**DATASETS**

1. The experimental data has been processed and the extracted features are in these tables.

They are python-pickled (file is pandas dataframe) for easier portability. Description of columns are at the end of this document.

pickletable\_HippoPvalb\_pd

pickletable\_HippoPyr\_pd

pickletable\_V1Pvalb\_pd

pickletable\_V1Pyr\_pd

pickletable\_V1SST\_pd

pickletable\_HumanCells\_pd

**JUPYTER NOTEBOOKS**

2. These are the codes (in jupyter notebooks) used for analysis and for plotting.

* Code has been originally developed under Python 2.7 and associated older package dependencies. Work is in progress to transfer code to Python3+.

Please see “package\_list.txt” to see how the miniconda environment is currently set up (it is very old)

1) Sub\_Sup\_entrainment\_core\_V1.ipynb

Sub\_Sup\_entrainment\_core\_hippo.ipynb

Sub\_Sup\_entrainment\_core\_human.ipynb

This is the core code that is assessing e-field entrainment.

This covers most of the subthreshold analysis (e.g. Figs1b, c, Fig 3)

This analyzes suprathreshold data: e.g. generating rose plots for Fig2 and getting the spike histograms for Fig 4b, etc. and extracts the circular statistics information.

2) Plots\_Rayleigh\_logp.ipynb

These are line plots plotting the Rayleigh p-values (e.g. Fig 2)

3) boxplots\_and\_lineplots.ipynb

This notebook is for making the boxplot data where data is plotted per-cell (e.g. Fig 2d, e)

These codes make use of data (control and 200 nA stim) in excel sheets—the large pandas dataframe was analyzed on a per-cell basis using the core entrainment codes, and then the numbers were put into excel sheets for convenience. Excel sheets names are below:

Pyr\_V1\_200\_boxplot\_lineplot\_nums.xlsx

Pvalb\_V1\_200\_boxplot\_lineplot\_nums.xlsx

SST\_V1\_200\_boxplot\_lineplot\_nums.xlsx

hippo\_200\_boxplot\_lineplot\_Pyr.xlsx

hippo\_200\_boxplot\_lineplot\_Pvalb.xlsx

V1\_200\_boxplot\_lineplot\_allclasses\_ttest.xlsx

Human\_200\_boxplot\_lineplot\_nums.xlsx

4) Angle\_SD.ipynb

This plots the standard dev. of spike-phase distribution for various amplitude/frequencies in V1 (Fig. S4).

5) bootstrapping\_meanVL.ipynb

This is the code for getting the bootstrapped mean VL values for doing the spike-ISIrate-ESfreq comparison. This is the code, and the extracted output is in excel files (to be used for plotting).

6) Barplots\_Bootstrap\_comparisons.ipynb

This code is for pyramidal cells (for V1 and human), where we bar-plotted out the bootstrapped mean VL values and plotted them by spike-freq-bins. (i.e. Figs 4c-d). It also plots the Welch’s test and cohen’s d values for the control vs. ES comparisons

**Regarding older-version code**

syl\_miniconda\_package\_list.txt

is a list of packages in my conda environment, and you’ll see that the packages are… quite old. The code still runs just fine under these conditions, but will require more testing with newer environments.

**DATAFRAME COLUMNS:**

filename: name of cell

sweep\_id: sweep id (this is a longer version of sweep\_number, has some info attached to sweep\_number, e.g. ES amplitude, etc)

sweep\_number: sweep number

ex\_el\_id: which electrode ID for extracellular recording

stim\_el\_id: which electrode ID for ES application

in\_el\_id: which electrode ID for intracellular recording

ex\_el\_distance\_mu: distance of extracellular electrode

spike\_tt: spike times

ex\_amp\_nA: ES amplitude

ex\_frequency: ES frequency

ex\_dur\_ms: duration of recording

ex\_delay\_ms: seconds before experiment starts

in\_amp\_pA: intracellular current injection amplitude

in\_dur\_ms: intracellular current injection duration

in\_delay\_ms: seconds before intracellular application starts

vext\_amp\_mV: Ve amplitude

vext\_phase: Ve phase from hilbert

vi\_amp\_mV: Vi amplitude

vi\_phase: Vi phase

vm\_amp\_mV: Vm amplitude

vm\_phase: Vm phase

avg\_vm\_mV: average Vm amplitude

spike\_phase: spike time matched to Ve phase

spike\_tt\_A: spike times after 0.5s

spike\_phase\_A: spike phases after 0.5 s

num\_spikes: number of spikes

num\_spikes\_A: number of spikes after 0.5 s

spike\_phase\_A\_corrected: spike-phase is 'normalized' to start at 0

Notes:

\*The “delay” periods are just when we start recording, then we record nothing for a few ms, and then the actual experiment (i.e. ES and/or intracellular current application) starts.

This was just to ensure that there is some stability in the recording before actual experiment starts.

\*A (naming in spike columns) is for the spiking data after the first 0.5s. As mentioned in the Methods, we start looking at our data after the first 0.5s. This is because as we inject intracellular current into the cell, there are sometimes other things happening due to the current injection itself, e.g. initial bursting, Ih, etc. To dissociate that from any actual ES-induced effects, we analyze the data after that first 0.5s.