  $A$  is a non-singular matrix and  $x$  and  $b$  are two vectors. The technique consists of decomposing the original matrix  $A$  as the product of simple matrices  $A = A_1 A_2 \dots A_n$ . It is of two types as follows:

- **Basic LU factorization:** This defines  $A$  as the product of a unit lower triangular matrix  $L$  and an upper triangular matrix  $U$ . So,  $A = LU$ .
- **LU factorization with pivot:** This defines  $A$  as the product of a permutation matrix  $P$ , a unit lower triangular matrix  $L$ , and an upper triangular matrix  $U$ . So,  $A = PLU$ .

## LDL decomposition

**LDL decomposition** for real matrices defines a real positive matrix  $A$  as the product of a lower unit triangular matrix  $L$ , a diagonal matrix  $D$ , and the transposed matrix of  $L$ , that is  $L^T$ . So,  $A = LDL^T$ .

## Cholesky factorization

The **Cholesky factorization** or Cholesky decomposition of real matrices is a special case of LU factorization [A:4]. It decomposes a positive definite matrix  $A$  into a product of a lower triangular matrix  $L$  and its conjugate transpose  $L^T$ . So,  $A = LL^T$ .

---

The asymptotic computational time complexity for the Cholesky factorization is  $O(mn^2)$ , where  $m$  is the number of features (model parameters) and  $n$  is the number of observations. Cholesky factorization is used in the linear least squares Kalman filter (refer to the *The recursive algorithm* section of *Chapter 3, Data Preprocessing*).

## Singular value decomposition

The **singular value decomposition (SVD)** of real matrices defines an  $m$  by  $n$  real matrix  $A$  as the product of an  $m$  square real unitary matrix  $U$ , an  $m$  by  $n$  rectangular diagonal matrix  $\Sigma$ , and the transpose  $V^T$  matrix of a real matrix. So,  $A=U\Sigma V^T$ .

The columns of the matrices  $U$  and  $V$  are the orthogonal bases and the value of the diagonal matrix  $\Sigma$  is a singular value [A:4]. The asymptotic computational time complexity for the singular value decomposition for  $n$  observations and  $m$  features is  $O(mn^2-n^3)$ . Singular value decomposition is used to minimize the total least squares and solve homogeneous linear equations.

## Eigenvalue decomposition

The Eigen decomposition of a real square matrix  $A$  is the canonical factorization as  $Ax = \lambda x$ .

$\lambda$  is the **eigenvalue** (scalar) corresponding to the vector  $x$ . The  $n$  by  $n$  matrix  $A$  is then defined as  $A = QDQ^T$ .  $Q$  is the square matrix that contains the eigenvectors and  $D$  is the diagonal matrix whose elements are the eigenvalues associated to the eigenvectors [A:5], [A:6]. Eigen decomposition is used in Principal Components Analysis (refer to the *Principal components analysis (PCA)* section of *Chapter 4, Unsupervised Learning*).


## Algebraic and numerical libraries

There are many more open source algebraic libraries available to developers as APIs besides Apache Commons Math, which is used in *Chapter 3, Data preprocessing*; *Chapter 5, Naïve Bayes Classifiers*, and *Chapter 6, Regression and Regularization*, and Apache Spark/MLlib used in *Chapter 12, Scalable Frameworks*. They are as follows:

- **jBlas 1.2.3** (Java) created by Mikio Braun under the BSD revised license. This library provides Java and Scala developers a high-level Java interface to **BLAS** and **LAPACK**. It is available at <https://github.com/mikiobraun/jblas>.
- **Colt 1.2.0** (Java) is a high-performance scientific library developed at CERN under the European Organization for Nuclear Research license. It is available at <http://acs.lbl.gov/ACSSoftware/colt/>.

- **AlgeBird 2.10** (Scala) developed at Twitter under Apache Public License 2.0. It defines concepts of abstract linear algebra using monoids and monads. This library is an excellent example of high-level functional programming using Scala. It is available at <https://github.com/twitter/algebird>.
- **Breeze 0.8** (Scala) is a numerical processing library using Apache Public License 2.0 originally created by David Hall. It is a component of the **ScalaNLP** suite of machine learning and numerical computing libraries, and it is available at <http://www.scalanlp.org/>.

The Apache Spark/MLlib framework bundles jBlas, Colt, and Breeze. The Iltb framework for conditional random fields uses Colt linear algebra components.



