Roadmap for opto data reformatting to use Plexon Offline Sorter (OFS)

Steps for rosenlab data (TytoLogy):

{summarize here, from document *Processing headfixed tytology data\_8.23.16.docx*}

Development plans for opto data spike sorting using Plexon OFS:

## Step 1: get working for single test of 1 cell from 1 animal

1. export opto *.dat* file to *.nex* file
2. import *.nex* file in OFS
3. export to *.plx* in OFS
4. sort in OFS
5. save sorted data as .*plx*
6. export data as *.mat*
7. incorporate spike times/sorted data/waveforms (?) into *.dat* file.
8. rework analysis program to use sorted data

Step 2: Adapt for use with *all* tests of 1 cell from 1 animal

Uses same general steps as used for single test, with some modifications

1. gather data from all relevant *.dat* and *.mat* files
   1. how to do this?
      1. Select files in GUI? Script? List of files in .txt file?
      2. Rosenlab technique is to copy all files into one directory and then program combines all relevant files
2. export opto *.dat* file to *.nex* file
   1. Rosenlab creates cellinfo.mat file in step 1 and 2 to store information that will be used here
3. import *.nex* file in OFS
4. export to *.plx* in OFS
5. sort in OFS
6. save sorted data as .*plx*
7. export data as *.mat*
8. incorporate spike times/sorted data/waveforms (?) into respective *.dat* file.
9. rework analysis program to use sorted data

Incorporating detected spikes into analysis

Options:

Output file format:

Plx

Mat

Help to have info from export\_for\_plexon() function?

One idea:

Output from OFS (as mat file) is (as noted in Rosenlab AddSpiketimesToMatFiles\_InclUnsort.m)

% 1) Read in .mat files exported by Plexon's Offline Sorter

% Column 1: unit number (where 0 is unsorted)

% Column 2: timestamp where spike crosses threshold (in seconds)

% Columns 3-34 (assuming waveform window of 1311us / 32 samples):

% waveform snippet, with or without prewindow as set in Offline Sorter

% (prewindow default: 494us / 12 samples)

% (window default: 1311us / 32 samples)

% This is in units of samples/sec of raw data file

% (24414.063 Hz based on settings in data acquisition program

% HPSearch or PresentStimCurve in RosenLab)

Note that sampling rate will be different and that timestamp is in seconds

Step 1: knowing each data file’s time “window” (in fileStartTime and fileEndTime), locate the timestamps within this window (column 2). These spikes can then be associated with the appropriate data file.

Step 2: associate each spike down to the appropriate sweep within that file and re-align the spike time to the start of the sweep. Use sweepStartBin and sweepEndBin cells, convert to time in seconds by subtracting 1 and dividing by sample rate