Group ICA of fMRI Toolbox (GIFT) Walk Through

The GIFT Documentation Team

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Introduction

This walk through is going to bring you through Group ICA analysis of functional MRI (fMRI) data ([1]). For a detailed explanation of the toolbox, please see the manual. The functional data for three subjects is located in the 'example_subjects.zip' file. More information on the task the subject performed while in the scanner is given in the Appendix A. The Appendix section also contains information on defaults used in the GIFT toolbox and other information. Please report suggestions or comments to vcalhoun@unm.edu or srachakonda@mrn.org.

For quick information on a particular topic click the *Help* button (Figure 1), this opens HTML help manual in the default web browser. GIFT-Help menu plotted on main figure windows opens the HTML page for that topic in the web browser. Each example subject also contains a functional data set, which contains only one brain slice. If you are having problems with this toolbox you may test this with a smaller data set.

Installing GIFT

Unzip the file 'GroupICATv2.0d.zip' to your local machine and add GIFT directories to the MATLAB search path or run the 'gift.m' file to automatically add GIFT directories. After the GIFT path is set, GIFT toolbox (Figure 1) opens in a new figure window. There is also an option to run group ICA using a batch script (See manual). Batch script is very useful for running large data sets.

Installing Example Subjects

Download the 'example_subjects.zip' file and unzip into an appropriate directory. Included in this file are three subject's preprocessed fMRI data from a visuomotor task (Appendix A). Whole brain and single slice data (for rapid testing) are provided.

Figure 1: Group ICA of fMRI Toolbox
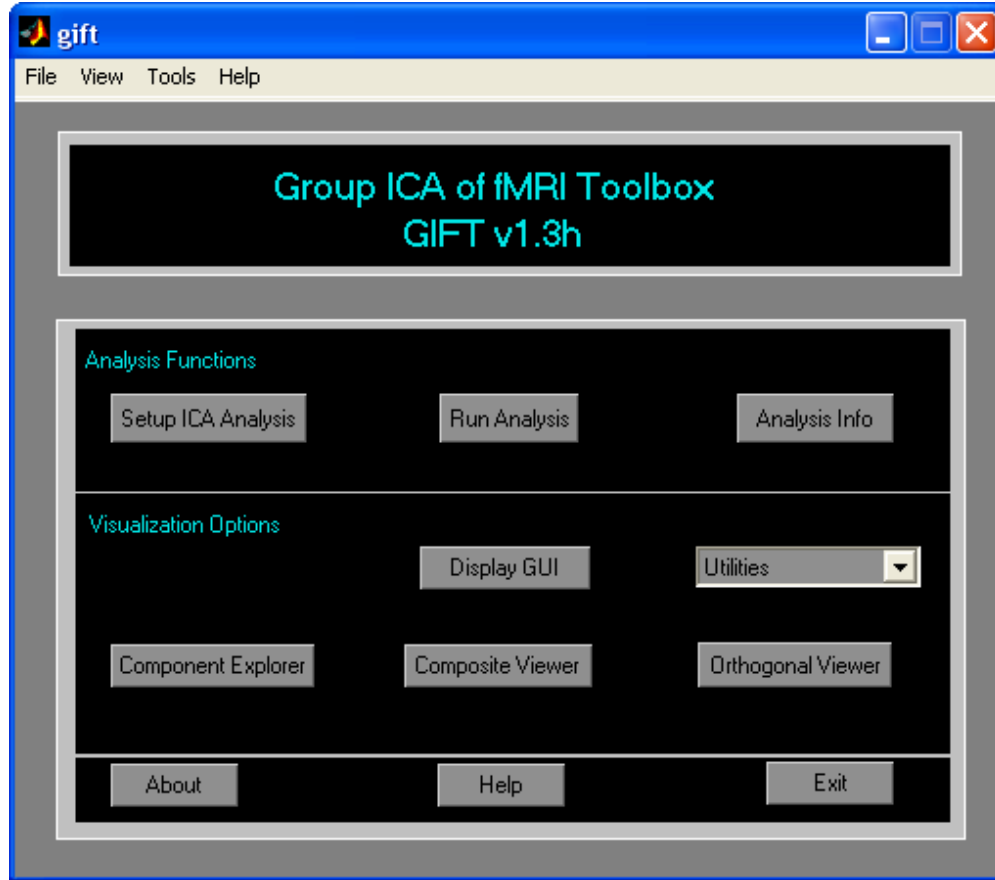
Steps involved in GIFT

The GIFT mainly consists of analysis functions and visualization options. This document takes the reader step-by-step first through the analysis and then onto the visualization parts of GIFT.

I. Analysis Functions:

1. *Setup ICA Analysis* 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 Analysis* button, a figure window (Figure 2) will open to select the analysis output directory. All the output files will be stored in this directory. For more information on file selection window please refer to the Appendix F. After the directory is selected, a parameter select window will open. Figure 3 shows the initial parameter select window. Some of the user interface controls (Figure 7) are shielded from the user and plotted in "SetupICA-Defaults" menu. The parameters are explained below:
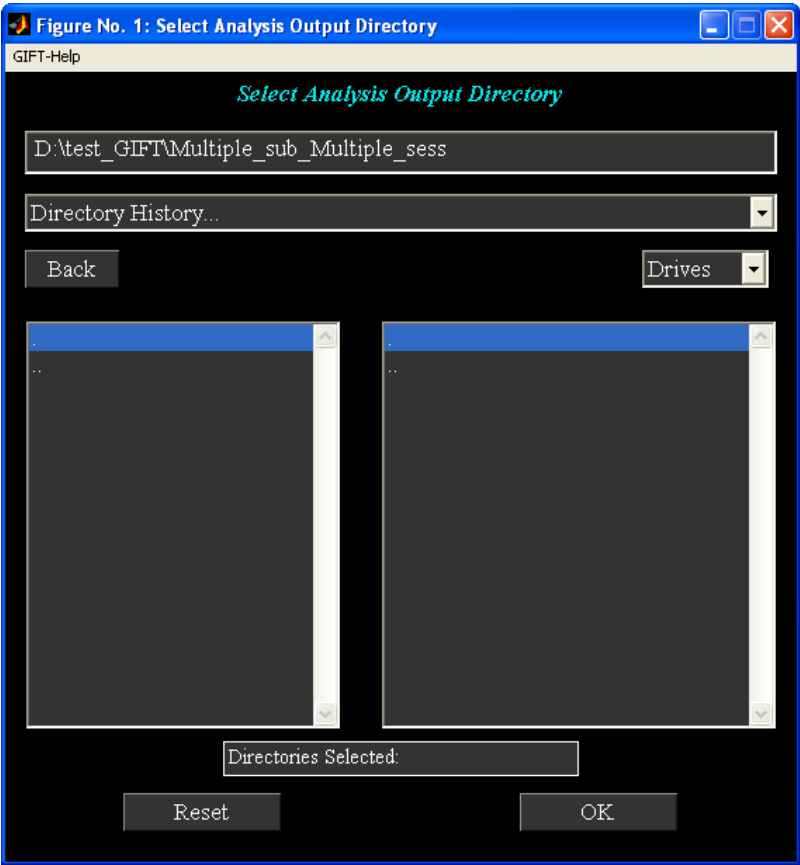
Figure 2: Directory Selection Window

Figure 3: Initial Parameter Selection Window

Main User Interface Controls:

1) 'Enter Name (Prefix) Of Output Files' is the prefix string to all the output files created by GIFT. Enter 'Visuomotor'.

2) 'Have You Selected the fMRI Data Files?' Click on the pushbutton *Select* and this will open a new figure (Figure 4) 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 5) will open to select the root folder for subjects and sessions. The selected root folder has three subject sub folders with the whole brain functional data and each subject folder has single slice data in sub-sub-folder. After the root directory for subjects and sessions is selected, another figure window (Figure 6) appears to enter the file pattern and an additional question to select the data in subject folders (whole brain) or session folders (Single Slice). Select '*.img' for 'Select file pattern for reading data' and 'No' for 'Are session folders inside subject folders'. Option is provided to enter a subset of files instead of using all files. 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.
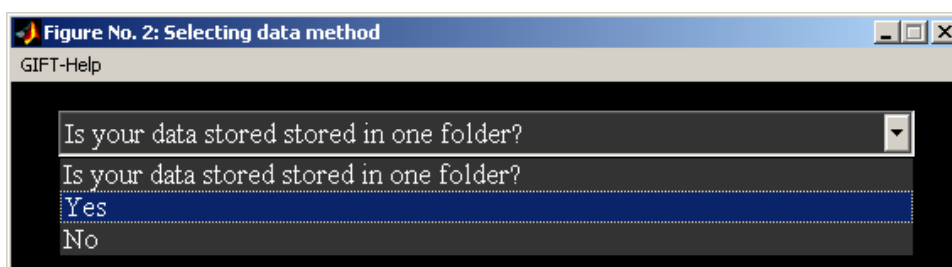
Figure 4: Selecting data method

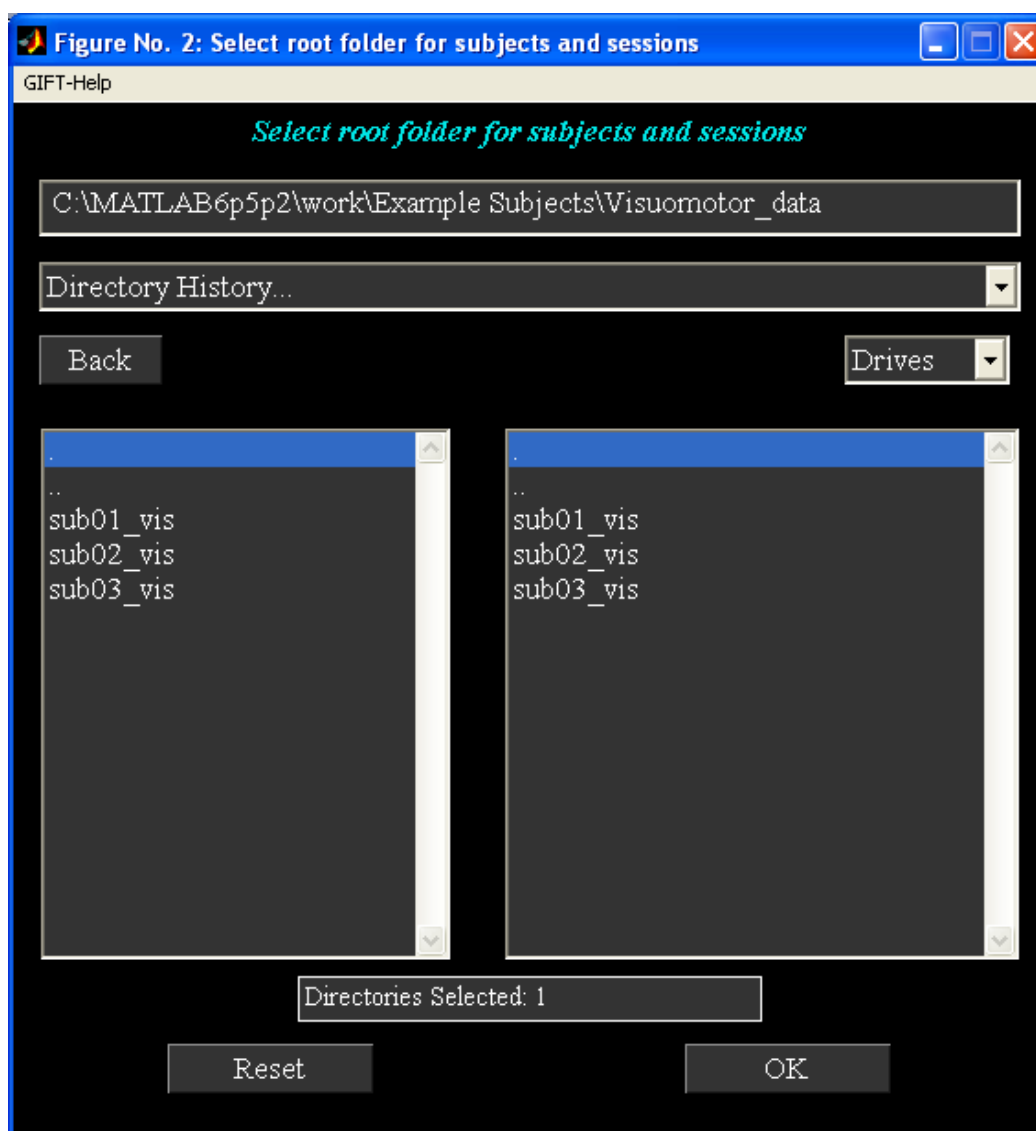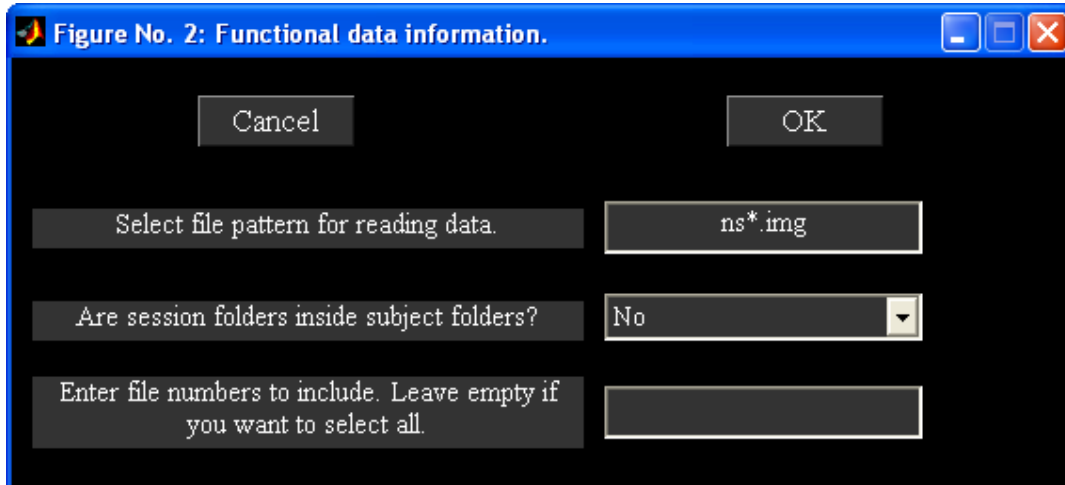Figure 5: Root folder for selecting subjects and sessions

Figure 6: 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 images.

3) 'Do you want to estimate the number of independent components?' Select 'Yes'. When this option is selected the components are estimated ([3]) from the fMRI data using the MDL criteria.
    i) 'Do you want to use all subjects to estimate the number of independent components?' Select 'No'.
    ii) 'Which subject you want to use for estimating components?' Select 'Subject 3 Session 1'. After estimation the number of components is displayed to the user. Click the push button *Plot* to view the plot of MDL where the minimum of MDL occurs is the estimated components. The number of estimated components is found to be 16.