**Alternative to Java/Scala libraries**

If your application or project needs a high-performance numerical processing tool under limited resources (CPU, RAM memory, and so on), and if portability is not a constraint, then using a C- or C++-compiled library is an excellent alternative. The binary functions can be accessed through the **Java Native Interface (JNI)**.

## First order predicate logic

**Propositional logic** is the formulation of axioms or propositions. There are several formal representations of propositions:

- Noun-VERB-*Adjective*: "Variance of the stock price EXCEEDS 0.76" or "Minimization of the loss function DOES NOT *converge*"
- Entity-value = *Boolean*: " Variance of the stock price GREATER+THAN 0.76 = *true*" or "Minimization of the loss function converge = *false*"
- Variable *op* value: "Variance\_stock\_price > 0.76" or "Minimization\_loss\_function != converge"

Propositional logic is subject to the rules of Boolean calculus. Let's consider three propositions  $P$ ,  $Q$ , and  $R$  and three Boolean operators NOT, AND, OR. So the following rules apply:

- NOT (NOT  $P$ ) =  $P$
- $P$  AND false = false,  $P$  AND true =  $P$ ,  $P$  OR false =  $P$ ,  $P$  OR true =  $P$
- $P$  AND  $Q$  =  $Q$  AND  $P$ ,  $P$  OR  $Q$  =  $Q$  OR  $P$
- $P$  AND ( $Q$  AND  $R$ ) = ( $P$  AND  $Q$ ) AND  $R$

**First-order predicate logic**, also known as first-order predicate calculus, is the quantification of propositional logic [A:7]. The most common formulations of the first order logic are as follows:

- IF P THEN action rules
- Existential operators

First order logic is used to describe the classifiers in learning classifier systems. Refer to the *XCS rules* section of *Chapter 11, Reinforcement Learning* for more information.

## Jacobian and Hessian matrices

Let's consider a function with  $n$  variables  $x_i$  and  $m$  outputs  $y_j$  such that  $f: \{x_i\} \rightarrow \{y_j = f_j(x)\}$ .

The **Jacobian matrix** [A:8] is the matrix of the first order partial derivatives of the output values of a continuous, differential function:

$$J(f) = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \dots & \frac{\partial f_1}{\partial x_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial f_m}{\partial x_1} & \dots & \frac{\partial f_m}{\partial x_n} \end{bmatrix}$$

The **Hessian matrix** is the square matrix of the second order of partial derivatives of a continuous, twice differentiable function:

$$H(f) = \begin{bmatrix} \frac{\partial^2 f}{\partial x_1^2} & \dots & \frac{\partial^2 f}{\partial x_1 \partial x_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial^2 f}{\partial x_n \partial x_1} & \dots & \frac{\partial^2 f}{\partial x_n^2} \end{bmatrix}$$

An example is as follows:

$$f(x, y) = x^2 y + e^{-y} \quad J(f) = [2xy, x^2 - e^{-y}] \quad H(f) = \begin{bmatrix} 2y & 2x \\ 2x & e^{-y} \end{bmatrix}$$



## Summary of optimization techniques

The same comments regarding linear algebra algorithms apply to optimization. Treating such techniques in depth would have rendered the book impractical. However, optimization is critical to the efficiency and, to a lesser extent, the accuracy of the machine learning algorithms. Some basic knowledge in this field goes a long way to build practical solutions for large data sets.

## Gradient descent methods

### Steepest descent

The **steepest descent** (or gradient descent) method is one of the simplest techniques used to find a local minimum of any continuous, differentiable function  $F$  or the global minimum of any defined, differentiable, and convex function [A:9]. The value of a vector or data point  $x_{t+1}$  at the iteration  $t + 1$  is computed from the previous value  $x_t$  using the gradient  $\nabla F$  of function  $F$  and the slope  $\gamma$ :

$$x_{(t+1)} = x_{(t)} - \gamma \nabla F(a)$$

The steepest gradient algorithm is used for solving systems of non-linear equations and minimization of the loss function in the logistic regression (refer to the *Numerical optimization* section of *Chapter 6, Regression and Regularization*), in support vector classifiers (refer to the *The nonlinear SVM* section of *Chapter 8, Kernel Models and Support Vector Machines*), and in multilayer perceptrons (refer to the *The multilayer perceptron (MLP)* section of *Chapter 9, Artificial Neural Networks*).

