

NeuroSorter Users' Manual

Version 2.0

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Overview

- This manual is a quick guide to getting started on analyzing your neural recording data.
- Once you have collected your data using NeuroPhys or JAGA basic software with our hardware JAGA16, you can import your data into NeuroSorter ([NeuroSys, LLC](#)) for offline in-depth analysis.
- The data acquisition software NeuroPhys has online spike sorting capabilities. This is a popular tool for many neurophysiologists as online spike sorting feature is a tremendous time-saver.
- Please contact us at software@jinga-hi.com or tom.neurosysllc.com with your inquiries.

Getting Started

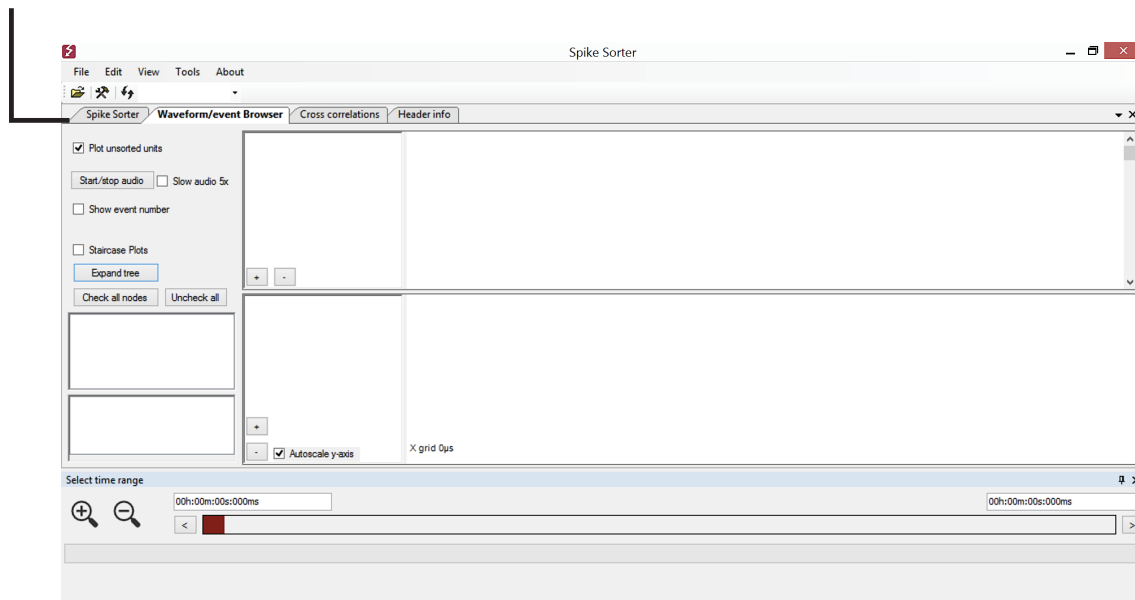
Once you have installed NeuroSorter on your computer,

1. Open NeuroSorter by double-clicking on icon.



2. You will have a window with a row of tabs as shown below. The tabs are briefly described below.

tabs



Spike Sorter

Select this tab if your data is spike-sorted data.

Waveform/event Browser

Select this tab if your data is raw (not spike sorted) or is LFP/EEG data.

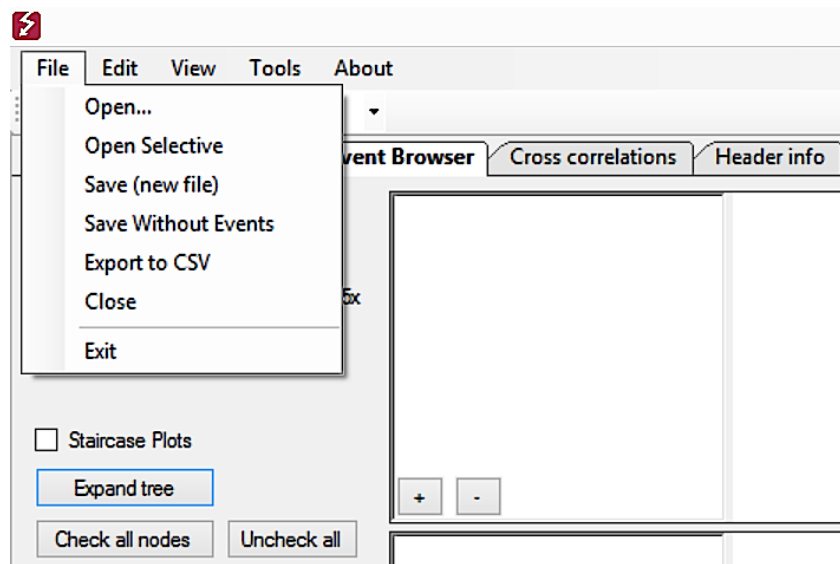
Cross correlations

This tab will show the correlation of spikes on a longer time scale.

