Diego's data/analysis

Here is information on how to analyze the data. I have included examples of tetrode data acquired with Measurement Computing's DT3010

Data file examples are found under:

https://www.dropbox.com/sh/q0asw7t2eno4fuk/AAB6oseEYsIRbLGFkqz_EtFqa?dl=0

Note: the .dg files are acquired with DT3010, the .rhd files are acquired with INTAN's RHD2000.

71117261367isominnl.dg was acquired by Daniel and has LFP data for mice engaged in differentiating isoamylacetate from mineral oil in the go-no go task as described in the Frontiers in Cellular Neuroscience paper (Ramirez-Gordillo et al., 2018).

O10130330.dg is acquired by Anan and has good single unit data (Li et al., 2015).

In order to look at the data run drta and open O10130330.dg. In the drtaBrowseTraces window choose 300-5000 (this shows data in the 300 Hz to 5000 Hz range: spikes) and then change your y range to 50. Channels 1 and 2 are dead, but other channels have nice spikes. The data in channel 11 is pretty nice. Each tetrode has four channels so channel 11 is in the third tetrode that includes channels 9-12.

Because Do_wave_clus has already been run you can also run wave_clus. Open wave_clus and "Load data". Tetrode 3 is excellent.

dgstitch

If the data acquisition was performed in several runs of the data acquisition program for one experiment stitch the files before running drta using m/drta/dgstitch. It is important to enter the files into this program in the time sequence that was used in the experiment.

drta

When you type drta you get two windows showing the data in each trial: drtaBrowseTraces and a sample of snips chosen with the thresholds entered and turning off some trials/channels with drtaThresholdSnips.

In drtaBrowseTraces you can view the data with differential subtraction (top, left in drtaBrowseTraces).

drta is a program used to browse through data acquired and to set four parameters that are important for clustering the spikes using Do_wave_clus.

Inputs:

Two files called ‘name.dg’ and ‘name.mat’ (DT3010)

The .mat file has the all the acquisition parameters

The .dg file has all the binary data. It can be read as follows:

```
   fid=fopen(handles.p.fullName,'r');
   no_unit16_per_ch=floor(handles.draq_p.sec_per_trigger*handles.draq_p.ActualRate)
;
   data=fread(fid,no_unit16_per_ch*handles.draq_p.no_chans*handles.draq_d.noTrials,
'uint16');
   fclose(fid)
```

Or a file called ‘name.rhd’ (INTAN)

Outputs:

drta outputs all the user’s choices and excluded spike times, as well as all epochs for the go-no go experiment in a file called jt_times_name.mat

In the browse window the user can browse through the data, change the y-axis and x-axis ranges, display only one or all channels, and display 3xthe standard deviation.

Fist exclude the lick artifact that is found in all channels

Then decide on differential or raw data

Finally set thresholds (2.5xSD)

The following parameters can be set by the user: thresholds for spike generation, choose which channels are processed by Do_wave_clusdrdg, choose trials that are excluded in Do_wave_clusdrdg because of electrical artifacts

To save the settings and thresholds the user has set, the user must push on “save” making the right choice for the correct experiment used (e.g. dropcspm).

Do_wave_clus and wave_clus

These programs are used to cluster the waveforms of similar shape by performing wavelet decomposition and superparamagnetic clustering using the method and MATLAB software developed by Quiroga and coworkers (Quiroga et al., 2004). We made a few modifications to the software:

1. In addition to determining 18 wavelet coefficients used in the Quiroga program, our modified program also determined the first three coefficients of a PCA of the spikes and calculated the peak to valley ratio. As explained in Quiroga et al., the program then proceeded to determine which of these descriptors showed a multimodal distribution and used the ten best descriptors to separate the spikes into well defined clusters using superparamagnetic clustering. Our change is useful because in some experiments PCA or peak to valley does better than wavelet.
2. We have adapted Do_wave_clusdrdg for use with tetrodes.