### Conjugate gradient

The **conjugate gradient** solves unconstrained optimization problems and systems of linear equations. It is an alternative to the LU factorization for positive, definite, and symmetric square matrices. The solution  $x^*$  to the equation  $Ax = b$  is expanded as the weighted summation of  $n$  basis orthogonal directions  $p_i$  (or conjugate directions):

$$Ax = b \rightarrow \sum_{i=0}^{n-1} \alpha_i p_i x^* = b; \quad p_i \cdot p_j = 0$$

The solution  $x^*$  is extracted by computing the  $i^{\text{th}}$  conjugate vector  $p_i$  and then computing the coefficients  $a_i$ .

## Stochastic gradient descent

The **stochastic gradient** method is a variant of the steepest descent method that minimizes the convex function by defining the objective function  $F$  as the sum of differentiable, basis functions  $f_i$ :

$$F(x) = \sum_{i=0}^{n-1} f_i(x), \quad x_{t+1} = x_t - \alpha \sum_{i=0}^{n-1} \nabla f_i(x)$$

The solution  $x_{t+1}$  at iteration  $t+1$  is computed from the value  $x_t$  at iteration  $t$ , the step size (or learning rate)  $\alpha$ , and the sum of the gradient of the basis functions [A:10].

The stochastic gradient descent is usually faster than other gradient descent or quasi-Newton methods in converging towards a solution for convex functions. The stochastic gradient descent method is used in logistic regression, support vector machines, and back-propagation neural networks.

Stochastic gradient is particularly suitable for discriminative models with large datasets [A:11]. Spark/MLlib makes extensive use of the stochastic gradient method.

## Quasi-Newton algorithms

**Quasi-Newton algorithms** are variations of Newton's method of finding the value of a vector or data point that maximizes or minimizes a function  $F$  whose first order derivative is null [A:12].

Newton's method is a well-known and simple optimization method used to find the solution to equations  $F(x) = 0$  for which  $F$  is continuous and differentiable up to the second order. It relies on the Taylor series expansion to approximate the function  $F$  with a quadratic approximation on the variable  $\Delta x = x_{t+1} - x_t$  to compute the value at the next iteration using the first order  $F'$  and second order  $F''$  derivatives:

$$F(x_t + \Delta x) - F(x_t) \approx F'(x_t) \cdot \Delta x + \frac{1}{2} F''(x_t) \Delta x^2 \rightarrow x_{t+1} = x_t - \frac{F'(x_t)}{F''(x_t)}$$

Contrary to Newton's method, quasi-Newton methods do not require that the second order derivative, Hessian matrix of the objective function be computed. It just has to be approximated [A:13]. There are several approaches to approximate the computation of the Hessian matrix.

## BFGS

The **Broyden-Fletcher-Goldfarb-Shanno (BFGS)** method is a quasi-Newton iterative numerical method to solve unconstrained nonlinear problems. The Hessian matrix  $H_{t+1}$  at an iteration  $t+1$  is approximated using the value of the previous iteration  $t$  as  $H_{t+1} = H_t + U_t + V_t$  applied to the Newton equation for the direction  $p_t$ :

$$H_t p_t = -\nabla F(x_t), \quad x_{t+1} = x_t + \alpha_t p_t$$

The BFGS method is used in minimization of the cost function for the conditional random field, and  $L_1$  and  $L_2$  regression.

## L-BFGS

The performance of the BFGS algorithm can be improved by caching the intermediate computation in memory in order to approximate the Hessian matrix. The obvious drawback is that the memory becomes a limiting factor in the scalability of the optimizer.

The **Limited memory Broyden-Fletcher-Goldfarb-Shanno** algorithm or **L-BFGS** is a variant of BFGS that uses a minimum amount of computer RAM. The algorithm maintains the last  $m$  incremental updates of the values  $\Delta x_t$  and the gradient  $\Delta G_t$  at iteration  $t$ , and then computes those values for the next step  $t+1$ :

$$x_{t+1} = x_t + \Delta x_t; \quad \nabla F(x_{t+1}) = \nabla F(x_t) + \Delta G_t \quad \text{with} \quad \Delta G_t = \Delta(\nabla F(x_t))$$

It is supported by the Apache Commons Math 3.3 and above, Apache Spark/MLlib 1.0 and above, Colt 1.0 and above, and liitb CRF libraries. L-BFGS is used in minimization of the loss function in conditional random fields. For more information, refer to the *Conditional random fields* section of *Chapter 7, Sequential Data Models*.

