

## MATLAB Assignment #4

Be sure to save the line codes to submit as .m file for grade.

For your previous homework you had to load and filter electrophysiology data. Spike crossings were also detected and snippets extracted. For this homework, you will extend these tools to explore spike quantification methods. A checklist is included at the end of the problem set indicating the items that will be graded. Remember to save your work as you proceed (use the save command). You can explore provided functions by using the help, type or edit commands. Accompanying questions are included at the end of each part to tie the algorithms with the neurophysiological information they intend to capture. As a guideline, answers to each question should consist of 1 to 5 sentences depending on their complexity.

### Spike Detection

#### **Part I:** Basic spike data analysis using peri-stimulus spike histograms (PSTHs)

Load one of the data files, you may use the same one you used previously. Plot the entire raw data from one channel of your choosing. Inspect the data, does it look ok? Are potentials and spikes evident if you zoom in? Make sure you create an appropriate time vector as the x-axis using the variable samprate.

1. Filter the data using a high-pass Butterworth filter, use an appropriate order and frequency cut-off. Use the butter and filter commands. Make sure the data is of type double precision prior to filtering. Calculate the mean and standard deviations of the filtered data. Justify your selection.

2. Use the TrigON variable to find the spacing between stimuli, then re-organize the data into a new variable that has dimensions of (trial\_data,stimulus#). Since the trigger indicates the time of stimulus, make sure you grab some time prior to stimulation (e.g. 0.5sec below). You can achieve this using this pseudo-code.

```
new_indeces = [1 : round(stim_time*samprate)] - round(0.5*samprate) ];
for m = 1 : n_stimulations,
    stimloc = find( t > TrigON(m) ,1);
    newdata(:, m) = data( stimloc + new_indeces );
end;
```

3. Find the negative spike deflections using a threshold of your choosing. Justify your selection. Applying this threshold to the data generates the raster plot data (binary). Recall that the raster only indicates a single point where the data crosses the threshold (see pseudo-code below). Generate a raster plot of one or more stimulation trial traces. You can use the plot\_raster function provided.

```
ii=find(newdata(:,m)<threshold);
```

```

id=find(diff(ii)>1);
ii=[ii(1);ii(id+1)];
raster=zeros(size(newdata));
raster(ii)=1;

```

4. Make a new time vector where the spacing between time points is the bin-width of the histogram you wish to generate (typical values range between 25 and 200 ms). You can achieve this using the following pseudo-code (also included in function plot\_psth provided). Generate the histogram plot of the same raster selection used above and compare them.

```

time_psth=[-0.5: psth_dt: stim_separation];
for m=1:length(time_psth),
    search_index=find( (time>=time_psth(m)) & (time<time_psth(m)+psth_dt) );
    psth(m,:)=sum(raster(search_index,:),1);
end;

```

5. Plot the average PSTH. What is the average increase in spike rate before and during stimulation?

6. Repeat this procedure for the data from all channels. Plot the average increase in spike rate evoked by stimulation as a function of channel (depth).

### **Accompanying questions:**

7. What are the three main cell types present in the brain? Which of these cells are electrically excitable? Which of these cells change their membrane potential? How are these cells different?
8. How can you separate synaptic potentials from action potentials in intra-cellular recordings? What are common filter ranges to isolate synaptic potentials? What are common filter ranges to isolate action potentials?
9. How would you implement a PSTH for electrophysiology data that does not have an evoked stimulus? You can think about ways that only employ the data available, or you can think about a complementary recording that may be available.

### **Assignment Checklist**

#### **Part I: PSTH**

1. Plot data from a channel of your choosing before and after filtering using a high-pass butterworth filter.
2. Calculate the mean and standard deviation of the filtered data. Justify your frequency cut-off selection.
3. Reorganize data relative to TrigON (trigger) and generate raster plot for one or more trials. Justify your threshold selection.

4. Generate histogram (PSTH) for one or more trials
5. Generate average histogram (PSTH) for all trials in one channel. What is the average spike rate before and during stimulation?
6. Generate average histogram (PSTH) for all trials in all channels and plot the average change in spike rate (during vs. before) as a function of depth (channel#).
7. Answer accompanying questions 7, 8 and 9