When processing a number of experiments the approach is to use Do_wave_clusdrdg to perform batch processing and then follow-up with wave_clus to refine the clustering (i.e. merging two clusters).

Overall strategy. Before you cluster spikes using these programs you must read the Quiroga paper to understand how it generates separate spike clusters using superparamagnetic clustering (Quiroga et al., 2004). Please pay particular attention to how changing temperature affects clustering as you will use this actively in wave_clus.

Here is the strategy:

- Using drta (see above) set thresholds for spike detection, choose which channels you will analyze, exclude trials that have noise, and exclude multichannel spikes.
- Double check that all your data have been saved correctly by drta by opening the file again in drta and making sure all thresholds that you set have been saved correctly.
- Run Do_wave_clusdrdg (or Do_wave_clus)
- Run wave_clus for each channel to make a final decision on single units and muti unit.
- If you think you need to change your thresholds you must run drta to change the thrsholds, go to Do_wave_clusdrdg and then use wave_clus. Doing drta followed by wave_clus (without Do_wave_clusdrdg) does not result in re-processing using different thresholds.

Do_wave_clus

Do_wave_clus is a batch file that will process data in a large number of .dg or .rhd files with thresholds chosen by drta. This program does superparamagnetic clustering that then allows you to choose single units and multiunit using wave_clus. You must have all files in the same

output files:

'joint_name.mat' (this is the input to wave_clus)

'jt_times_name.mat' (this is the input to drs and Do_drs)

histograms, etc in a subdirectory called ‘name’

VERY IMPORTANT: If you use a long name for the dg file, or if you use directories with spaces between names you will likely get an error in run_cluster.m when this function calls the c program that does superparamagnetic clustering (cluster.exe or cluster_maci.exe).

An example of this error:

"error:
at line 74 of 'param.c': too long"

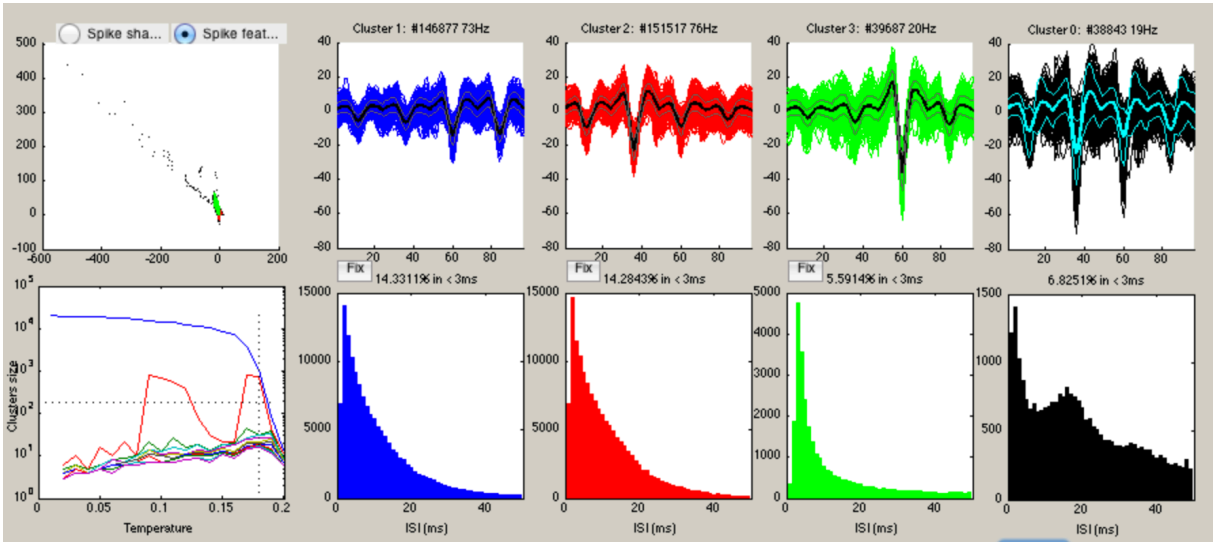
wave_clus. You must follow up the results of Do_wave_clus with wave_clus. Open the joint file by pressing load data and loading the joint file. You do this one channel at a time.

