**Filter framework Analysis Notes – HPExpt**

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***1) DFSsj\_HPexpt\_getripalignspiking.m***

- Calls DFAsj\_getripalignspiking.m (requires sj\_getripples\_cellinfo.m, a variant of getripples.m)

- For run sessions, gets ripple-aligned spiking for all cells. I am running separately for PFC and CA1 cells.

- After filter script is done, bottom portion of code combines data for cells across run epochs, and does a significance test based on mean rate in response and bck window using a shuffle method. I am using 0-150ms, and -500 to -350ms as the windows. Data is saved in \*\_gather files

- You have option to plot individual cell response

- At end, population response is plotted.

***2) DFSsj\_HPexpt\_getripalignspiking\_sleep.m***

- Same for sleep sessions.

- Keeping pre-sleep (1st epoch), and post-sleep (last epoch) separate. Not doing intermediate rest sessions.

***3) DFSsj\_HPexpt\_getripalignspiking\_perepoch.m***

- Storing ripple aligned responses for cells in each epoch separately. Saves a “ripplemod” structure file for each day, just like a “ripples” or “spikes” file.

- This will make it easy to just load this data in filter framework rather than re-computing everytime.

***4) sj\_addripplemodtag.m***

- For PFC and CA1 cells, goes through run and sleep epochs (separately), and adds a tag to each cell based on whether they are significantly modulated or not.

- For run epochs, tag is added based on data combined across epochs

- For sleep epochs, pre and post sleep are kept separate

***5) DFSsj\_plotthetamod.m***

- Calls DFAsj\_plotthetamod.m

- Get theta modulation of cells during run epochs. For both PFC and CA1, reference is CA1 theta on dCA1 reference electrode.

- I run separately for PFC and CA1 cells for run sessions. Data is combined across runs, and saved in “\*\_gather” files with summary data which can be loaded and plotted. Combines data across run epochs and computes fits and stats of circular concentration as well. Plots for single cells as well as population summary

***5) sj\_combine\_thetaandripplemod2.m***

- Plots comparisons of theta and ripple modulation in a population.

***6) sj\_combine\_runandsleepripplemod2.m***

- Plots comparisons of awake and rest/ sleep modulation in a population.

***7) DFSsj\_HPexpt\_ripresp\_corrandcoactz.m***

- Calls DFAsj\_HPexpt\_getripresp\_corrandcoactz.m

* Get correlations and co-activez scores for pairs of cells, and plots population summary.

***8) sj\_addthetamodtag.m***

- Similar to sj\_addripplemodtag

***9) DFSsj\_HPexpt\_ThetaCovOnly.m***

- Calls DFAsj\_getthetacrosscov.m

- Get PFC-CA1 theta covariance for different categories of cells. For each PFC cells, get the mean standardized cc from all its corresponding CA1 pairs. Threshold implantation for cc is like Siapas (2005) currently. I will change it to using shuffled data to account for Poisson statistics as in Wierzynski (2009)

***10) sj\_HPexpt\_ThetaCov\_ByRipModln.m***

- Gets theta covariance files and SWR modulation files and compares the two.

***11) DFSsj\_HPexpt\_ThetacorrAndRipresp.m***

- Calls DFAsj\_HPexpt\_getripresp\_corrandcoactz.m and DFAsj\_getthetacrosscov.m

- Need to update still to compute CC peaks, etc.

- Compare theta covariance and rip cross-corrln. Pairwise or for different categories of cells.