

Group ICA of EEG Toolbox (EEGIFT) Walk Through

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Introduction

This walk-through guides you step by step in analyzing EEG data based on the group ICA framework initially suggested by Calhoun for spatial ICA of fMRI, which was recently adapted for event related EEG time-domain data in the context of EEG-fMRI integration (Calhoun, Adali, Pearlson, & Pekar, 2001; Eichele, et al., 2008). Complementary to the toolbox we have provided a batch script (See Section VIII) for analyzing large data sets. A HTML help manual is also provided to complement this walk-through. For the walk-through we have provided 3 example subjects from an auditory oddball task to illustrate the use of the software. The full oddball dataset with EEG from 30 subjects is available upon request, hybrid data to test this software can also be provided. More information on this task is given in Appendix A. Results from a test of this software with hybrid data is in Appendix B. A formal description of the group model is given in Appendix C. Information about output files generated by EEGIFT is given in Appendix D. EEG defaults are explained in Appendix E. For any questions or suggestions, please contact vcalhoun@unm.edu, tom.eichele@psybp.uib.no or srachakonda@mrn.org.

Installing the Software

- Unzip ‘GroupICATv2.0a.zip’ file and add icatb folder and its sub folders on MATLAB path. You can also add path when you run ‘groupica.m’ or ‘eegift.m’ file and this will automatically add folders and sub-folders at the bottom of the MATLAB path to fix the menu problem for figures.
- Type eegift or groupica eeg at the MATLAB command prompt to open group ICA of EEG toolbox (Figure 1).

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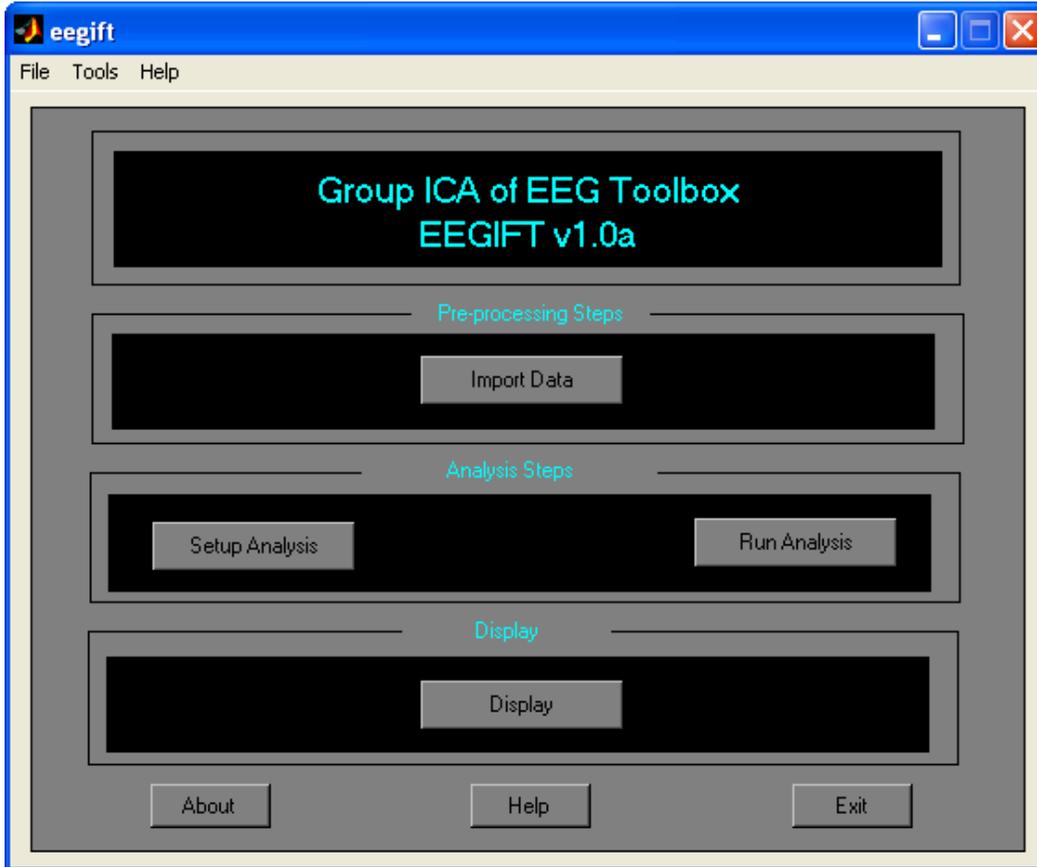
Installing Example Subjects

Unzip ‘eeg_example_subjects.zip’ file and this contains three subjects from oddball task in .SET format. The dimensions of the data are 512 time points by 400 trials by 64 electrodes. Also contained in the zip file is the EEG channel locations file from EEGLAB (‘oddball_locs.locs’) which will be used during display of group ICA components. More information on the task is given in appendix A.

Data Format

- We use MAT file format for reading EEG data and writing component data (time courses, topographies). Each subject must contain only one MAT file whose dimensions are time points by trials by electrodes.
- *Import Data* pre-processing step uses single subject epoched data in SET or DAT file format created by EEGLAB (<http://sccn.ucsd.edu/eeglab/>). Note: This software is intended solely for post-processing and here in particular for extraction of time-locked components that contribute to the event related potential. We assume that users employ EEGLAB or other appropriate software for individual pre-processing, e.g. filtering, epoching, threshold based artifact rejection, single subject ICA for reduction of ocular and other artifacts, and other necessary denoising (Delorme & Makeig, 2004; Jung, et al., 2000). This is to reduce the variability contributed by some noise sources that are not time-locked within, and across subjects. However, additional removal of sources representing typical background rhythms, e.g. posterior alpha and central mu is not necessary to improve extraction of event-related activity in the group model in our experience. EEGIFT requires that the data dimensions are same across subjects and sessions i.e., time points by trials by electrodes. Missing trials are padded using the mean of the surrounding trials.

Figure 1: Group ICA of EEG Toolbox



The main user interface controls in figure 1 are *Import Data*, *Setup Analysis*, *Run Analysis* and *Display*. Each user interface control is explained below:

I) *Import Data*

This step imports EEGLAB .SET data and saves them as .MAT files. Here, EEG trials can also be smoothed across trials using a moving window average. This is useful to further denoise the data when one predominantly wants to look at slower dynamics across trials. Smoothing does not dramatically alter the outcome of the group ICA.

When you click on *Import Data* button, a figure (Figure 2) will open to select the EEG files in a data format that EEGLAB toolbox uses. After selecting the data files, an input dialog box will open (Figure 3) to enter the following parameters.

- ‘Enter vector to correct baseline (ms)’. Enter time range in milliseconds to remove the baseline.

- ‘Do you want to smooth the EEG trials?’ Selecting ‘Yes’ means that the trials will be smoothed using the selected moving window.
- ‘Enter a number for moving point average?’ Trials will be averaged using the selected window length. For now leave it as 3.
- ‘How Do You Want To Sort Trials?’ You have the option to sort trials based on condition and latency. For now leave it as ‘No’. Note that trial sorting makes sense when (a) trial structure is different across subjects (b) sources are vastly different between conditions and or behavioral outcomes. Sorting trials makes it easier to identify components of interest in the display GUI, it does for the most part not critically affect the accuracy of individual component reconstruction, for illustration, in a typical oddball experiment, one can run the group ICA on unsorted trials, and then sort the resulting components according to individual RTs, which reconstructs the RT-dependency of later components that belong to the P300 complex. EEGIFT can sort by RT and trial category, and employs the EEG.event structure from EEGLAB for this.
- ‘Enter file name (not full path) for writing data.’ Data will be written in MAT file format that EEGIFT uses for analyzing EEG data. The data will be saved in the specified output directory (Figure 4) and the data set directory name will be the same as the file name.

