JRCLUST manual

Janelia Rocket Clust (ver. 3)
Updated on 2017 Jun 20

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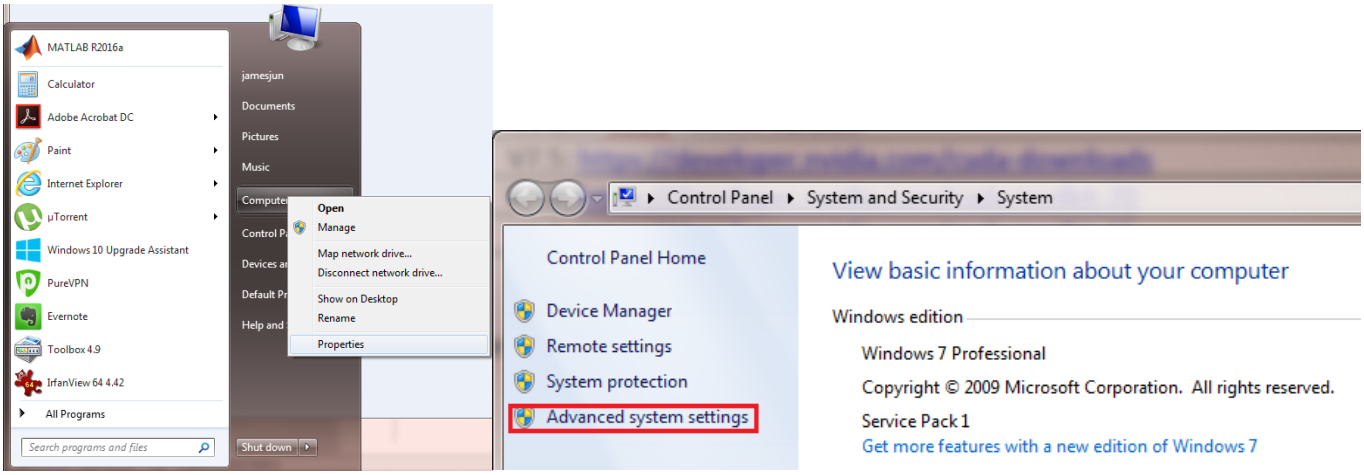
Installation instruction

[Requirements]

1. Matlab (R2014b+) and toolboxes: Parallel computing, Signal processing, Image processing.

2. RAM should be larger than ¼ of the recording file size.

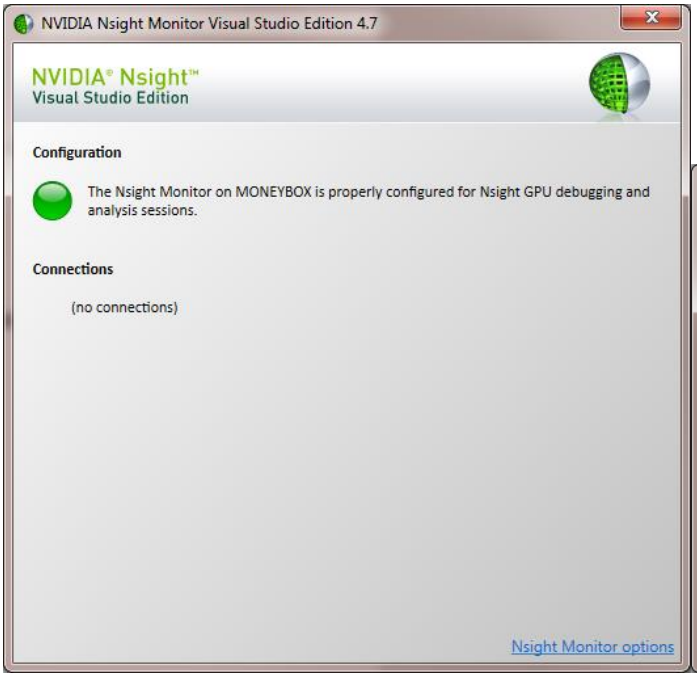
3. Install [Microsoft Visual Studio Express 2013 (V12)] to compile the CUDA codes (C-code for GPU).

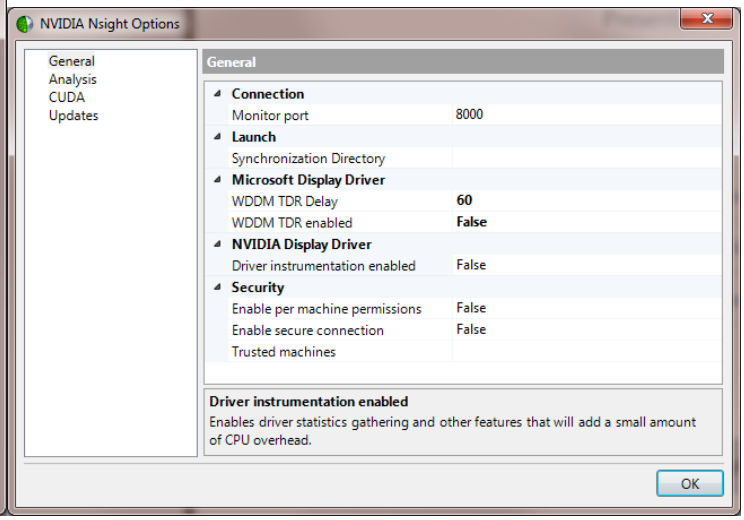


3. Install a correct version of the NVIDIA CUDA toolkit. You can find the version supported by the Parallel Computing Toolbox by running "gpuDevice" in Matlab and check "ToolkitVersion".

Matlab version	NVIDIA CUDA Toolkit version
R2017a	V8.0: https://developer.nvidia.com/cuda-downloads
R2016a,b	V7.5: https://developer.nvidia.com/cuda-75-downloads-archive
R2015b	V7.0: https://developer.nvidia.com/cuda-toolkit-70
R2015a	V6.5: https://developer.nvidia.com/cuda-toolkit-65
R2014b	V6.0: https://developer.nvidia.com/cuda-toolkit-60

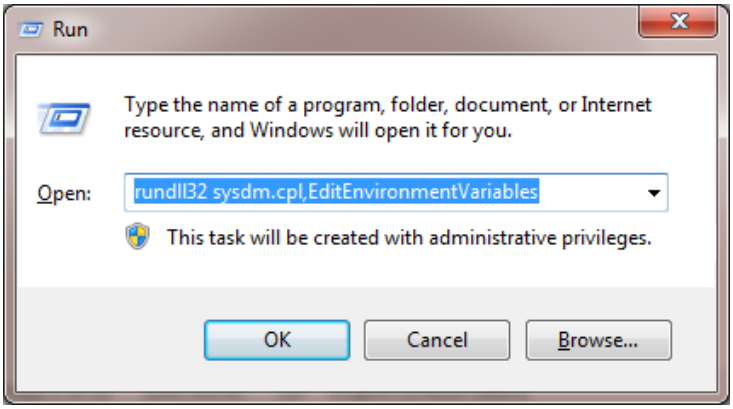
4. Disable the GPU timeout by running “Nsight Monitor”; navigate to “options” located at bottom-left; set "WDDM TDR enabled" to “false”.