Header info

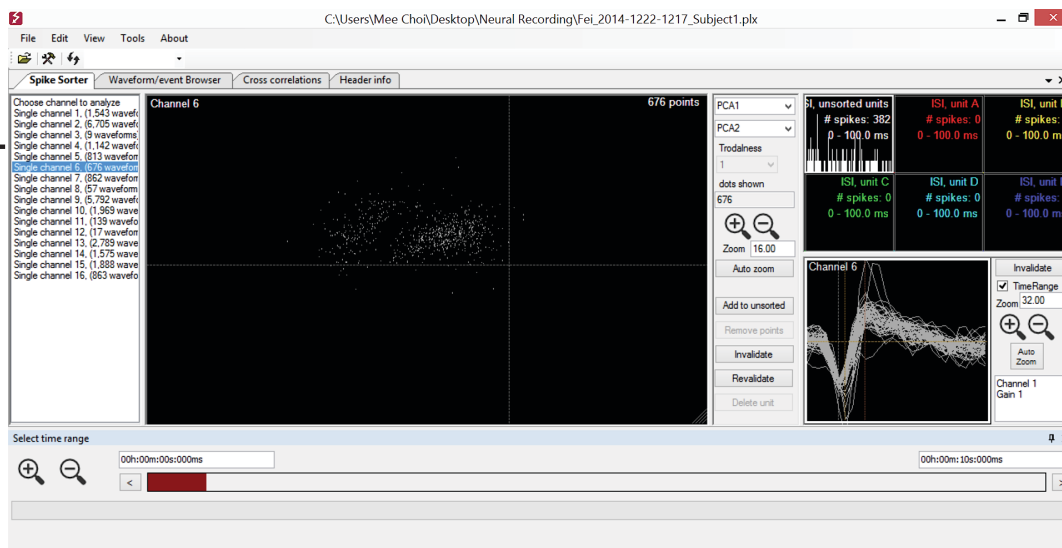
Select this tab if you want to obtain basic file information (*e.g.* sampling rate, bit resolution, file-creation time, maximum voltage range).

3. Select file obtain from NeuroPhys, by going to **File>Open**

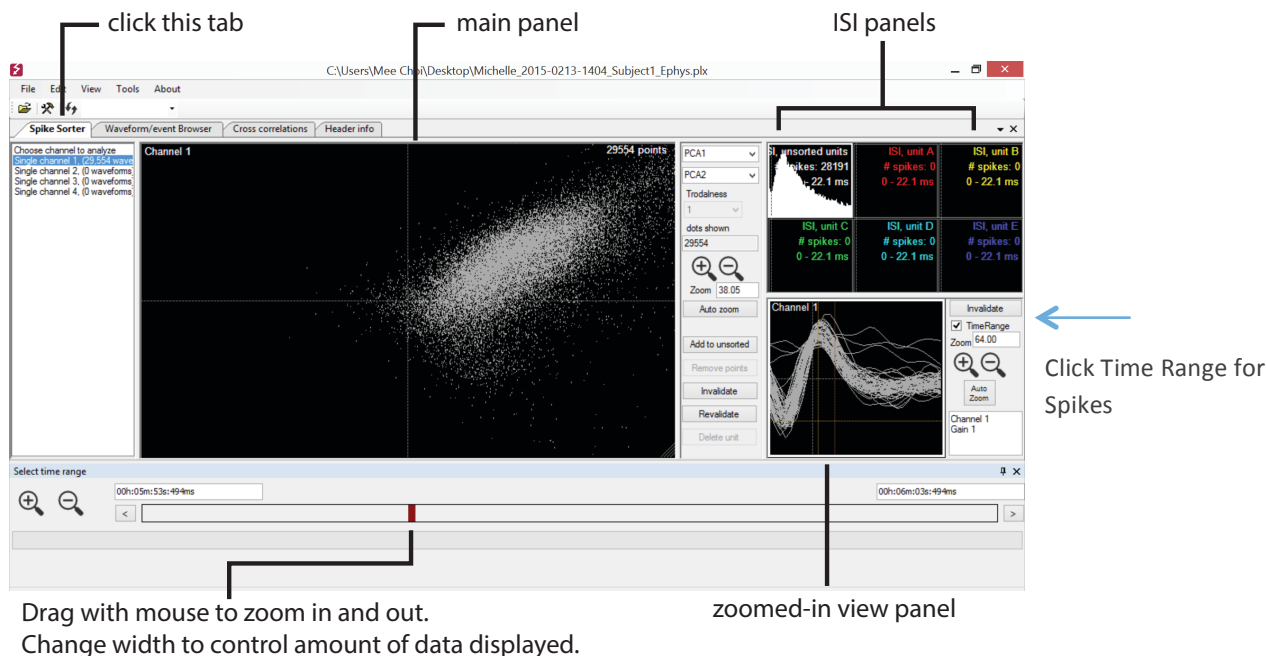


4. NeuroSorter automatically detects the number of channels that were used in your recording and lists them in the left-most panel. In the example below, there are 16 channels listed. Click to select the channel of interest.