4) 'Number of IC'. Enter '16'. This refers to the number of independent components extracted from the data.

5) '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. If there are more than or equal to two data reduction steps, initial data reduction numbers are set to 30. For now leave the options as 'Yes'.

6) 'Which ICA Algorithm Do You Want To Use?' Select 'Infomax'. There are 14 algorithms implemented in the toolbox like Infomax, FastICA, Erica, Simbec, Evd, Jade Opac, Amuse, SDD ICA, Semi-blind Infomax, Constrained ICA (Spatial), Radical ICA, Combi, ICA-EBM and FBSS. A detailed explanation of algorithms like Infomax, FastICA, Erica, Simbec, Evd, Jade Opac and Constrained ICA (Spatial) is given in the manual.

Note: If you are using Constrained ICA (Spatial) as ICA algorithm, the number of independent components will be set to the number of spatial reference or template files selected. Example reference files like 'ref_right_visuomotor.nii', 'ref_left_visuomotor.nii' and 'ref_default_mode.nii' are provided in folder icatb/icatb_templates.

7) 'Which Group ICA Analysis You Want To Use?' Options are 'Regular' and 'ICASSO'. When you select 'ICASSO', ICA is run several times and the best estimate for each component is used. For now select 'Regular'.

Hidden User Interface Controls

These user interface controls (Figure 7) will be shown after you click 'Setup ICA-Defaults' menu (Figure 3). The parameters in Figure 7 are explained below:

1) 'Select Type Of Data Pre-processing' - Data is pre-processed prior to the first data reduction. Options are discussed below.
   a. 'Remove Mean Per Timepoint' - At each time point, image mean is removed.
   b. 'Remove Mean Per Voxel' - Time-series mean is removed at each voxel.
   c. 'Intensity Normalization' - At each voxel, time-series is scaled to have a mean of 100. Since the data is already scaled to percent signal change, there is no need to scale the components.
   d. 'Variance Normalization' - At each voxel, time-series is linearly detrended and converted to Z-scores.
2) 'What Mask Do You Want To Use?' There are two options like 'Default Mask' and 'Select Mask'.
   a. 'Default Mask' - Mask is calculated using all the files for subjects and sessions or only the first file for each subject and session depending upon the variable DEFAULT_MASK_OPTION value in defaults. Boolean AND operation is done to include the voxels that surpass the mean of each subject's session. For now select 'Default Mask'.
   b. 'Select Mask' - You can specify a mask containing the selected regions for the analysis. This mask must be in Analyze or Nifti format.
3) 'Select Type Of PCA' - There are three options like 'Standard', 'Expectation Maximization' and 'SVD'. For now use standard PCA. Please see manual for more information.
4) 'Select The Backreconstruction Type' - Options are 'Regular', 'Spatial-temporal regression', 'GICA3' and 'GICA'. GICA is the preferred method for reconstructing subject components.
5) 'Do You Want To Scale The Results?' The options available are 'No Scaling', 'Scale to original data(%)', 'Z-scores', 'Scaling in timecourses' and 'Scaling in maps and timecourses'.
   a. 'Scale to original data(%)' - Each subject component image and time course will be scaled to represent percent signal change. Select 'Scale to original data(%)'.
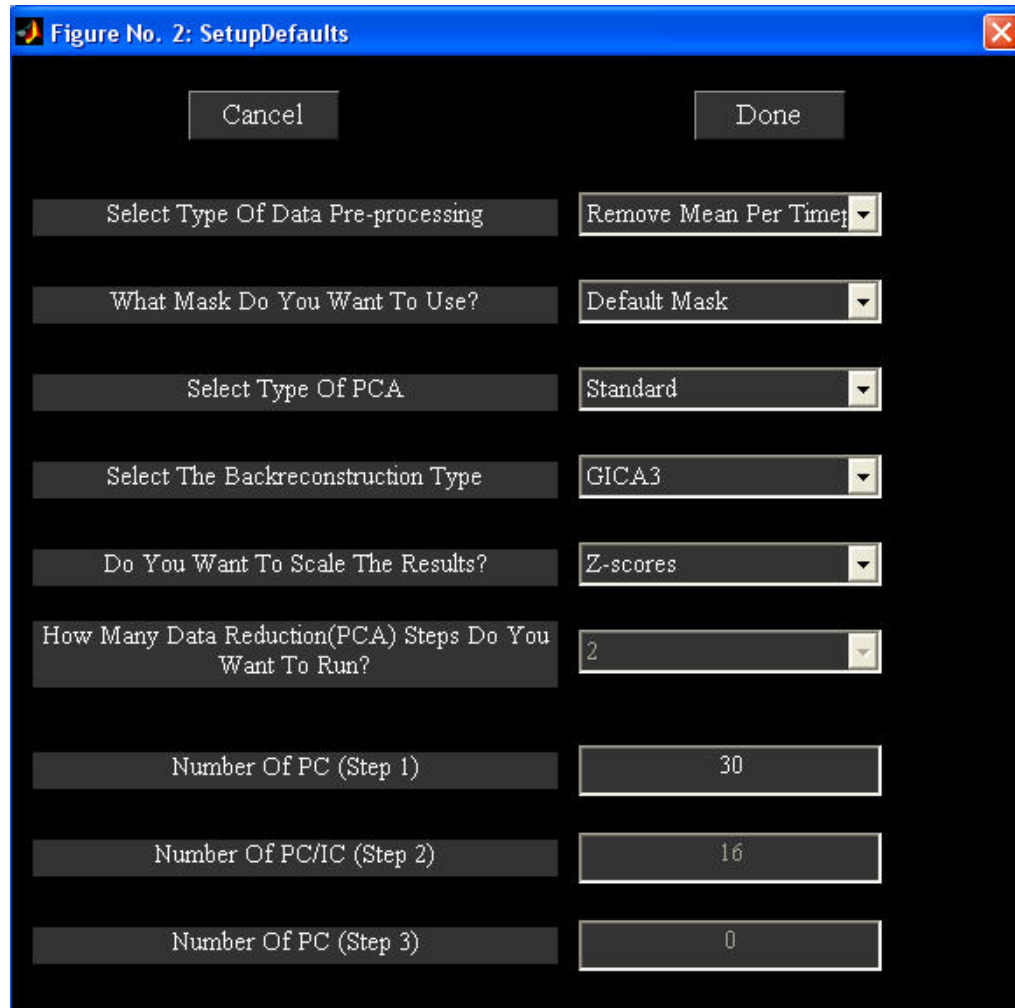
b. 'Z-Scores' - Each subject component image and time course will be converted to z-scores. Standard deviation of image is calculated only for the voxels that are in the mask.

c. 'Scaling in timecourses' - Spatial maps are normalized using the maximum intensity value and the maximum intensity value is multiplied to the timecourses.

d. 'Scaling in maps and timecourses' - Spatial maps are scaled using the standard deviation of timecourses and timecourses are scaled using the maximum spatial intensity value.

Note: By default, subject component images are centered based on the peak of the distribution. Please see variable CENTER_IMAGES in 'icatb_defaults.m'.

6) '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. For the example data-set two reduction steps are automatically selected.

7) '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.

8) '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.

9) '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.

Figure 7: Hidden User Interface Controls

Figure 8: Completed Parameter Select Window

b) Figure 8 shows the completed parameters window. Click *Done* button after selecting all the answers for the parameters. This will open a figure window (Figure 9) 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 (Appendix C). Currently, the dialog box is only available for the Infomax, FastICA, Optimal ICA, Semi-blind ICA and Constrained ICA (Spatial) algorithms. After selecting the options, parameter file for the analysis is created in the working directory with the suffix 'ica_parameter_info.mat'.

Figure 9: Options of the ICA algorithm

2. *Run Analysis* contains initializing parameters along with the steps involved in the group ICA.

1) After the *Setup ICA analysis* is done click on the *Run analysis* button, a screen will pop up asking you to select the parameters file. The parameters file is the same file that you entered all the analysis information. It is named as 'ica_parameter_info.mat'. Once the parameter file is selected a figure (Figure 10) will pop up showing the options for *run analysis*.

2) Select 'All***'. You can run all the group analysis steps at once or run each one separately. To run them all at once select 'All***', to run then separately select the desired step. The steps must be done in order and you must run each step.

Figure 10: Run Analysis
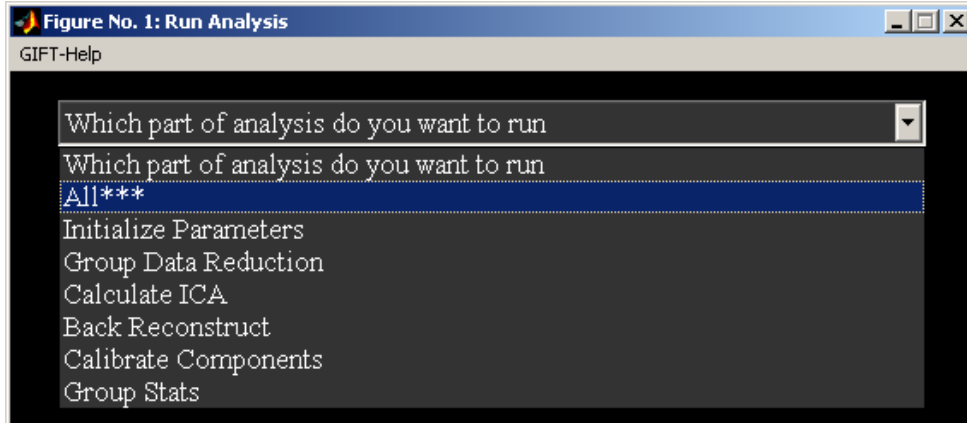
3) Results during each of the steps are printed to the MATLAB command window. Before the group analysis can take place the parameters file must be initialized. At this stage variables that were entered through the GUI are parsed and initialized as needed for the group ICA analysis. Error checking is 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.

3. *Analysis Info* contains the information about the parameters, data reduction and the output files. Once the analysis is done, click on the *Analysis Info* button on the GIFT main window and select the parameter file that you want to look at. Then a figure (Figure 11) will pop up showing the information contained within this window is dependent on whether or not the parameters file has been initialized or just created.

Figure 11: Analysis Information


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Figure No. 1: Analysis Information                        _ □ X
GIFT-Help

Group ICA Parameter Information

Got Parameters From User: YES
Parameters Initialized: YES
Number of Subjects : 3
Number of Sessions : 1
Number of Independent Components : 16
ICA Algorithm : Infomax
Number Of Scans/Timepoints : 220
Mask File : Default Mask Created From Functional Data
Data Pre-processing Type : Remove Mean Per Timepoint
PCA Type : Standard
Back Reconstruction Type : GICA3
Scaling Components : Z-scores