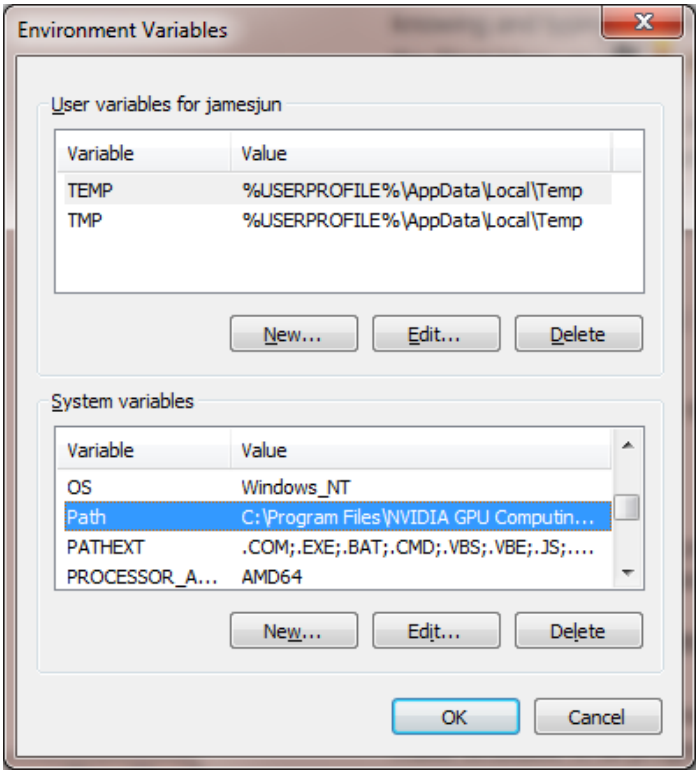




5. Add paths for the NVIDIA and Microsoft compilers in the system path. Each entry in path should be separated by ";". See below for the instructions for setting the system path in Windows:

Press win+R and type "rundll32.exe sysdm.cpl,EditEnvironmentVariables" and press OK.





Select “Path” under System variables and add the following:

Program	Path
Microsoft Visual Studio 2013	C:\Program Files (x86)\Microsoft Visual Studio 12.0\VC\bin
NVIDIA CUDA Toolkit	*select a correct version from below:* C:\program files\NVIDIA GPU Computing Toolkit\CUDA\v8.0\bin (Matlab R2017a) C:\program files\NVIDIA GPU Computing Toolkit\CUDA\v7.5\bin (Matlab R2016a,b) C:\program files\NVIDIA GPU Computing Toolkit\CUDA\v7.0\bin (Matlab R2015b) C:\program files\NVIDIA GPU Computing Toolkit\CUDA\v6.5\bin (Matlab R2015a) C:\program files\NVIDIA GPU Computing Toolkit\CUDA\v6.0\bin (Matlab R2014b)

Requirement	Comments	Tested
Matlab	Required toolboxes: parallel processing, statistics and machine learning, signal processing, image processing toolboxes	Version R2015b to R2017a
CUDA	Download NVidia CUDA toolkit Set	Version 6.5 to 8.0
Graphics card	CUDA-compatible NVidia GPU	Titan X (12 GB) and GTX 980 Ti (6 GB)
CPU	Multi-core CPU runs multiple threads	Dual Xeon 3.0 GHz CPU (Quad-core)
RAM	Larger than ¼ of the recording file size	16 GB+ recommended
Hard drive	Fast I/O speed recommended	RAID or SSD

[Install JRCLUST]

1. Copy JRCLUST folder in the Dropbox folder (e.g. "C:\Dropbox\jrclust") to another location (e.g. "C:\jrclust_user"). Latest JRCLUST version can be also obtained from www.jrclust.org. Download the .zip file and extract to a folder (e.g. “C:\jrclust_user”).

2. Start Matlab and "cd" to the copied location (e.g. "C:\jrclust_user").

3. Run "jrc install". This will compile all the CUDA codes. You can later recompile by running “jrc compile”

4. Edit "path_dropbox" in "user.cfg" and specify the path to the Dropbox folder containing JRCLUST (e.g. "C:\Dropbox\jrclust").

5. (optional) Download example files (sample.bin and sample.meta) by running “jrc download sample”.

6. Further details can be found in “install.txt”.

A. Step-by-step tutorial

Step 1. Make a parameter file from a default template (default.prm)

Syntax:

```
>> jrc makeprm [myrecording.bin] [myprobe.prb]
```

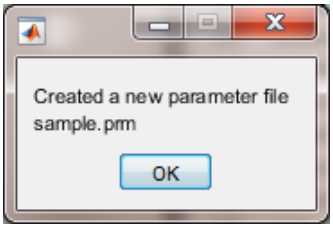
This creates a new parameter file (myrecording_myprobe.prm) for a WHISPER recording (myrecording.bin) that uses a probe configuration file (myprobe.prb).

Example:

```
>> jrc makeprm sample.bin sample.prb
```

Result:

```
Created a new parameter file
      sample_sample.prm
```



default.prm

```
% Default parameters for jrclust (default.prm)
% James Jun, 2017 May 12


% Recording file format
vcFile = '';    % raw file path (D:\Chronic2\ANM305341\20150828-1915-A2.bin)
csFile_merge = {};          % list of files to merge if running batch
probe_file = 'imec2.prb';   % probe file
nChans = 120;               % # channels stored
vcDataType = 'int16';       % raw data format
sRateHz = 25000;            % sampling rate
uV_per_bit = 0.305176;      % uV per bit resolution
vcFile_prm = '';            % Default: current file name if left empty (*.prm)
viChan_bin = [];            % channel translation order for bin file
viChan_aux = [];            % aux and sync channels
vcDate_file = '';           % date string. e.g. '19-May-2016 13:02:18'
nBytes_file = [];           % file byte size
duration_file = [];         % recording duration in seconds
cviShank = {};              % Shank channel group
fTranspose_bin = 1;         % file ordered by channels first and time second (whisper format)
template_file = '';         % use template file to copy settings
fInverse_file = 0;          % flip polarity of set to one
vcFile_gt = '';             % Ground truth file. Default: *_gt.mat

% Display parameters
tlim = [0, .2];             % Time range to display
nSkip_show = 1;            % Show 1 in n samples when plotting traces
fSpike_show = 1;            % show spikes in the trace view
fText = 1;                  % Show text description
LineStyle = '';             % Line style string
maxAmp = 250;               % Amplitude range in uV (spike band)
fShowAllSites = 0;          % Show mean traces from all sites
fAddCommonRef = 0;          % add common ref
nShow = 200;                % Maximum number of traces to show
corrLim = [.9 1];           % Correlation color plot range
iClu_show = [];             % cluster to display %show all by default
nSpk_show = 30;             % show spike waveforms for manual clustering
nShow_proj = 500;           % Show 1000 spikes in projection view max
maxSite_show = [];          % uses maxSite if empty.
tlim_lfp = [0, 5];          % lfp viewing range
maxAmp_lfp = 1000;          % Amplitude range in uV (LFP)
freqLim_corr = [15 150];    % LFP correlation frequency limit
vcFet_show = 'vpp';         % Feature to show in time plot {'vpp', 'cov', 'pca'}
time_tick_show = [];        % Time interval tick marks in secondds, [] for auto
viChan_show = [];           % Show all if empty
fWav_raw_show = 0;          % Show raw waveform (0 to show filtered);
mrColor_proj = [.75 .75 .75; 0 0 0; 1 0 0];     % background, select, compare color
```

Note:

1. JRCLUST will search within the current folder if full-path is not provided. Surround the full-path with a pair of single quotation if it contains blank characters.

   ```
   >> jrc makeprm 'C:\Dropbox (HHMI)\Git\jrclust_alpha\sample.bin' sample.prb
   ```

2. JRCLUST supports **merging multiple binary files**. If you provide a wild-card ("*" character), JRCLUST will replace * with "all" and generate a merged binary file. See below example:

   ```
   >> jrc makeprm 'D:\myfolder\myrecordings_*.bin' sample.prb
   ```

   This command will generate following files: "myrecordings_all.bin", "myrecordings_all.prm" and "myrecordings_all.meta".

