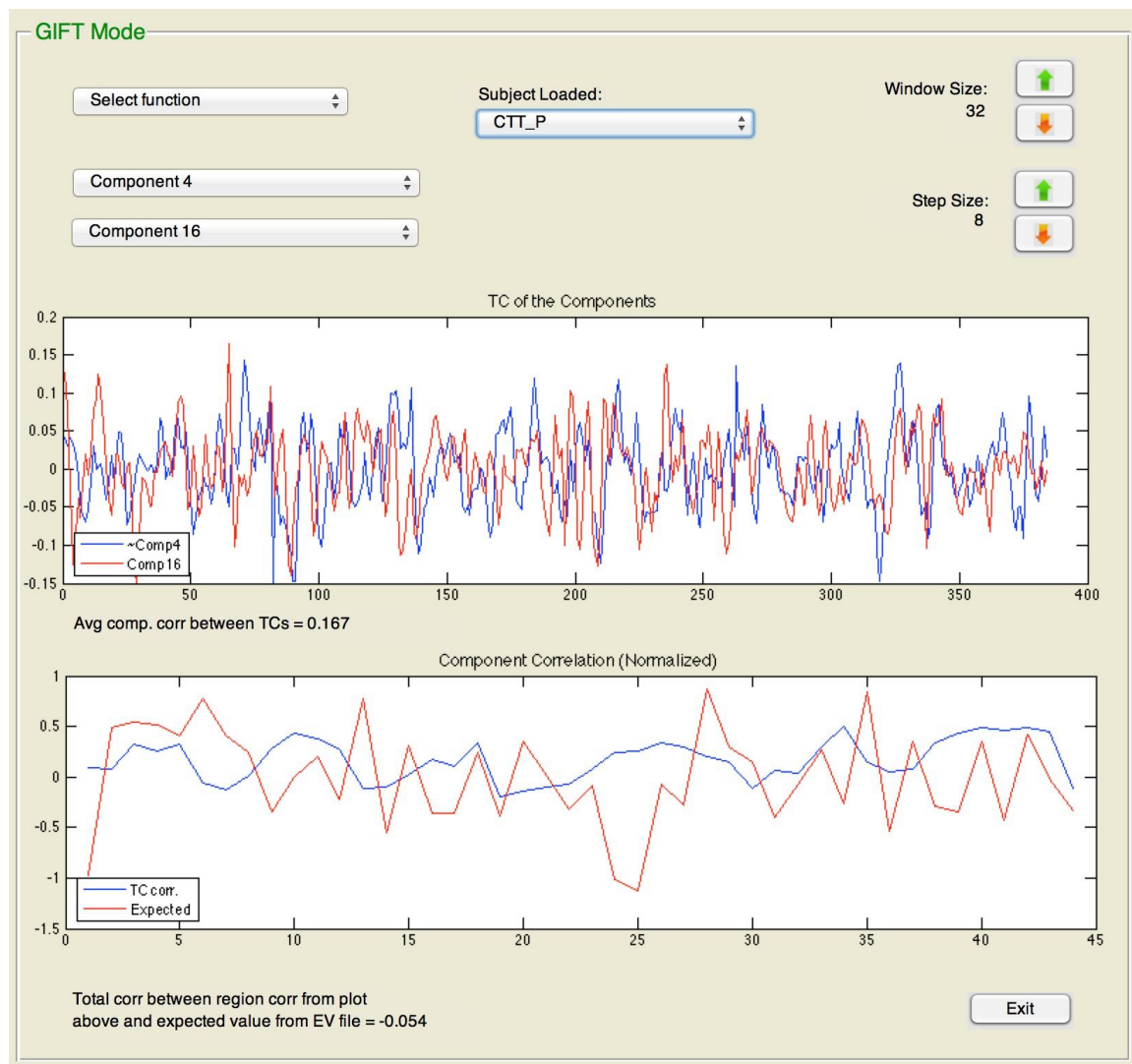# DynaConn Users Guide

Dynamic Function Connectivity Graphical User Interface

Table Of Contents

Chapter 1 – Introduction

1.1 – Introduction

DynaConn is a graphical toolkit written in MATLAB for analysis of fMRI data using dynamic functional connectivity (DFC) analysis and dynamic functional network connectivity (DFNC) analysis. It follows the methods prescribed in Sakoglu et al., (2010) entitled A method for evaluating dynamic functional network connectivity and task---modulation: application to schizophrenia. DFC identifies correlation between activities in various brain regions by correlating two time courses (TCs) in a sliding time window as shown in Figure 1.

coses   (TCs)in   a   sliding   time   wFigdow 1.
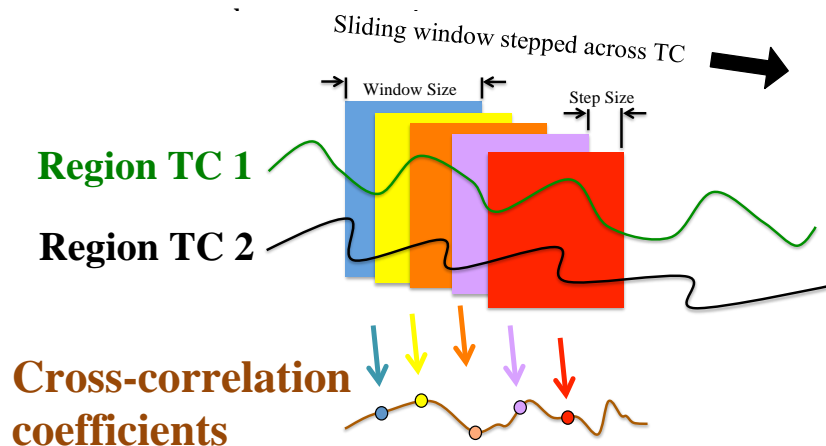
Figure 1. DFC using a sliding time window.