## Nonlinear least squares minimization

Let's consider the classic minimization of the least squares of a nonlinear function  $y = F(x, w)$  with  $w_i$  parameters for observations  $\{y, x_i\}$ . The objective is to minimize the sum of the squares of residuals  $r_i$ :

$$\mathcal{L}(w) = \sum_{i=0}^{m-1} r_i(w)^2; \quad r_i = y_i - F(x_i, w)$$

## Gauss-Newton

The **Gauss-Newton** technique is a generalization of Newton's method. The technique solves nonlinear least squares by updating the parameters  $w_{t+1}$  at iteration  $t+1$  using the first order derivative, or Jacobian:

$$w_{(t+1)} = w_{(t)} - \left\| \frac{\partial r_i(w_t)}{\partial w_i} \right\|_{ij}^{-1} r(w_{(t)})$$

The Gauss-Newton algorithm is used in logistic regression. For more information, refer to the *The logistic regression* section of *Chapter 6, Regression and Regularization*.

## Levenberg-Marquardt

The **Levenberg-Marquardt** algorithm is an alternative to the Gauss-Newton technique for solving nonlinear least squares and curve fitting problems. The method consists of adding the gradient or Jacobian terms to the residuals  $r_i$  to approximate the least squares error:

$$\mathcal{L}(w + \delta) \approx \sum_{i=0}^{m-1} \left( r_i(w) - \frac{\partial F(x_i, w)}{\partial w} \delta \right)^2$$

The Levenberg-Marquardt algorithm is used in the training of logistic regression. For more information, refer to the *The logistic regression* section of *Chapter 6, Regression and Regularization*.

## Lagrange multipliers

The **Lagrange multipliers** methodology is an optimization technique to find the local optima of a multivariate function, subject to equality constraints [A:14]. The problem is stated as *maximize  $f(x)$  subject to  $g(x) = c$ , where  $c$  is a constant and  $x$  is a variable or features vector*.

This methodology introduces a new variable  $\lambda$  to integrate the constraint  $g$  into a function, known as the Lagrange function  $\mathcal{L}(x, \lambda)$ . Let's note  $\nabla \mathcal{L}$ , which is the gradient of  $\mathcal{L}$  over the variables  $x_i$  and  $\lambda$ . The Lagrange multipliers are computed by maximizing  $\mathcal{L}$ :

$$\begin{aligned}\mathcal{L}(x, \lambda) &= f(x) + \lambda(g(x) - c) \\ \nabla_{x, \lambda} \mathcal{L}(x, \lambda) &= 0 \\ \nabla \mathcal{L} &= \left[ \frac{\partial \mathcal{L}}{\partial x_i}, \frac{\partial \mathcal{L}}{\partial \lambda} \right]\end{aligned}$$

An example is as follows:

$$\begin{aligned}f(x, y) &= x^2 + y^2 \text{ subject } x - y = 2 \\ \frac{\partial \mathcal{L}}{\partial x} &= 2x + \lambda, \frac{\partial \mathcal{L}}{\partial y} = 2y - \lambda, \frac{\partial \mathcal{L}}{\partial \lambda} = x - y - 2 \\ x = 1, y &= -1, \lambda = -2\end{aligned}$$

Lagrange multipliers are used in minimizing the loss function in the non-separable case of linear support vector machines. For more information, refer to *The nonseparable case (soft margin)* section of *Chapter 8, Kernel Models and Support Vector Machines*.

## Overview of dynamic programming

The purpose of **dynamic programming** is to break down an optimization problem into a sequence of steps known as **substructures** [A:15]. There are two types of problems for which dynamic programming is suitable.

The solution of a global optimization problem can be broken down into optimal solutions for its subproblems. The solutions of the subproblems are known as **optimal substructures**. Greedy algorithms or the computation of the minimum span of a graph are examples of decomposition into optimal substructures. Such algorithms can be implemented either recursively or iteratively.

The solution of the global problem is applied recursively to the subproblems if the number of subproblems is small. This approach is known as dynamic programming using **overlapping substructures**. Forward-backward passes on hidden Markov models, the Viterbi algorithm (refer to the *The Viterbi algorithm* section of *Chapter 7, Sequential Data Models*), or the back-propagation of error in a multilayer perceptron (refer to the *Step 3 - error backpropagation* section of *Chapter 9, Artificial Neural Networks*) are good examples of overlapping substructures.