Figure 2: EEG File Selection

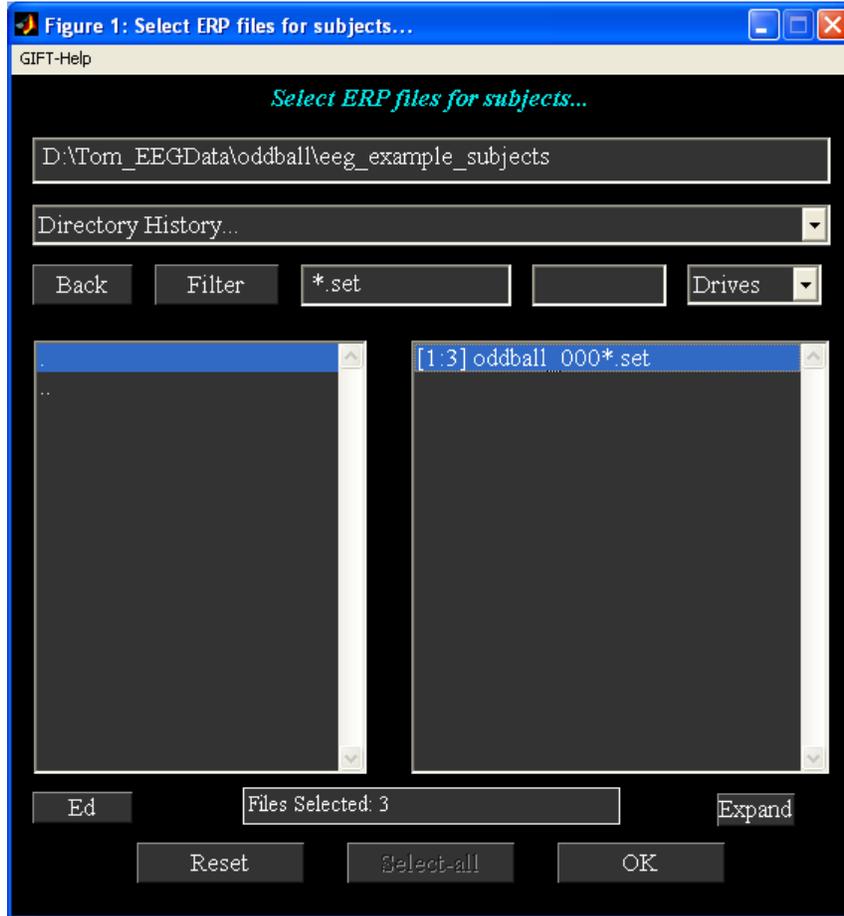


Figure 3: EEG Parameters

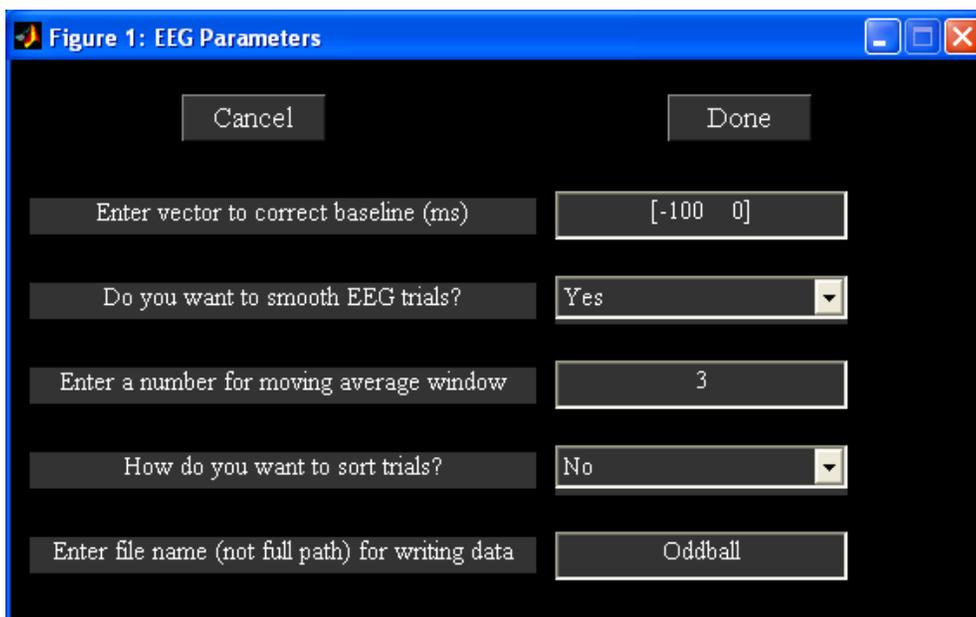
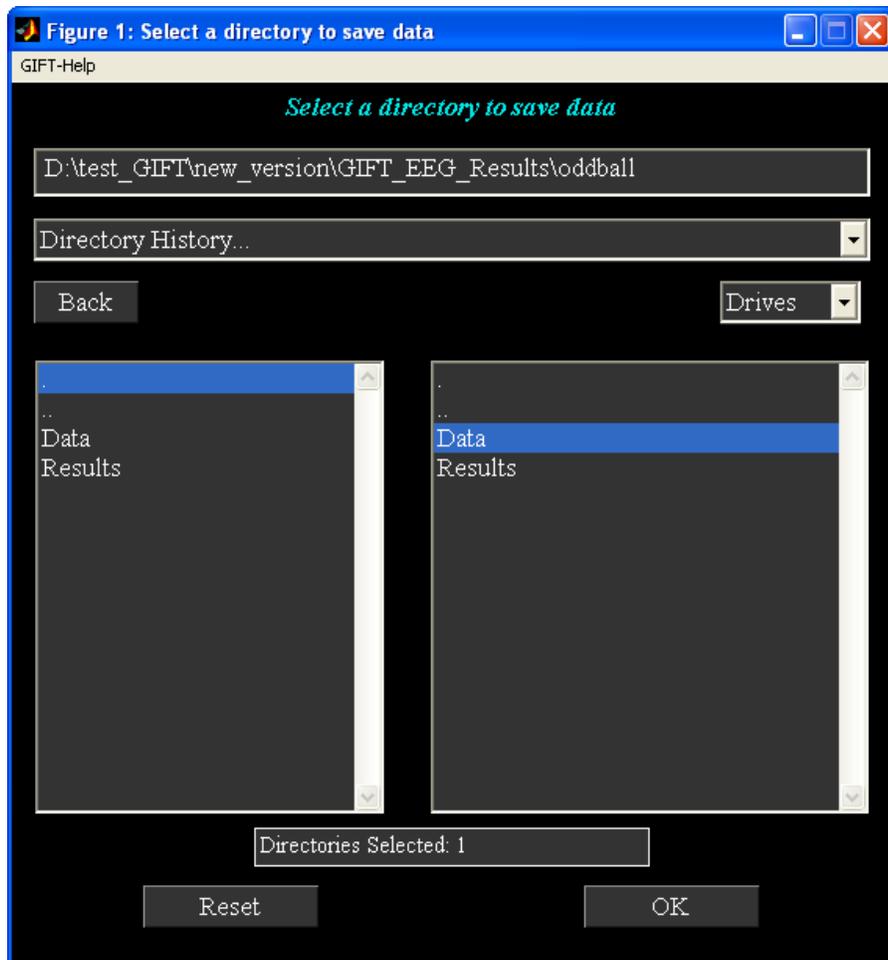


Figure 4: Output directory for saving the data



II) Setup ICA

Setup ICA involves entering parameters for the group ICA analysis. The following are the steps involved in this process:

a.) When you click on the *Setup ICA* button (Figure 1), a figure window (Figure 5) will open to select the analysis output directory. All the output files will be stored in this directory. After the directory is selected, a parameter select window will open. Figure 6 shows the initial parameter select window. Some of the user interface controls (Figure 10) are shielded from the user and plotted in "SetupICA-Defaults" menu. We explain the main user interface controls followed by hidden user interface controls.

Figure 5: Analysis Output Directory

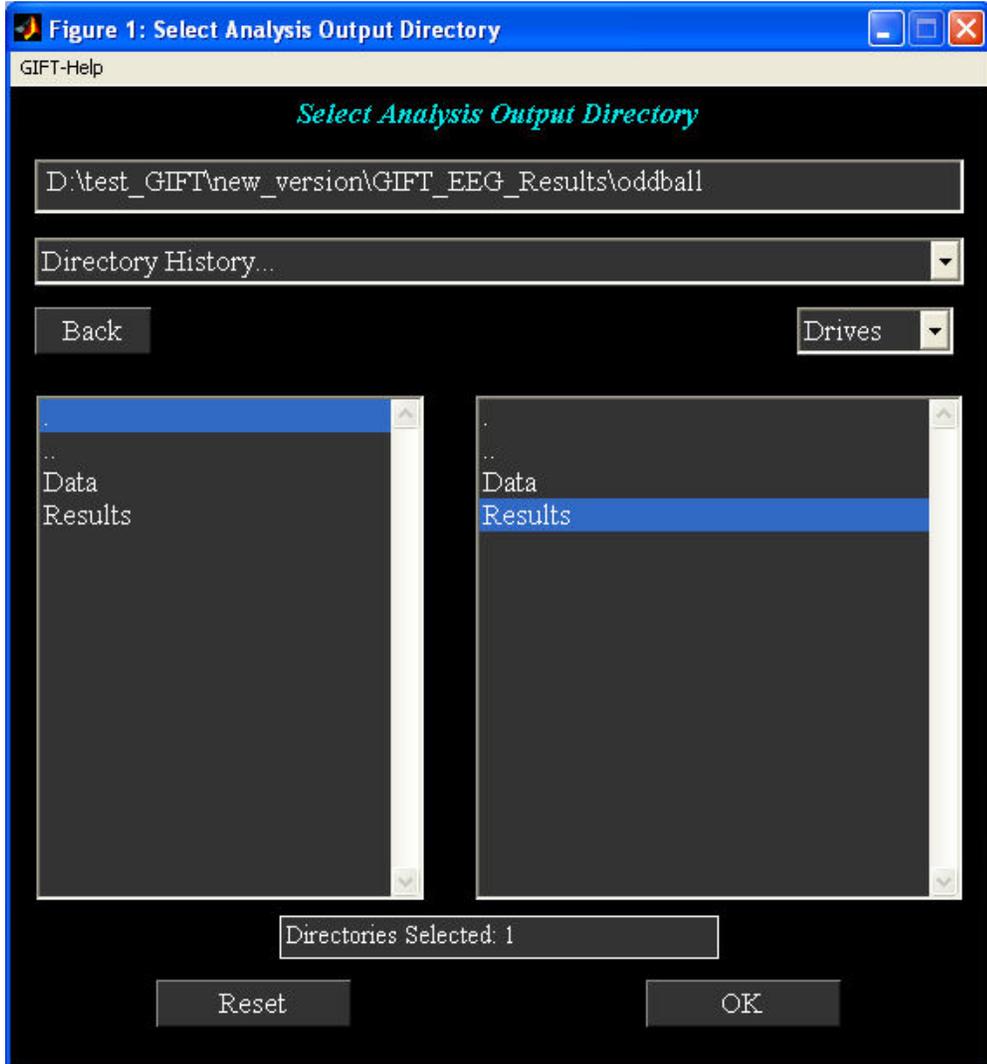
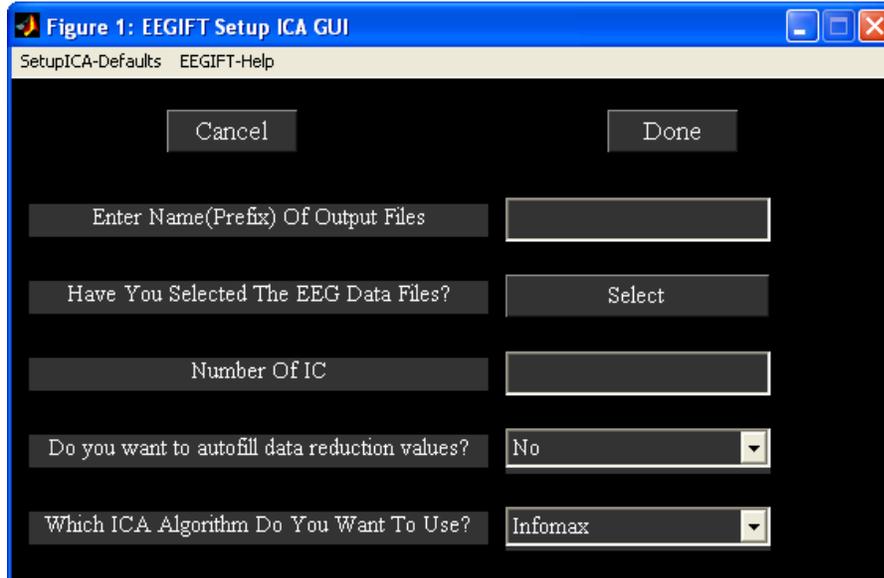


Figure 6: Initial Parameter Selection Window



Main User Interface Controls:

- 1) 'Enter Name (Prefix) Of Output Files' – All the output files created by EEGIFT will be saved using this prefix. Enter 'Oddball'.
- 2) 'Have You Selected the EEG Data Files?' When you click the pushbutton *Select* a new figure window (Figure 7) will open where the data-sets can be selected. There are two options for selecting the data. For now select the first option. After selecting 'Yes', another figure window (Figure 8) will open to select the root folder for subjects and sessions. The selected root folder has three subject folders and each subject contains one MAT file. After the root directory for subjects and sessions is selected, another figure window (Figure 9) appears to enter the file pattern and an additional question to select the data in subject folders or session folders. Select 'Oddball.mat' for 'Select file pattern for reading data' and 'No' for 'Are session folders inside subject folders?' The data will be read from each subject folder with the specified file pattern. The selected subjects and sessions will be printed to the MATLAB command prompt. The number of subjects and sessions selected for the analysis are 3 and 1.