3. JRCLUST opens the newly generated parameter file as shown above. This text file is interpreted by Matlab, and thus it must follow a Matlab script format. The first section of the parameter values ("recording file format") are computed based on the meta file (.meta) generated by SpikeGL/X. If needed, edit "probe_file = 'sample.prb';" to

change the probe configuration. For recordings generated by other than SpikeGL/X, it needs to be edited manually.

Step 2. Show the probe layout

Syntax:

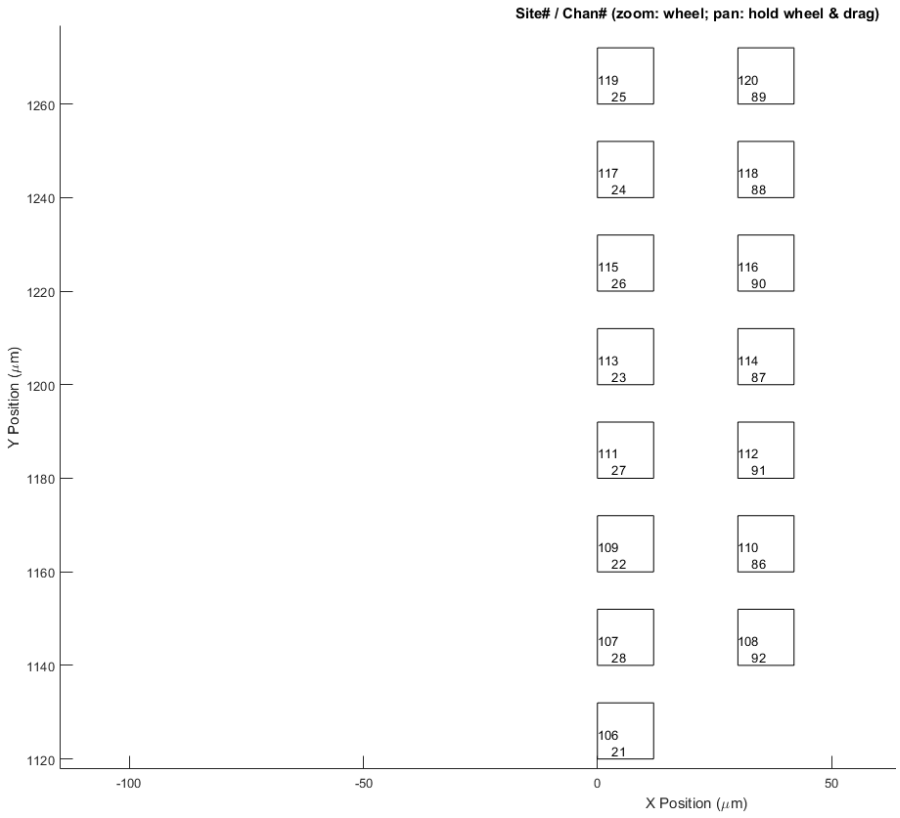
```
>> jrc probe [myprobe.prb or myrecording.prm]
```

Example:

```
>> jrc probe sample.prb
```

```
>> jrc probe sample_sample.prm
```

Result:



```
% Order of the probe sites in the recording file
channels = 1 + [40  103 39  104 41  102 38  105 42  101 37  106 43  100 36  107, 44

% Site location in micrometers (x and y)
geometry = zeros(128, 2);
geometry(1:2:end,1) = 0;
geometry(2:2:end,1) = 28;
geometry(1:2:end,2) = 20*(0:63);
geometry(2:2:end,2) = geometry(1:2:end,2);

% Reference sites are being excluded
ref_sites = [1 18 33 50 65 82 97 114];
channels(ref_sites) = [];
geometry(ref_sites,:) = [];

% Recording contact pad size in micrometers. Height x width
pad = [12 12];

% Default prm
maxSite = 4.5;
um_per_pix = 20;

% Shanks
% shank = ones(size(channels)); shank(geometry(:,1)>0)=2;
```

Note:

1. To zoom, use a mouse wheel. To pan, hold down the wheel and move.
2. displays the probe configuration file (.prb) that is plotted above. Make necessary changes if a different channel order is used. The above shows the IMEC Phase II probe configuration used in Janelia.
3. The probe configuration file (.prb) contains the following variables and is interpreted by MATLAB.
4. Write a command on a single line only. Do not use a Matlab line break "…".

Variable (case sensitive)	**Description**
channels: [1, nSites]	A channel map to translate from the site number to the recorded order. Each number corresponds to the order of appearance in the binary file. The sites are linearly arranged from the bottom to top, left to right. For example, the first element in the "channels" array corresponds to the bottom left site, the second element corresponds to the bottom right sites, the third element corresponds to the second bottom left site.
geometry: [nSites, 2]	Location of each site in micrometers. The first column corresponds to the width dimension and the second column corresponds to the depth dimension (parallel to the probe shank).
pad [1, 2]	Dimensions of the recording pad (height by width in micrometers).
ref_sites (optional)	This indicates reference or disconnected sites to eliminate.
shank (optional)	Shank number for each site #. For example shank=[1,1,1,1,2,2,2,2] will assign site 1-4 to shank 1 and site 5-8 to shank 2.

Step 3. Plot traces

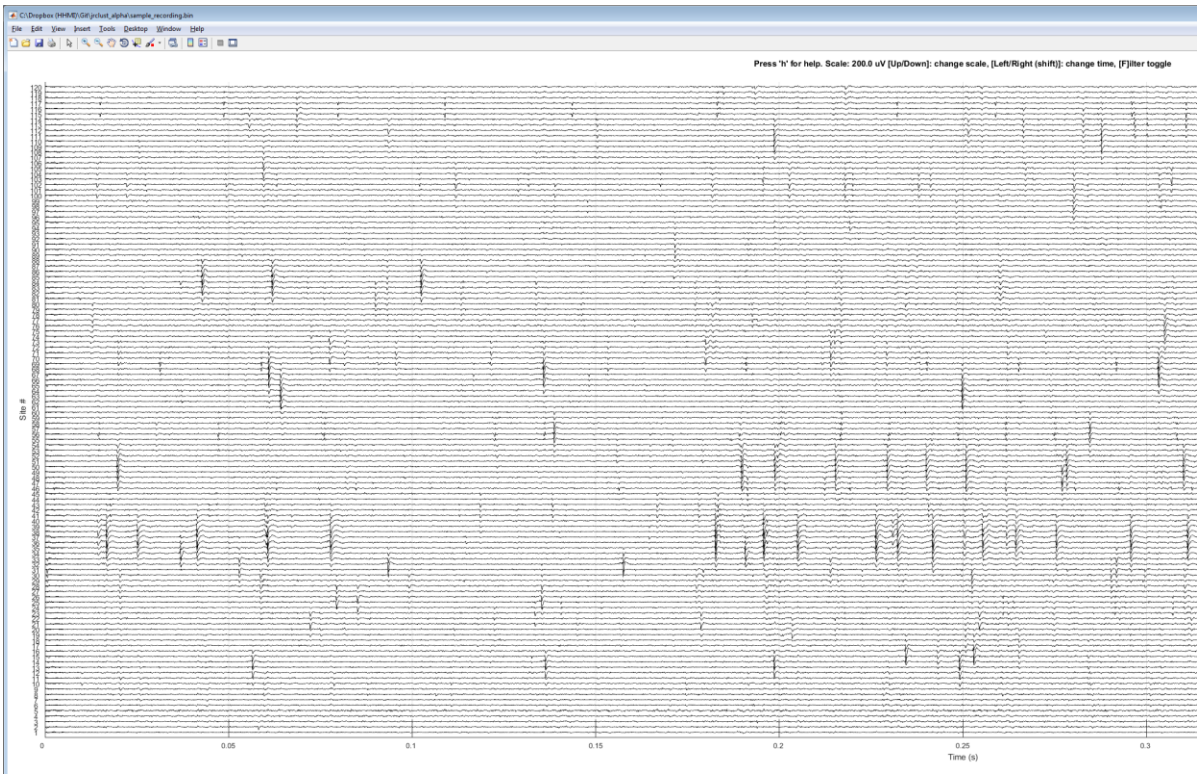
Syntax:

```
>> jrc traces [myrecording.prm]
```

Example:

```
>> jrc traces sample_sample.prm
```

Result:



Note: Change the amplitude scale using up/down keys and change time using left/right keys. Zoom using mouse wheel and pan by holding down the wheel and drag. Switch between spike-band vs. full-band by pressing 'F' key. Press 'H' for further help.