        Parameter Info        Data Reduction Info        File Output Info
```

II. Visualization Methods:

GIFT contains three main ways of visualizing the components after analysis like the component explorer, the composite viewer and the orthogonal viewer. These three visualization options can be used independently or collectively using the *Display GUI*. This visualization tool provides the user an easy way to explore all the three visualization options along with subject component explorer.

The selected visualization method will be highlighted in colored text. By default, *Component Explorer* (Figure 14) visualization method will be selected after selecting the parameter file. Some of the user-interface controls are shielded from the user and these are plotted in "Display Defaults" menu (Figure 14). Explanation of the main user interface controls is given below followed by explanation of visualization methods:

1) 'Sort Components' – Components will be sorted spatially or temporally. This control will be enabled only for *Component Explorer* visualization method.
2) 'Viewing Set' – This is the component viewing set to look at like subject 1 session 1, mean for session 1, etc and will be disabled for *Subject Explorer* visualization method.
3) 'Component number' – Component number/numbers to look at. This will be disabled for *Component Explorer* visualization method.
4) *Load Anatomical* – *Load Anatomical* button is used to select anatomical image. Component images will be overlaid on this anatomical image. By default, first image of functional data will be used as an anatomical image.
5) *Display* – *Display* button is used to display the components of different visualization methods.
6) Display Defaults menu – Hidden display parameters will be shown in a figure when you click on "Display Defaults" menu. This figure contains parameters like 'Image Values', 'Anatomical Plane', 'Threshold', 'Slice Range', 'Images Per Figure'.
7) "Display GUI Options" menu can be used to change design matrix and selecting the text file that contains regressor information for temporal sorting.
    i. Select 'Design Matrix' for selecting design matrix for temporal sorting. There are three options for selecting design matrix (Figure 12) like 'Same regressors for all subjects and sessions', 'Different regressors over sessions' and 'Different regressors for subjects and sessions'. Here only two are shown because there are three subjects and one session. For now select 'Same regressors for all subjects and sessions' and then a figure window (Figure 13) will open to select the design matrix.

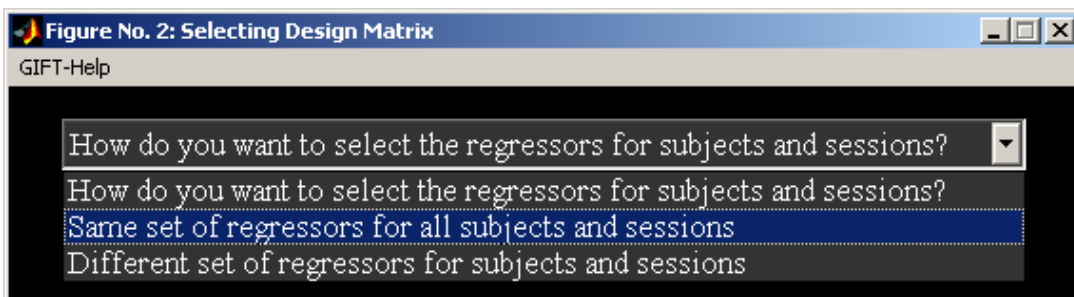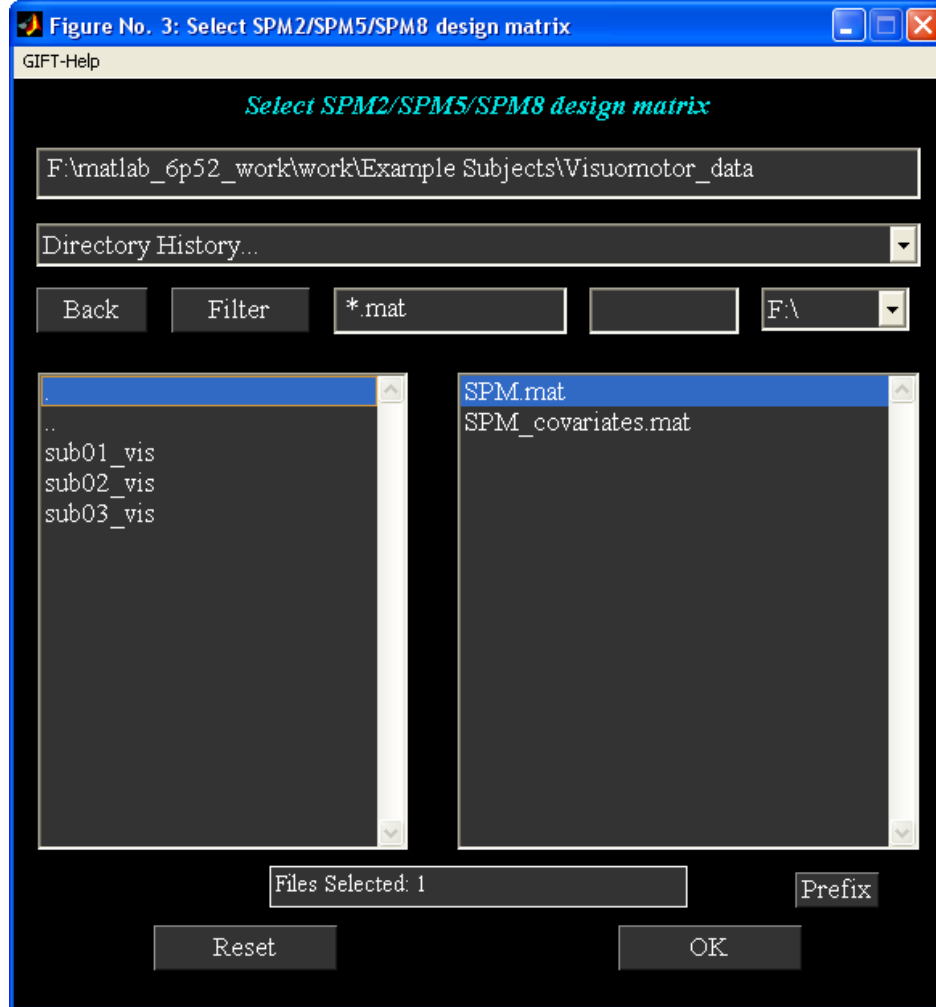Figure 12: Specifying Type of Regressor Selection

Figure 13: SPM File Selection

A. Component Explorer

1) *Component Explorer* is used to display all components of a particular viewing set. Therefore, 'Component Number' control will be disabled for this visualization method.
2) 'Viewing Set'. Select viewing set 'visuo_mean_component_ica_s_all'. This is the mean for all subjects and sessions.
3) 'Sort Components'. Sort the components based on temporal or spatial models. Leave this on 'No'.
4) Figure 14 shows the selected parameters for the *Component Explorer*.
5) Click on *Display* button and wait for the figures containing spatial maps to pop up.
6) Figure 15 shows all the components of mean for all subjects and sessions in groupings of four. By default, slices in axial plane are plotted in mm. You can change these parameters when you click "Display Defaults" menu.

Figure 14: Selected Parameters for the Component Explorer
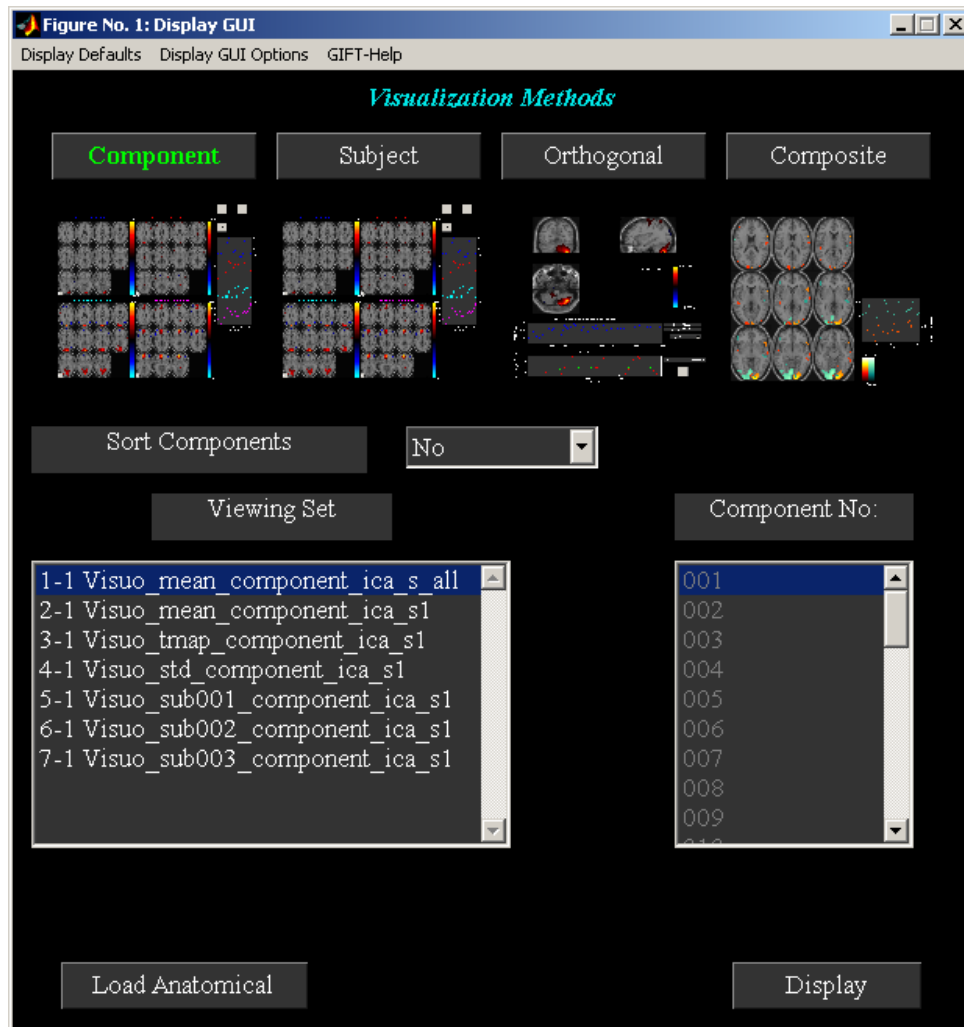
7) The time course for each component is displayed on the top of the figure (Figure 15). The color bar for each component is displayed next to it. Click on the time course for an enlarged view.

8) Look through the components by clicking on the arrow keys at the bottom of each figure. Find the components of interest and take a note. With this data set you should find two task related components and one transiently related component. The task related components show activation in the visual cortex. The act of classifying components becomes more difficult with more complex tasks and is the motivation for adding the sorting option.

Figure 15: Components 1 to 4 of 'Mean for all subjects and sessions' Not Sorted
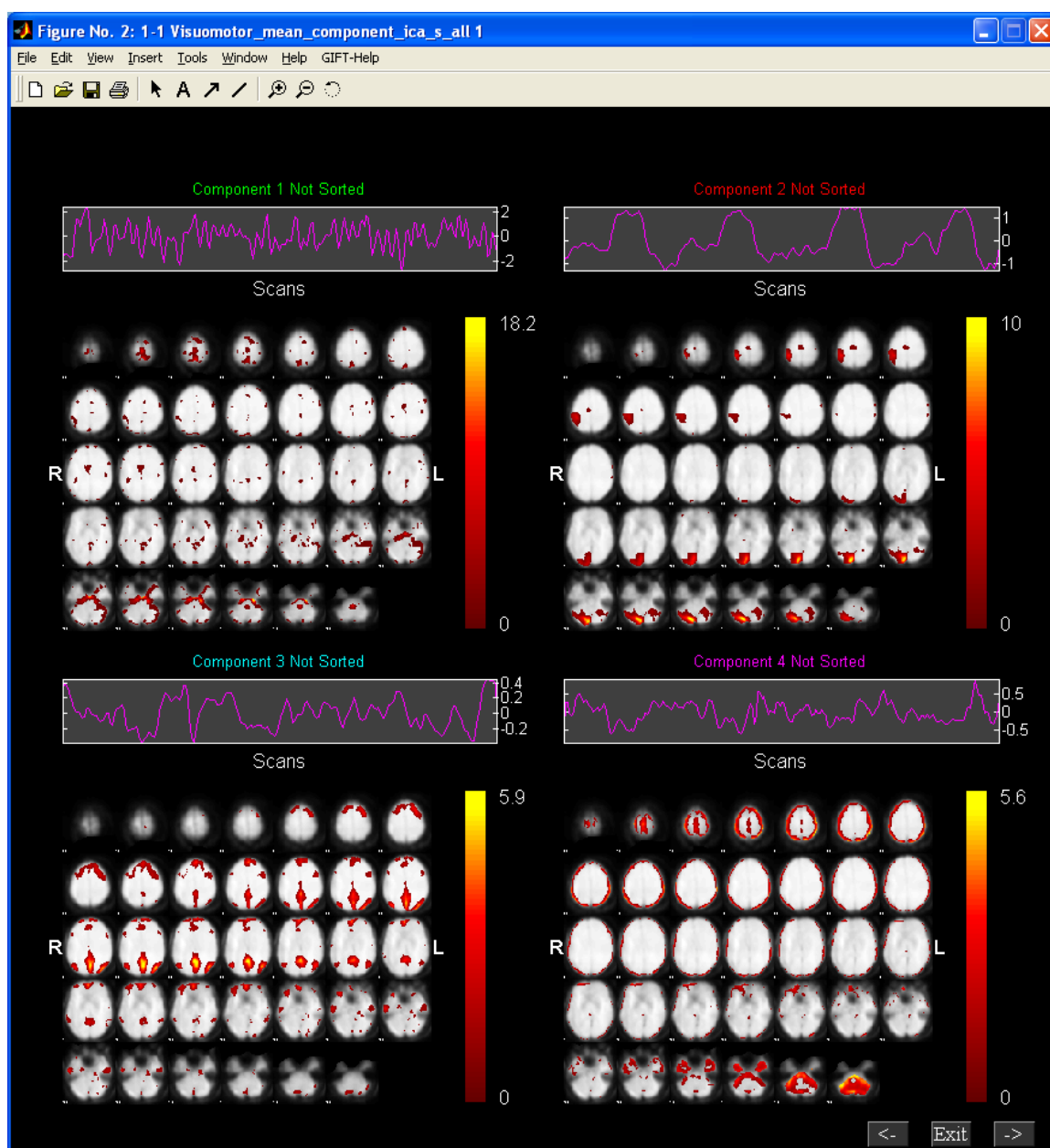
B. Subject Component Explorer

1) Click *Subject* button to select *Subject Explorer* method. This method is used to display a specific component for all subjects, sessions, mean etc. Therefore, viewing set control is disabled for this visualization method.
2) 'Component Number' - This will let you select which component number you want to look at. Select component '001'.