The output of Do_wave_clus is a cluster size vs. temperature plot that allows you to choose where in this plot you set a point to make wave_clus calculate clusters. If you press “change temp” you can go anywhere within this plot and re-calculate the clusters. When you do this there is always a “cluster 0” that has the excluded spikes (spikes that do not fit any cluster templates). In addition there are n clusters (clusters 1 to n). These are the templates that are supposed to have clusters with spikes of different shapes. In the cluster size vs temperature there are different lines. There always is a blue line that includes the multiunits. In addition, if you choose a point below any of the lines with other colors you will get clusters that are candidates for single units. How to go about choosing a point in this plot is explained in the Quiroga paper.

Single units will show a refractory period in the ISI plot. The multiunit cluster will not show a refractory period.

Once you choose where in the plot your point will fall you have to decide whether you want to merge some clusters. Suppose you think clusters 2 and 3 are the same single unit. If you press “join” you can join these two clusters in one. After you do this make sure that the ISI plot leaves a refractory period indicating this indeed is one single unit.

Figure of use of wave_clus



Usually there are different spikes if you choose a point in clusters size vs. temperature under red on the left side vs. a point under red on the right side. See for example the figure shown here. Thus it makes sense to get the spikes defined by both the point under the left side and the point under the right side of the red line. To do this you have to first choose “change temp” and choose one of the two points (say the point under the right red). Then “fix” the point under the red. Then follow up with changing the temp to a point under the other red line (say left). At this point choose “force” and you will get a figure such as that one shown here. Then press “save clusters”. Repeat this for all four tetrodes.

Once you have a set of clusters that represent a single unit (or units) and a multiunit you can “force” some of the spikes that are in the excluded spikes (cluster 0) into clusters 1 to n. If some of the excluded spikes fall within x standard deviations (S.D.) of a cluster they are moved from cluster 0 to that cluster. Notice you can change the S.D. We generally use 1.5 to 3.

Once you are done, you save the clusters by pressing “save clusters”.

Input files: ‘joint_name.mat’

Output files:

‘joint_name.mat’ (this is the input to wave_clus)

‘jt_times_name.mat’ (this is the input to drs and Do_drs)

Quiroga RQ, Nadasdy Z, Ben Shaul Y (2004) Unsupervised spike detection and sorting with wavelets and superparamagnetic clustering. Neural Comput 16:1661-1687.

Bypass wave_clus

If you want to look at LFP, not spikes using drgMaster:

-Open the file in drta. Save with the appropriate choice (i.e. dropcspm)

-In drgMaster choose “Open jt”