You can change the time range to display (default 0.5 s) by editing a line in a .prm file:

```
tlim = [0, .5];
```

Step 4. Excluding bad sites manually

You can manually identify bad sites and exclude them from analysis by editing a .prm file. The below line excludes bad sites #1 and #5:

```
viSiteZero = [1 5];
```

If there is no bad site to exclude then set:

```
viSiteZero = [];
```

If you wish to auto-detect the bad sites using a confidence threshold of 4.5, then edit as below:

```
fCheckSites = 1;
viSiteZero = [];
maxLfpSdZ = 4.5;
```

Step 5. Detect spikes

Syntax:

```
>> jrc detect sample_sample.prm
```

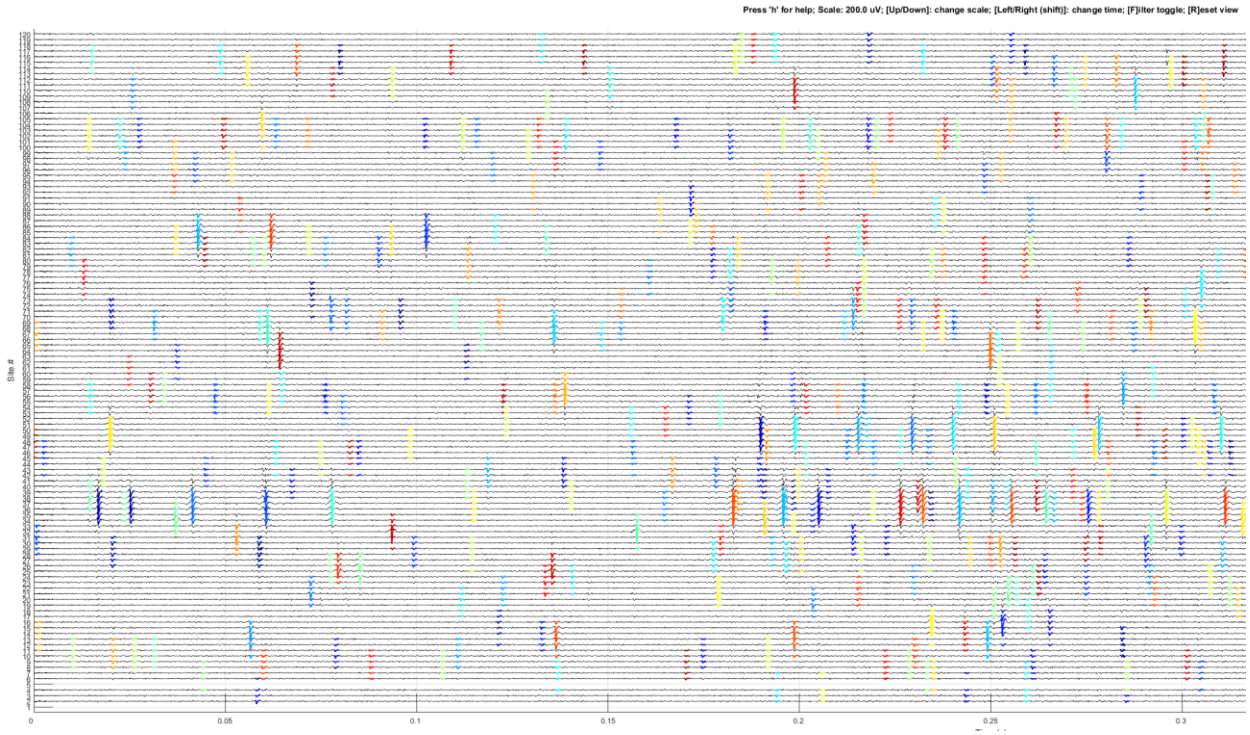
Output:

```
13:39:57 [W] Loading .\sample.bin
Loading .\sample.bin...took 5.3s (1950.0 MB, 365.5 MB/s)
Sites 1, 5, set to zero.
Filtering... Subtracting common ref...took 8.1s
took 22.6s
Exported to .\sample.spk (took 38.4s)
assigned 'mrWav' to workspace
13:40:36 [W] Wrote to .\sample.spk
Detecting spikes...
Detecting 1131433 spikes took 14.8s.
Merging spikes...
Merging 338263 spikes took 3.7s
assigned 'Sevt' to workspace
Saving to .\sample_evt.mat... took 9.1s
13:41:04 [W] Wrote to .\sample_evt.mat
assigned 'Sevt' to workspace
assigned 'mrWav' to workspace
Logged to .\sample.log
```

Note: Confirm the spike detection by plotting the traces:

```
>> jrc traces sample_sample.prm
```

Output:



Note: The traces from excluded sites are not shown (white gaps).

Step 6. Cluster automatically

Command:

```
>> jrc sort sample_sample.prm
```

Output:

```
14:00:02 [W] Loading .\sample.bin
Loaded .\sample_evt.mat from cache
Calculating rho...took 0.5s
Calculating delta...took 1.1 s
clustering took 2.2 s
.\sample.spk loaded from workspace cache
Computing cluster mean waveform... took 8.0s.
Saving to .\sample_clu.mat... took 1.1s
14:00:16 [W] wrote to .\sample_clu.mat
Recording file
    Recording file          .\sample.bin
    Recording Duration      300.0s
    #Sites                  120
Event
    #Spikes                 338263
    Feature                 amp
    #Sites/event            6
Cluster
    #Clusters               325
    min. spk/clu            50
    Cluster run-time        2.2s
assigned 'Sevt' to workspace
assigned 'Sclu' to workspace
assigned 'mrWav' to workspace
Logged to .\sample.log
```