3) Figure 16 shows the selected parameters. Click *Display* button. Figure 17 shows the component '001' of all the entries in the 'viewing set'.

Figure 16: Selected Parameters for Subject Component Explorer
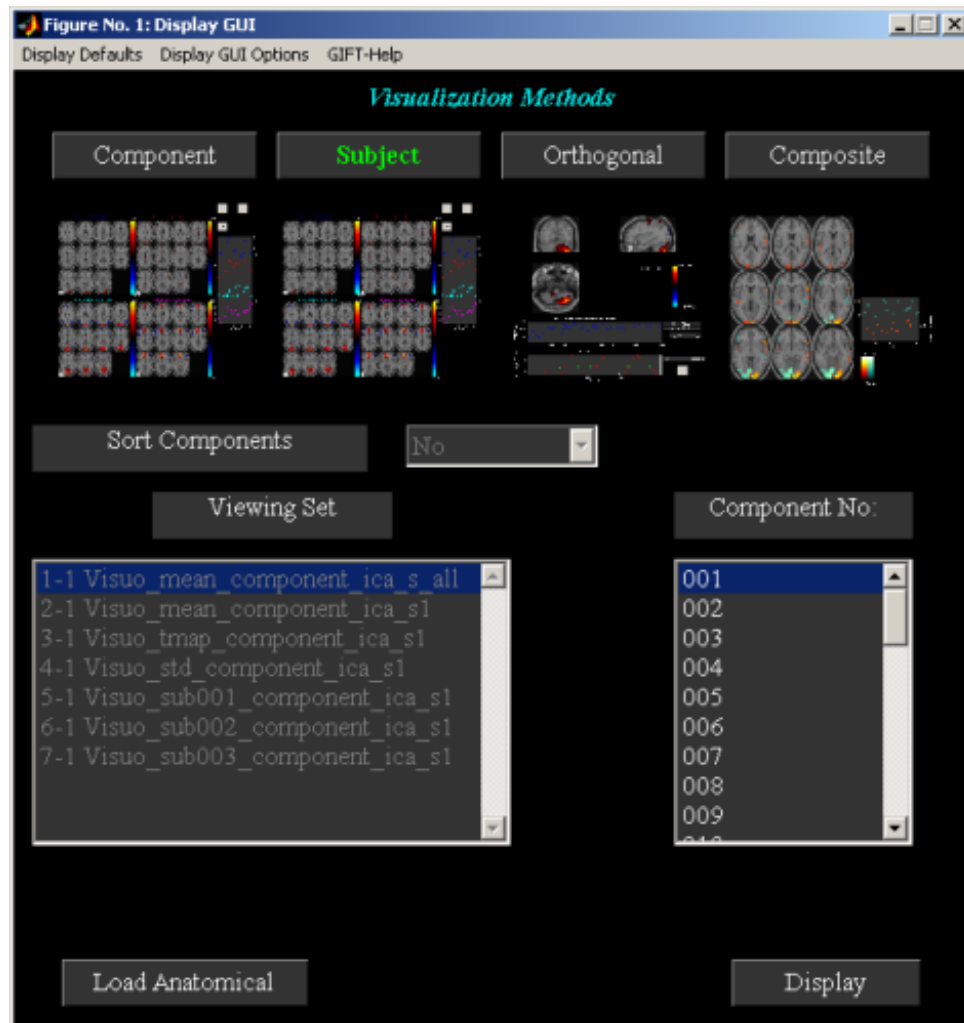
Figure 17: Component '001' of all the entries in the viewing set
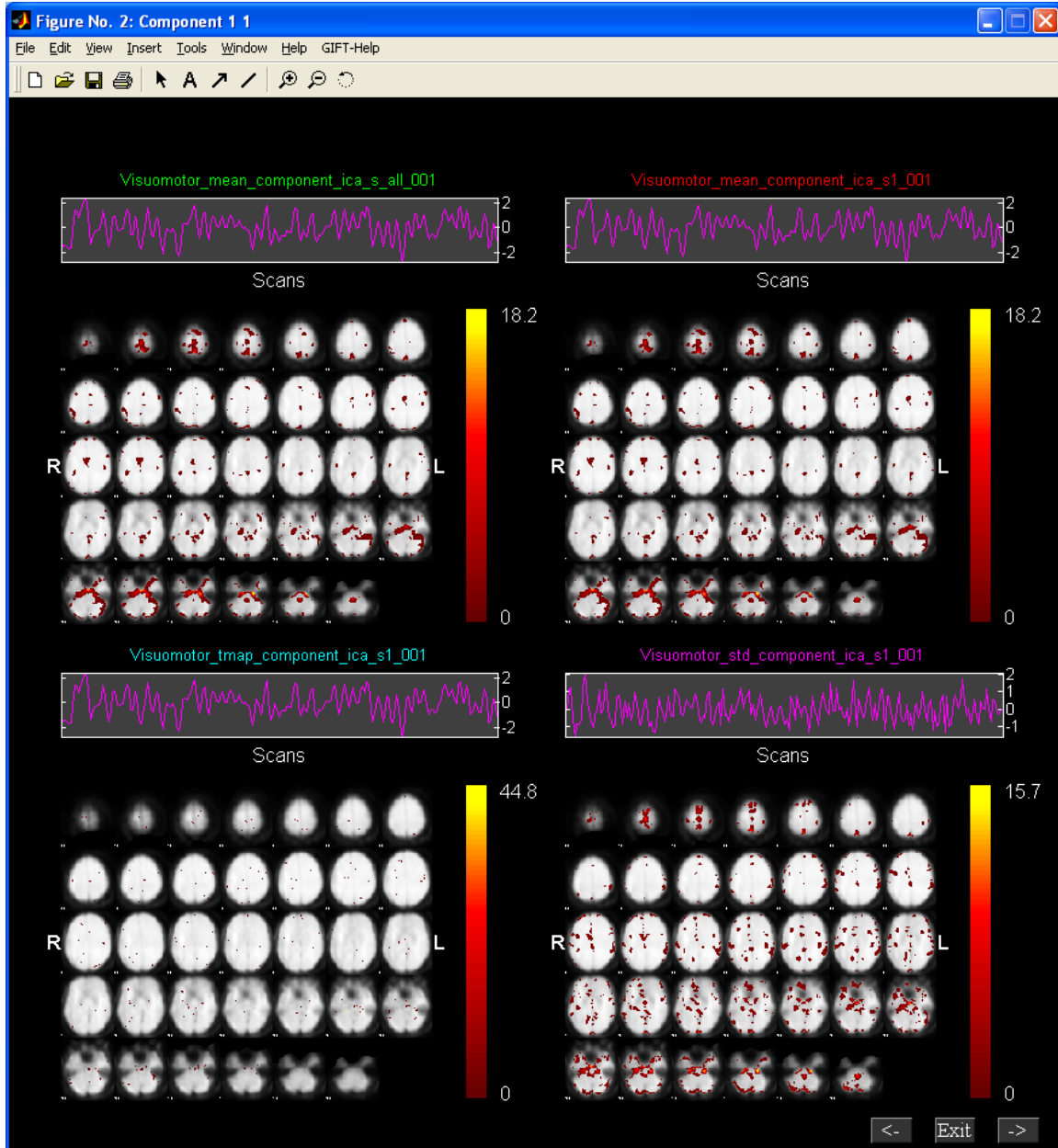
C. Orthogonal Viewer

1) Click *Orthogonal* button to select *Orthogonal Viewer* method. This method is used to look at a component and compare it to the functional data. Select viewing set as 'Visuo_mean_component_ica_s_all'.

2) Select one of the task related components in the 'Component Number' user interface control. Figure 18 shows the selected parameters and click on *display* button.

3) Figure 19 shows one of the task related components. Upper plot is the BOLD time course for the selected data-set in the popup window at the current voxel. You can interactively select voxel by clicking on any of the slices. Lower plot shows the ICA time course for

the maximum voxel (red), minimum voxel (dotted red) and the selected voxel (green). When you click on *Plot* button top five components (of the selected viewing set) for the selected voxel will be displayed. Option is provided in the figure 19 (Options Menu) to enter the current voxel position (real world coordinates) instead of navigating around the brain. To get the updated BOLD time course plot you need to select the subject in the drop down box.

4) Maximum voxel intensity and its location are printed to the command prompt. Voxel intensity and its coordinates at the current voxel are also printed to the command prompt.

Figure 18: Selected Parameters for Orthogonal Viewer
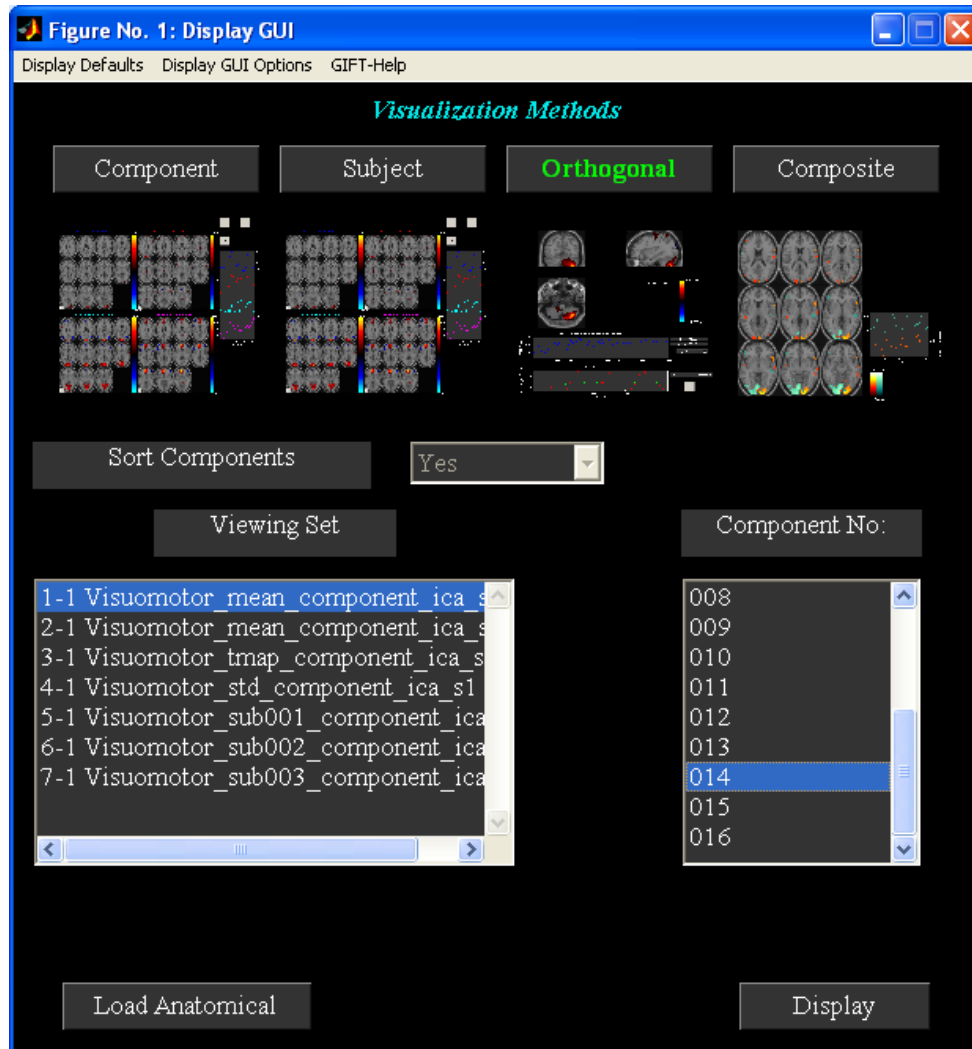
Figure 19: Plot of one of the task related components using Orthogonal Viewer
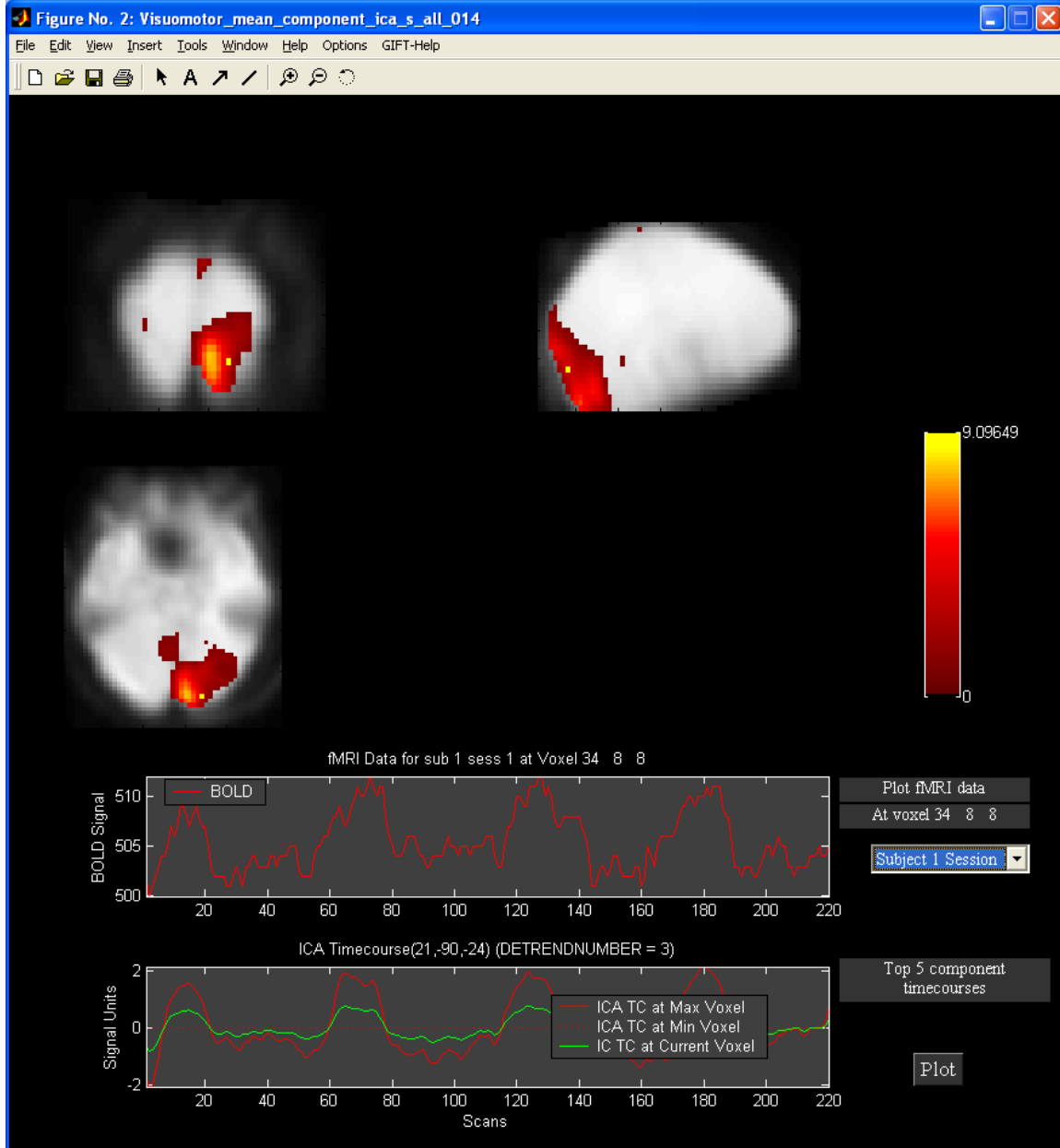
D. Composite Viewer

1) Click on *Composite* button to select *Composite Viewer* method. *Composite viewer* is used to look at multiple components of interest. Use the component explorer to find the task related components.
2) In the 'Component Number' user interface control, select the two components that are task related. At most five different components can be overlaid on one another.
3) Select anatomical image 'nsingle_subj_T1_2_2_5.nii' from icatb/icatb_templates folder using *Load Anatomical* button to overlay component images on anatomical image.

4) Figure 20 shows the selected parameters. Click *Display* button, then the figure 21 will open in a new window.

Figure 20: Selected parameters for Composite Viewer
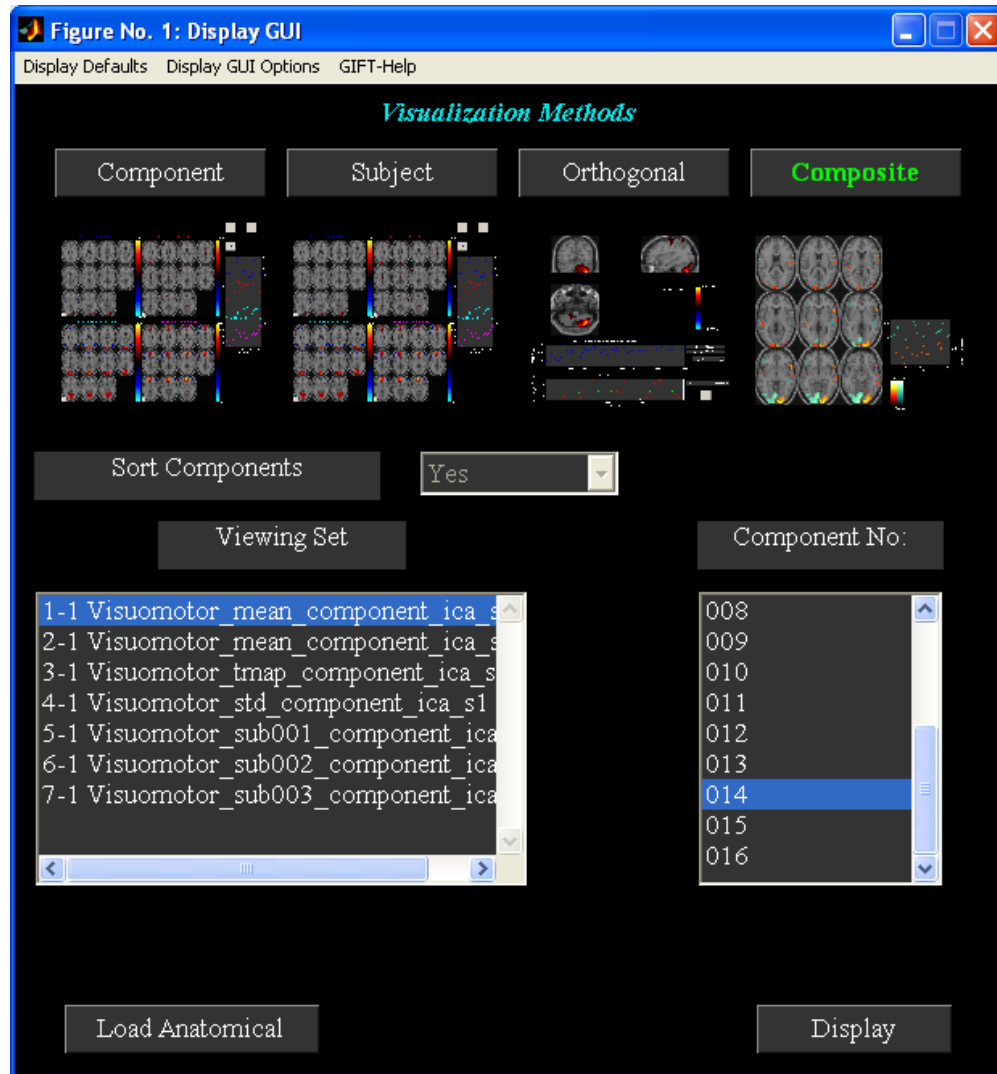
Figure 21: Plot of two task related components using Composite Viewer
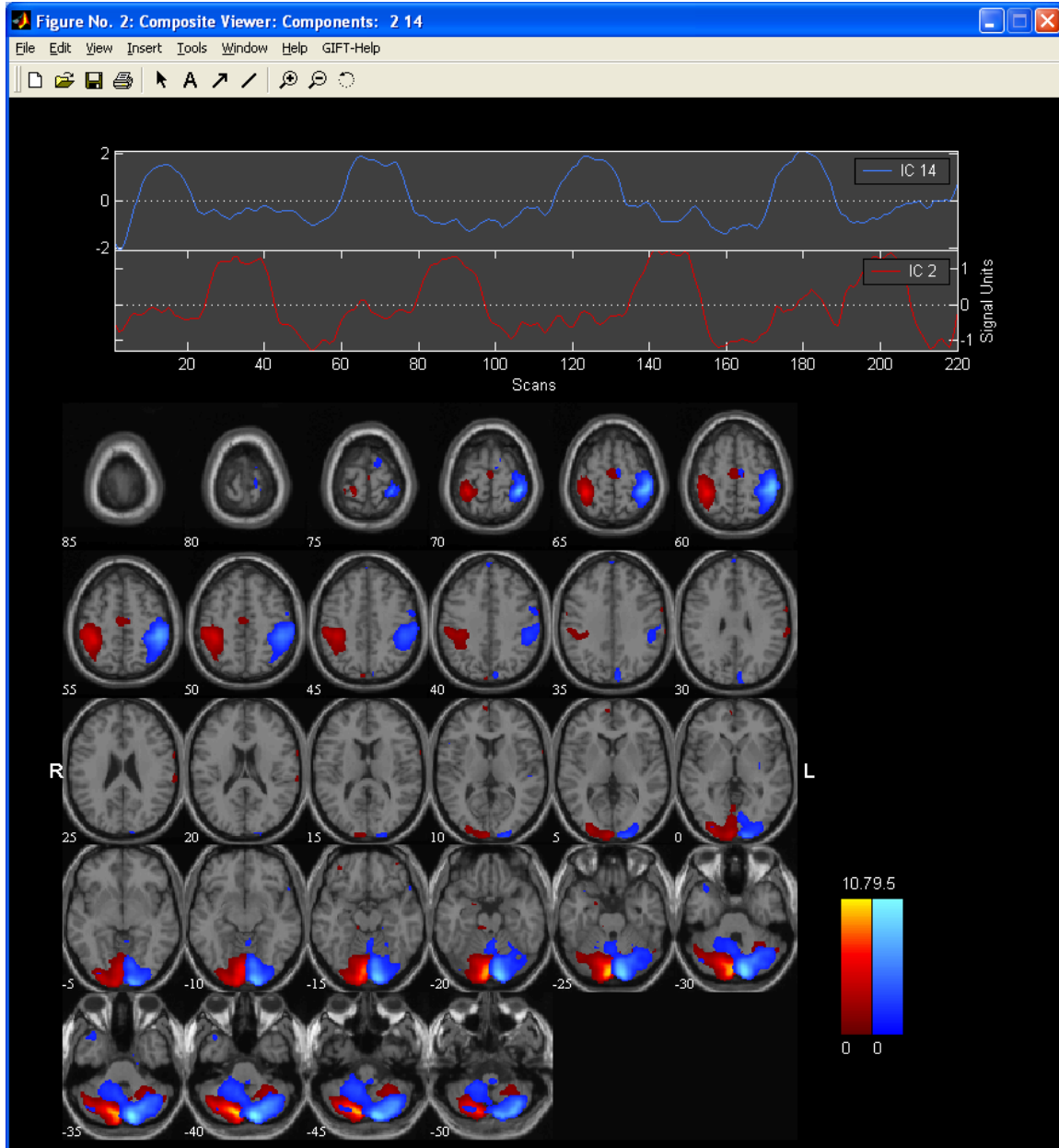
III. Sorting Components:

Sorting is a way to classify the components. The components can be sorted either spatially or temporally. For every independent component spatial maps and time courses are generated. Temporal sorting is a way to compare the model's time course with the ICA time course whereas spatial sorting classifies the components by comparing the component's image with the template. When you click *Component* button, 'Sort Components' popup box will be enabled. Select 'Yes' for 'Sort Components'. Click *Display* button then a figure (Figure 22)

will open in a new window. We have implemented three different types of sorting criteria like Correlation, Kurtosis and Multiple Linear Regression (MLR). MLR can be a very useful method in separating the two task related components. First, temporal sorting is explained followed by spatial sorting. The following are the steps involved in sorting components:

a. Temporal Sorting

1) Select the 'sorting criteria'. Select for now 'Multiple Regression'.
2) Select 'Sorting Type'. Select 'Temporal'.
3) 'What do you want to sort?' Select 'All DataSets'. Explanation of this option – You will select all data sets and correlate with model time courses.
4) A list dialog box with regressors will be shown after you click *Done* button. Select both 'Sn(1) right*bf(1)' and 'Sn(1) left*bf(1)' time courses. Explanation for this option – You have a good measure to separate the task related components depending on the model time course.
5) Figure 23 shows the components sorted based on the MLR sorting criteria in groupings of four. Here you can see that the first two components are task related. For a larger view of the time course plot (Figure 24) click on the time course plot in the main window. A list of menus is plotted on the time course plot. The explanation of each menu will be explained below:
    a) Utilities: Utilities contain options like "Power Spectrum", "Split-time courses" and "Event-Average". For now click on sub menu "Split-time courses", a new figure (Figure 26) will open showing the split of the concatenated data-sets. Click on sub menu "Event Average" and select 'Sn(1) right*bf(1)' reference function to plot the event averages (Figure 28) of the ICA time courses. Explanation of the event average is given in Appendix E.
