**CC\_Longitudinal\_wPLI.m**: This is the main analysis script. It is broken up into the following sections:

* Setup Environment: Initialize the work environment by defining file paths and default function parameters.
* wPLI Analysis: Segments the recording periods for each alertness state into segments of length “segment\_l” defined in the above section. The wPLI is calculated for each of these segments using subsegments of length “trial\_l”, also defined in the above section.
* Add Networks: Networks are constructed from the adjacency matrices calculated above. For each subject the percolation threshold is calculated on the most alert state, the absolute value at this threshold is then used as the threshold for all other states on a within subject basis. Weighted networks are labeled “Thresholded’ while unweighted networks are labeled “Binarized”.
* Calculate Network Stats: Average Degree, Transitivity, Characteristic Path Length, Assortivity Coefficient, Clustering Coefficient, Modularity, and Small World Propensity are calculated.
* Plot Graph Metrics: This section will plot the results of a chosen graph metric for each subject and each frequency band. These are useful for looking at changes between alertness states.
* Calculate Confidence Intervals and one-way-ANOVA: Generates a “GraphStats” object with 95% confidence intervals and results of one-way-ANOVA testing. Also generates a summary matrix titled “GraphStatsMat” containing the ANOVA p-values as well as FDR and Bonferroni corrected p-values.
* 3D Brain Plotting Demo: A short demo of the “plotbrain” function for plotting a given network and subject electrodes on a 3D template brain.

**Longitudinal\_wPLI\_ParamEstimation.m**: This script was used to examine the effects of varying the length of the segment time window on the mean wPLI. It is broken into the following sections:

* Setup Environment: Initialize the work environment by defining file paths and default function parameters.
* wPLI Parameter Screen: Calculates the mean wPLI using a series of segment lengths defined in “seglengths”. The results are stored in a variable titled “VarTrack”.
* Plot wPLI Means: This section will plot the results stored in “VarTrack” as either a function of time or segment length using the “plotmeanvar” function.

PercolationThr.m: This function calculates the percolation threshold for a given adjacency matrix in one of two ways. ‘iterativeEdge’ will compute the “true” percolation threshold by iteratively removing the weakest edges until the threshold is found. ‘cutoff’ will approximate the threshold by screening relative thresholds to a 0.001 accuracy and performs much faster.

**plotmeanvar.m:** This function plots the results of “Longitudinal\_wPLI\_ParamEstimation.m”. The X-axis will either be start time of each segment, if ‘time’ is chosen, or the segment length itself, if ‘seglen’ is chosen.

Ex.



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**plotmetric.m:** This function plots a desired graph metric for a desired subject, grouped and color coded by alertness state.

Ex.



**plotbrain.m:** This function plots a subject’s electrodes on a 3D template brain along with the connections between the electrodes in a network.

Ex.



The following functions written by others but used in the above scripts are also included:

adj2edge.m: converts an adjacency matrix to a list of edges.

bonf\_holm.m: applies Bonferroni correction to a list of p-values.

fdr\_bh.m: applies Benjamini-Hochberg correction to a list of p-values.

small\_worldness\_propensity.m: calculates the SWP of a network.