DFNC is a specific type of DFC analysis where DFC is applied to brain networks such as those obtained by spatial independent component analysis (ICA). In particular, this tool performs DFNC analysis on results from group ICA performed by GIFT (from MiaLabs: http://mialab.mrn.org/software/gift).

DynaConn features include:
- Load 4D NIfTI fMRI Data
- Load post ICA NIfTI from GIFT
- Co---registration between ICs and anatomical brain regions via brain atlas.

- Visualization of ICs in axial slice window
- Visualization of individual and aggregate DFC/DFNC results.
- Export data in various DFC formats to MATLAB matrix. DynaConn is a collection of GUI blocks that connect to each other. The Main GUI is the entry point to DyanConn. It also is the display for individual DFC results and provides data export functionality. Setup is the tool used to specify which subject, group designations, EV files, brain atlases, and brain masks to use in the analysis. The component / region viewer is a tool used to see the 3D IC maps or 3D region maps. The viewer also lists which anatomical brain regions are associated with the ICs. The DFC matrix display is a visual representation of a matrix composed of DFC results from all subjects and all the IC or region combinations.
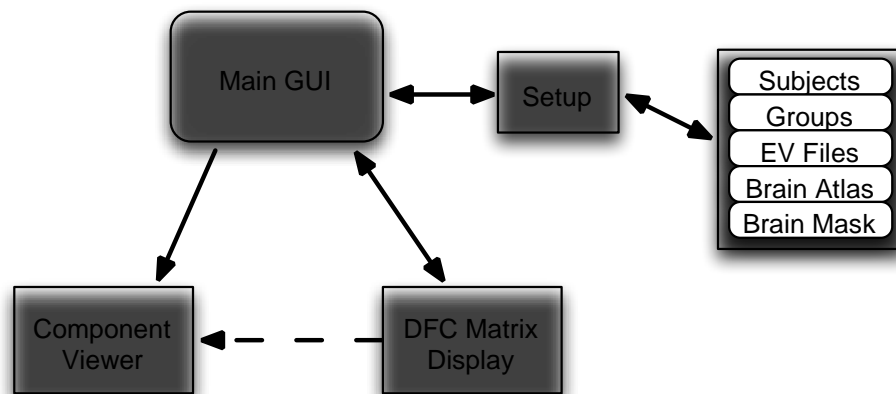
Figure 2. DynaConn topology overview.

1.2 – Running DynaConn

DynaConn is stored on a GitHub (github.org) repository, which is a git repository. Therefore you need to install git (http://git-scm.com/downloads) first. In order to copy the source code to your local machine is to clone the repository as described in https://www.atlassian.com/git/tutorial/git-basics#!init.

The first step to cloning the repository is to create a git directory on your local machine. Run the init command at the directory that you wish to contain the repo.

$RepoDir> git initi

Once the git repo is initialized, clone the DynaConn repository to your local directory using the clone command.

$RepoDir> git clone https://github.com/dynaconn/Dynaconnv2.git

The clone command will create a folder called DynaConn in your repo directory.

In MATLAB change to this new directory and run the command to start DynaConn:

>> cd RepoDir/dynaconn >> dynaconn

The main GUI, shown in Figure 3, should become visible.

The style of the GUI may change slightly based on the operating system and version of MATLAB being used. The only functions that can be run at this point is to either change the mode or to configure the setup.
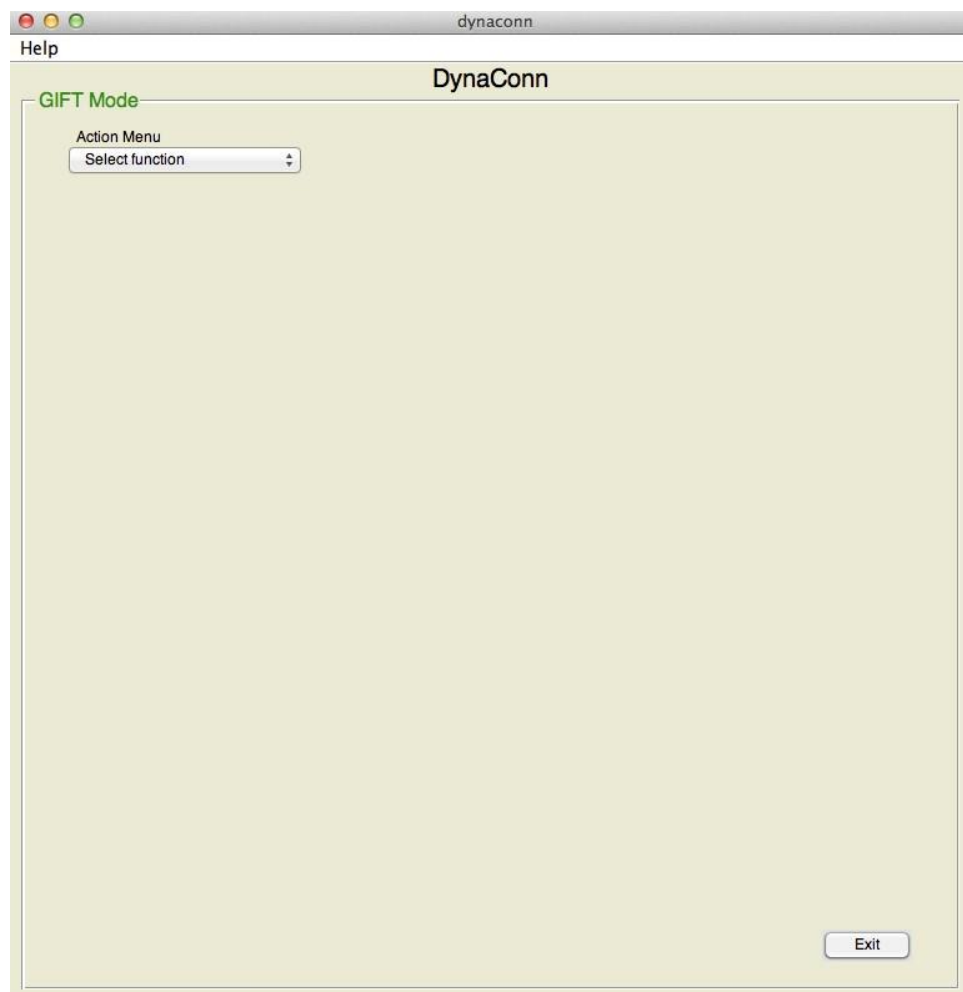
Figure 3 --- Main GUI at startup.