-Only behavior and LFP functions will work

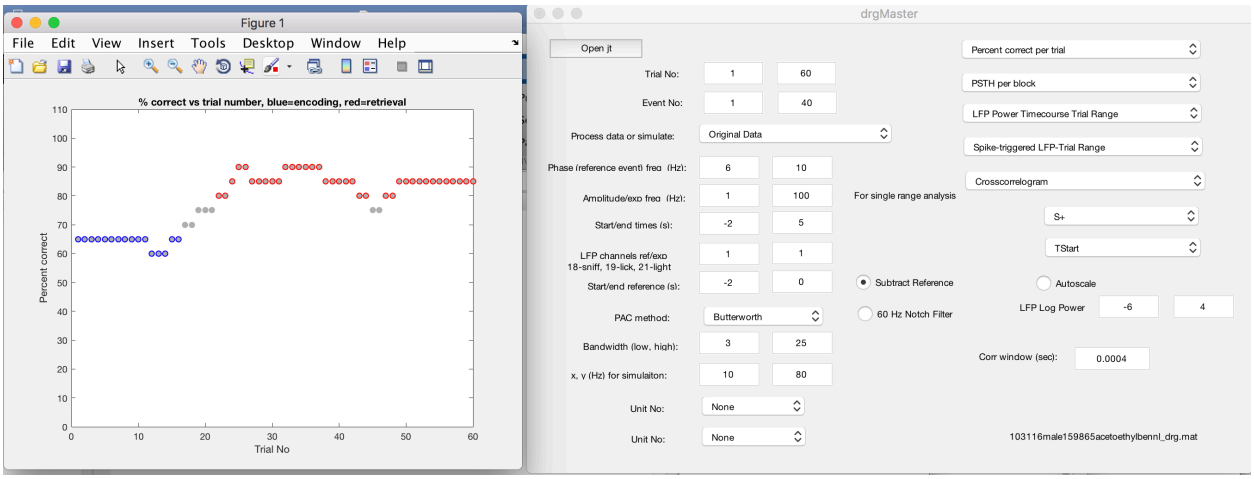
-At a later date you can do wave_clus to find the spikes

David Gire’s data/analysis
MClust does spike sorting
Load MClust 3.5 from http://redishlab.neuroscience.umn.edu/MClust/MClust.html
If you are working on a Mac get the mex files and add them to the MClust-3.5\MClust\LoadingEngines. Make sure to load the 32 or 64 depending on how you have your computer running.

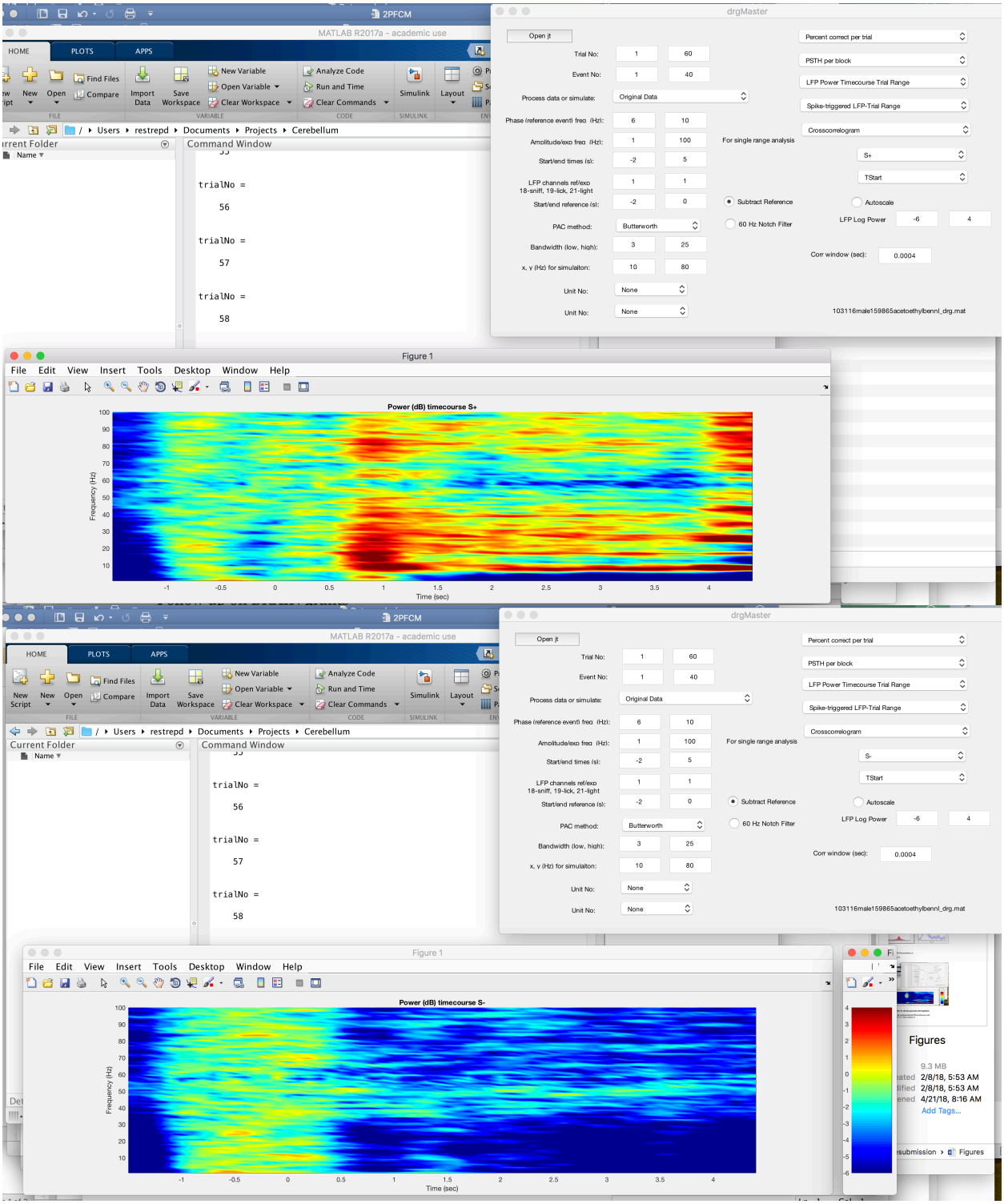
drgMaster is a comprehensive program that allows single experiment data processing using the jt_times file. If wave_clus has not been run then spikes cannot be analyzed; only the behavior and LFP functions will work.