Note: Run "jrc ***describe*** sample_sample.prm" to display summary information

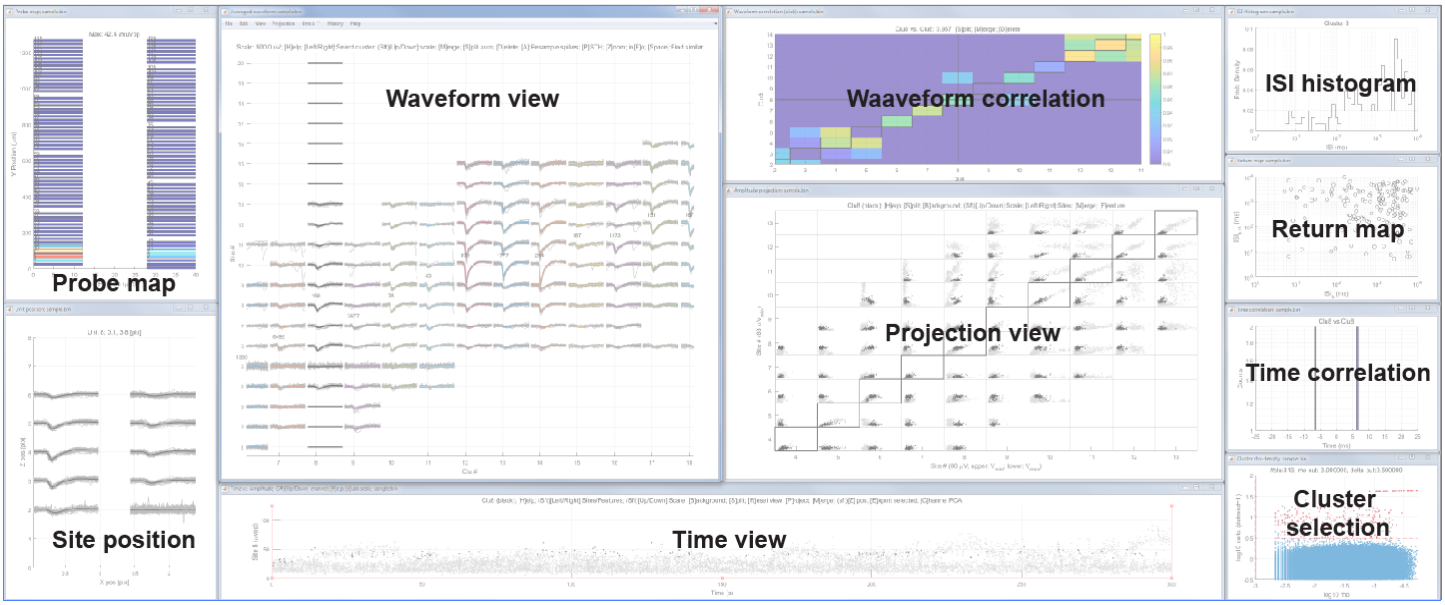
```
>> jrc2 describe sample_sample.prm
Recording file
    Recording file          sample.bin
    Probe file              sample.prb
    Recording Duration      300.0s
    #Sites                  120
Events
    #Spikes                 285963
    Feature                 spacetime
    #Sites/event            10
Cluster
    #Clusters               313
    min. spk/clu            10
    Cluster run-time        2.1s
Runtime (s)
    Detect + merge          21.3s
    Feature + Sort          18.8s
    Total                   40.1s
    Runtime speed           x7.5 realtime
```

Step 7. Manual curation

Command:

```
>> jrc manual sample_sample.prm
```

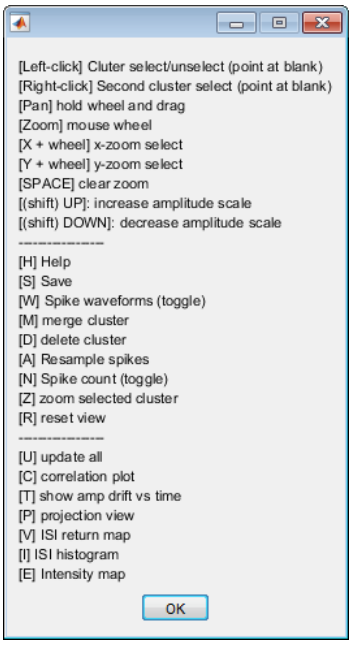
Output:



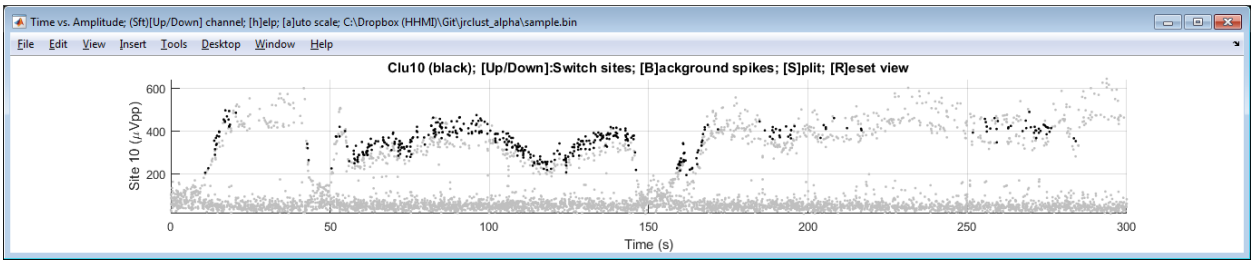
Waveform view (Interactive):

Select a cluster by clicking with a left click. Click between traces and do not directly click on the traces. The selected cluster is shown in black. Zoom in/out using a mouse wheel and pan by pressing down the wheel and drag.

Change **scale** by pressing **Up/Down** keys. Press '**H**' to display help.



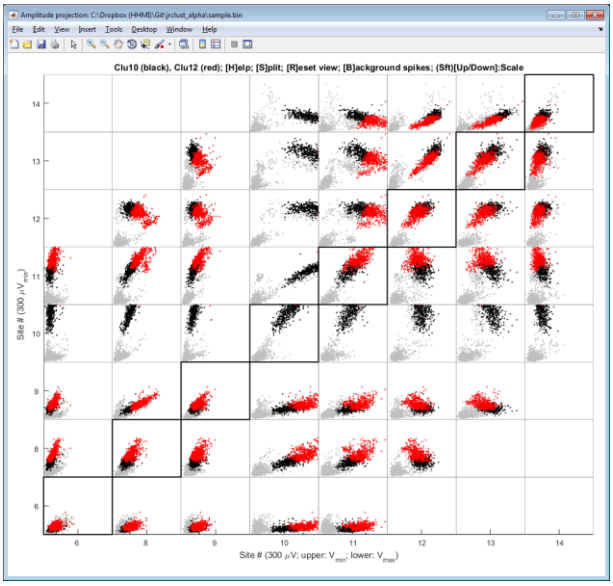
Time view (Interactive):



This view allows a check for probe drift over time. Press Up/Down arrows to switch sites.

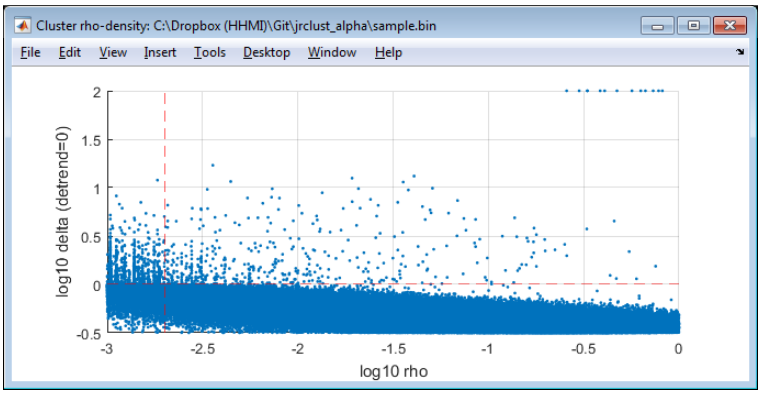
Note: You can split a cluster by pressing '**S**' and draw a polygon. Splitting is enabled when only one cluster is selected. Press '**B**' to show or hide the background spikes shown in gray. Press '**M**' to merge two clusters.

Projection view (Interactive):



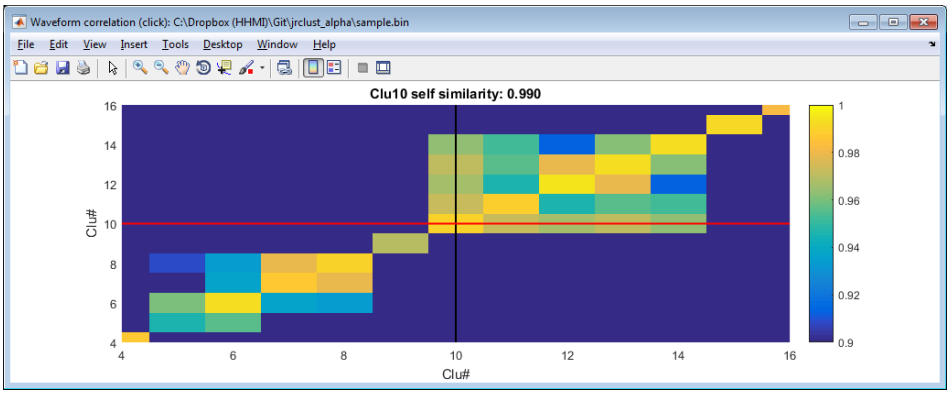
Press '**S**' to split a cluster by drawing a polygon. Splitting is enabled when only one cluster is selected. Press '**B**' to show or hide the background spikes (gray). Press '**M**' to merge two clusters.