Chapter 2 - Configuring DFC GUI

2.1 – Configure setup options

Before any analysis functions are accessible, the setup must be configured. This is accomplished by choosing the Configure setup option in the action drop down menu as shown in Figure 4.   The configure setup option will bring up the configure setup window which is shown in Figure 5.

A directory selection window will pop-up asking the user to select the directory in which to store any results and previous saved states. If the directory that is selected has a previously saved state, the user will be asked if they wish to use the previous setup.
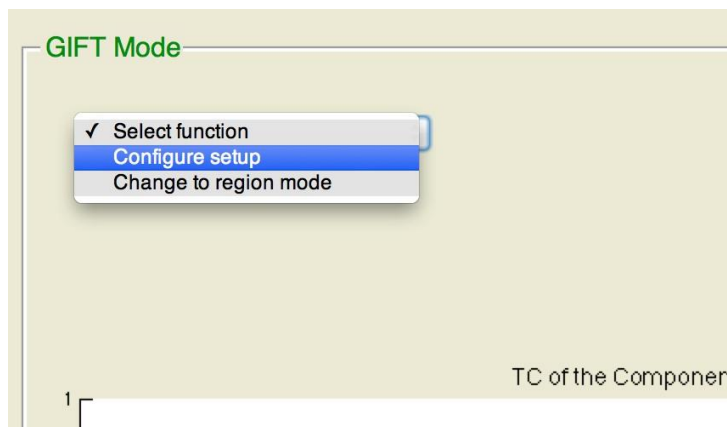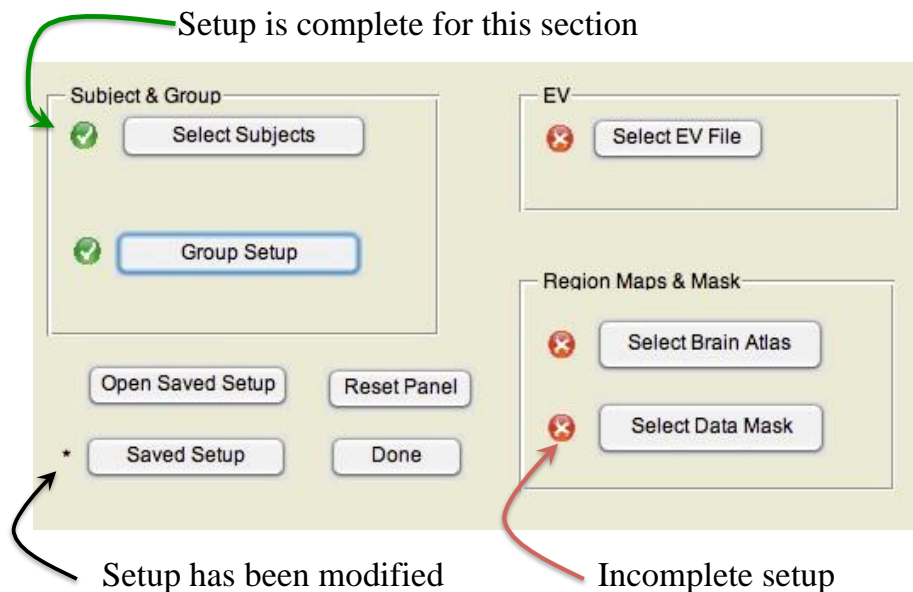

Figure 4. Selecting configure setup.

Figure 5. Setup window.

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The setup configuration window has five sections of configuration. Once a section is completed the red X will change to a green check mark showing that the section was completed successfully. If a previous setup is loaded, then the sections that were previously completed will show a green check mark. A small asterisk will appear next to the saved setup button if any of the setup has been modified. This is to remind the user that they need to save the modified setup.

- Select Subject – Enter all of the subjects to be analyzed. This section is required to do any analysis and for any analysis function to become available through the action menu in the main GUI.

- Group Setup – This section is where you choose which group (ie. class/category) each subject belongs to. This section is not mandatory but neither the Component Region Matrix function, nor any of the Data Output functions will be available if there is not group setup.

- Select EV File – EV File selection links an EV (expected value/task modulation) file with each subject. This section is not mandatory, but the Output EV Modulated data function will not be available. In the bottom component correlation window of the main GUI, the TC or group average will be shown, but not the EV/Task modulation average, if the Select EV File section is not completed.

- Select Brain Atlas – This section allows the introduction of a brain atlas or brain region map in order to give an anatomical label to which parts of the brain are active. This section is mandatory, however if no brain atlas is given, DFC GUI will load the default AAL (Anatomical Automatic Labeling) brain atlas.

- Select Data Mask – The section allows the selection of a binary 3d mask to be applied to the subject files. This section is mandatory, but if no data mask is entered a standard MNI space map will be loaded.

- Saved Setup – The function allows you to save the current setup to a directory.