    b) Options: Options menu has sub menus like "Timecourse Options", "Adjust ICA", "Save Figure Parameters" and "Load Figure Parameters". Menus like "Timecourse Options" and "Adjust ICA" will be explained below:
        a) Timecourse Options: When you click on sub menu Timecourse Options, a new figure window will open that contains options for detrending the ICA time course, model time course and options for event average. Explanation of this figure window is given in the Appendix D. Leave the defaults as shown in the figure.
        b) Adjust ICA: When you click on sub menu Adjust ICA, a list dialog box will open to select the reference function. For now select the 'Sn(1) right*bf(1)' time course. The ICA time course is adjusted by removing the line fit of the model with the ICA time course where model contains nuisance parameters and other than the selected reference function. After the ICA time course is adjusted the plot is shown in the expanded view time course plot (Figure 25). Click on the sub menu Split-time courses in Utilities menu, a new figure window (Figure 27) showing the split of the adjusted ICA time courses will be shown. Similarly click on sub menu "Event-Average" in "Utilities" menu and select the 'Sn(1) right*bf(1)' reference function to view the event averages (Figure 29) of the new ICA time courses.

Note:

1. After temporal sorting, the beta weights (slopes of regressors) and regression values are printed to a text file and MAT file. You can use these beta weights to determine the task-relatedness (Appendix G) of the components.
2. Event average can also be done without sorting components (See Utilities drop down box in Figure 1).
3. For using all the regressors to sort the components, set METHOD_ENTERING_REGRESSORS variable in 'icatb_defaults.m' to 'AUTOMATIC'. For large number of data-sets regressors can be entered through a text file (Appendix C).

b. Spatial Sorting

1) Select the 'sorting criteria' as 'Multiple Regression' in Sorting GUI (Figure 22).
2) Select 'Sorting Type' as 'Spatial'.
3) A figure window will open to select the templates after pressing *Done* button. Select both right visual and left visual templates[1] with the file names 'LeftTemplate.nii' and 'RightTemplate.nii' in the 'icatb_templates'[2] folder.
4) Select 'component set to sort'. Select 'subject1 session 1 components' and wait for components to be displayed.
5) Figure 30 shows the components sorted based on the MLR sorting criteria in groupings of four. Here you can see that the first two components are task related.

Figure 22: Sorting GUI

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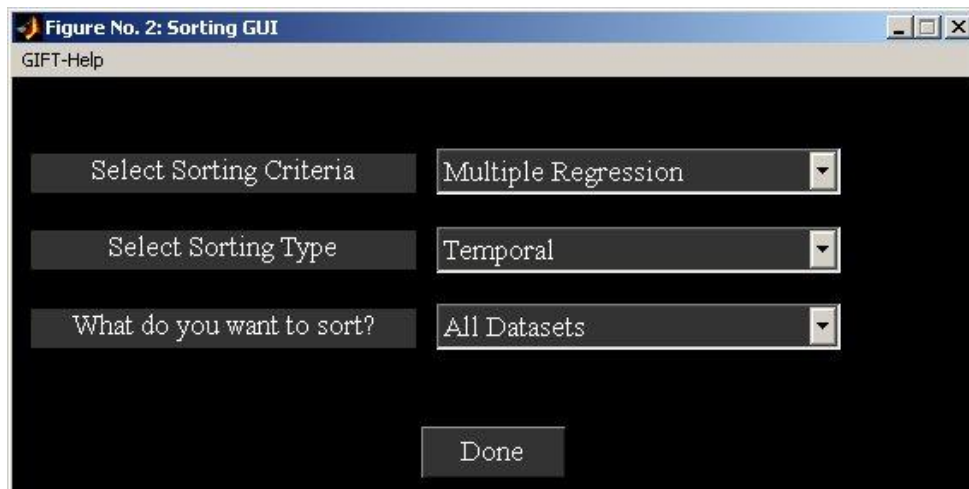
[1] Template – Spatial template shows the regions of interest or task-related regions
[2] icatb_templates – Folder obtained when you unzip the file 'gift'.

Figure 23: Sorted components of 'all subjects and sessions' using Temporal Sorting
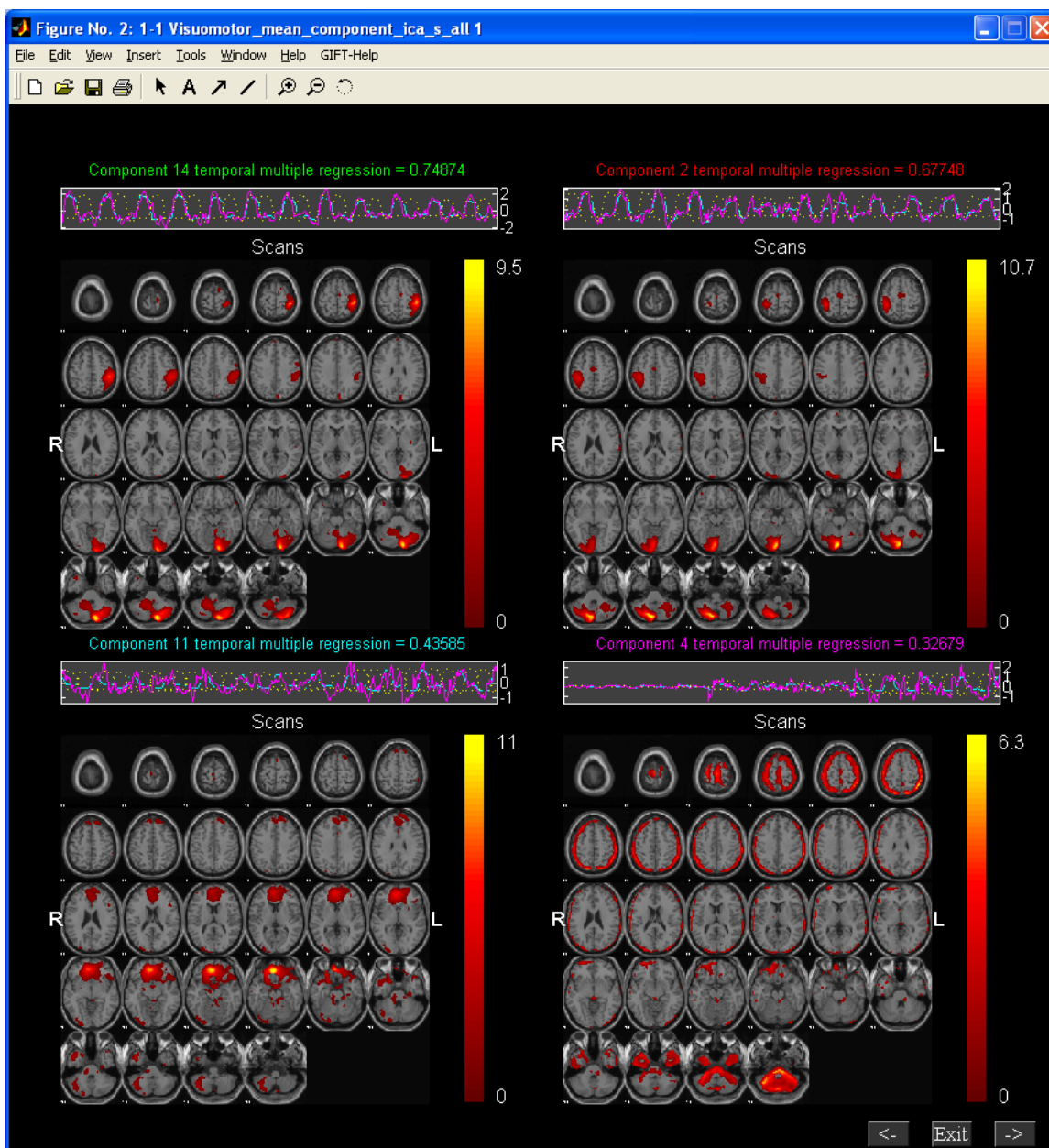
Figure 24: Expanded view of "Sn(1) right*bf(1)" time course

Figure 25: Expanded view of adjusted "Sn(1) right*bf(1)"time course

Figure 26: Split of subject time courses for the "Sn(1) right*bf(1)" time course

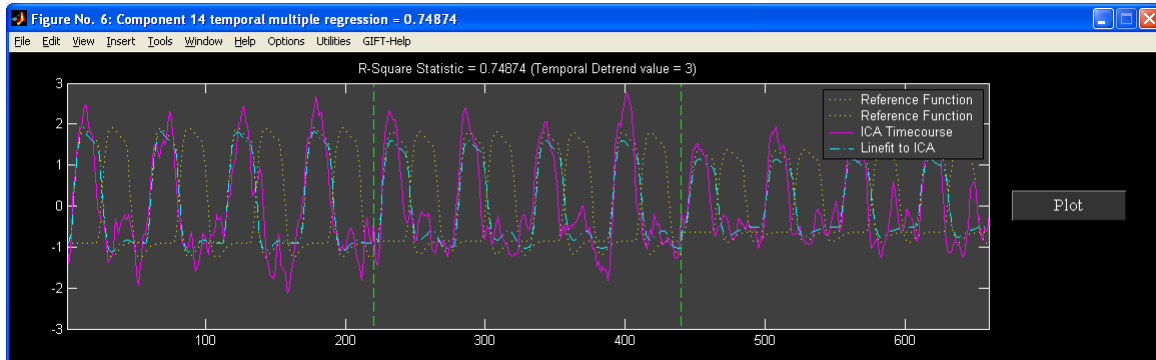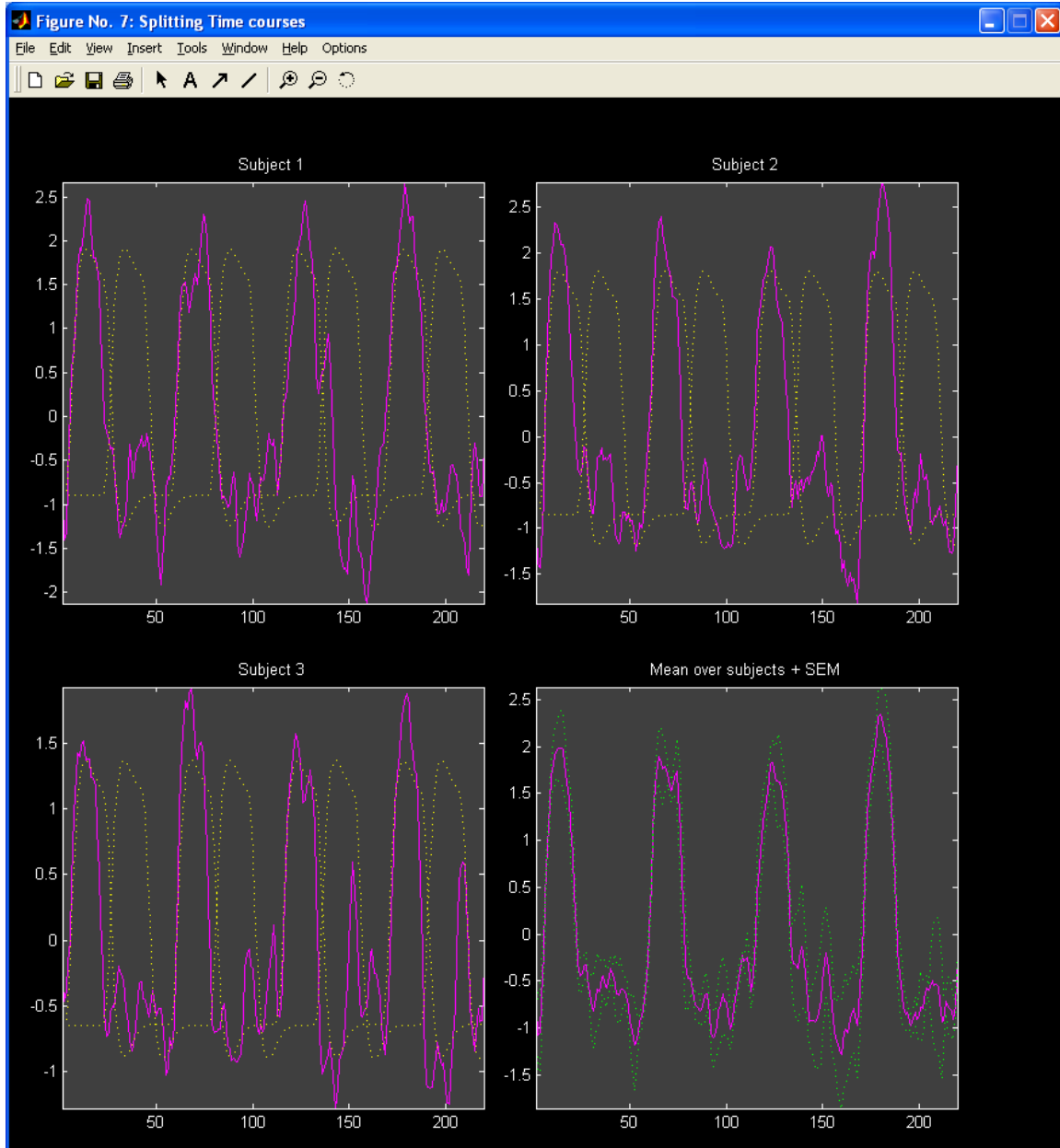Figure 27: Split of adjusted ICA time courses for the "Sn(1) right*bf(1)" time course
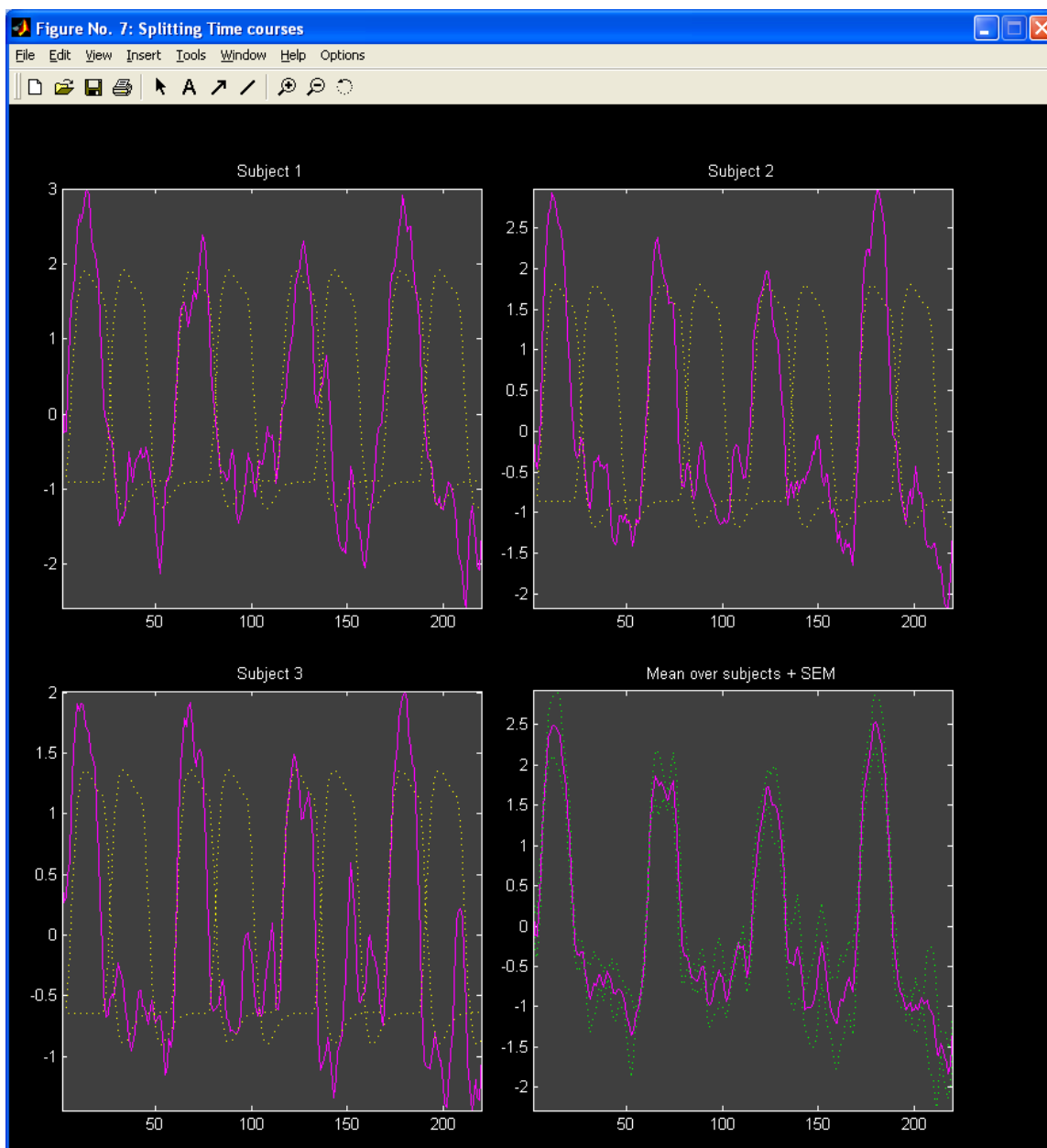
Figure 28: Event related average of the "Sn(1) right*bf(1)" time course
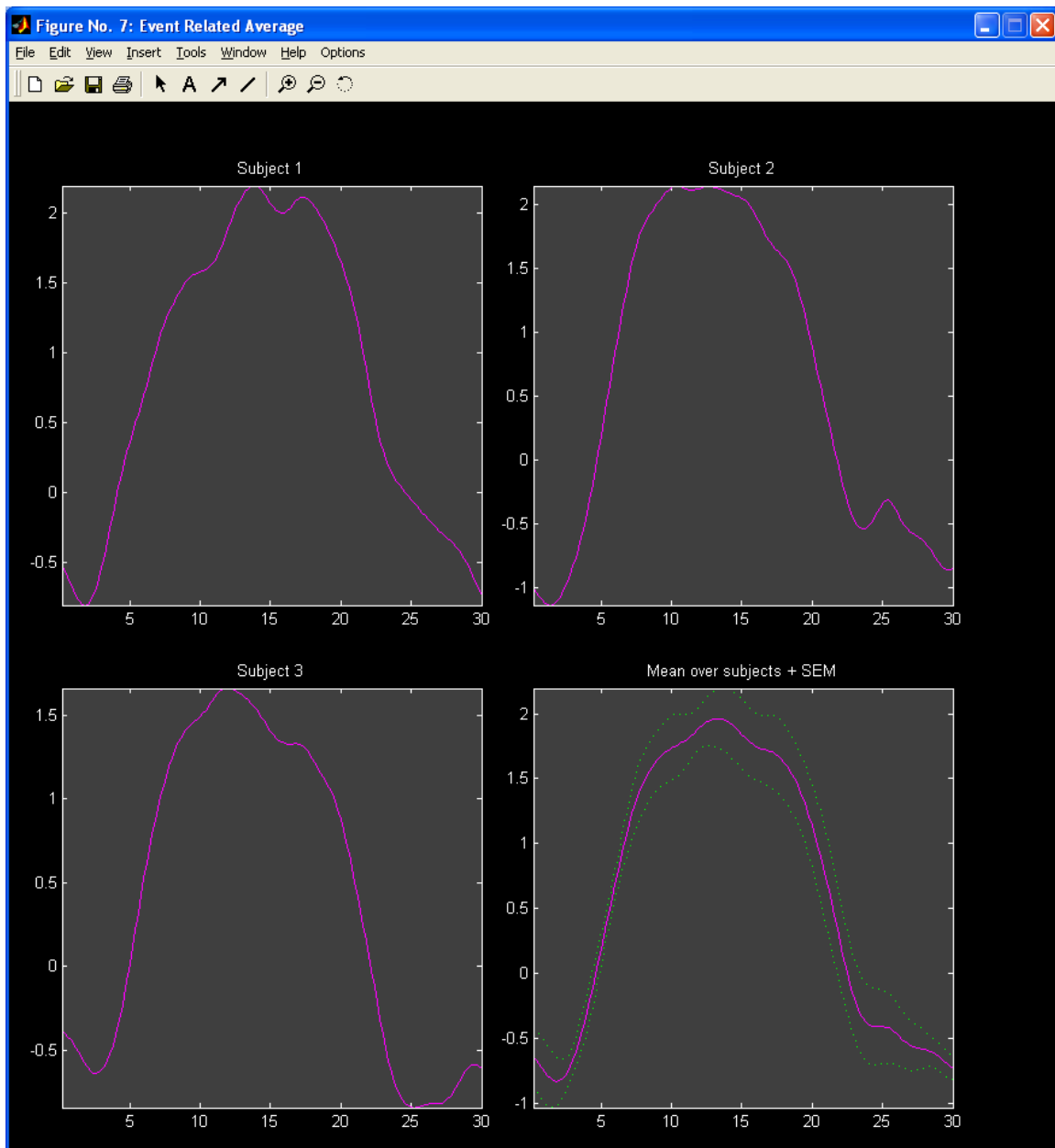
Figure 29: Event related average of adjusted "Sn(1) right*bf(1)" time course
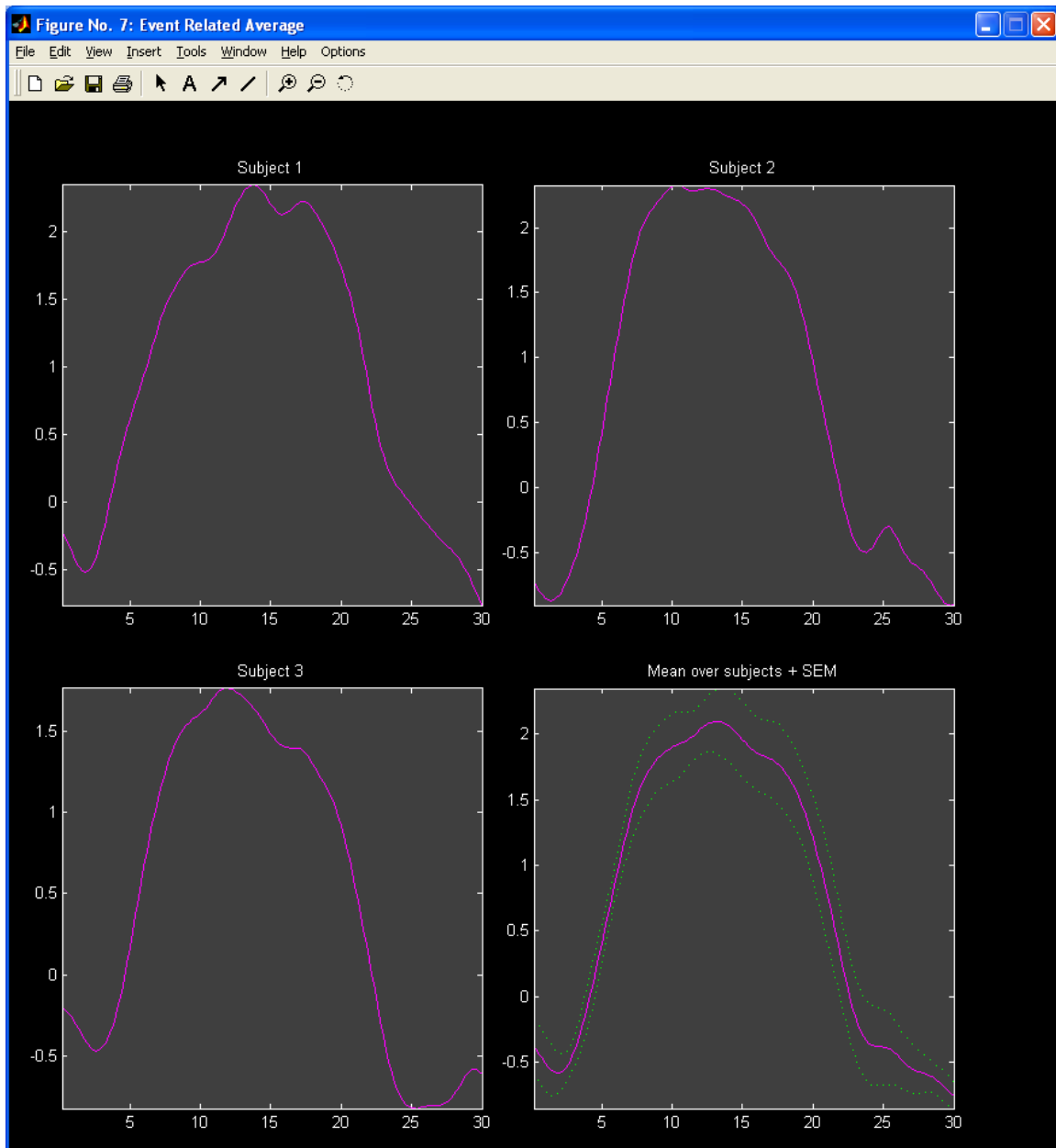
Figure 30: Sorted components of 'subject 1 session 1' using Spatial Sorting
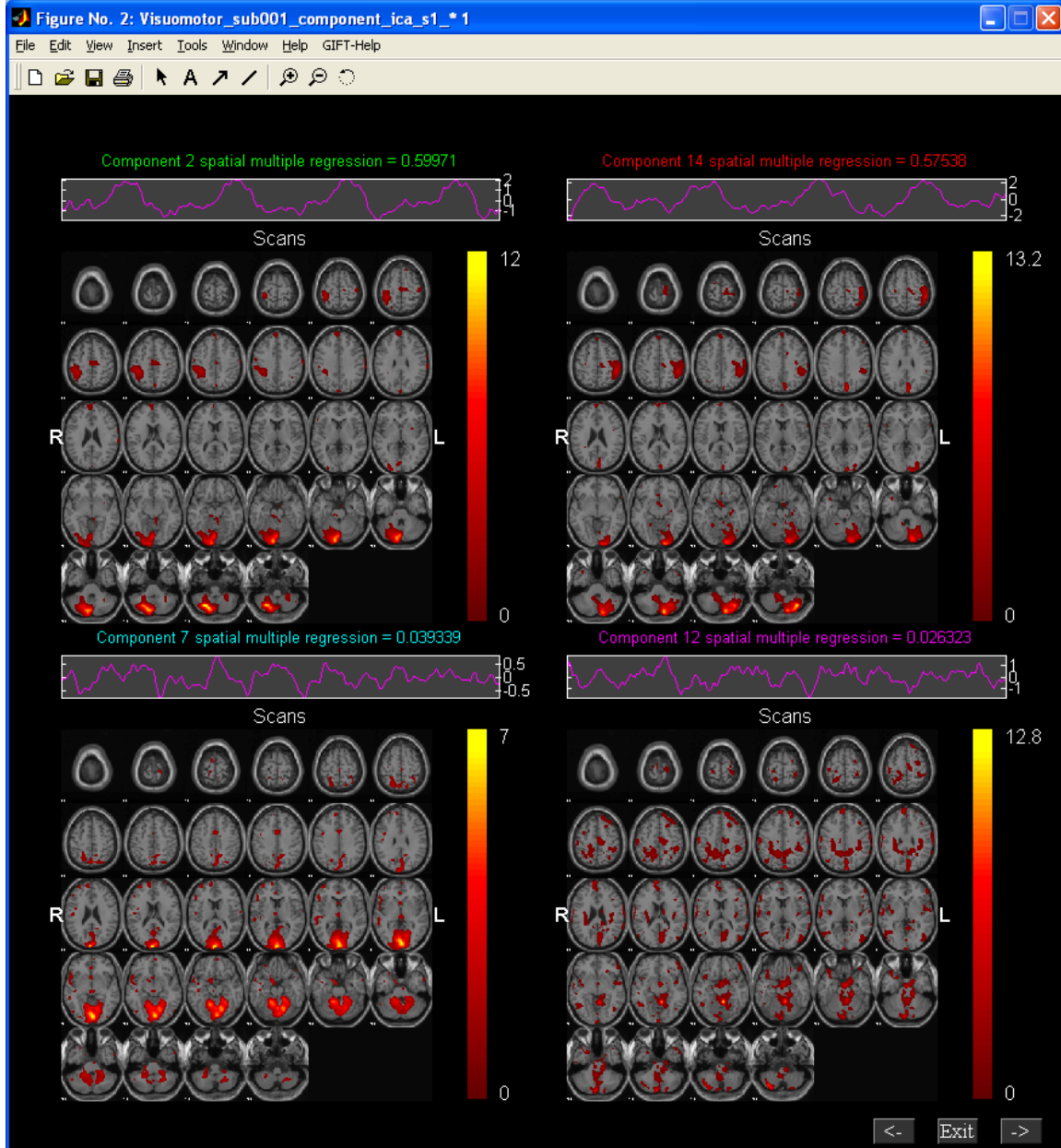
c. *Spatial Sorting using Maximum Voxel Criteria*

Components can be spatially sorted based on the maximum voxel criteria. Create a template defining the regions of interest. A maximum of all the voxels for each component is taken for the regions inside the template. The components are then sorted based on the maximum voxel. The procedure for using maximum voxel criteria is explained below:

1) Select 'Sorting Criteria' as 'Maximum Voxel' in Sorting GUI (Figure 22).
2) Press *Done* button, a figure window will open to select the template. Select 'VisuomotorMask.img' in the output analysis directory as template. A list dialog box will

open to select the component set used for sorting. Select 'subject1 session 1 components' and wait for the components to be displayed.

3) Figure 31 shows the components spatially sorted using maximum voxel criteria. The real world coordinates of the maximum voxel for each component are stored in a file with the suffix 'max_voxel.txt'.