The mathematical formulation of dynamic programming solutions is specific to the problem it attempts to solve. Dynamic programming techniques are also commonly used in mathematical puzzles such as the Tower of Hanoi.

## Finances 101

The exercises presented throughout this book are related to historical financial data and require the reader to have some basic understanding of financial markets and reports.

### Fundamental analysis

Fundamental analysis is a set of techniques to evaluate a security – stock, bond, currency, or commodity – that entails attempting to measure its intrinsic value by examination related to both macro and micro, financial and economy reports. Fundamental analysis is usually applied to estimate the optimal price of a stock using a variety of financial ratios.

Numerous financial metrics are used throughout this book. Here are the definitions of the most commonly used metrics [A:16]:

- **Earnings per share (EPS):** This is the ratio of net earnings to the number of outstanding shares.
- **Price/Earnings ratio (PE):** This is the ratio of the market price per share to earnings per share.
- **Price/Sales ratio (PS):** This is the ratio of market price per share over gross sales or revenue.
- **Price/Book value ratio (PB):** This is the ratio of market price per share over total balance sheet value per share.
- **Price to Earnings/Growth (PEG):** This is the ratio of price/earnings per share (PE) over annual growth of earnings per share.
- **Operating income:** This is the difference between the operating revenue and operating expenses.
- **Net sales:** This is the difference between the revenue or gross sales and cost of goods or cost of sales.
- **Operating profit margin:** This is the ratio of the operating income over net sales.
- **Net profit margin:** This is the ratio of net profit over net sales (or net revenue).
- **Short interest:** This is the quantity of shares sold short and not yet covered.

- **Short interest ratio:** This is the ratio of the short interest over total number of shares floated.
- **Cash per share:** This is the ratio of the value of cash per share over market price per share.
- **Pay-out ratio:** This is the percentage of the primary/basic earnings per share excluding extraordinary items paid to common stockholders in the form of cash dividends.
- **Annual dividend yield:** This is the ratio of sum of dividends paid during the previous 12-month rolling period, over the current stock price. Regular and extra dividends are included.
- **Dividend coverage ratio:** This is the ratio of income available to common stockholders, excluding extraordinary items, for the most recent trailing twelve months, to gross dividends paid to common shareholders, expressed as percent.
- **Gross Domestic Product (GDP):** This is the aggregate measure of the economic output of a country. It actually measures the sum of value added by the production of goods and delivery of services.
- **consumer price index (CPI):** This is an indicator that measures the change in the price of an arbitrary basket of goods and services used by the Bureau of Labor Statistics to evaluate the inflationary trend.
- **Federal Fund rate:** This is the interest rate at which banks trade balances held at the Federal Reserve. The balances are called Federal Funds.

## Technical analysis

*Technical analysis is a methodology used to forecast the direction of the price of any given security through the study of past market information derived from price and volume. In simpler terms, it is the study of price activity and price patterns in order to identify trade opportunities [A:17]. The price of a stock, commodity, bond, or financial future reflects all the information publicly known about that asset as processed by the market participants.*

## Terminology

- **Bearish or bearish position:** A bear position attempts to profit by betting that the prices of the security will fall.
- **Bullish or bullish position:** A bull position attempts to profit by betting that the price of the security will rise.
- **Long position:** This is the same as bullish.

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- **Neutral position:** A neutral position attempts to profit by betting the price of the security will not change significantly.
  - **Oscillator:** An oscillator is a technical indicator that measures the price momentum of a security using some statistical formulae.
  - **Overbought:** A security is overbought when its price rises too fast as measured by one or several trading signals or indicators.
  - **Oversold:** A security is oversold when its price drops too fast as measured by one or several trading signals or indicators.
  - **Relative strength index (RSI):** The RSI is an oscillator that computes the average of number of trading sessions for which the closing price is higher than the opening price over the average of number of trading sessions for which the closing price is lower than the opening price. The value is normalized over  $[0, 1]$  or  $[0, 100\%]$ .
  - **Resistance:** A resistance level is the upper limit of the price range of a security. The price falls back as soon as it reaches the resistance level.
  - **Short position:** This is the same as bearish.
  - **Support:** A support level is the lower limit of the price range of a security over a period of time. The price bounces back as soon as it reaches the support level.
  - **Technical indicator:** A technical indicator is a variable derived from the price of a security and possibly its trading volume.
  - **Trading range:** The trading range for a security over a period of time is the difference between the highest and lowest price for this period of time.
  - **Trading signal:** A signal is triggered when a technical indicator reaches a predefined value, upwards or downwards.
  - **Volatility:** This is the variance or standard deviation of the price of a security over a period of time.