- Open Saved Setup – This function allows you to open a previously saved setup. All of the setup fields that were previously saved will changed to green check marks.

If you wish to clear the previous setup state, the Reset Panel button will change the state of each setup section to be incomplete.

2.2 - SELECT SUBJECTS

The select subject menu is where you enter all of the subjects to be analyzed. This section is required for any analysis function to become available through the action menu in the main GUI.

The select subject form will differ depending on whether you are in GIFT Mode or Region Mode.

In GIFT mode, as shown in Figure 6, the only option is to select the GIFT output directory which contains all of the results from a group ICA run. The format must be GIFT 3.0 or later. Once the directory contents have been read, click the Done button to save the subjects and return to the setup window.
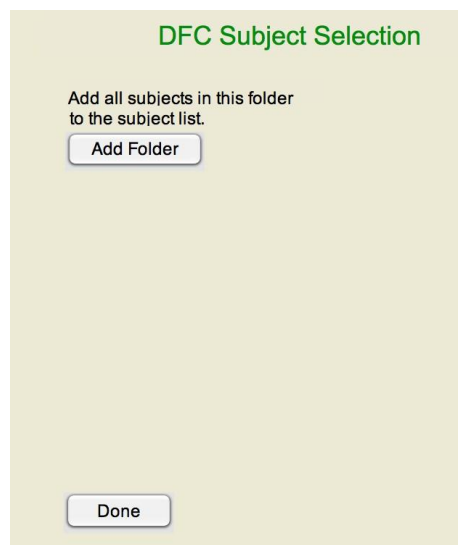
Figure 6. Select Subject in GIFT mode.

In Region Mode, the form will look like Figure 7. In this mode there are several ways to add new subjects. In general, the button aid in adding the path to each subject in the text window in the right-hand side. The subjects in the window will be loaded once the Done button is used.

The format for the subject list is the full path to each subject, per line. For example, here, subject 2 and 5 will be loaded.

       C:\filepath\subject2.nii
   C:\filepath\subject5.nii

Below is a list of the functions available in the *Select Subject* form in Region Mode:

- Add Folder – The add folder button will prompt you to select a directory that contains all of the NIfTI (.nii) subject files that you wish to add to the list of subjects for analysis. The immediate directory and one level down of

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subdirectories will be searched. Once the folder has been read, the path to each NIfTI file will be added to the text window.

- Add Subject - The add subject button will prompt you to select a single subject NIfTI file. The path to the file will be added to the text window.

- Load – This function allows you to select a text file which has the path to all the subject NIfTI files you wish to load. Once the subject list has been read the paths will be placed in the text window.

- Save – The save function will save all the text from the text window to a text file.

- Done – Once all the subjects that you wish to load are in the text window, click done to have the subjects scanned and return to the setup window.

Note that you can manually enter the path to any subjects you wish to load into the text window before clicking the Done button.
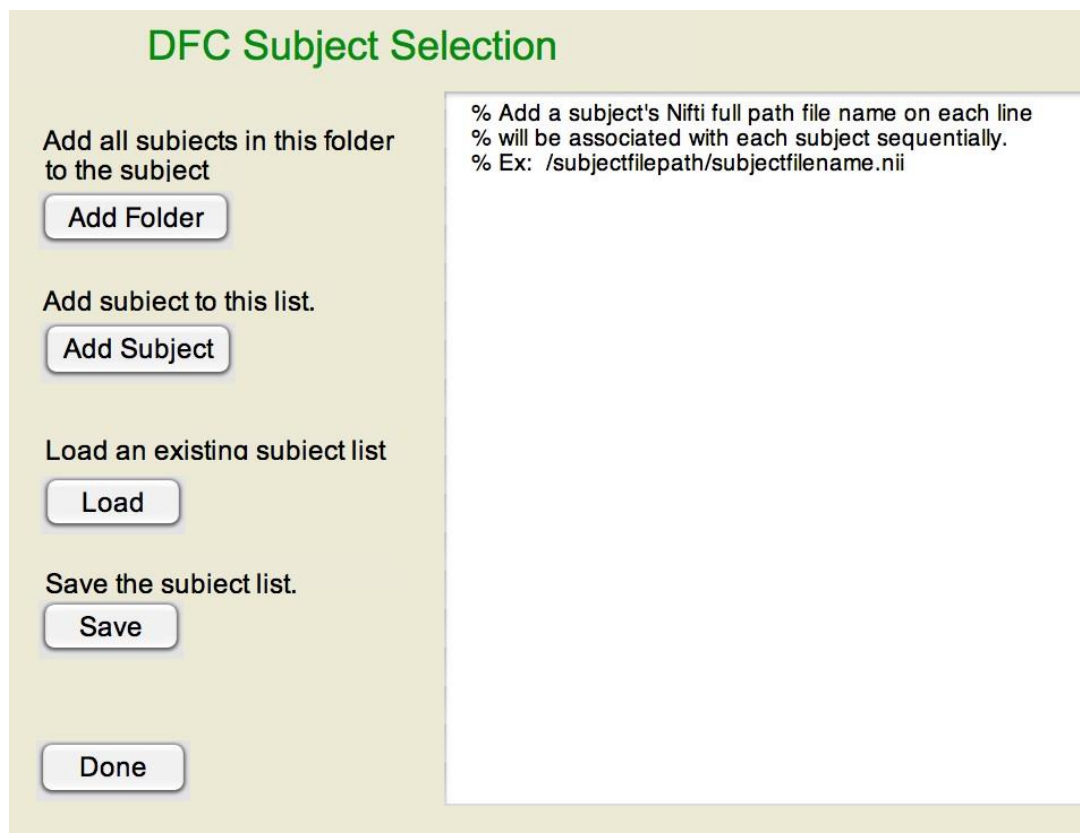
Figure 7. Select Subject in Region mode

2.3 - GROUP SETUP

The Group setup form determines which group (i.e. class/category) each subject belongs to. The group information is used in data output functions and the component region matrix function.