Figure 31: Spatial Sorting using Maximum Voxel Criteria
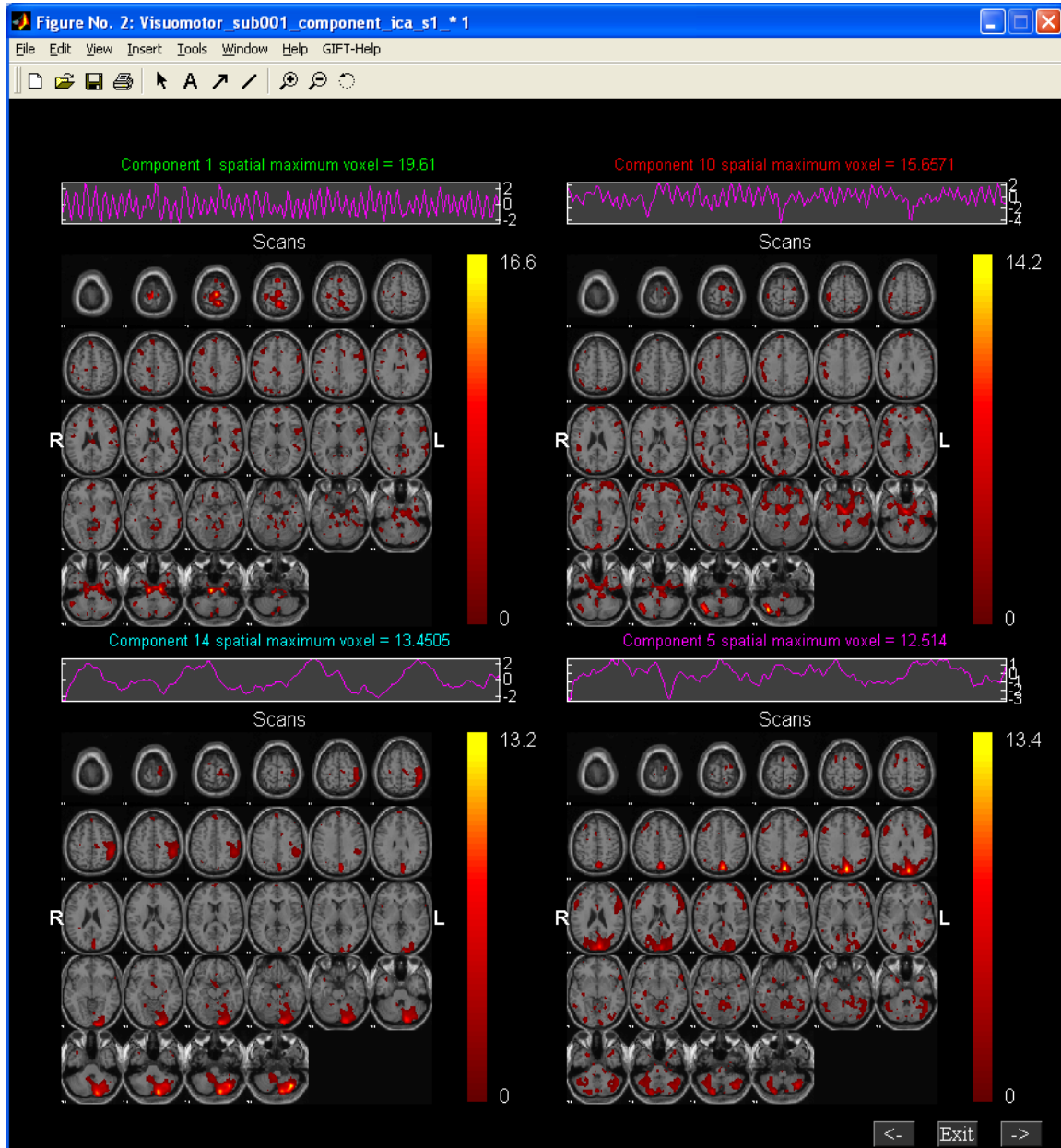
References

1. V. D. Calhoun, T. Adali, G.D. Pearlson, and J.J. Pekar, A Method for Making Group Inferences From Functional MRI Data Using Independent Component Analysis Hum. Brain Map., vol. 14, pp. 140-151, 2001.

2. V. D. Calhoun, T. Adali, J.J. Pekar, and G.D. Pearlson, Latency (in) Sensitive ICA: Group Independent Component Analysis of FMRI Data in the Temporal Frequency Domain NeuroImage, vol. 20, 2003.

3. Y. Li, T. Adali, and V. D. Calhoun, "Sample Dependence Correction For Order Selection In FMRI Analysis," in Proc. ISBI, Washington, D.C., 2006.

Appendix

A. Experimental Paradigms

The GIFT contains an example data-set which employs visuomotor paradigm (Figure 32). The paradigm contains two identical but spatially offset, periodic, visual stimuli, shifted by 20 seconds from one another. The visual stimuli were projected via an LCD projector onto a rear-projection screen subtending approximately 25 degrees of visual field, visible via a mirror attached to the MRI head coil. The stimuli consisted of an 8 Hz reversing checkerboard pattern presented for 15 seconds in the right visual hemifield, followed by 5 seconds of an asterisk fixation, followed by 15 seconds of checkerboard presented to the left visual hemifield, followed by 20 seconds of an asterisk fixation. The 55 second set of events was repeated four times for a total of 220 seconds. The motor stimuli consisted of participants touching their right thumb to each of their four fingers sequentially, back and forth, at a self-paced rate using the hand on the same side on which the visual stimulus is presented. FMRI data from this paradigm, when analyzed with standard ICA, separates into two different task-related components (one in left visual and motor cortex, one in right visual and motor cortex).

Figure 32: Visuomotor paradigm
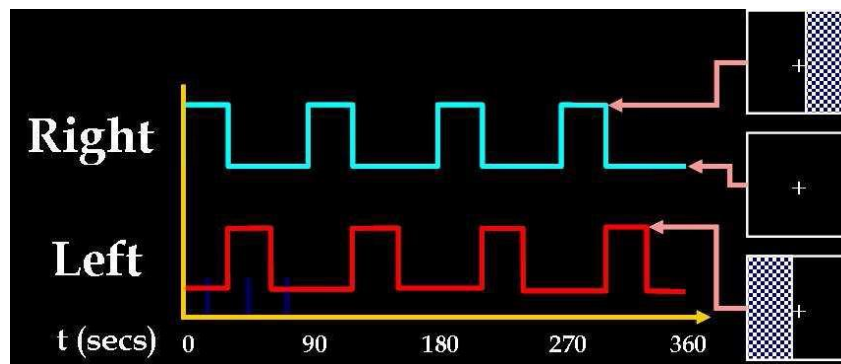
B. SPM Design Matrix

SPM design matrix (SPM2 or SPM5) contains information about the time courses and onsets for the regressors. Multiple regression and correlation sorting criteria in GIFT use SPM design matrix to sort components temporally. The SPM design matrix filename should be in .mat format. Type load(filename) at the MATLAB command prompt to view the SPM structure. GIFT uses the following fields in SPM structure:

Field	Description
nscan	Refers to the number of scans. For multiple sessions, nscan should look like a row vector.
xX.X	Regressor time courses in a matrix where number of rows equals the sum of the scans and number of columns equals the number of regressors.
xX.name	Contains the regressor names in a cell array. Number of regressors is equal to length of the cell array.
xY.RT	Refers to the inter-scan interval (TR).
xBF.UNITS	Refers to units in seconds or scans.
Sess	Contains information like onsets, regressor names in a session. Length of SPM.Sess is equal to the number of sessions.

Note: GIFT extracts session specific regressors only when the regressor names contain the session number like Sn(1) right_visual_hemisphere*bf(1) where 1 after Sn(refers to the session number.

C. Defaults

Defaults used in the GIFT toolbox are in 'icatb_defaults.m' file. The variable names are in capital letters. Explanation of some of the variables is given below:

- Colors: Colors are RGB values i.e., [0 0 0] means black. Background color can be changed by changing variable values. The variable names are listed below for figures and user interface controls:
    - Figure background color: BG_COLOR .
    - User Interface controls background color except push button: BG2_COLOR.
    - User Interface controls font color except push button: FONT_COLOR.
    - Push button background color: BUTTON_COLOR.
    - Push button font color: BUTTON_FONT_COLOR.
    - Fonts for user interface controls:
        - Font Name: UI_FONTNAME = 'times'
        - Font Units: UI_FONTUNITS = 'points'
        - Font Size: UI_FS = 12
- Display Defaults: Defaults in display GUI are plotted first. These can be changed by accessing variables like:
    - SORT_COMPONENTS: Options available are 'No' to 'Yes'.

- o IMAGE_VALUES: Options available are 'Positive', 'Positive and Negative', 'Absolute Value' and 'Negative'.
  - o CONVERT_Z: Options are 'Yes' and 'No'.
  - o THRESHOLD_VALUE : Threshold value to use voxels above or equal to the threshold
  - o IMAGES_PER_FIGURE: Options are '1', '4', '9', '16', '25'.
  - o ANATOMICAL_PLANE: 'axial', 'sagital' and 'coronal'.
- Detrend Number: Detrend defaults for ICA time courses can be changed by changing the variable DETRENDNUMBER value. Options are 0, 1, 2 and 3.
