**Pupil/ECoG Correlation Pipeline**

**About:**

This pipeline is adapted from Harry Sha’s pupil\_pipeline. It plots pupil data and ECoG HFB on the same axis. Pupil Data outputted from Harry’s pipeline is smoothed using a sliding average, and then plotted with the ECoG HFB average outputted from Su’s preprocessing pipeline. Additionally it can also create a graph that plots pupil diameter vs HFB signal for all time points and calculates the r value. There is also an option to plot the change pupil diameter vs the change in HFB signal.

**Pupil Data:**

The pipeline will prompt you to select two files. The Pupil Data should be in the form of the .pkl file exported from Harry’s pupil pipeline (called merged\_<name>).

**ECoG Data:**

The ECoG Data should be in the form of a .mat file that contains two variables. The first is called ‘plot\_time’ and contains a 1x1000 matrix with all the time points of the ECoG measurements (assuming there are 1000 time points). The second is called ‘temp\_mean’ and contains a 1000x3 matrix with the HFB power at each recorded time point for each condition to be plotted (assuming there are 1000 time points and 3 conditions to be plotted. It should work for other values as well as long as temp\_mean and plot\_time are congruent).

**Getting the ECoG Data from Su’s Preprocessing Pipeline:**

The ECoG .mat file can be easily manufactured by adding the following code to line 49 of Plot\_script.m in Su’s pipeline (under ‘temp\_std(:,j)=…’) and running the pipeline:

plot\_time = t(window);

save(fullfile(D{1}.path,strcat('pupil\_',name,'.mat')),'temp\_mean','plot\_time');

This code will save a .mat in the proper format for every channel. To select only one channel, run Su’s pipeline with chanp = <index value of channel> (line 4 of Plot\_script.m) in addition to the above code. The index value can be found in D.channels(1).label of Su’s outputted MfffdECoG…mat file.

**Parameters:**

Parameters can be specified by passing a .py file as an argument when running the pipeline. The file parameters\_default.py contains the default parameters and will be run automatically if no argument is passed. To change parameters, either change them in the file parameters\_default.py or create a new file with the format of parameters\_default.py and pass it as the argument when running the pipeline.

**Parameter Options:**

There are a number of options that can be specified using the parameters file. If all\_channels is set to True, the pipeline will prompt you to select a folder and will run for all .mat files in that folder. This way you can run all channels at once. If scatter is set to ‘normal’ or ‘derivative’, it will create a scatter plot of pupil diameter vs HFB or the change in pupil diameter vs the change in HFB respectively.

**Running the pipeline:**

1. Download python 3.7 from (https://www.python.org/downloads/)
2. Clone this repository
3. Put Pupil and ECoG Data in a convenient folder. An output folder will be created in the same folder that the .mat file comes from.

**Run the pipeline with Terminal or Command Prompt (same as Harry’s pipeline):**

1. Open terminal (mac, linux) or command prompt (windows)
2. cd into the pipeline
3. type `python correlation.py <parameters>`, where `<parameters>` is replaced with the name of the parameters file. You can also leave it empty to run the pipeline with the default parameters.

**Run the pipeline with Atom (this will only work with default\_ parameters but default\_parameters can easily be changed and run consecutively):**

1. Download atom (<https://atom.io/>) and the scripts package within atom
2. Open the pipeline folder in atom
3. Select the correlation.py file
4. Select Packages🡪Script🡪Run ( or CTRL, SHIFT, B)