The format for the group file is a subject on each line followed by a number reference to the associated group. For example, subject2 below will belong to group 1 and subject5 will belong to group 2.

> C:\filepath\subject2.nii 1
> C:\filepath\subject5.nii 2

Figure 8. Group setup window

Below is a list of the functions available in the *Group Configuration* form:

- Build – This function creates a list of all subjects previously loaded and adds a default group number after the subject path. You can then change the group number to the correct group number.

- Load – Load prompts the user to select a text file that has a list of subjects and group numbers. The text file contents will be loaded into the text window.

- Save – This function saves the text in the text window to a text file.

- Done – Once all subjects with a group number have been entered into the text window. Then clicking the Done button will store the group info and close the group setup window.

Note that you can manually enter the path to any subjects along with the group number into the text window before clicking the Done button.

2.3 – SELECT EV FILE

An EV file or expected value file is a text file that has a minimum of one column and a maximum of three columns. The first column is the time that a task occurs. The time can be either time in milliseconds or scan number. The optional second column is the scan duration. The optional third column is a binary successful test identifier. Only the first column of the EV file is used by Dynaconn.

The Select EV File form, shown in Figure 9, is used to input a list of EV or expected value files for each subject. The format is a full path to an EV file per line. Once completed and the Done button is used, each EV file will be associated with each previously loaded subject in sequential order. There must be the same amount of EV file listings as there are subjects unless the one EV file for all subjects is used.
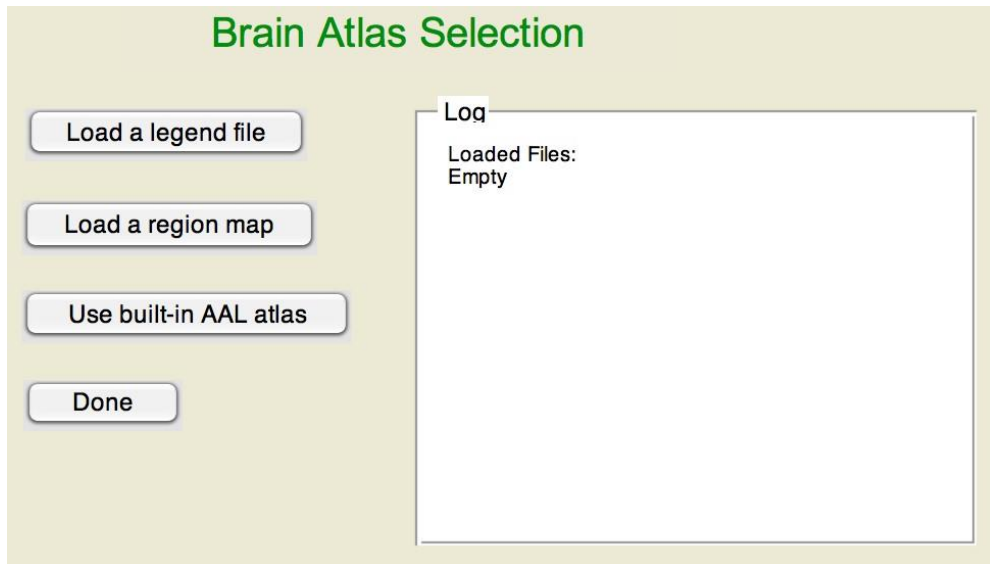
Below is a list of the options for the EV map setup:

- EV file units are seconds – Use this option is the 1st column of the EV file lists the event times in milliseconds.

- EV file units are scan numbers - Use this option if the first column of the EV file lists the event times in scan number.

- TR – Repeat time in milliseconds. DFC GUI uses TR to convert scan number into seconds and vice versa.

- TA – Acquisition time in milliseconds. TA is currently not used, but the option is for future use.

- Use one EV file for all subjects – This option associates all subjects with the one EV file listed in the EV file list text window as opposed to listing a different file for each subject. There must be only one EV file listed in the EV file list text window if this option is selected or there must be as many EV files listed as there are subjects if the option is not selected.

- Add – Prompts the user to select an EV file, which will then be added to the EV file list text window.

- Load – Prompts the user to select a previously populated text EV file list. The EV file list will be loaded into the EV file list text window.

- Save – Saves the text in the EV file list text window into a text file for later retrieval.

- View subject list – This function retrieves a list of the currently loaded subjects so that the EV files can be matched against.

- Done – Once all the desired EV files are loaded, clicking the Done button will parse and load the EV files from the EV file text window. The number of EV

files will also be checked to match the number of subjects unless the "Use one EV file for all subjects" option is selected.

2.4 - SELECT BRAIN ATLAS

The Brain Atlas Selection form is used for including brain atlas / region maps with associated brain region legend. The format of the brain atlas map is either 3D NIfTI in which the regions do not overlap (AAL atlas for example) or 4D NIfTI where there is a 3D map for each region (HarvardOxford probability map for example). The associated brain region legend, which names each region must be in XML format. DFC GUI uses 2mm space; however, if the map being imported is not 2mm it will automatically be rescaled to 2mm.

Figure 10. Brain Atlas Selection Form

The Brain Atlas selection form shown in Figure 10 has 2 functions to load external brain atlases, or it can load a default atlas:

- Load a legend file – This function prompts the user to locate a XML legend file. Once loaded the text log will note how many regions (levels) were found. If prior to using this function, a region map was loaded, these region labels will be applied to the region map levels.

- Load a region map – This function prompts the user to locate a region map NIfTI file. Once loaded the text log will note how many regions (levels) were found. If

prior to using this function, a legend file was loaded, then the prior loaded legends will be applied to this region map.