Figure 7: Selecting data method

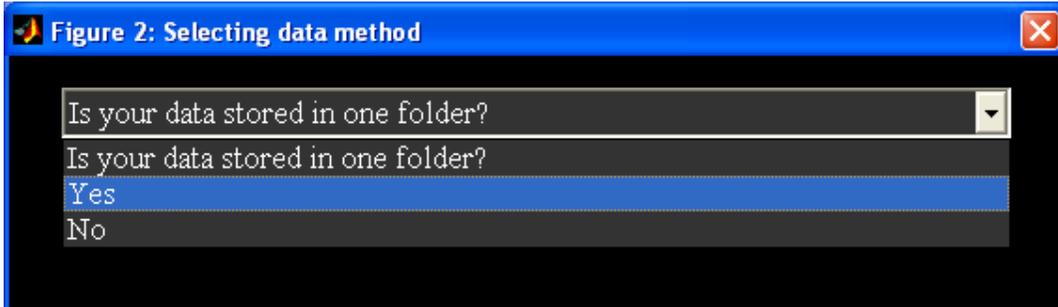


Figure 8: Root folder for selecting subjects and sessions

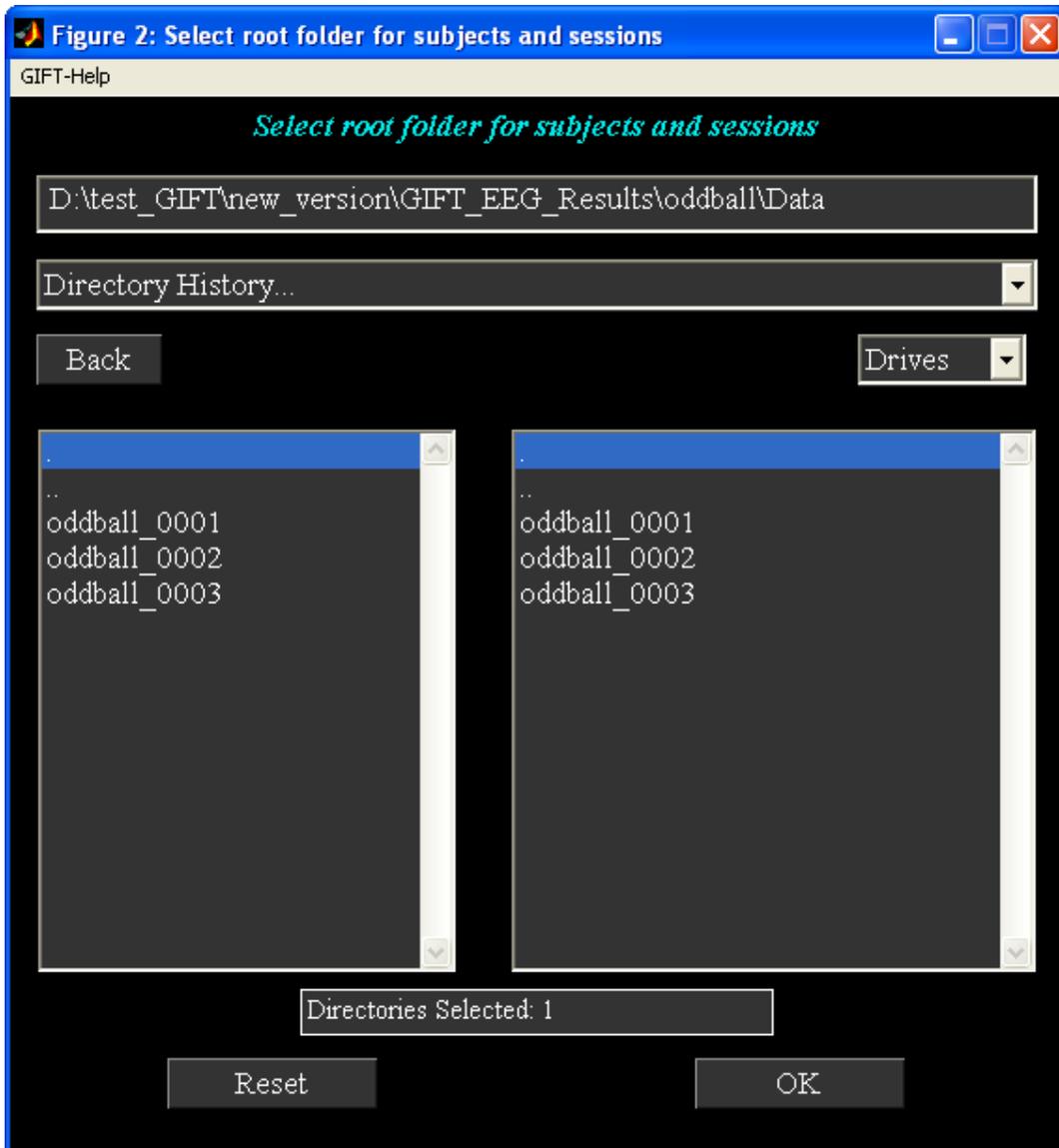
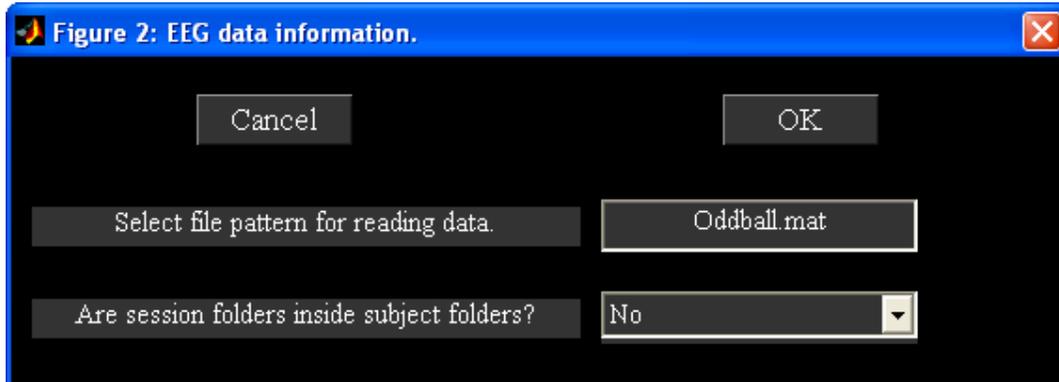


Figure 9: File pattern and question for selecting data



Note: After the data is selected the pushbutton *Select* will be changed to popup window with ‘Yes’ and ‘No’ as the options. ‘No’ option means the data files can be selected again. ‘Yes’ option updates the data reduction parameters if the parameter file is previously selected. The number of components will be auto filled to 20 depending on the number of channels or electrodes.

- 3) ‘Number of IC’. Enter ‘20’. This refers to the number of independent components extracted from the data.
- 4) ‘Do you want to auto fill data reduction values?’ By default this option is set to ‘Yes’ when the data is selected and the ‘Number of IC’ is set to 20. For now leave the options as ‘Yes’.
- 5) ‘Which ICA Algorithm Do You Want To Use?’ Select ‘Infomax’. Presently there are 9 algorithms in the toolbox that can be used for EEG data like Infomax, FastICA, Erica, Simbec, Evd, Jade Opac, Amuse, SDD ICA and Radical ICA. A detailed explanation of algorithms like Infomax, FastICA, Erica, Simbec, Evd and Jade Opac is given in the GIFT manual and in related journal publications. By default, we employ Infomax since this algorithm has been used most frequently in electrophysiology and neuroimaging to our knowledge. The performance of the different algorithms is not remarkably different when applied to aggregate EEG time domain data (See Appendix B).

Hidden User Interface Controls

These user interface controls (Figure 10) will be shown after you click 'Setup ICA-Defaults' menu (Figure 6). The parameters in Figure 10 are explained below:

- 1) 'Do You Want To Scale The Results?' The options available are 'No', 'Calibrate' and 'Z-scores'.
 - a. 'Calibrate' – Components will be scaled to original data units by doing a multiple regression using the time domain average of the component as model and the average of the EEG signal from the original data as observation. For each component, EEG signal from the original data is computed by selecting the electrode that has the maximum absolute value. For now select 'Calibrate'.
 - b. 'Z-Scores' – Components will be converted to Z-scores.
- 2) 'How Many Reduction (PCA) Steps Do You Want To Run?' A maximum of three reduction steps is provided. The number of reduction stages depends on the number of data-sets (Table 1). For the example data-set two reduction steps are automatically selected.
- 3) 'Number Of PC (Step 1)' - Number of principal components extracted from each subject's session. For one subject one session this control will be disabled as the number of principal components extracted from the data is the same as the number of independent components.
- 4) 'Number Of PC (Step 2)' - Number of principal components extracted during the second reduction step. This control will be disabled for two data reduction steps as the number of principal components is the same as the number of independent components.
- 5) 'Number Of PC (Step 3)' – This user interface control is disabled and set to 0 for the example data-set as there are only two data reduction steps. For data sets with typical study sizes (e.g. 10-20 subjects), the number entered here determines the number of independent components that are extracted. By default, the number of principal components retained in the reduction steps equals the number of independent components. This can be changed, e.g. from a set of 20 principal components, one can extract e.g. 10 independent

components. While estimating lesser components can be reasonable in some situations, extracting more independent components than principal components is not recommend.

Figure 10: Hidden User Interface Controls

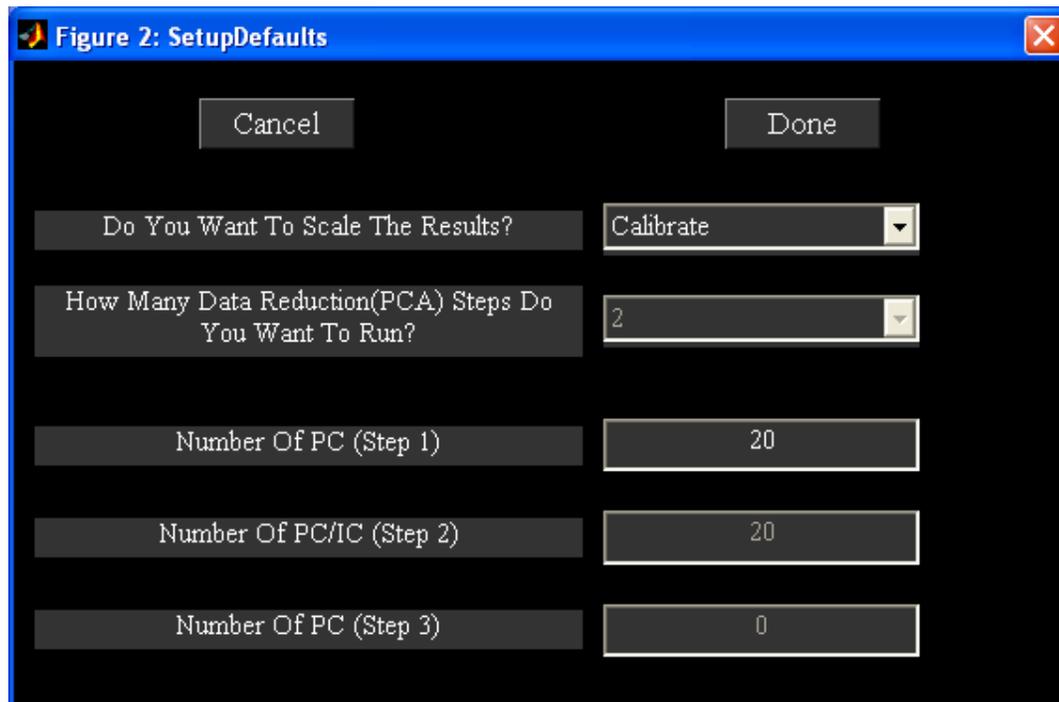


Table 1: Shows how groups are formed depending upon the number of data-sets

Number of Data-Sets (n)	Number of groups or reduction steps
n = 1	1
n < 4	2
4 <= n <= 10	User specified number (2 or 3) in "Setup ICA-Defaults" menu.
n > 10	3

b) Figure 11 shows the completed parameters window. Click *Done* button after selecting all the answers for the parameters. This will open a figure window (Figure 12) to select the ICA options. You can select the defaults, which are already selected in the dialog box or you can change the parameters within the acceptable limits that are shown in the prompt string. ICA options window can be turned off by changing defaults. Currently, the dialog box is only available for the Infomax, FastICA, and SDD ICA. After selecting the options, parameter file for the analysis is created in the working directory with the suffix ‘ica_parameter_info.mat’.