## Trading signals and strategy

The purpose is to create a set variable  $x$ , derived from price and volume;  $x = f(\text{price}, \text{volume})$  then generate predicates,  $x \text{ op } c$ , where  $\text{op}$  is a Boolean operator, such as  $>$  or  $=$ . The  $\text{op}$  operator compares the value of  $x$  to a predetermined threshold  $c$ .



Let's consider one of the most common technical indicators derived from price: the relative strength index  $RSI$ , or the normalized  $RSI$ ;  $nRSI$ , whose formulation is provided here for reference:

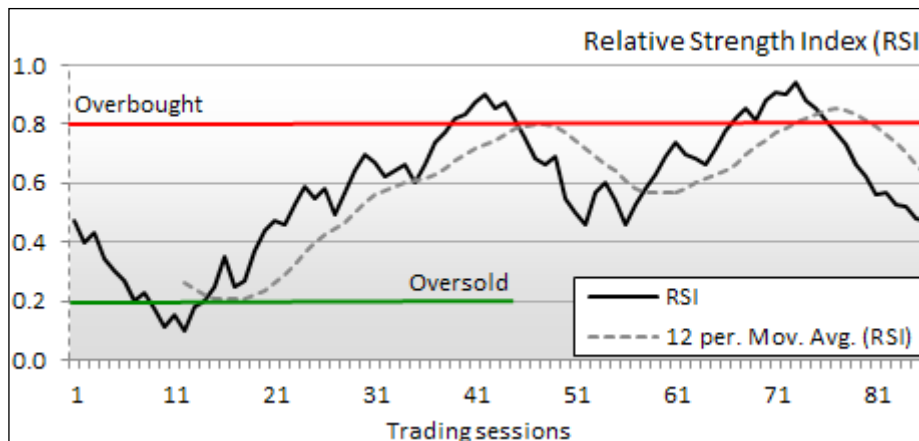
The  $RSI$  for a period of  $T$  sessions, with opening price  $p_o$  and closing price  $p_c$  is given by:



$$U_T = \sum_{t=0}^{T-1} (p_c(t) > p_o(t))$$

$$RSI_T = 100 - \frac{100}{1 + \frac{U_T}{T - U_T}} \quad nRSI_T = RSI_T / 100$$

A **trading signal** is a predicate using a technical indicator  $nRSI(t) < 0.2$ . In trading terminology, a signal is emitted for any time period,  $t$ , for which the predicate is true. Have a look at the following graph:



Traders do not usually rely on a single trading signal to make a rational decision.

As an example, if  $G$  is the price of gold,  $I10$  is the current rate of the 10-year Treasury bond, and  $RSI_{sp500}$  is the relative strength index of the S&P 500 index, then we can conclude that the increase in the exchange rate of the US\$ to the Japanese Yen maximizes for the trading strategy:  $\{G < \$1170 \text{ and } I10 > 3.9\% \text{ and } RSI_{sp500} > 0.6 \text{ and } RSI_{sp500} < 0.8\}$ .

## Price patterns

Technical analysis assumes that historical prices contain some recurring albeit noisy patterns that can be discovered using the statistical method. The most common patterns used in the book are the trend, support, and resistance levels [A:18], as illustrated in the following chart:

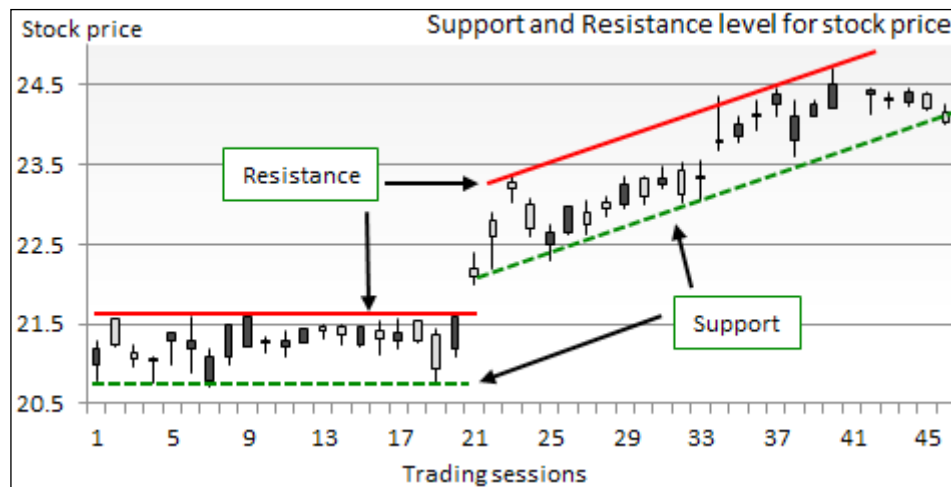


Illustration of trend, support, and resistance levels in technical analysis

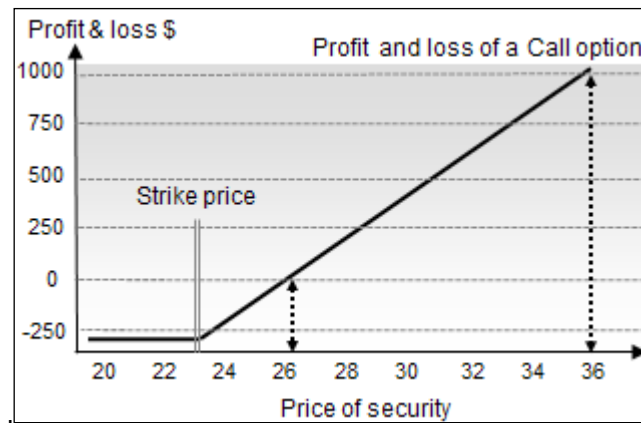
## Options trading

An option is a contract that gives the buyer the right but not the obligation to buy or sell a security at a specific price on or before a certain date [A:19].

The two types of options are calls and puts:

- A call gives the holder the right to buy a security at a certain price within a specific period of time. Buyers of calls expect that the price of the security will increase substantially over the strike price before the option expires.
- A put option gives the holder the right to sell a security at a certain price within a specific period of time. Buyers of puts expect that the price of the stock will fall below the strike price before the option expires.

Let's consider a call option contract on 100 shares at a strike price of \$ 23 for a total cost of \$ 270 (\$ 2.7 per option). The maximum loss the holder of the call can incur is the loss of premium or \$270 when the option expires. However, the profit can be potentially almost unlimited. If the price of the security reaches \$ 36 when the call option expires, the owner will have a profit of  $(\$ 36 - \$ 23) * 100 - \$ 270 = \$ 1030$ . The return on investment is  $1030/270 = 380$  percent. Buying and then selling the stock would have generated a return on investment of  $36/24 - 1 = 50$  percent. This example is simple and does not take into account transaction fee or margin cost [A:20]. Have a look at the following graph:



## Financial data sources

There are numerous sources of financial data available to experiment with machine learning and validation models [A:21].

- Yahoo finances (stocks, ETFs, and indices) available at <http://finance.yahoo.com>
- Google finances (stocks, ETFs, and indices) available at <https://www.google.com/finance>
- NASDAQ (stocks, ETFs, and indices) available at <http://www.nasdaq.com>
- European Central Bank (European bonds and notes) available at <http://www.ecb.int>
- TrueFx (forex) available at <http://www.truefx.com>
- Quandl (economics and financials statistics) available at <http://www.quantl.com>
- Dartmouth University (portfolio and simulation) available at <http://mba.tuck.dartmouth.edu>

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## Suggested online courses

- *Practical Machine Learning*. J. Leek, R. Peng, B. Caffo. Johns Hopkins University, available at <https://www.coursera.org/jhu>
- *Probabilistic Graphical Models*. D. Koller. Stanford University, available at <https://www.coursera.org/course/pgm>
- *Machine Learning*. A. Ng. Stanford University, available at <https://www.coursera.org/course/ml>

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# Bibliography

This Learning path is a blend of text and projects, all packaged up keeping your journey in mind. It includes content from the following Packt books:

- Scala for Data Science, Pascal Bugnion
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