Cluster confidence view:



If over-split, increase "**delta1_cut**" value in .prm file (default 0.5). If recording is too noisy, increase "**rho_cut**" value (default -3). Close and re-open the manual view by running "jrc manual *myparam.prm*".

Waveform correlation view:



Diagonal entries show self-similarity. Low score indicates you need to split (press '**S**' in the projection view). Off-diagonal entries show between-cluster similarities. High score indicates you need to merge (press 'm' in the waveform view).

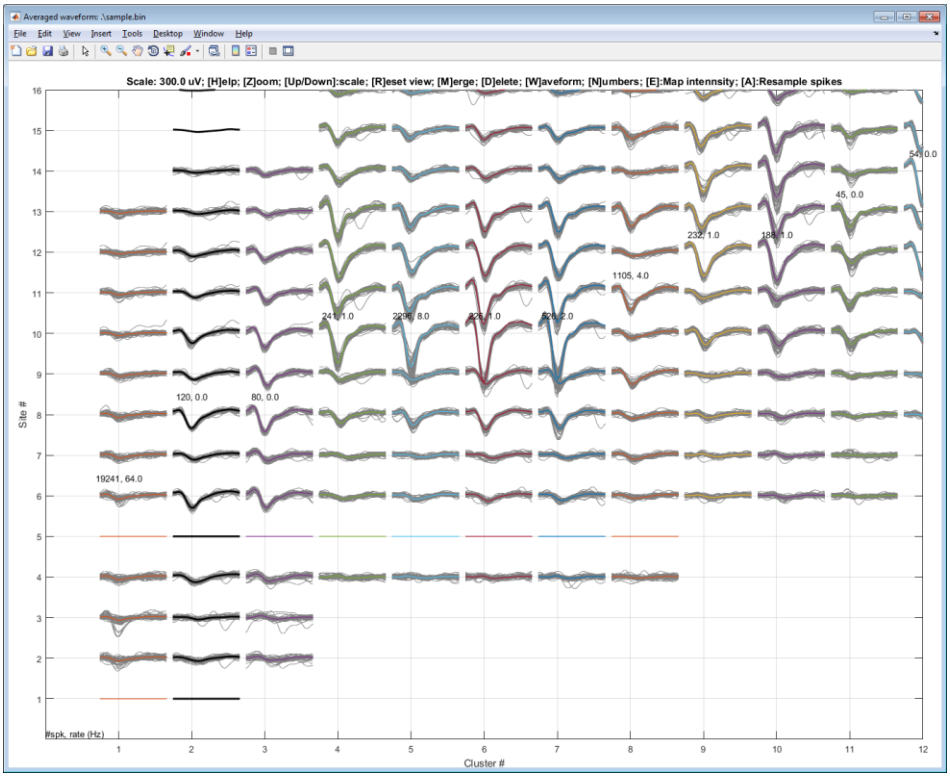
You can navigate using mouse (wheel to zoom, drag while pressing the wheel). If clusters appear over-split, increase the "maxWavCor" value (default 0.975) in the .prm file.

Probe view:

This displays the peak-to-peak amplitude of the averaged cluster waveform in each sites on the probe.

Step 8. Delete a noisy cluster

Select a cluster with a left click and hit '**delete'** key.

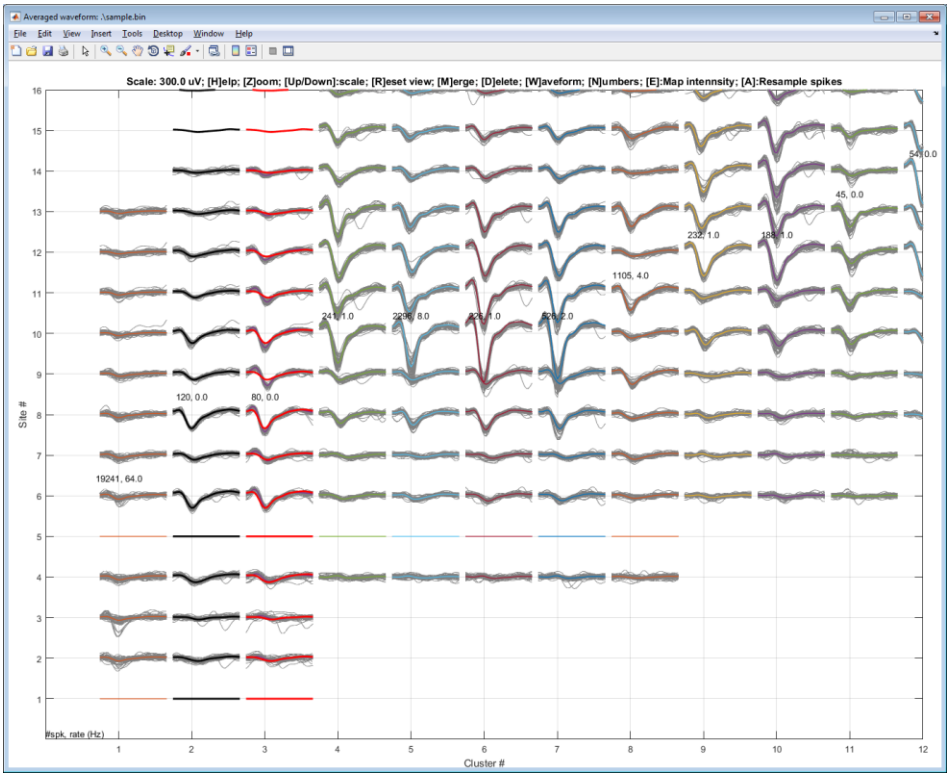


The selected cluster waveform is shown in black.

Note: You must click the white space between lines. Nothing will happen when you click on the waveform lines. You can hide the spike waveforms by pressing '**W**' to only display the averaged waveforms.

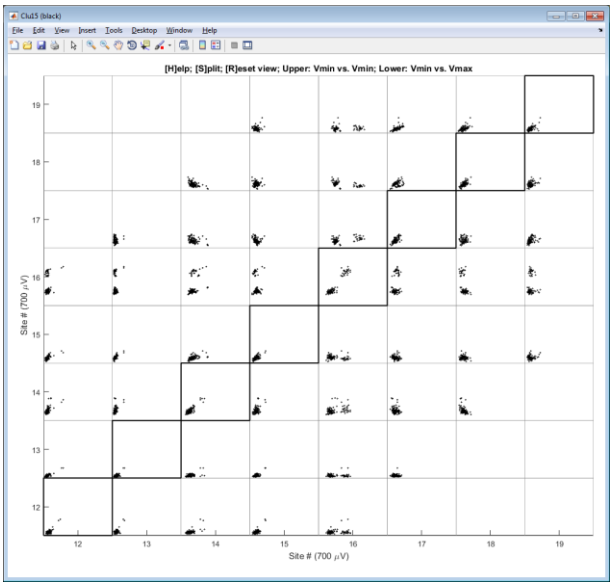
Step 8. Merge two clusters

Select a cluster with a left-click and a second cluster with a right-click and hit '**M'** key. Mean waveforms of the black cluster is copied to the red cluster for comparison.