Figure 11: Completed Parameter Select Window

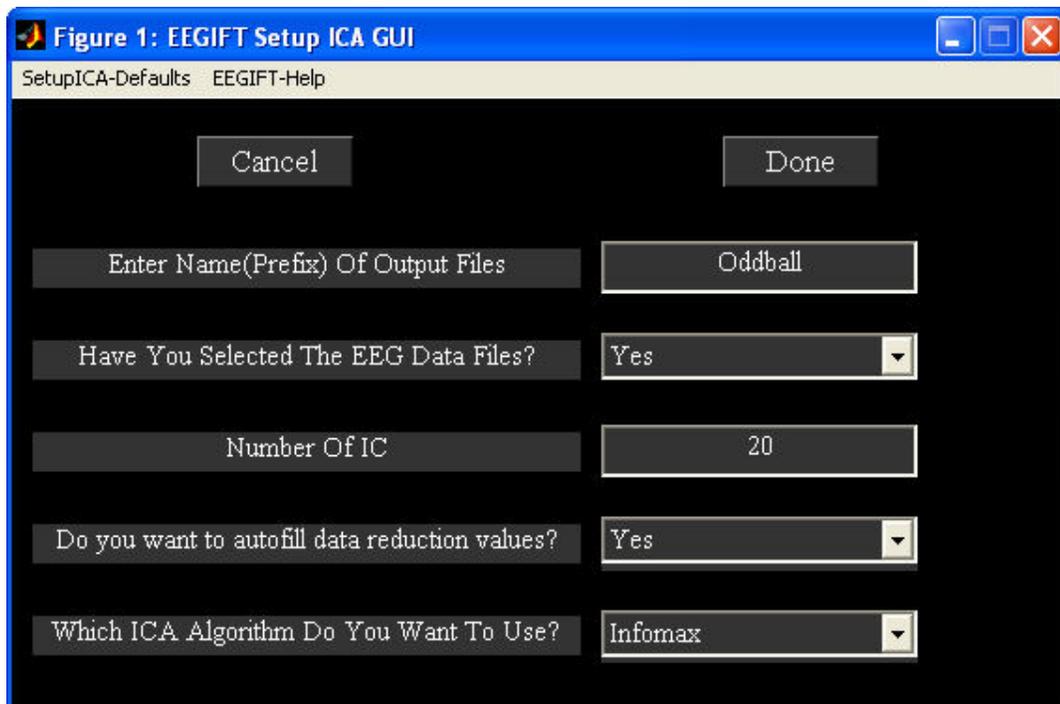
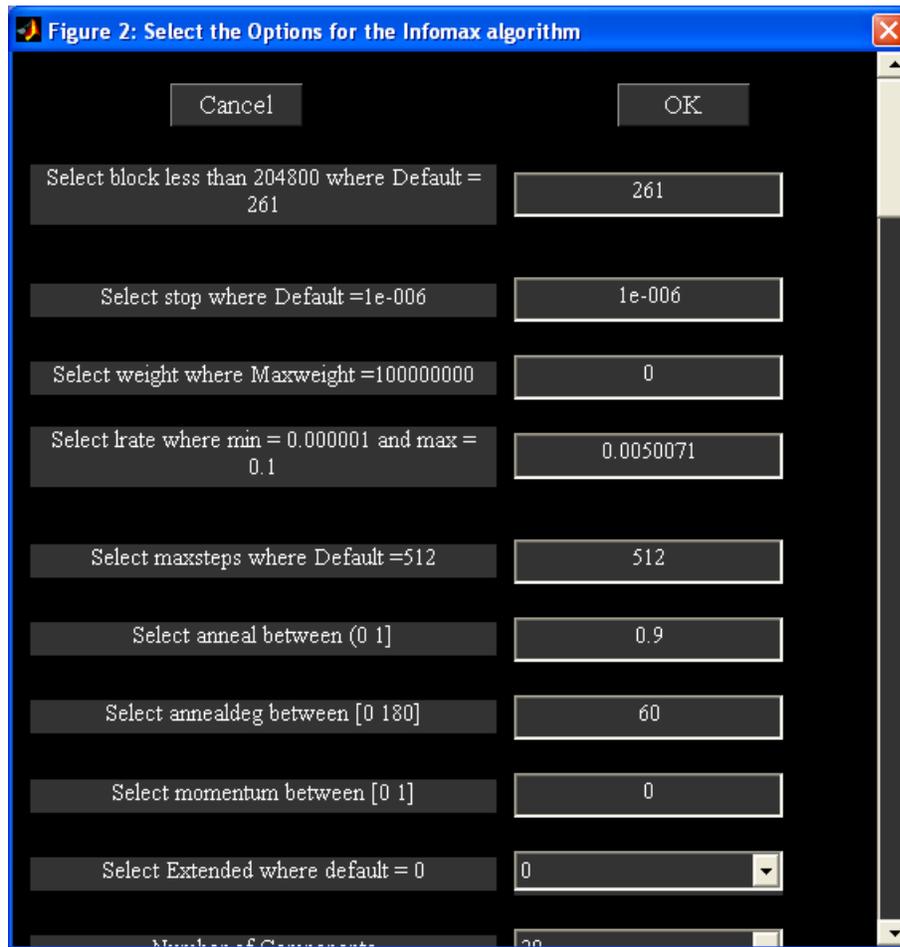


Figure 12: Options of the ICA algorithm



III) *Run Analysis*

Run Analysis contains initializing parameters along with the steps involved in the group ICA. When you click on *Run Analysis* button, a figure window will open to select the ICA parameter file. After selecting the ICA parameter file, figure 13 will open and contains the following options:

- 1) 'All***' - You can run all the group analysis steps at once or run each one separately. To run all steps at once select 'All***', to run each step separately select the steps in order. For now select 'All***'.
- 2) 'Parameter Initialization' - All the variables that are needed later on or during the analysis are declared and initialized. A parameter error check is also preformed to try and catch errors before the group analysis begins.

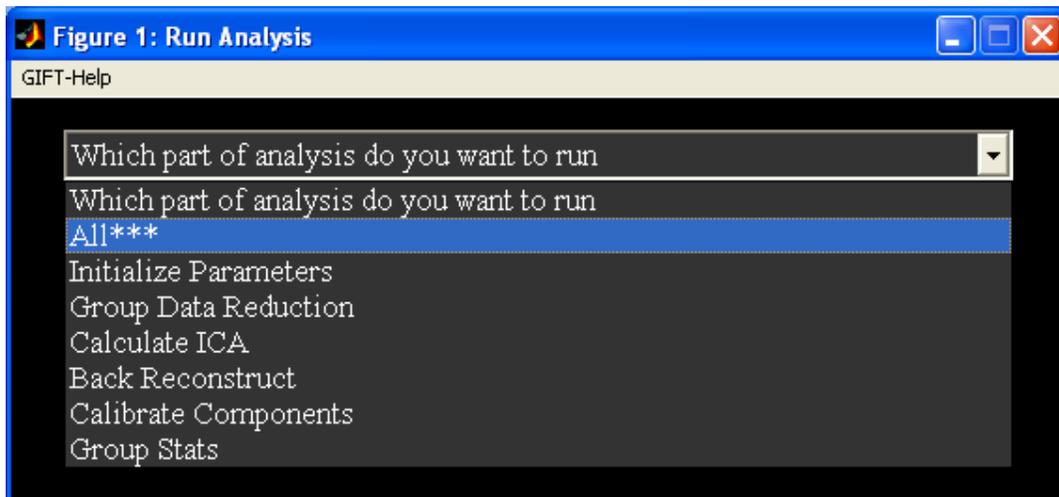
- 3) 'Data Reduction' - Each data-set is reduced using Principal Components Analysis (PCA). These reduced data-sets are then concatenated into a group or groups depending on the number of data reductions steps selected, this process is repeated. Each reduced data is saved in a MAT file and will be used in the back reconstruction step. The second data reduction step demands most computing resources (RAM) but works well for most current desktop/laptop PC configurations and MATLAB versions. If an 'out of memory error' from MATLAB occurs, try the usual steps to improve performance, e.g. clear the workspace, terminate unused programs and background processes. If it still does not work, reduce the number of principal components or change the input data (e.g. lower sampling rate).
- 4) 'Calculate ICA' - The concatenated data from the data reduction step is used and the aggregate ICA components are saved in MAT file format. Each component consists of EEG time domain signal and weights.
- 5) 'Back Reconstruction' - The aggregate components and the results from data reduction are used to compute the individual subject components. The individual subject components are saved in MAT file format.
- 6) 'Calibrating Components' - The original EEG data is used to scale the components from arbitrary units to data units or Z-scores.
- 7) 'Group Stats' - The individual back reconstructed components are used to compute statistics on components like mean, standard deviation and t-test. Each component consists of EEG time domain signal and topographic weights. For the t-test weights of a session used is the same as the mean of weights of that session. These group stats components are calculated for each session and are saved in MAT file format.

Results during each of the steps are printed to the MATLAB command window. Before the group analysis can take place the parameters file must be initialized. At this stage variables that were entered through the GUI are parsed and initialized as needed for the group ICA analysis. Error checking is also performed so that mistakes can be caught before the analysis starts. After the analysis is completed, Display GUI (Figure 14) will open automatically for visualizing components. You can turn off this option by setting variable value of OPEN_DISPLAY_GUI to 0 in 'icatb_defaults.m' file.

Note:

- All the analysis information is stored in the '_results.log' file. This file gets appended each time you run the analysis with the same prefix for the output files.
- Output files information and variables contained in MAT files are explained in Appendix D.

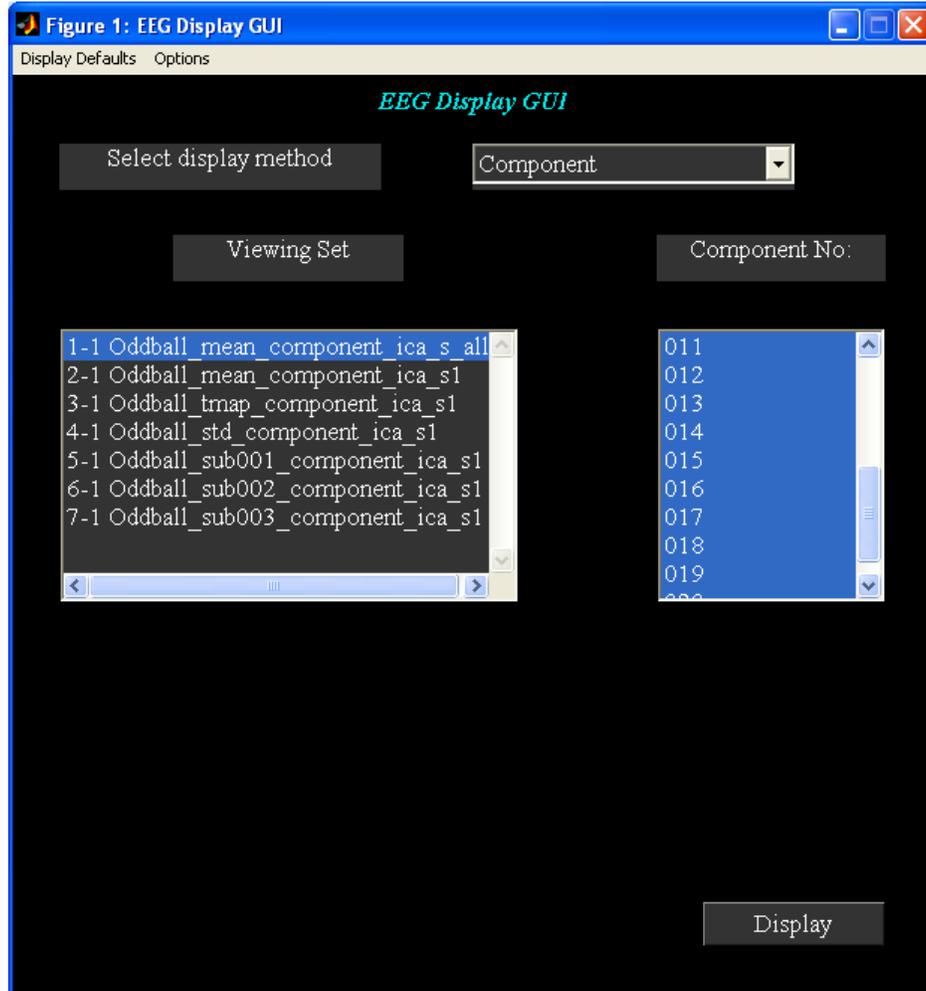
Figure 13: Run Analysis



IV) Display

Figure 14 will open when you click *Display* button (Figure 1) and had selected the ICA parameter file. The parameters in the display GUI are explained below:

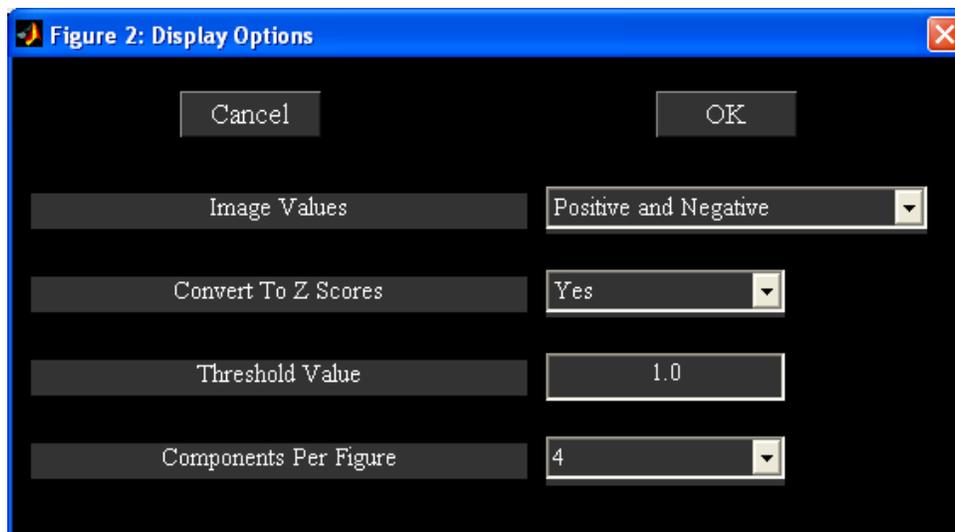
Figure 14: EEG Display GUI



1. 'Select display method.' There are two display methods like component and subject. Each display method is explained below:
 - a. Component display method displays all components of a viewing set. You can also select the components of interest in the component list box.
 - b. Subject display method displays a component of all viewing sets.
2. 'Viewing Set' – You can look at mean of all data sets, mean of one session, individual data set components, etc.
3. 'Component No.:' – Component numbers you want to look at. For subject display method only one component can be selected whereas for component display method more than one component can be selected.