- Use built-in AAL atlas – Loads the AAL (Anatomical Automatic Labeling) atlas map and labels which come with DFC GUI.

- Done – Once all region maps and labels are loaded click the Done button to store use them in DFC GUI.

Note that more than one set of region labels and map can be used. For instance, the user could load 20 label HarvardOxford cortical file followed by a 20 region HarvardOxford cortical probability map, then load a 30 label HarvardOxford sub-cortical file followed by a 30 region Harvard Oxford sub-cortical probability map. DFC GUI would then use 50 regions in its analysis.

2.4 - SELECT DATA MASK

The Select Data Mask function is a prompt to either select a data mask or used the default 2mm MNI mask as shown in Figure 11.
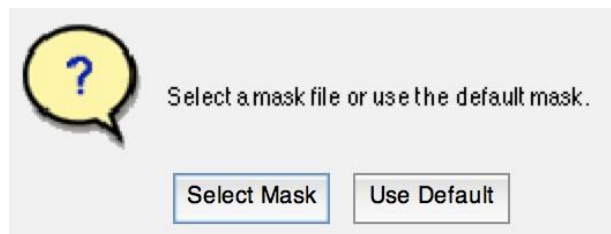

Figure 11. Select data mask prompt

- Select Mask – This function prompts the user to select a NIfTI data mask. The mask must be a 3D binary MNI mask. If the selected mask is not 2mm it will automatically be rescaled to 2mm.

- Use Default – This function loads a standard 2mm MNI mask.

## Chapter 3 – Using the Main GUI

3.1 – Main GUI after setup

After the setup has been configure the upper part of the Main GUI should look similar to Figure 12, Figure 13, or Figure 14, depending if the GUI is in GIFT mode, Region mode, or Group Mode respectively. The main difference between the GIFT and region mode is that in GIFT mode, components are selected instead of regions. The difference between GIFT mode and group mode, is that in group mode, the average of all the groups is displayed instead of individual subject results.
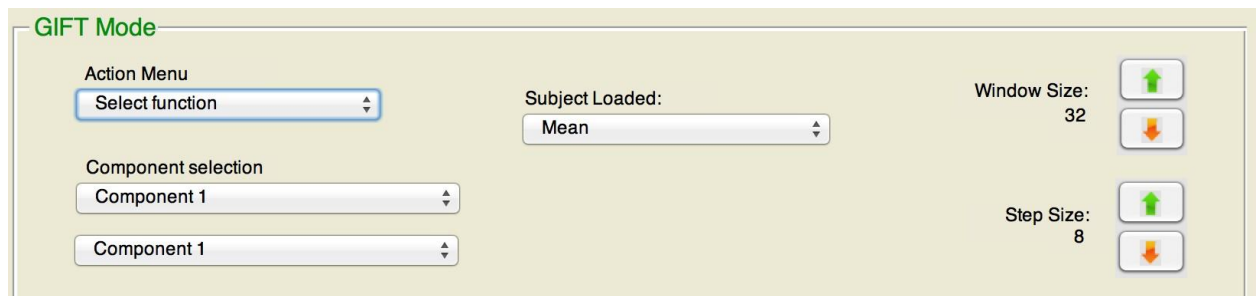
**Figure 12. Menu section of Main GUI in GIFT Mode.**
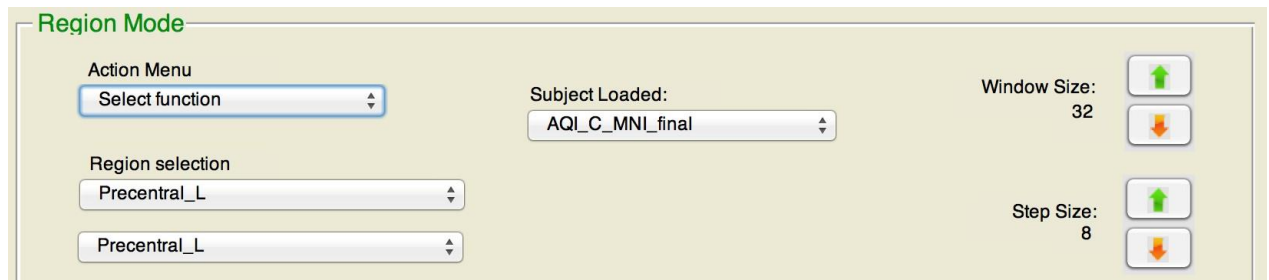
Figure 13. Menu section of Main GUI in Region Mode.
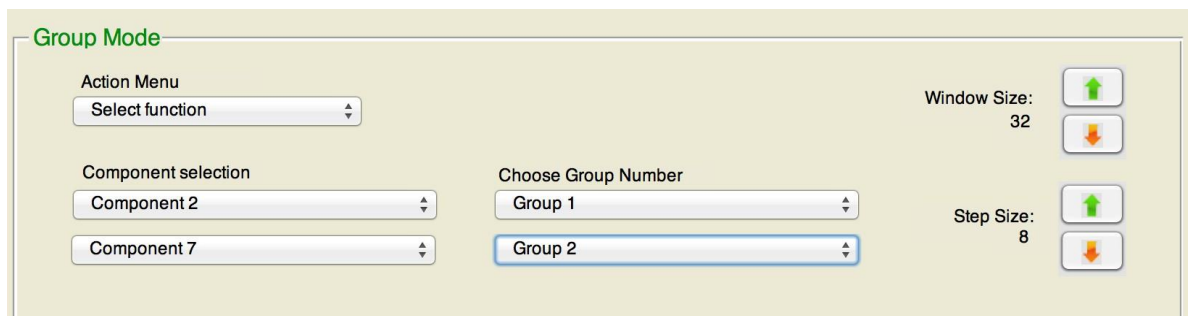
Figure 14. Menu selection of Main GUI in Group Mode.