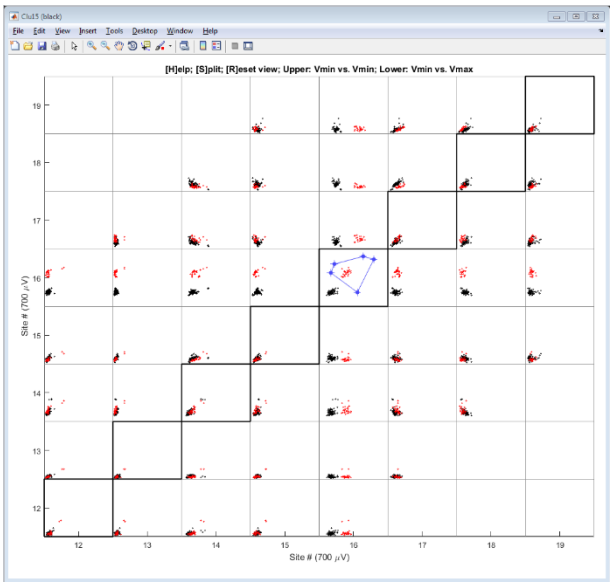


Step 9. Split a cluster

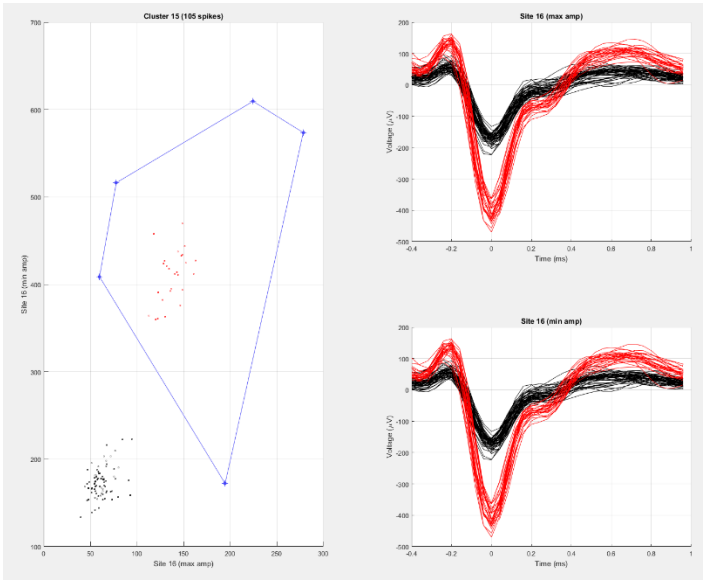
Select a projection view and press 's' to draw a polygon. Zoom in.



Draw a polygon



Edit and Confirm

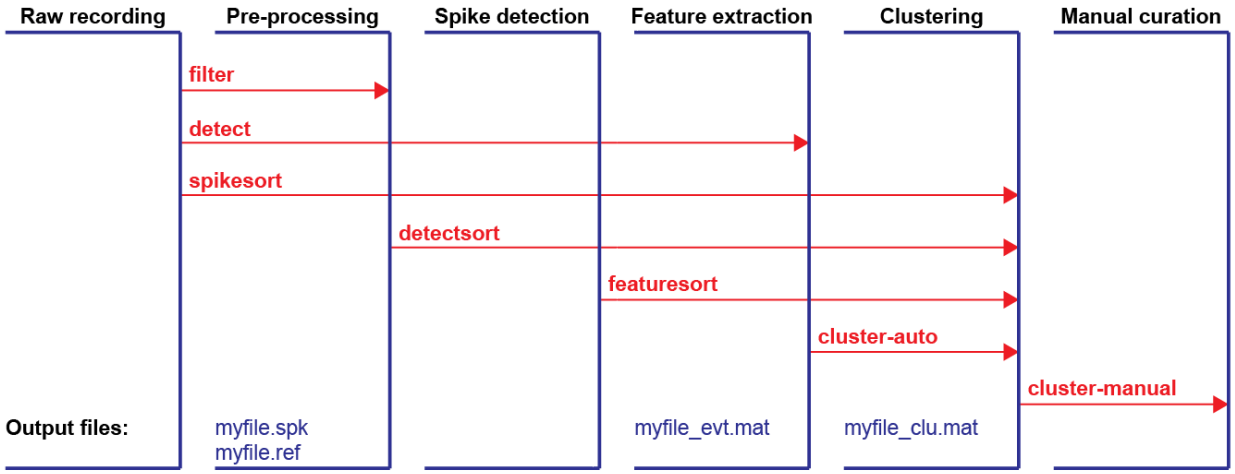


*__Note__: Press '__B__' to toggle all the background spikes.

*__Note__: Press '__S__' in the waveform view to save results.

B. Command listing

Type "**jrclust** ***command*** myfile.prm"



Syntax: "jrc ***command*** input"

Command	Input	Output / behavior
General		
help		Display help
probe	.prm or .prb file	Plot probe layout
traces	.prm file	Plot raw traces
detect	.prm file	Perform spike detection and feature extraction
exportcsv	.prm file	Spike timing, cluster number and max. site locations are saved
describe	.prm file	Displays summary information about the analysis
Clustering		
cluster	.prm file	Automatically cluster
manual	.prm file	Manual curation
spikesort	.prm file	Redo filtering, detection and sort
detectsort	.prm file	Redo spike detection to sort
Raster		
maketrial	.prm file	Generate time alignment marker from a TTL channel Output: "_trial.mat"
raster	.prm and _trial.mat	Plot rastergram and PSTH
Advanced		
cluster-verify	.prm file and _gt.mat	Compare against ground truth file

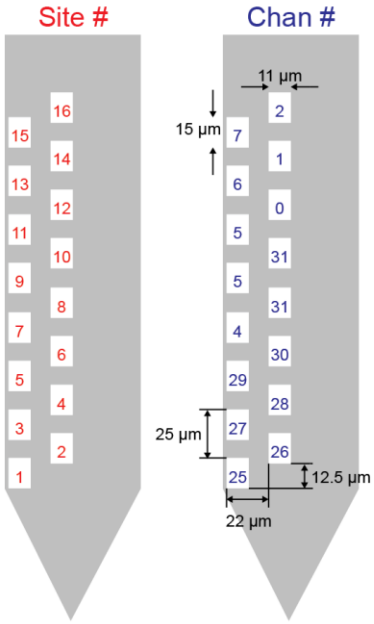
C. File format

Extension	Content	Format
Input files		
.prm	Parameter file	Plain text
.prb	Probe file	Plain text
.bin or .dat	Raw recording file	Binary file (SpikeGL)
.meta	Meta file for the raw recording (SpikeGL)	Binary file
_gt.mat	Ground truth file	Matlab data file
_trial.mat	Trial time	Matlab data file
Output files		
.spkwav	Filtered spike waveforms from a subset of channels	Binary file (16-bit integer)

.spkraw	Raw spike waveforms from a subset of channels	Binary file (16-bit integer)
_jrc.mat	Spike timing, location and cluster numbers. Cluster-specific information is stored in “S_clu” struct.	Matlab data file
_log.mat	Log file for manual operations	Matlab data file
.log	Program log file	Plan text
.csv	Spike time, cluster number, max site	Comma separated file

C1. Create a probe file

Probe file (.prb) describes channel ordering and site locations.



Site #	Chan #
1	25
2	26
3	27
4	28
5	29
6	30
7	4
8	31
9	5
10	32
11	6
12	1
13	7
14	2
15	8
16	3

Site numbers are assigned from the bottom to top of the probe, and left to right order. Channel numbers specify the order of file storage. For example, site #1 which appears at the bottom of the probe is stored in the 25th column of the file. Note that channel numbers start from 1, not from zero.

