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