**Version Notes**

* *Updated by SPJ on 02-12-14.*

*Added* ***sj\_addripmodtag4.m*** *and* ***sj\_combine\_thetaandripplemod2\_ver4var.m***

*All scripts and functions named with suffix “ver4” or “4”*

* *Updated by Gideon on 02-11-14.*

*Codes version4 onwards*

**Filter framework Analysis Notes – HPExpt**

***1) DFSsj\_HPexpt\_getripalignspiking\_ver4.m***

- Files stored with \_feb14 in name now

- Calls DFAsj\_getripalignspiking4.m (requires sj\_getripples\_tetinfo.m, a variant of getripples.m, which gets ripples by looking across all tetrodes: “GLOBAL RIPPLE”)

***2) DFSsj\_HPexpt\_getripalignspiking\_perepoch\_ver4.m***

- Files stored with \_feb14 in name now

- 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.

***3a) sj\_addripmodtag4.m and sj\_addripmodtag\_var4.m***

*- First code adds ripplemodtag for HPa,b,c for all epochs for all animals and for both PFC and CA1 based on mean difference statistics. Also adds type = “exc” and “inh”. Currently only being run for PFC cells in run epochs. Once “getripalign” is run for sleep sessions and CA1 cells, can run this code for those as well.*

*- Second code (one being more important now) adds “ripplemodtag2” based on the new variance measure for PFC called for run epochs for all animals.*

- 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

***4) DFSsj\_plotthetamod4.m. Still the same***

- Calls DFAsj\_plotthetamod4.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\_ver4.m*** *and* ***sj\_combine\_thetaandripplemod2\_ver4var.m***

*does the comparison with the newest “var” measure*

*1st code can be changed to compare with the old measures*

***6) sj\_addthetamodtag4.m Same as before***

- Similar to sj\_addripplemodtag. Does all animals, including Ndl, now

***7) DFSsj\_HPexpt\_ThetacorrAndRipresp\_ver4.***

- Calls DFAsj\_HPexpt\_getripresp\_corrandcoactz4.m and ~~DFAsj\_getthetacrosscov.m/~~ DFAsj\_getthetacrosscov\_timecondition4.m

***8) DFSsj\_HPexpt\_glm\_theta4.m***

* Calls DFSsj\_glm\_ripalign\_dataForTheta4 and DFSsj\_glm\_thetaGR4
* Does a glmfit of “ripplemod” data and a glmfit of theta data to ripple firing

- NOTE: DFSsj\_HPexpt\_glm\_ripalign4 does only the ripple part of the GLM. Calls DFAsj\_glm\_ripalign4

***9) sj\_getPFC\_CA1\_sigcorridxs4.m and sj\_getPFC\_CA1\_sigidxs4***

- Gets indices of significant correlations based on the pairwise correlations (or glm fits based on ripple glmfit for the 2nd file).

**10) Place filed correlations based on the significant correlations: Demetris has code.**