4. “Display Defaults” menu - Display defaults are plotted in a figure which will open when you click “Display Defaults” menu. The parameters in figure 15 are explained below:
 - a. ‘Image Values’ – There are four options like ‘Positive and Negative’, ‘Positive’, ‘Absolute’ and ‘Negative’. For now select ‘Positive and Negative’.
 - b. ‘Convert To Z-scores’ – You have the option to convert EEG signal of all trials to Z-scores. For now select ‘Yes’. If you are looking at t-statistic images, do not convert to Z-scores.
 - c. ‘Threshold Value’ – Z threshold applied on image. Select ‘1.0’.
 - d. ‘Components Per Figure’ – Options are ‘1’, ‘4’ and ‘9’. Select ‘4’.

Figure 15: Display Defaults



5. “Options” menu contains items like ‘Select EEG channel locs file’ and ‘Select time scale’. Each item is explained below:
 - a. When you click ‘Select EEG channel locs file’, a figure (Figure 16) will open to select the channel locations file for doing topography plots for components. The default color map for topography plot is in ‘icatb_defaults.m’ file with the variable name EEG_TOPOPLOT_COLORMAP.

- b. 'Select time scale' – This utility is optional. EEG signal time axis in milliseconds can be loaded from an ASCII or a SET file (Figure 17).

Figure 16: Select EEG channel location file

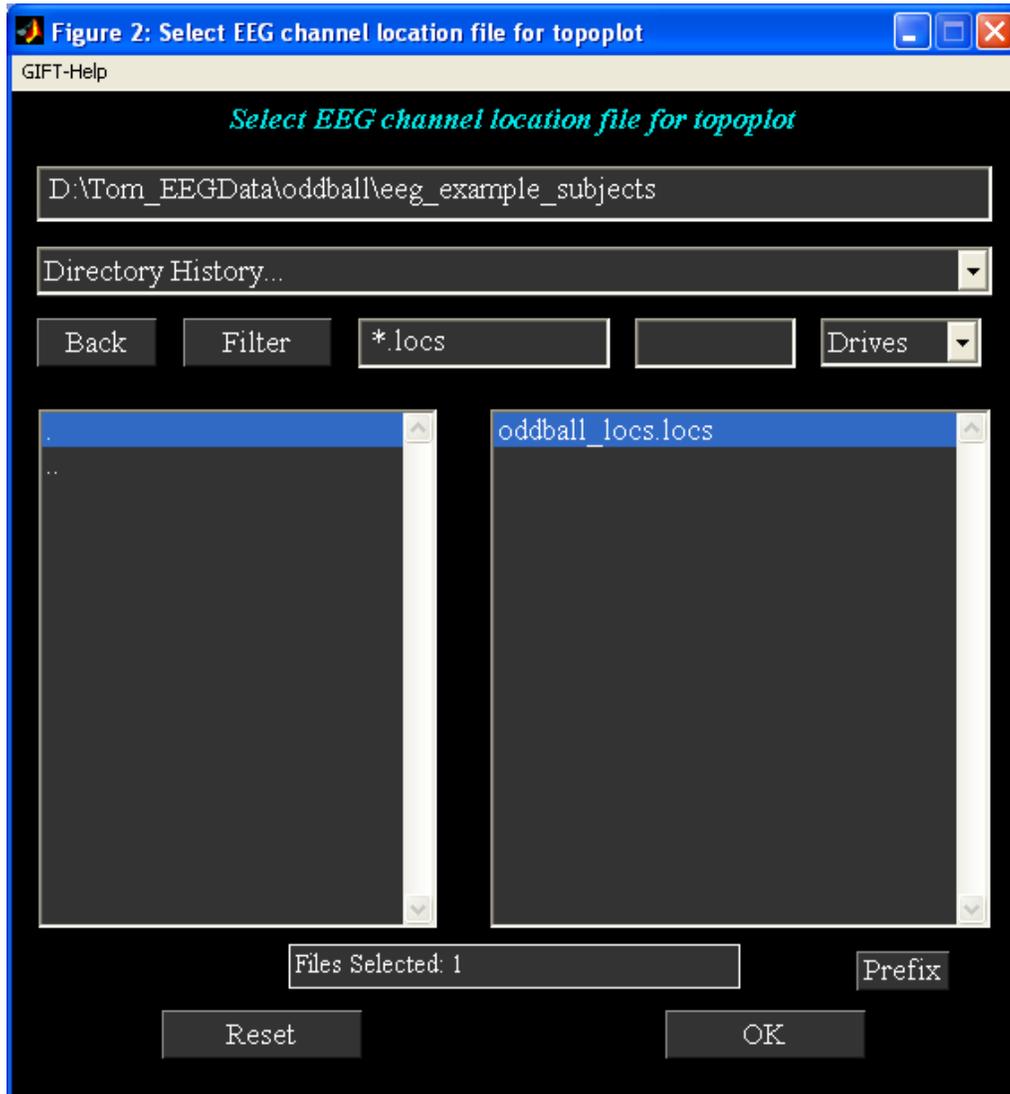
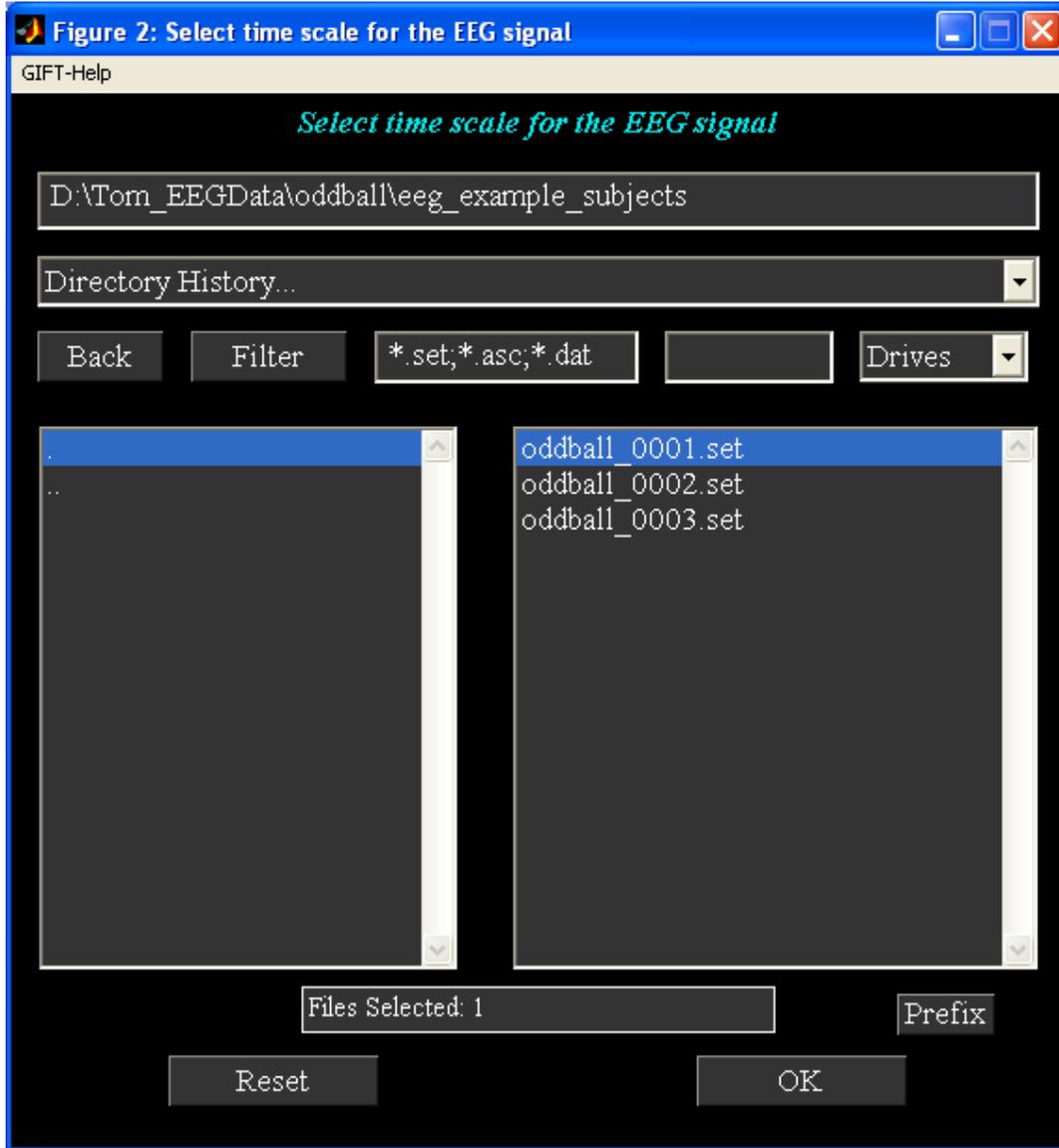


Figure 17: Select time scale for plotting EEG signal



V) Component Display Method

When you select 'Component' under 'Select display method' (Figure 14) and select all components and click *Display* button, figure 18 will open showing components in groupings of four. Each component consists of a topography plot of weights, an 'erpimage', i.e. a stacked single trial plot and the component ERP. When you use left click or double click of mouse on each plot, an enlarged view of that plot (Figure 19) is

shown in a new figure. You can browse around figures by using left arrow and right arrow buttons at the end of the figure.