- Smoothing parameters: When SMOOTHPARA variable is changed to 'Yes' the time courses are smoothed by the value indicated in the variable SMOOTHINGVALUE.
- Flag for acknowledging creators: FLAG_ACKNOWLEDGE_CREATORS variable is used to display acknowledgement for creators. You can turn off the dialog box by changing variable FLAG_ACKNOWLEDGE_CREATORS to 'off'.
- Flag for displaying ICA Options Figure: ICAOPTIONS_WINDOW_DISPLAY variable is used to display ICA options window. You can turn off the figure window by changing variable ICAOPTIONS_WINDOW_DISPLAY to 'off'.
- Flag for storing directories in file selection window: When STORE_DIRECTORY_INFORMATION variable is changed to 'Yes', directories specified in cell array DIRS_TO_BE_STORED are stored in the file selection window.
- Variable for compressing image files in zip format: When ZIP_IMAGE_FILES is set to 'Yes', the component images will be compressed to a zip file based on their viewing set.
- Variable for entering regressors: METHOD_ENTERING_REGRESSORS variable has three options like 'AUTOMATIC', 'GUI' and 'BATCH' for temporal sorting. Each option is explained below:
  - o 'AUTOMATIC' – Regressors in SPM.mat file will be used directly. For 'Different regressors over sessions' or 'Different regressors for subjects and sessions' session related regressors will be used.
  - o 'GUI' – Figure window will open to select regressors.
  - o 'BATCH' – Regressors can be entered using a text file by specifying the file name for variable TXTFILE_REGRESSORS. This is the best way to enter regressors if you have many data-sets and if you have selected 'Different regressors over subjects and sessions'.
- FLIP_ANALYZE_IMAGES: Flip parameter for the analyze images. Default value is 0.
- NUM_RUNS_GICA: Number of times ICA will be run. Default is 1.
- DEFAULT_MASK_OPTION: Mask is calculated by doing a Boolean AND of voxels that surpass or equal the mean. By default first file for each subject is used. You can use all files by changing variable value to 'all_files'.
- OPEN_DISPLAY_GUI: Option is provided to open the display GUI automatically after the analysis. You can turn off the option by changing variable value to 0.
- CENTER_IMAGES: A value of 1 means subject spatial maps will be centered based on the peak of the distribution.
- PREPROC_DEFAULT: Data pre-processing default.
  - o 1 - Remove mean per time point
  - o 2 - Remove mean per voxel

- o 3 - Intensity normalization
- o 4 - Variance normalization
- PCA_DEFAULT - PCA default.
  - o 1 - Standard
  - o 2 - Expectation Maximization
- BACKRECON_DEFAULT: Back reconstruction default.
  - o 1 - Regular
  - o 2 - Spatial-temporal Regression
  - o 3 - GICA3
  - o 4 - GICA
- SCALE_DEFAULT - Scaling components default.
  - o 0 - No scaling
  - o 1 - Percent signal change
  - o 2 - Z-scores
  - o 3 – Scaling in timecourses
  - o 4 – Scaling in maps and timecourses

D. Options Window

When you click "Timecourse Options" sub menu in "Options" Menu (Figure 24), options window (Figure 33) appears with the defaults used from the 'icatb_defaults.m'. There are three categories in the left list box like Model Time course, ICA Time course and Event Average. The explanation of each option in the list box is explained below:

Model Time course:
1) Normalize Model Timecourse: Model time course is normalized and the ICA time course is used as a reference.
2) Linear detrend Model Time course: Linear trend is removed in model time course.

ICA Time course:
1) Detrend Number: ICA time course is detrended with the number specified in popup control.
2) Flip ICA Time course: ICA time course is flipped.
3) Smoothing Parameter: ICA time course is smoothed if the option is set to 'Yes'.
4) Smoothing Value: ICA time course is smoothed using the value specified in edit control.

Event Average:
1) Window size in seconds: Window size to display the event average of ICA time course.
2) Interpolation factor: Factor to interpolate the ICA time course.

The function of each button in the figure window is shown below:

OK

> The values in the controls are used and the time courses are plotted in the expanded view of time course (Figure 23).
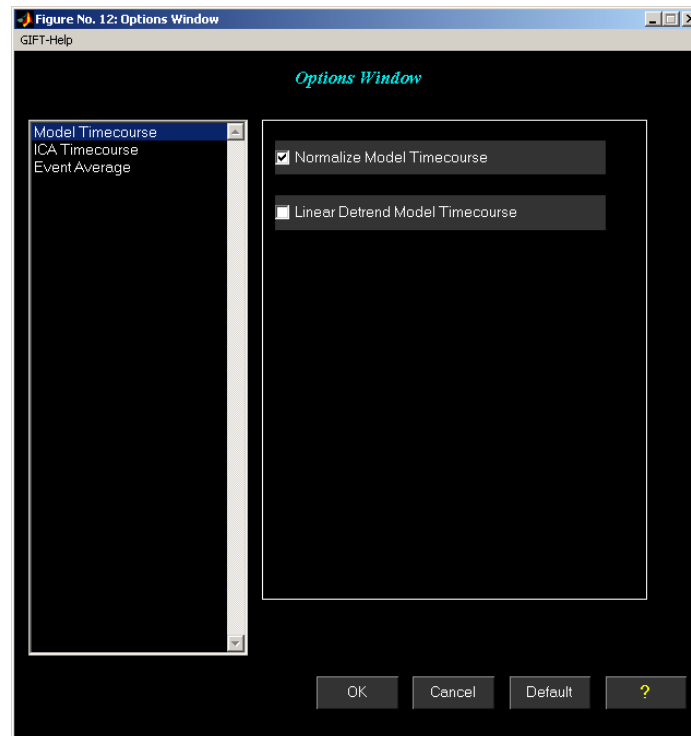
Cancel

> Figure window will be closed.

Default

> Defaults will be used from 'icatb_defaults.m' file.

Figure 33: Timecourse Options Window

E. Event Related Average

Events are calculated based on the onsets of the selected reference function or model time course. The parameters needed for event average are window size and interpolation factor (specified in options window). The procedure for calculating the event average is given below:

1) The interpolation factor is multiplied with TR (Appendix B). The ICA time course is interpolated by the scaled interpolation factor.
2) Onsets of the selected model time course will be used. If the units are in seconds, the selected onsets are divided by TR.