Examples of analysis:

Percent correct per trial shows the percent correct calculated in a 20 trial window.



LFP Power Timecourse Trial Range uses spectrogram to compute the timecourse for LFP power for the trial range.



For drg batch processing:

drgRunBatch does all the processing that needs long computer time. After drgRunBatch is run the output file can be used to display different analyses using different functions

dropc

These programs control the Restrepo olfactometer, a modification of the Slotnick olfactometer (Slotnick and Restrepo, 2005).

get mccdaq-2.exe from the mcc web site
https://www.mccdaq.com/daq-software/MATLAB-Support.aspx
Error # 1 is definitely bubbling up from the Measurement Computing InstaCal driver. First, close MATLAB and Launch InstaCal. Be sure the DAQ board tests OK (can flash the LED, for example) in InstaCal, and note the logical board number assigned. Then close InstaCal and re-launch MATLAB ... insure that the MATLAB aplication references that particular logical board number.

daq.getDevices
open matlab as administrator
daqregister('mcc')

Finally, try the software at your own risk ☺ Not all functions are tested!! Also, I want to thank Nick George for steering me towards GitHub.

Diego

Li, A., Gire, D.H., and Restrepo, D. (2015). Y spike-field coherence in a population of olfactory bulb neurons differentiates between odors irrespective of associated outcome. J Neurosci *35*, 5808-5822.
Quiroga, R.Q., Nadasdy, Z., and Ben Shaul, Y. (2004). Unsupervised spike detection and sorting with wavelets and superparamagnetic clustering. Neural Comput *16*, 1661-1687.
Ramirez-Gordillo, D., Ma, M., and Restrepo, D. (2018). Precision of Classification of Odorant Value by the Power of Olfactory Bulb Oscillations Is Altered by Optogenetic Silencing of Local Adrenergic Innervation. Front Cell Neurosci *12*, 48.
Slotnick, B.M., and Restrepo, D. (2005). Olfactometry with mice. In Current Protocols in Neuroscience, J.N. Crawley, C.R. Gerefen, M.A. Rogawski, D.R. Sibley, P. Skolnick, and S. Wray, eds. (New York: John Wiley and Sons, Inc), pp. 1-24