Figure 18: Components of mean of all data sets

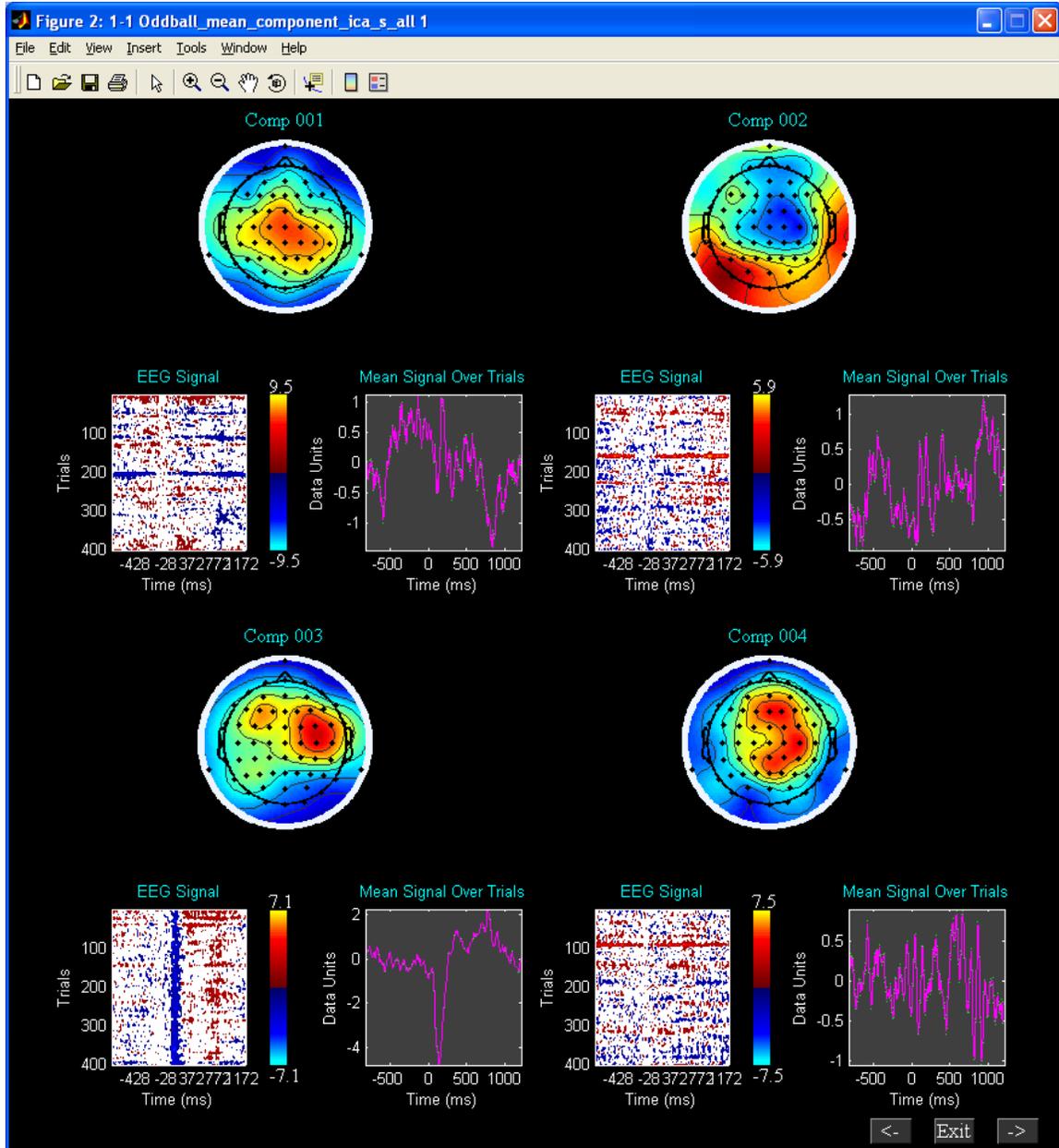
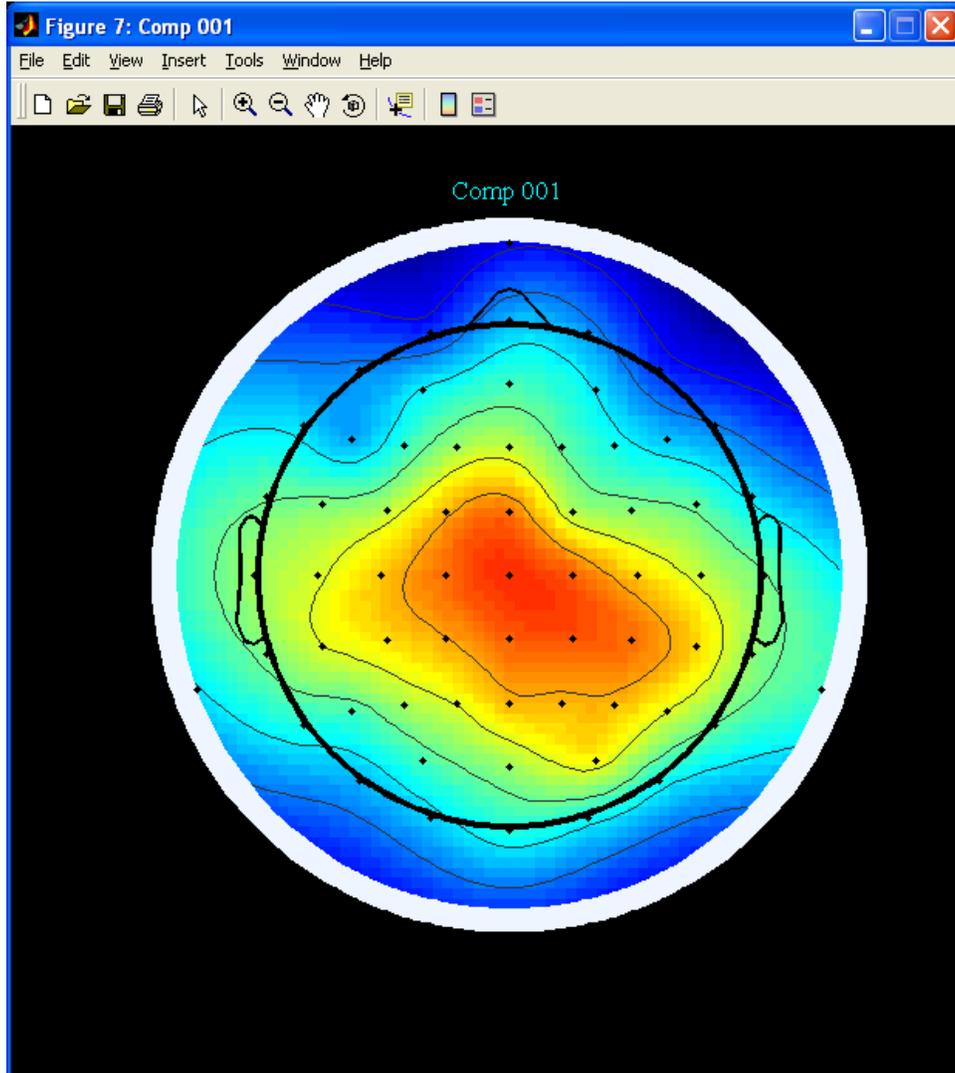


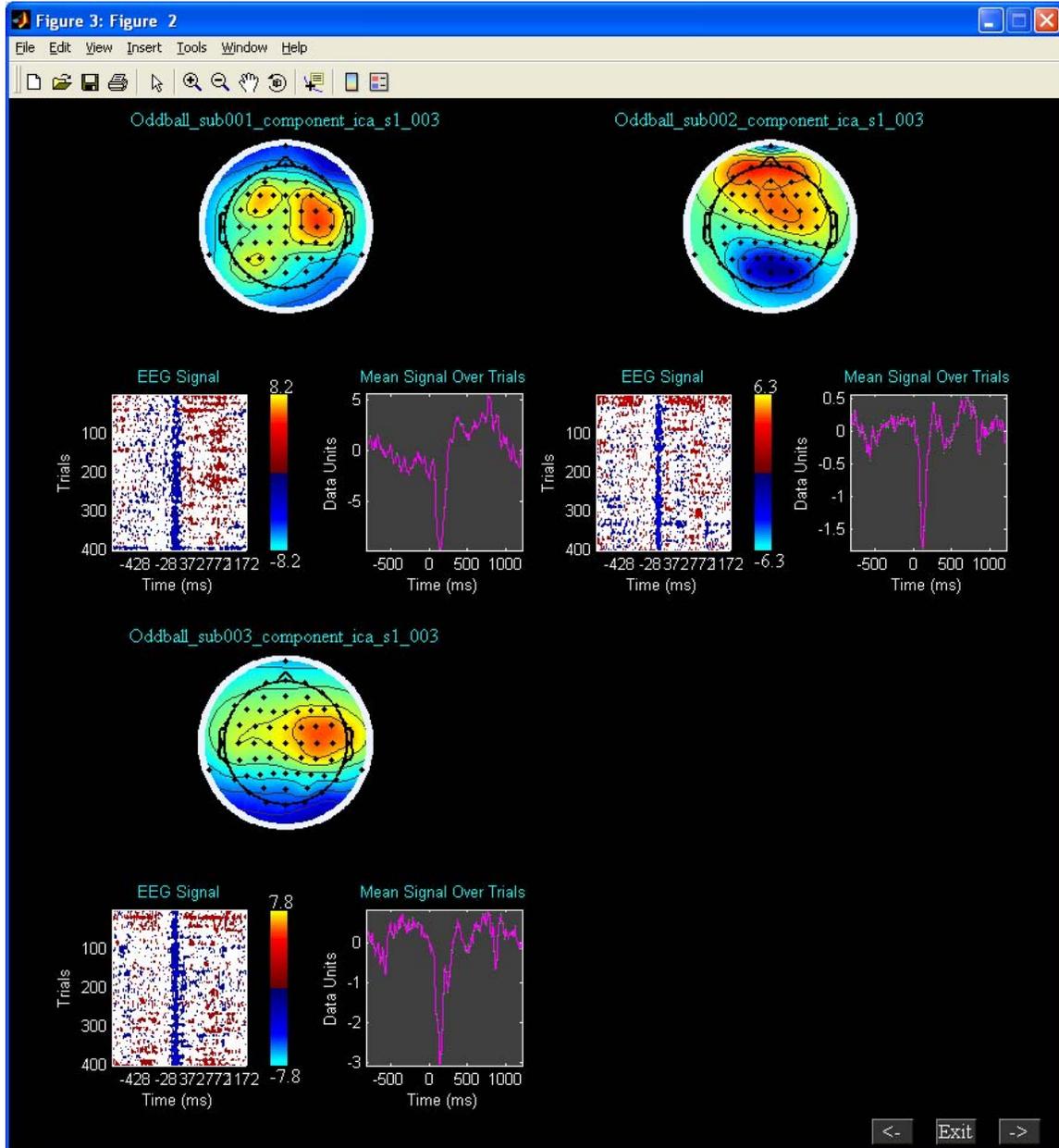
Figure 19: Enlarged view of topography plot of component '001'



VI) Subject Display Method

You have the option to view all data sets of a particular component when you select 'Subject' under 'Select display method' (Figure 14). Figure 20 shows individual subjects task related component results in groupings of four.

Figure 20: Task related component of 3 subjects



VII) Group ICA on 15 subjects

We have done group ICA analysis on 15 subjects and extracted 20 components from the data. Figures 21 and 22 show task related component results using subject display method.