Below is a brief description of what the different function of the menu section are used for. A more in-depth description is in the following sub chapters.

- Action Menu – This dropdown box has various functions to analyze the current data set such as showing a matrix of component combination correlation and showing the components or regions selected in a graphical window. There are also options for outputting the data and changing the mode to either GIFT or Region mode.

- Subject Loaded – This dropdown box allows you to change current subject to any of the other subjects that were previously loaded during setup.

- Component/Region selection – These dropdown boxes show which 2 components or regions are currently going to be shown in the graph section of the Main GUI (bottom of Figure 15). Note that initially nothing is shown in the graph area but once a component or region is selected, the graph will be updated.

- Window size – The window size is the size in data points of the sliding correlation window used to calculate dynamic functional connectivity (DFC). The result of changing the window size can be immediately seen in the bottom (Region Correlation) window.

- Step Size – The step size is the size in data points that the sliding correlation window move to the left after every correlation in order to calculate dynamic functional connectivity (DFNC). The result of changing the window step size can be immediately seen in the bottom (Region Correlation) window.

- Choose Group Number – In Group Mode, the user can select which two groups to display in the plot windows. The group average DFC results from the selected groups will be displayed in the top window. The null-hypothesis and p-values will be displayed in the lower plot window.
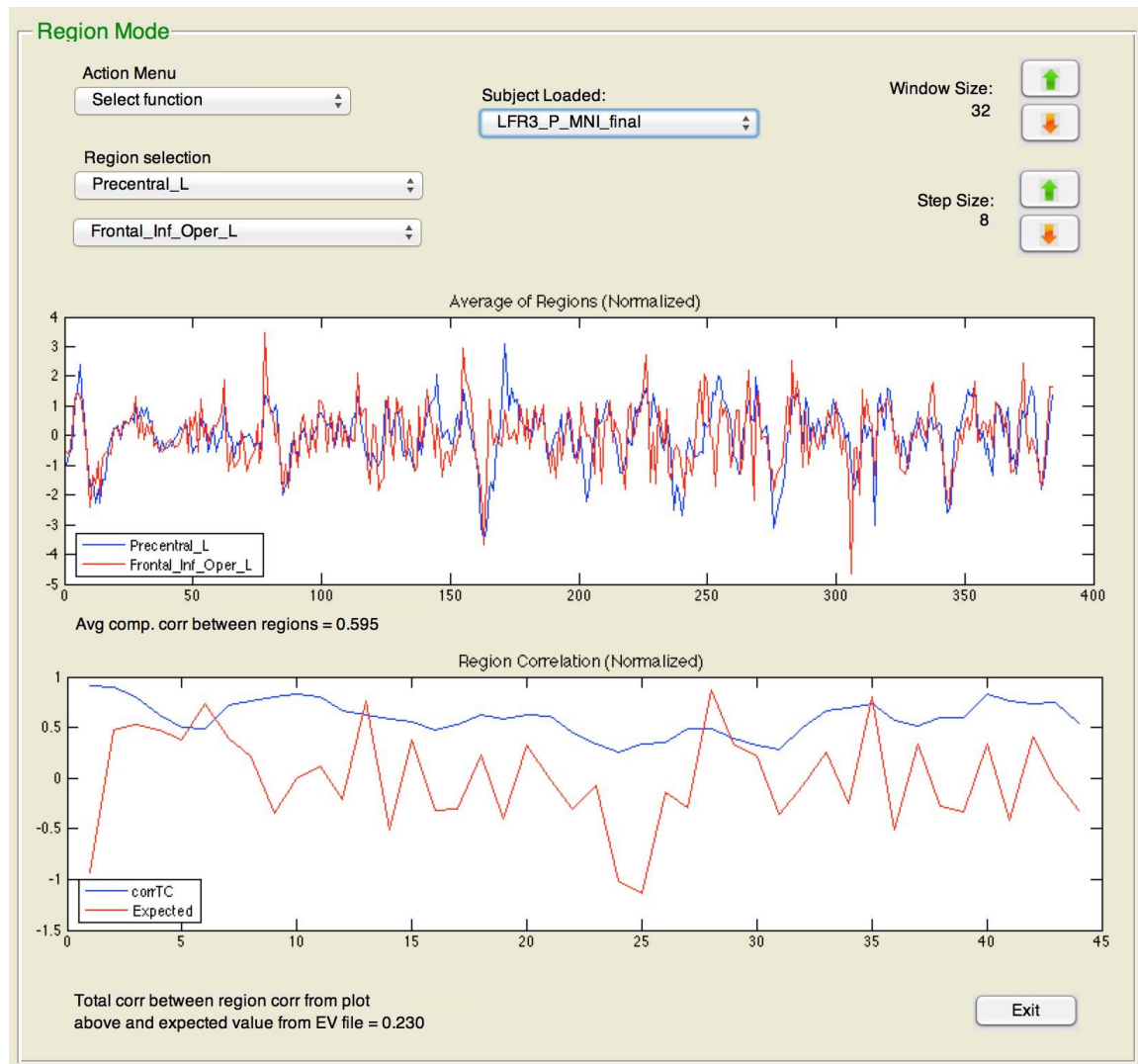
Figure 15. Main GUI in Region Mode

3.2 – Action Menu

There are 10 functions available from the action menu as shown in Figure 16.
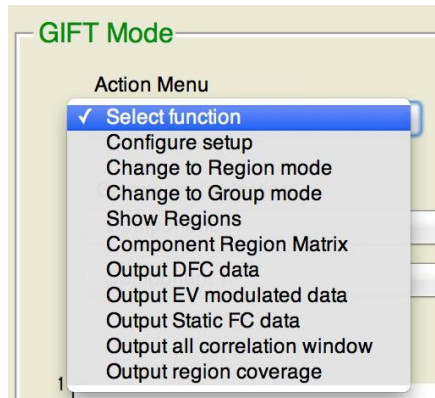
Figure 16. Action menu in the main GUI.