Create a new probe file and type the information below:

Command:

```
>> edit example.prb
```

Content of example.prb:

```
% Order of the probe sites in the recording file
channels = [25 26 27 28 29 30 4 31 5 32 6 1 7 2 8 3];

% Site coordinate (x,y) in micrometers
geometry = [...
    0,  0;
    22, 12.5;
    0,  25;
    22, 37.5;
    0,  50;
    22, 62.5;
    0,  75;
    22, 87.5;
    0,  100;
    22, 112.5;
    0,  125;
    22, 137.5;
    0,  150;
    22, 162.5;
    0, 175;
    22, 187.5];

% Recording contact pad size in micrometers. Height x width
```

```
pad = [15 11];

% Single shank contains site 1-16
shank = ones(1,16);
```

Verify the probe layout by typing:

```
>> jrc probe example.prb
```

Note: Define a shank group by editing "***shank***". The line below describes a two-shank probe containing 16 sites each:

```
shank = [repmat(1,1,16), repmat(2,1,16)];
```

D. Parameter settings (.prm file)

Name	Content	Values permitted
Recording file format		
vcFile	File path to a raw recording or a directory	'filepath.bin or .dat'
probe_file	File path to a probe settings	'filepath.prb'
nChans	Number of channels recorded	Integer
vcDataType	Number precision recorded	'int16', 'uint16', 'single', 'double'
uV_per_bit	Microvolts per bit	Positive real (set to 10 for single or double precision)
Pre-processing		
freqLim	Frequency range to filter in Hz	[low_cut, high_cut] (default [500 3000])
freqLimNotch	Notch frequency range. You can specify multiple ranges	{[low,high], [low,high], …} Default {}
fElliptic	Use elliptic filter. Butterworth filter otherwise	0 or 1
vcCommonRef	Common reference method	'mean', 'median', 'none', 'trimmean', 'holtzman'
viSiteZero	Bad recording sites to exclude	[array of integers] (default [])
fCheckSites	Flag for auto-detecting bad sites	0 or 1 (default 1)
maxLfpSdZ	Z-score cutoff for LFP-based bad site detection	Real number
fSaveSpk	Flag for saving filtered traces (.spk)	0 or 1 (default 1)
Spike detection/grouping		
spkThresh_uV	Spike detection threshold in microvolts	Positive real ([]: auto)
spkThresh_max_uV	Maximum spike amplitude permitted	Positive real ([]: ignore)
qqFactor	Quian-Quiroga automatic threshold factor	Positive real (default 4.5)
qqSample	Quian-Quiroga median subsample	Positive integer (default 4)
spkRefrac_ms	Refractory period for spike in milliseconds	Positive real (default 1)
vcSpatialFilter	Denoise using neighboring sites	'none', 'subtract', 'average'
maxSite	Max. distance to neighboring sites to consider merging	Integer or half-integer (default 2.5)
fSaveEvt	Flag for saving event file (_evt.mat)	0 or 1 (default 1)
Feature extraction		
vcFet	Features to extract	'vpp', 'amp', 'pca', 'slope', 'energy'
spkLim_ms	Spike time range in milliseconds (0 at the negative peak)	[min, max] (default: [-.40, .96])
nMinAmp_ms	Minimum amplitude search range in msec	Positive real (default 0)
nPcPerChan	Number of principal components per channel	Positive integer (default 3)
slopeLim_ms	Time range for slope calculation in msec (0 at the negative peak)	[min, max] (default: [.1, .6])
Clustering		
vcCluDist	Distance function	'euclidean', 'citblock', 'correlation' Default: euclidean
dc_factor	Controls merging or splitting. Higher means more merging.	1 +/- .5
min_count	Minimum spikes allowed per cluster	Default:30 Set to [] to ignore

E. Output file format

"_jrc.mat" file

Contains S0 struct. You can obtain the current S0 struct by running "*jrc export*". Run "*jrc export varname*" to export specific variables within S0 struct.

Name	Content	Data format
General		
viTime_spk	Spike timing in ADC sample unit	nSpikes x 1: int32
viSite_spk	File path to a probe settings	nSpikes x 1: int32
vrAmp_spk	Spike amplitude (local min. after filtering)	nSpikes x 1: int16
cviSpk_site	Cell of spike index (for *_spk* prefix) per site	Cell of vector of int32
vrThresh_site	Detection threshold per site	1 x nSites: single
dimm_spk	Dimensions for spike waveforms (stored in _spkwav.bin file)	Vector of double
dimm_raw	Dimensions for the raw spike waveforms (stored in _spkraw.bin file)	Vector of double
dimm_fet	Dimensions for the features (stored in "*_fet.bin*" file)	Vector of double
dimm_fet_sites	Dimensions for the feature sites (stored in "*_fet_sites.bin*" file)	Vector of double
runtime_detect	CPU time to run spike detection in sec	double
runtime_sort	CPU time to run spike sorting in sec	double
Cluster output: "S_clu" struct		
nClu	Number of clusters	double
viClu	Cluster index for each spike (0 is a noise cluster, negative numbers are deleted clusters)	nSpikes x 1: int32
viClu_auto	Automated output for cluster index	nSpikes x 1: int32
viSite_clu	Center site for each cluster	1 x nClu: double
vrPosX_clu	Center x position for each cluster	Vector of double
vrPosY_clu	Center y position for each cluster	Vector of double
csNote_clu	Manual annotation for each cluster	Cell string
trWav_spk_clu	Mean filtered waveforms for each cluster (centered, nSites_spk=2 x maxSites + 1)	nSamples x nSites_spk x nClusters: single
tmrWav_spk_clu	Mean filtered waveforms for each cluster (all sites)	nSamples x nSites x nClu: single
trWav_raw_clu	Mean raw waveforms for each cluster (centered)	2xnSamples x nSites_spk x nClu: single
tmrWav_raw_clu	Mean raw waveforms for each cluster (all sites)	2xnSamples x nSites x nClu: single
mrWavCor	Waveform correlation between clusters	nClu x nClu: double
vnSite_clu	Cluster quality: number of sites exceeding the detection threshold	nClu x 1: double
vrVmin_clu	Cluster quality: negative peak voltage per cluster	1 x nClu: single
vrSnr_clu	Signal to noise ration for each cluster (SNR = Vpeak / Vrms)	nClu x 1: single
rho	DPCLUS density parameter	1 x nSpikes: single
delta	DPCLUS distance to the nearest neighbor having a greater rho	1 x nSpikes: single
ordrho	DPCLUS index ordered by the density (rho)	1 x nSpikes: souble
dc	DPCLUS distance cut-off	1 x nSpikes: single

nneigh	DPCLUS nearest neighbor	1 x nSpikes: uint32
icl	DPCLUS	nClu x 1: double
P	Parameter struct used for automated clustering	struct
Parameters: "P" struct (Copied from .prm file)		

"_spkwav.bin" file

Binary file containing filtered waveforms per spike. Dimension is described in S0.dimm_spk
Format: nSamples x nSites_spk x nSpikes: real.

"_spkraw.bin" file

Binary file containing raw waveforms per spike. Dimension is described in S0.dimm_raw
Format: 2xnSamples x nSites_spk x nSpikes: real.

"_fet.bin" file

Binary file containing a feature matrix per spike.
Format: nFet x nSites_spk x nSpikes: real. Dimension is described in S0.dimm_fet

"_fet_sites.bin" file

Binary file containing site numbers for the feature matrix per spike.
Format: nFet x nSites_spk x nSpikes: real. Dimension is described in S0.dimm_fet_sites

"_log.mat" file

Stores the latest state of the program for each manual operation.