Figure 21: Mean, standard deviation and t-map results

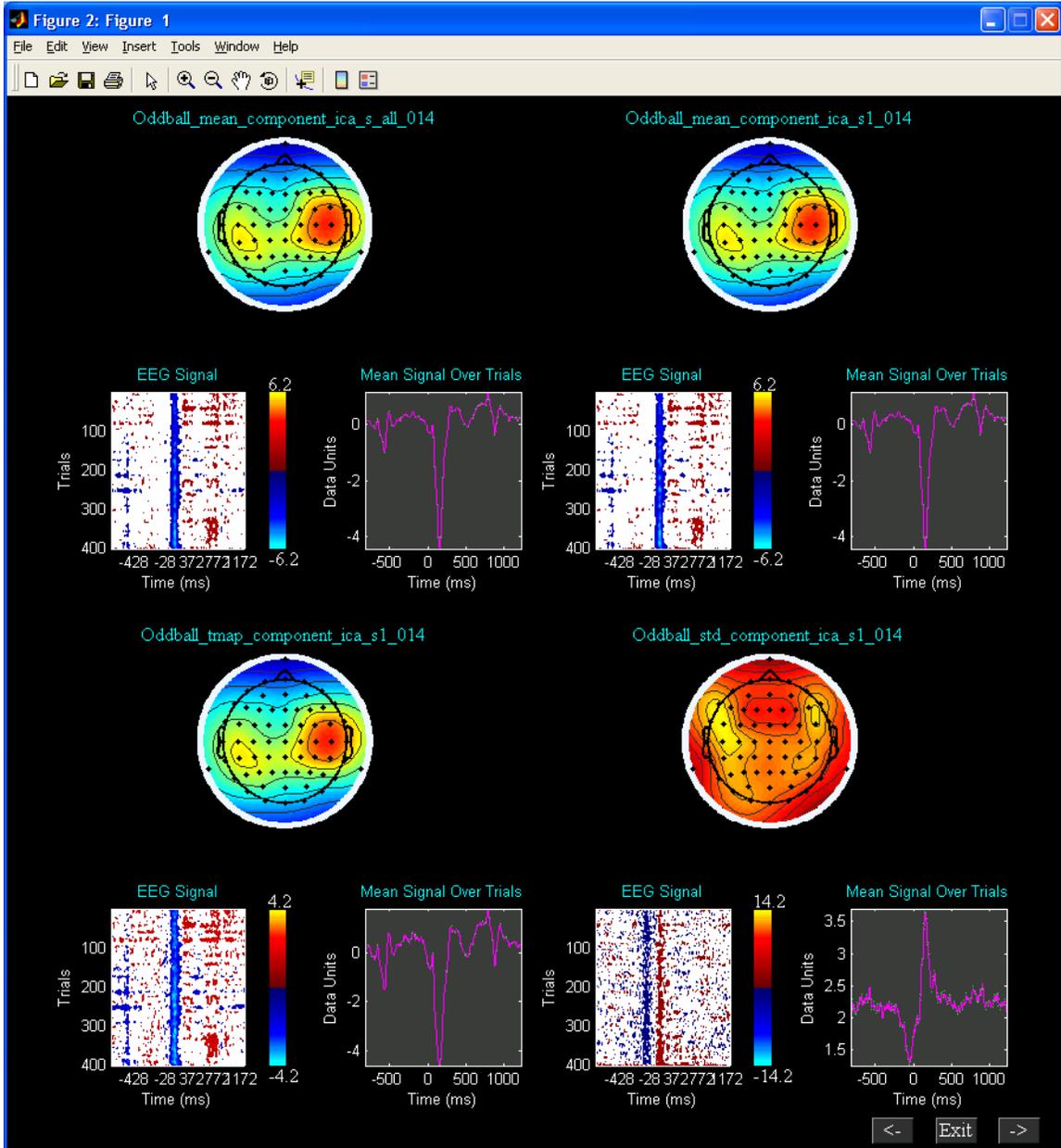
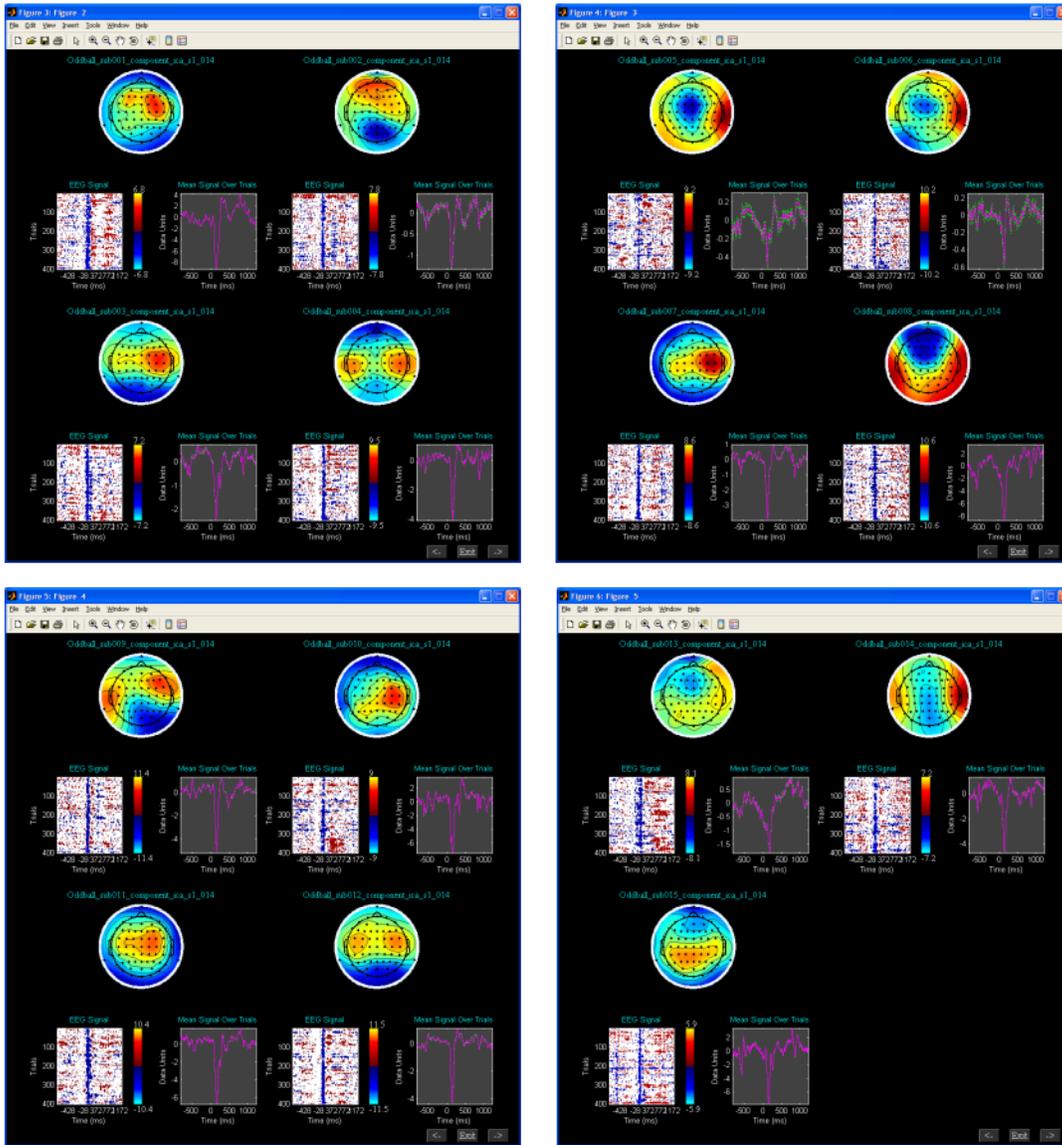


Figure 22: Task related component of individual subjects



VIII) Batch Script

Batch script is an alternative way to run the group ICA. We have provided two example input files like 'Input_eeg_data_subjects_1.m' and 'Input_eeg_data_subjects_2.m' in folder `icatb/toolbox/eegiftv1.0a/icatb_eeg_batch_files`. The function for running the batch file is 'icatb_batch_file_run'. Type `icatb_batch_file_run(inputFile)` at the MATLAB command prompt where `inputFile` is the full file path of the input file. We explain below the parameters in the input file.

- modalityType - Modality type. Enter 'EEG'.
- dataSelectionMethod - There are two ways to select the data. Options are 1 and 2. Each option is explained below:
 - 1 - Data will be selected automatically if you specify the root folder for subjects and sessions, file pattern and a flag. Options for flag are 'data_in_subject_folder' and 'data_in_subject_subfolder'.
 - 'data_in_subject_subfolder' - Data is selected from the subject sub-folders. Number of sessions is equal to the number of sub-folders containing the specified file pattern.
 - 'data_in_subject_folder' - Data is selected from the subject folders. The number of sessions is 1 and the number of subjects is equal to the number of subject folders containing the specified file pattern.
 - 2 - This option can be used when all the data is not in one directory. You need to specify the data directory for each subject and session followed by file pattern. The required variables are selectedSubjects and numOfSess. selectedSubjects contains the arbitrary names of subjects (s1 refers to subject1, s2 refers to subject 2, etc) and numOfSess contains the number of sessions. Subject 1 session 1 data information must be entered in variable s1_s1 and subject 2 session 2 information must be entered in variable s1_s2.
- outputDir - Output directory of the analysis.
- prefix - All the output files will be pre-pended with this prefix.
- numReductionSteps - The number of reduction steps used and is dependent on the number of data-sets used. A maximum of three reduction steps is used.
- numOfPC1 - Number of PC for reduction step 1.
- numOfPC2 - Number of PC for reduction step 2.
- numOfPC3 - Number of PC for reduction step 3.
- scaleType - Options are 0, 1 and 2. 0 means don't scale, 1 means scale components to data units and 2 means scale components to Z-scores.

- algoType - Currently there are 9 ICA algorithms available in the EEGIFT toolbox. The algorithms are as follows:
 - 1 - Infomax
 - 2 - FastICA
 - 3 - ERICA
 - 4 - SIMBEC
 - 5 - EVD
 - 6 - JADE OPAC
 - 7 - AMUSE
 - 8 - SDD ICA
 - 9 - Radical ICA

Appendix

A. Auditory Oddball Paradigm

The Auditory Oddball Paradigm (AOD) consisted of detecting an infrequent target sound within a series of frequent regular sounds. The stimuli were presented via headphones, and participants were asked to respond as quickly as possible by pushing a mouse button with their right index finger. The standard stimulus was a center-panned 500 Hz tone, the target stimuli were left or right-panned location deviants, respectively. Targets occurred with a probability of 0.20, 0.10 for each location; the standard stimuli occurred with a probability of 0.80. Stimulus duration was 75 ms and the inter-stimulus interval was 700 ms, with no immediate repetitions of targets. In the example data, the epochs contain a sequence of standard – target – standard sounds, to dissociate between obligatory stimulus related and target related components, respectively. All stimuli were presented at approximately 65 decibels above threshold. Response times ranged from 250-500 ms, the overall accuracy was larger than 98%.

Participants - 32 healthy right-handed undergraduates were recruited, and took part in the experiment after providing a written statement of informed consent. Participants were sitting in a comfortable recliner in an electro-magnetically shielded and sound-attenuated testing chamber (Rainford EMC Systems, Wigan, UK). Participants were fitted with 63 Ag/AgCl scalp electrodes mounted in an elastic cap (EasiCap, Falk Minow Services, Breitenbrunn, Germany) according to the 10-20 System: FP1, FP2, F7, F3, Fz, F4, F8, T7, C3, Cz, C4, T8, P7, P3, Pz, P4, P8, O1, OZ, O2, with additional intermediate sites at Fpz, AF7, AF3, AFz, AF4, AF8, FT7, FC5, FC3, FC1,

FCz, FC2, FC4, FC6, FT8, C5, C1, C2, C6, TP7, CP5, CP3, CP1, CPz, CP2, CP4, CP6, TP8, P5, P1, P3, P6, PO7, PO3, POz, PO4, PO8, including mastoid sites TP9 and TP10. All channels were referenced to the nose, with a ground electrode on the cheek, and impedances were kept below 10k Ω . Vertical eye movement (EOG) was acquired from a bipolar derivation between Fp1 and an additional electrode placed below the left eye, horizontal EOG was acquired from a F7-F8 bipolar montage. EEGs were recorded continuously at 500 Hz sampling frequency with a band-pass from 0.01-250 Hz with BrainAmp DC amplifiers (BrainProducts, Munich, Germany).

EEGs were down-sampled to 250 Hz, filtered with a zero-phase Butterworth filter from 1-45 Hz (24 db per octave), and re-referenced to common average reference. The data were then segmented from -800 to 1200 ms around target stimuli and baseline activity was defined from -300 to 0 ms around stimulus onset, and trials with amplitudes exceeding $\pm 150\mu\text{V}$ on any of the channels were excluded from further analysis. Concatenated single sweeps around target onset, including the previous and the following standards were subjected to single subject independent component analysis (ICA, Infomax algorithm), implemented in EEGLAB (Delorme & Makeig, 2004) running in MATLAB. Components with topographies attributable to eye movement and frontotemporal muscle activity were identified and removed from the data (Jung, et al., 2000). For each dataset, we kept 20 components. Missing trials were padded with the mean from surrounding trials. Hereafter, single-trials were additionally denoised with a wavelet filter (Quiñero Quiroga & Garcia, 2003). Wavelet coefficients used for the reconstruction of the single trials were selected on the basis of the grand-averaged response, and were the same for all electrode sites and participants. Hereafter, group ICA was computed, estimating 20 PC/ICs.

