**Supplementary Materials**

**S2. DEEP Additional Functions**

**S2.1 Surrogate data functions**

One important step in analyzing the hyperscanning datasets is to run control analyses checking for spurious correlations between the two EEG signals. The current version of the pipeline employs two surrogate analysis methods: between-dyad and within-dyad shuffling approaches. Using the between-dyad shuffling approach, the ***DEEP\_permtest\_dyad.m*** script generates random dyads, for example, by pairing data of mothers with randomly assigned infants. The script checks whether the randomly generated pairs are from the same dyad and discards these values from the surrogate analyses. The script then calculates either the cross-frequency PLVs or PLVs for these randomly generated dyads for each channel combination and frequency band for a particular condition. The user can choose for which condition and frequency band they want to run the surrogate analyses.

For the within-dyad shuffling approach the pipeline uses two scripts. ***DEEP\_permtest\_plv.m*** script first conducts a paired-sample t-test at the level of averaged PLVs. If this test shows a significant result, a permutation test follows. Here, the permutation test is done at the level of single PLVs. All values in the two conditions for one dyad are combined in a single set. The script then generates separate permutation distributions for all dyads, which is followed by paired sample t-tests. The number of drawn PLVs per condition for each permutation is the same and is kept identical with the original distribution.

***DEEP\_permtest\_mplv.m*** script first runs a paired-sample t-test, which is followed by a permutation test, if the result of the t-test is significant. Unlike the *DEEP\_permtest\_plv.m* script, here, the permutation is done on the level of averaged PLVs. In this script, the permutation is done by randomly interchanging the values of the two conditions within the dyads. We recommend the users to use this script, only if the number of PLV segments is almost the same in both conditions for a single dyad. Within dyad shuffling surrogate scripts will be adjusted for cross-frequency PLV calculations in future versions of the pipeline.

**S2.3 Plot functions**

 Several plotting functions are available in the pipeline. A function can be started using the command “***function\_name (cfg, dataset)***”. The averaged results obtained at step 9 can be used for the plotting functions. To execute one of these functions, the specific dataset (either data of one participant or averaged data of several participants) should be located in the workspace in MATLAB. Each function can be configured individually using the settings described in Table S2.3.

Table S2.3: A combined list of configurations and their descriptions for the entire plot functions. Please note that different plot functions have slightly different configurations.

|  |  |
| --- | --- |
| cfg.part: | Identifies the participants. Options: 'mother' or 'child' (default: 'mother'). |
| cfg.condition: | Determines the conditions (default: 11 or 'DFreePlay', see DEEP\_datastructure.m, for the current dataset). |
| cfg.baseline: | Baseline condition (default: []). Any valid condition can be used as the baseline condition. The values of the baseline condition are subtracted from the values of the selected condition (see cfg.condition). |
| cfg.log: | Uses a logarithmic scale for the y axis. Options: 'yes' or 'no' (default: 'no').  |
| cfg.powlim:  | Sets the limits for power dimension to use, 'maxmin' or [pmin pmax] (default: 'maxmin').  |
| cfg.trial: |  Number of trials (default: 1). |
| cfg.freqlim: | Sets the limits for the frequency range to use, [begin end] (default: [2 30]).  |
| cfg.timelim: | Sets the limits for the time interval to use, [begin end] (default: [4 116]).  |
| cfg.electrode: | Electrodes of interest (e.g., {'C3', 'Cz', 'C4'}, default: 'all'). |
| cfg.elecorder | Describes the order of electrodes (‘default’ or specific order, i.e., 'DEEP\_01'). |
| cfg.elecPart: | Number of electrodes for the first participant, e.g., the mother (default: 'Cz'). |
| cfg.elecPart2: | Number of electrodes for the second participant, e.g., the child/infant (default: 'Cz'). |
| cfg.avgelec: | Plots the average over selected electrodes, options: 'yes' or 'no' (default: 'no').  |
| cfg.zlim: | Sets limits for color dimension, 'maxmin', 'maxabs', 'zeromax', 'minzero', or [zmin zmax] (default: 'maxmin').  |
| cfg.showeogv: | Show vertical eye electrodes in topo plot, options: 'yes' or 'no' (default: 'no'). |

**S2.3.1 DEEP\_easyPlot.m**

 This function plots the raw or preprocessed continuous EEG data for one participant (e.g., adult or child) in a particular condition and trial for a particular electrode.

**S2.3.2 DEEP\_easyPLVPlot.m**

This function plots the PLVs for one dyad or the average PLVs across dyads in a particular condition for particular electrode combinations. The user can choose to plot each electrode combination separately or plot the average PLVs over the selected electrode combinations. If applicable, a baseline can be specified to subtract the data of the baseline from the condition selected for plotting. We will include plotting functions for cross-frequency PLV results in future versions of the pipeline.

**S2.3.3 DEEP\_easyPowPlot.m**

 This function plots the power spectrum values for one participant or average power spectrum values across participants in a particular condition for a particular electrode. If applicable, a baseline can be specified to subtract the data of the baseline from the condition selected for plotting.

**S2.3.4 DEEP\_easyTFRPlot.m**

 This function plots the time-frequency responses for one participant or average time-frequency responses across participants in a particular condition for a particular electrode. If applicable, a baseline can be specified to subtract the data of the baseline from the condition selected for plotting.

**S2.3.5 DEEP\_easyTopoPlot.m**

 This function plots a topo plot for one participant or values across participants in a particular condition within a particular frequency range. If applicable, a baseline can be specified and data during this baseline is then subtracted from the condition selected for plotting.

**S2.3.6 DEEP\_easyMPLVplot.m**

 This function plots the PLVs for the average of dyads in a particular condition separately for each available electrode combination. If applicable, a baseline can be specified and data for this baseline will be subtracted from the condition selected for plotting.

**S2.3.7 DEEP\_easyMultiPowPlot.m**

 This function plots the power spectrum for one participant or an average of power values across participants in a particular condition within a particular frequency range for all electrodes on a head model. If applicable, a baseline can be specified and data for this baseline will be subtracted from the condition selected for plotting.

**S2.3.8 DEEP\_easyMultTFRPlot.m**

This function plots the time-frequency responses for one participant or the average values across participants in a particular condition within a particular frequency range separately for each available electrode.

**S2.4 Export functions**

**S2.4.1 DEEP\_exportPow\_general.m**

 With this function, the user can export the power spectrum data for selected participants and conditions for a certain frequency range or several frequency ranges. In addition, the user can choose whether to export the average power value over the selected electrodes (i.e., “cluster average”) or the power values from each individual electrode for each frequency.

**S2.4.2 DEEP\_exportPLV\_general.m**

Similar to the power spectrum values, the pipeline allows the users to export the PLVs for selected participants and conditions for a certain frequency range or over several frequency ranges. Moreover, the user can select whether to export particular electrode combinations or the average PLV over the selected electrode combinations for each frequency. Using the same script, the users can also export the PLVs for the surrogate data generated with a between-dyad shuffling approach.

**S2.4.3 DEEP\_exportcrossPLV\_general.m**

With this script, users can export cross-frequency PLVs for selected participants and conditions for a certain frequency range or over several frequency ranges. All of the above functionalities of DEEP\_exportPLV.m script can be performed for cross-frequency PLVs using DEEP\_exportcrossPLV\_general.m script.