list of channels



Analyzing your spike data



If you are working with data that has already been spike sorted, select the tab **Spike Sorter** and you will see a window like this:

On the left panel **Choose channel to analyze**, select the channel of interest. The following is a description of what is going on in each of the panels:

Main panel

- This window shows a collection of dots. Each dot represents an identified spike event. The x and y axis can be a PCA component in one direction or timestamp.
- You can zoom in and out of this image using the bar located at the bottom of the screen. The width of the red line indicates the slice of time; by dragging your mouse over the red line, you can control the width and hence the amount of data that is displayed.

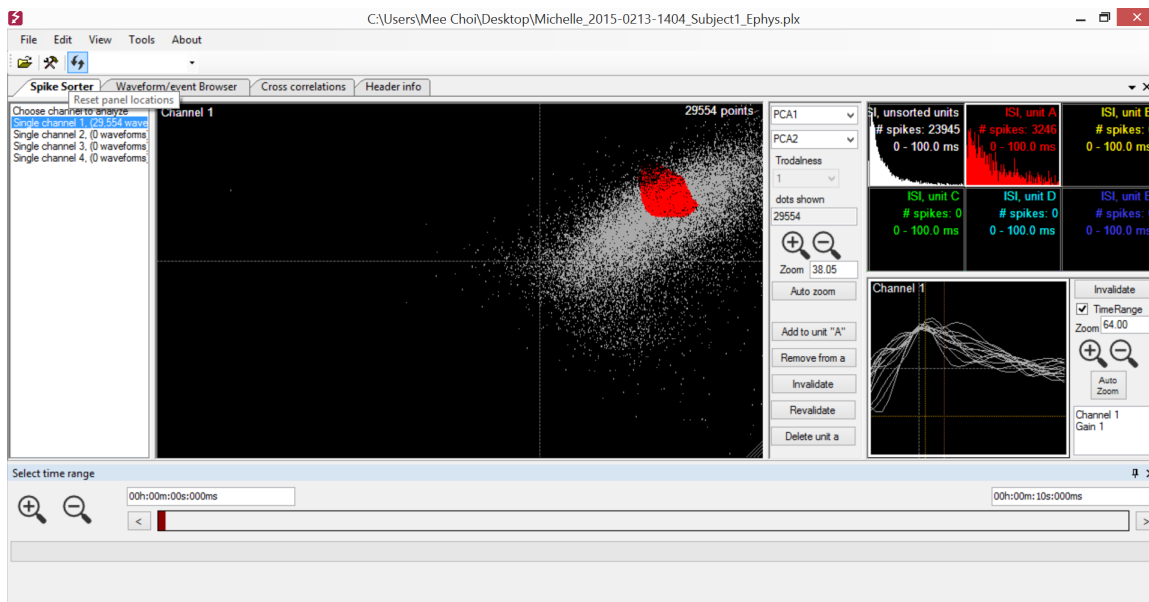
Zoomed-in view panel

In this bottom-right panel, you will see individual waveforms as you zoom in and out using the time bar.

ISI panels

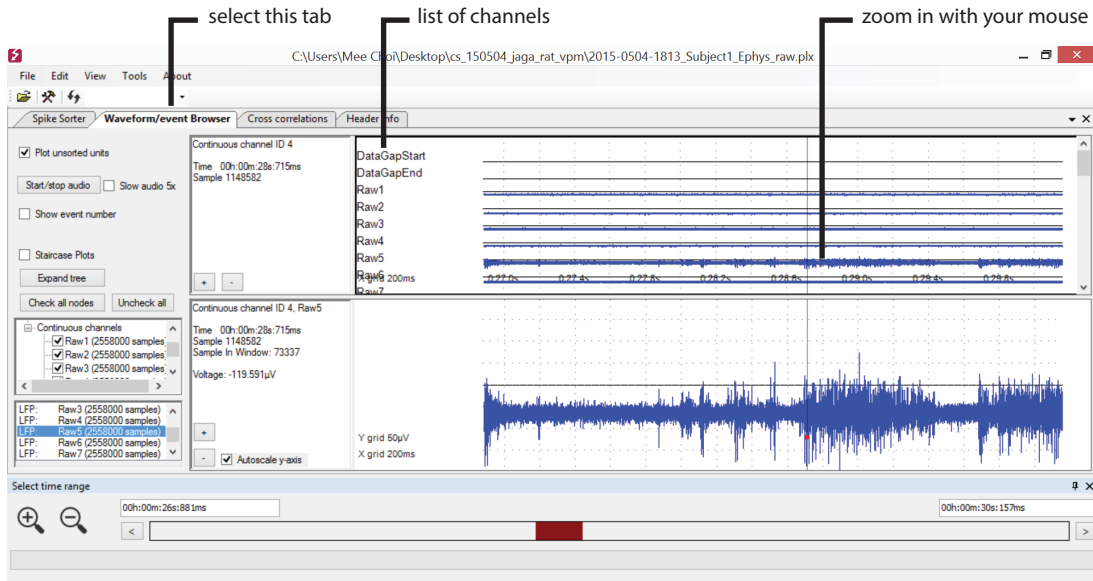
- The top-right section of the screen shows 6 separate ISI (inter spike interval) histograms.
- The first ISI window shows the result of analyzing the entire data set. Here, you can again use (roll) the mouse to zoom in and out of the data.