B. Hybrid Results

Unlike the general linear model, ICA is not naturally suited to generalize results from a group of subjects. The solution that we selected here is to create aggregate data containing observations from all subjects, estimate a single set of components and then back-reconstruct these in the individual data. For estimation of the group temporal ICA we employ the rationale proposed by Calhoun (Calhoun, Adali, Pearlson, & Pekar, 2001), where the concatenation of multiple datasets into one matrix is instantiated via two data reduction steps prior to estimation of independent components. PCA is used for dimensionality reduction on the single trial data from all EEG channels in each participant, and subsequently on aggregated data. Hereafter ICA is performed, estimating a single set of components, thus identifying and ordering the same components in different subjects in the same way. The component time courses for individual subjects are back-

reconstructed from the aggregate mixing matrix by multiplying the partition of W corresponding to the respective subject with the corresponding partition of the data. The individual un-mixing matrices are separable across subjects and the back-reconstructed data is a function of primarily the data within subjects (See figure 24). When used for EEG time series analysis, the accuracy of component detection and back-reconstruction with this group model is dependent on the degree of intra and inter individual time and phase-locking of event related EEG processes. We illustrate this dependency here by generating hybrid data for 20 datasets that consist of three simulated event-related sources with varying degrees of latency jitter and variable topographies (S1-S3, see figure 24, As top left and to right for examples of two individual datasets), mixed with real EEG data (See figure 24, x middle), and compute the group ICA solution (See figure 24, Wy bottom). Reconstruction accuracy, expressed as the variance of the source accounted for by the reconstructed IC averaged across the 20 datasets (R^2) was tested for latency jitter 1, 2 and 3 times the FWHM of the source ERPs for a number of algorithms (Table 2). The results show that group ICA is adequate for decomposition of single trial ERPs with physiological jitter, and will reconstruct such sources with approx. 70-90% accuracy both temporally, and spatially.

Figure 24: Hybrid Data ICA Results

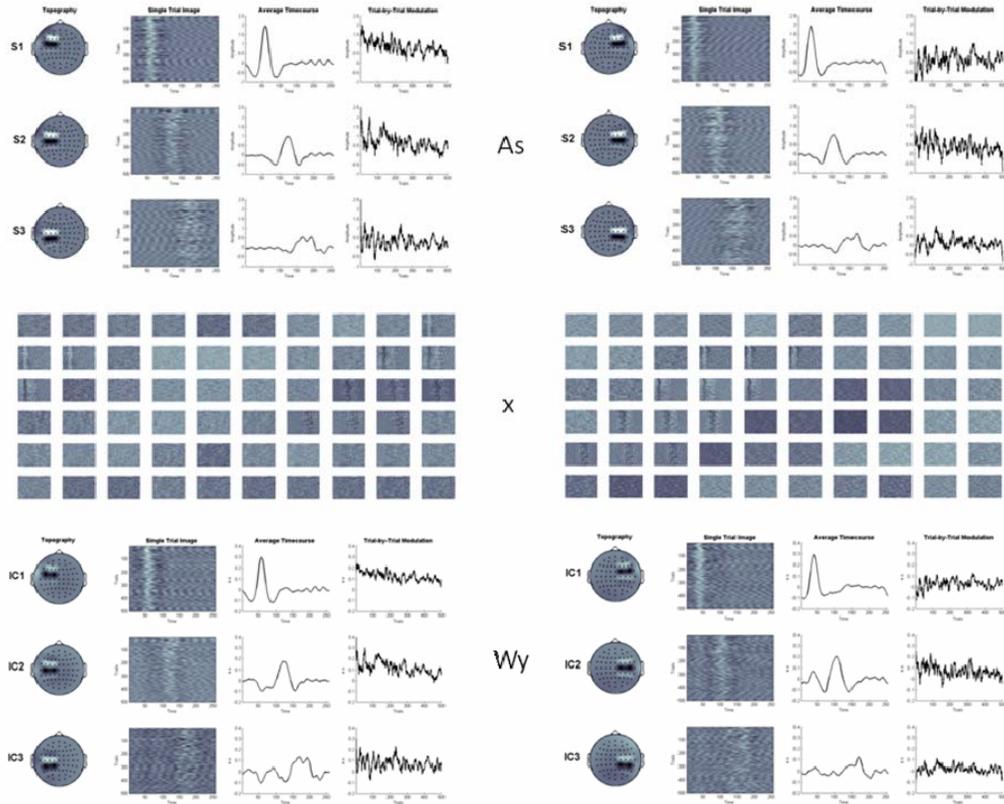


TABLE 2 <i>Algorithm</i>	<i>temporal</i>			<i>spatial</i>		
	<i>S1</i>	<i>S2</i>	<i>S3</i>	<i>S1</i>	<i>S2</i>	<i>S3</i>
Infomax (single subject)	0,99	0,99	0,99	0,89	0,89	0,90
Infomax (group)	0,91	0,87	0,69	0,87	0,83	0,74
Erica (group)	0,92	0,85	0,62	0,86	0,76	0,71
Jade Opac (group)	0,85	0,87	0,59	0,87	0,78	0,77
FastICA (group)	0,90	0,87	0,68	0,87	0,84	0,74
Simbec (group)	0,91	0,88	0,65	0,87	0,79	0,75

C. Concatenation and Reconstruction

Data Reduction: For each individual separately, the pre-processed single trial data $y(j)$ are pre-whitened and reduced via principal component analysis (Figure 24, $R_1^{-1} \dots R_M^{-1}$) containing the major proportion of variance in the N uncorrelated time courses of $x(j) = [x_1(j), x_2(j), \dots, x_N(j)]^T$.

PCA whitening preconditions the data and simplifies ICA estimation due to the orthogonal projection, reduction of complexity, and de-noising, as well as compressing the data and thus reducing the computational load. Group data is generated by concatenating individual principal components in the aggregate data set G . In detail, let $X_i = R_i^{-1}Y_i$ be the L -by- V reduced data matrix from subject i where Y_i is the K -by- V data matrix containing preprocessed EEG epochs from all channels, R_i^{-1} is the L -by- K reducing matrix from the principal component decomposition, V is the number of time points (samples per epoch * trials), K is the number of scalp channels, and L is the size of the channel dimension following reduction. The next step is to concatenate the reduced data from all subjects into a matrix and reduce this matrix to N , the number of components to be estimated. The N -by- V reduced, concatenated matrix for the M subjects is

$$(1) \quad X = G^{-1} \begin{bmatrix} R_1^{-1}Y_1 \\ \vdots \\ R_M^{-1}Y_M \end{bmatrix}$$

Where G^{-1} is an N -by- LM reducing matrix from a second PCA decomposition and is multiplied on the right by the LM -by- V concatenated data matrix for the M subjects.

ICA Estimation: After concatenation of individual principal components in the aggregate data set G , this matrix is decomposed by ICA, estimating the optimal inverse of the mixing matrix \hat{A} , and a single set of source time courses (\hat{S}). Following ICA estimation, we can write $X = \hat{A}\hat{S}$, where \hat{A} is the N -by- N mixing matrix and \hat{S} are the N -by- V component time courses. Substituting this expression for X into equation (1) and multiplying both sides by G results in

$$(2) \quad GAS = \begin{bmatrix} R_1^{-1}Y_1 \\ \vdots \\ R_M^{-1}Y_M \end{bmatrix}$$

Partitioning and single subject reconstruction: Partitioning the matrix G by subject provides the following expression

$$(3) \quad \begin{bmatrix} G_1 \\ \vdots \\ G_M \end{bmatrix} AS = \begin{bmatrix} R_1^{-1}Y_1 \\ \vdots \\ R_M^{-1}Y_M \end{bmatrix}$$

We then write the equation for subject i by working only with the elements in partition i of the above matrices such that

$$(4) \quad G_iAS_i = [R_i^{-1}Y_i]$$

The matrix \hat{S}_i in equation 4 contains the single subject component timecourses for subject i , calculated from the following equation

$$(5) \quad \hat{S}_i = (G_i A)^{-1} R_i^{-1} Y_i$$

We now multiply both sides of equation 4 by R_i and write

$$(6) \quad Y_i \approx F_i G_i A \hat{S}_i$$

yielding the ICA decomposition of the data from subject i contained in the matrix Y_i . The N -by- V matrix \hat{S}_i contains the N component time courses, and the K -by- N matrix $F_i G_i A$ is the single subject mixing matrix, yielding the scalp maps for N components.

D. Output Files

1. Subject File – Subject file contains information about number of subjects, sessions and input files. It is saved with suffix ‘Subject.mat’. The following are the variables in the MAT file:

- numOfSub – Number of subjects.
- numOfSess – Number of sessions.
- files – Input files stored in a data structure.

2. Parameter File – Parameter file contains user input and analysis output files information. It is stored with suffix ‘_ica_parameter_info.mat’. The MAT file contains sesInfo data structure and the user input information is stored in sesInfo.userInput.

3. Data reduction (PCA) - After PCA step, the data reduction information is stored in a MAT file with suffix ‘_pca_ra-b.mat’ where a refers to reduction step number and b refers to data-set number. The following are the variables in the PCA file:

- V – Eigen vectors whose dimensions are electrodes by components.
- Lambda – Eigen values diagonal matrix of dimensions components by components.
- pcasig – Reduced data of dimensions time*trials by components.
- whiteM – Whitening matrix of dimensions components by electrodes.
- dewhiteM – Pseudo inverse of whitening matrix of dimensions electrodes by components. This will be used while reconstructing individual subject components during the back reconstruction step.

4. ICA - After ICA step, the aggregate components information is stored in a MAT file with the suffix ‘_ica.mat’. The following are the variables in the ICA file:

- W – Un-mixing matrix of dimensions components by components.
- A – Pseudo inverse of W and is of dimensions components by components.
- icasig – Independent source signals of dimensions components by time*trials.

5. Back reconstruction – Back reconstruction files are saved with suffix ‘_brn.mat’ where n refers to the data-set number. The MAT file contains compSet data structure with the following fields:

- timecourse - EEG signal of dimensions components by time*trials.
- Topography - Weights matrix of dimensions electrodes by components.

6. Calibrate – Calibrate step files are saved with suffix ‘*ca-b.mat’ where a refers to subject number and b refers to session number. The following variables are in the calibrate step file:

- timecourse - Scaled EEG signal of dimensions components by time*trials.
- topography - Scaled weights matrix of dimensions electrodes by components.

7. Group stats – Group stats files are saved with suffix ‘_component_ica_’ in MAT format. Each MAT file contains time courses (EEG signal) and topography (weights matrix) of the same dimensions as in the calibrate step file.

E. Defaults

EEG defaults are in ‘icatb_defaults.m’ file. In GIFT manual and walk-through we explained necessary variables required for analysis and display. We explain below EEG specific variables used in EEGIFT:

- EEG_RMBASE – Vector used for removing baseline from EEG signal during smoothing trials. The default value is [-100 0].
- EEG_IMAGE_VALUES – Image values used for displaying stacked EEG signal. The options available are ‘Positive and Negative’, ‘Positive’, ‘Absolute’ and ‘Negative’. The default value is ‘Positive and Negative’.
- EEG_CONVERT_Z – Option is provided to convert stacked EEG image to Z-scores during display. The default value is ‘Yes’.
- EEG_THRESHOLD_VALUE – Threshold used for displaying stacked EEG signal. The default value is ‘1.0’.
- EEG_IMAGES_PER_FIGURE - The number of components per figure that can be displayed. The options available are ‘1’, ‘4’ and ‘9’. The default value is ‘4’.
- EEG_TOPOPLOT_COLORMAP – Color map used for topography plot. The default value is ‘jet(64)’.

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