3) Window size is multiplied by the original interpolation factor. Event average is initialized to zero vector of length equal to the scaled window size.
4) Loop is done over the length of the selected onsets.
5) Starting index corresponds to current selected onset value multiplied by scaled interpolation factor. All the indices from starting index to length of the scaled

window size are used. Time course values of the corresponding indices are added to the event average.

6) Number of onset where ending index exceeds the size of the time course is determined.
7) End of loop over the selected onsets.
8) Event average is divided by number of onset where index exceeds the size of the time course.

F. Interactive Figure Window

Interactive figure window is used to select a directory, file or files for performing the group ICA. Figure 34 shows the file selection window with the ability to select more than one file. The explanation for each user interface control in the figure is explained below:

1) Directory text box shows the current directory or you can edit the text box. When enter key is pressed the sub-folders are displayed on the left list box and also the files or folders are displayed on the right list box.
2) Directory History shows the history of the directories recently visited in the MATLAB along with the path for the GIFT.
3) *Back* button returns to the previous folder in the same drive.
4) *Filter* button resets the filter text box to *.
5) Filter text box filters files based on the text entered. If you want to list files with different patterns, separate them with semi-colon as delimiter.
6) File numbers edit box adjacent to filter text box is used to enter the file numbers for a 4D Nifti file.
7) Drives show the drives available for the Windows operating system except the floppy drive. For other operating systems the root directory is displayed.
8) Sub-folders list box shows sub-folders in the left list box.
9) Files or sub-folders list box plotted on the right shows files with prefixes in the current directory. In case of directory selection, sub-folders in the current directory will be displayed.
10) *Ed* button is used to edit the files.
11) *Reset* button refreshes the drives in the Windows operating system and de-selects all the files previously selected.
12) *Expand* button lists files in expanded mode.
13) *Select-All* button selects all the files in the current working directory depending on the filter specified.
14) *OK* button closes the figure window when the entries on the right list box are selected.

Note: For single file selection or directory selection, the list box mode is set to inactive after the first selection. In order to select a different file or a directory *Reset* button should be used.

Figure 34: Interactive Figure Window for selecting Files or Directory
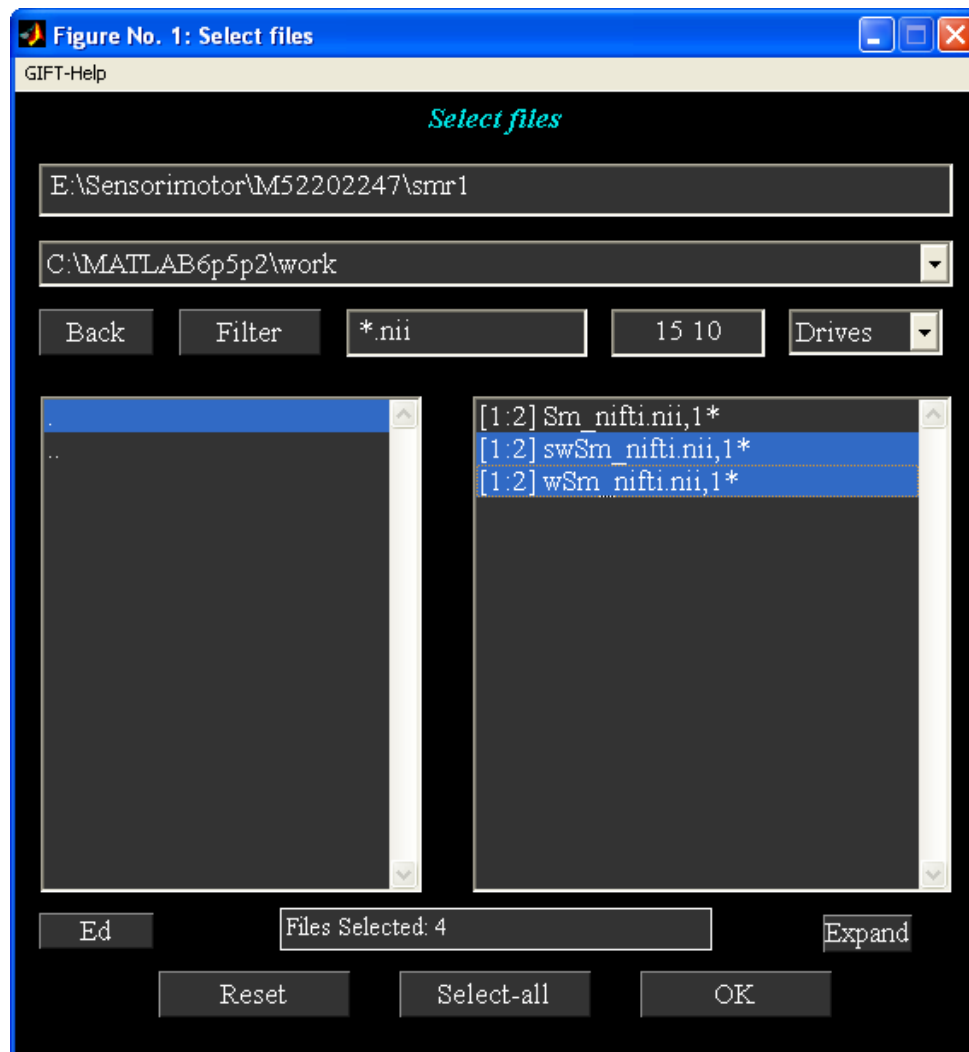
G. Statistical Testing Of Images and Time Courses

Two Sample t-test

Two sample t-test can be used to compare a component between subjects or sessions. For example for a particular component session 1 images can be treated as group 1 and session 2 images as group 2. You can use these images in SPM to do two sample t-test.

Regression Parameters

After performing temporal sorting, the fit regression parameters are saved in a file with suffix 'regression.txt'. This file can be quite useful in performing statistical tests to evaluate the task-relatedness of the components or to perform tests between components or groups. The text file contains a number for each component, regressor, subject and

session (Table 1). The numbers represent the 'fit parameter' from the regression. In order to use these numbers it is important to scale the ICA data. For example, if 10 subjects were analyzed with ICA and two regressors were used to sort, then one can test the degree to which the average amplitude of group 1 was greater than the average amplitude of group 2 by computing a two-sample t-test between the 10 parameters for group 1 and the 10 parameters for group 2. A separate test can be done for each component, and the components which show a significant difference can be determined.

Table 1: Table shows two sorted components parameters. Regression values for each component are shown followed by the beta weight of each condition with the ICA time course.

Component Numbers	7	3
Regression Values	0.74876543	0.67747138
Subject 1 Sn(1) right*bf(1)	2.3585817	0.55115175
Subject 1 Sn(1) left*bf(1)	0.097659759	2.158409
Subject 2 Sn(1) right*bf(1)	2.2468961	0.69208646
Subject 2 Sn(1) left*bf(1)	0.40444896	1.3045916
Subject 3 Sn(1) right*bf(1)	1.4413982	0.46694756
Subject 3 Sn(1) left*bf(1)	-0.045741345	1.6667349

Note: Statistics on images and time courses can be done using the GIFT toolbox. Please see manual for more information.