- c. In the figure above, you can see an ideal data set. The plot shows exponential decay – this corresponds to environmental noise, and there is a lack of data points in the initial time points (few mseconds). This “dip” corresponds to the latency period during neural activity, and is characteristic of recording data when a single neuron is being detected.
- d. If you want to select a portion of data for further analysis, click on an empty ISI box, then click **Add to unit A**. Move your mouse to the main window and circle the region of interest. The corresponding data will be automatically selected and will be displayed on a new ISI window.
- e. In the example below, the selected region in the main panel is shown in red. The corresponding histogram is also displayed in red.



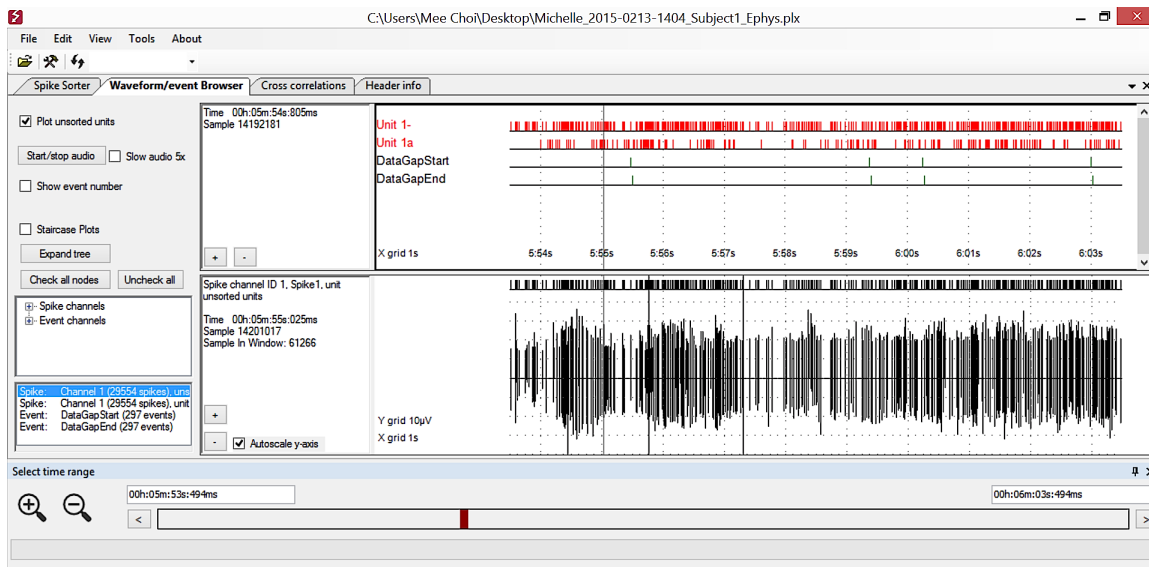
Analyzing raw or LFP data

If you are importing raw or LFP/EEG data, you will select the tab **Waveform/event browser**. This window will look as shown below.



Top panel: The top panel displays the channels used for recording. NeuroSorter software will automatically detect the channels from your data file. You can select a channel for analysis by clicking on it.

Bottom panel: The bottom panel displays data corresponding to the channel you selected. Place the mouse on the top panel and scroll the mouse to zoom in and out. The image displayed on the bottom panel can be zoomed in to further identify the region of interest. An example is shown in the figure below.



Converting file to csv format

Saving spike-sorted data into a csv format (comma separated value) enables your data file to be exported to other programs.

To save, go to **File > export to csv**. The format for csv output will be detailed in a separate file (see NeuroPhys_output_csv_format.pdf).