- Configure setup – This function calls the configure setup window that is discussed in chapter 2.

- Change to GIFT mode – This function changes the current operating mode to GIFT mode. If already in GIFT mode this option will not be visible.

- Change to region mode – This function changes the current operation mode to region mode. If already in region mode, this option will not be visible.

- Change to group mode – This function changes the current operation mode to group mode. If already in group mode, this option will not be visible.

- Show Regions/ Show components – This link brings up the region or component display window, which visually and numerically shows the components currently listed in the component/region selection part of the main GUI. The region/component display window is discussed in chapter 4.

- Component Region Matrix – This link brings up the Component Region Matrix GUI, which shows a matrix of all component or region combination correlations. The Component Region Matrix GUI is discussed in chapter 5.

- Output DFC data – This function builds a matrix of all subjects DFC or DFNC data. The data is saved as a .mat file. The format and construction of the data is shown in chapter 6.

- Output EV modulated data – This function builds a matrix of the DFC data correlated against the EV data to show if the DFC data is modulated by the EV data. The data is saved as a .mat file. The format and construction of the data is shown in chapter 6.

- Output static FC data – This function builds a matrix of the static functional connectivity for each subject. The data is saved as a .mat file. The format and construction of the data is shown in chapter 6.

- Output all correlation window – This function builds a matrix of all the points of the correlation between the 2 TCs from each component for each subject. The data is saved as a .mat file. The format and construction of the data is shown in chapter 6

- Output region coverage – This function outputs a text list showing the top five regions that are associated with all of the ICs that are loaded. The regions coverage's are determined by the currently loaded brain atlas.

3.6 – GIFT Mode

When the Main GUI is in GIFT mode, the top plot window will show the TC of the two components that are selected from the subject that is select. If the average correlation between the two components is higher with the first component inverted, then the first component TC will but multiplied by -1 and a "~" will appear in front of the component name in the plot legend.

In the bottom plot window is the cross-correlation between the two TCs displayed in blue. If an EV file is loaded, DynaConn will display the expected value along with the TC cross-correlation. Above the plot window is the average of the correlation. Below the plot window is the average correlation between the TC cross-correlation and the EVHRF waveform.

Since the polarity of the ICs are unknown we don't know what polarity to build each HRF waveform that goes into the EV-HRF plot.   Therefore we employ a method to improve the matching between the HRF and the TC correlation by testing whether adding a positive or negative HRF gives better correlation. We chose the higher correlation of the two as shown in Figure 17.
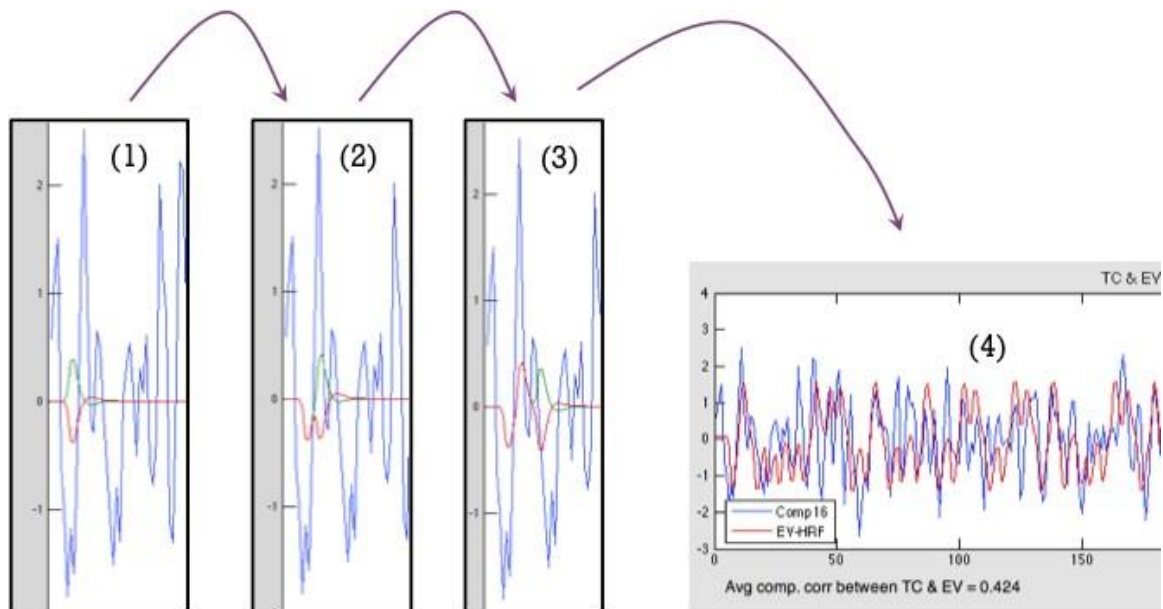
Figure 17. Construction of the EV---HRF waveform.

3.7 – Group Mode

When the Main GUI is in Group mode, as shown Figure 18, the top plot window will show the average DFNC results from the two groups that are selected. In other words, the DFC results are the average of the sliding time window analysis on the two TCs that are selected. How many groups are available in the Main GUI drop down box depends on how many groups were defined in the group setup.

In the bottom plot window is the p-values from a U-Test of the DFC results from the top window. The p-values are in blue. The red result in the bottom window is the nullhypothesis result of the p-values at 5%. When the value is 1, then the null-hypothesis is rejected for that section of the DFC results.
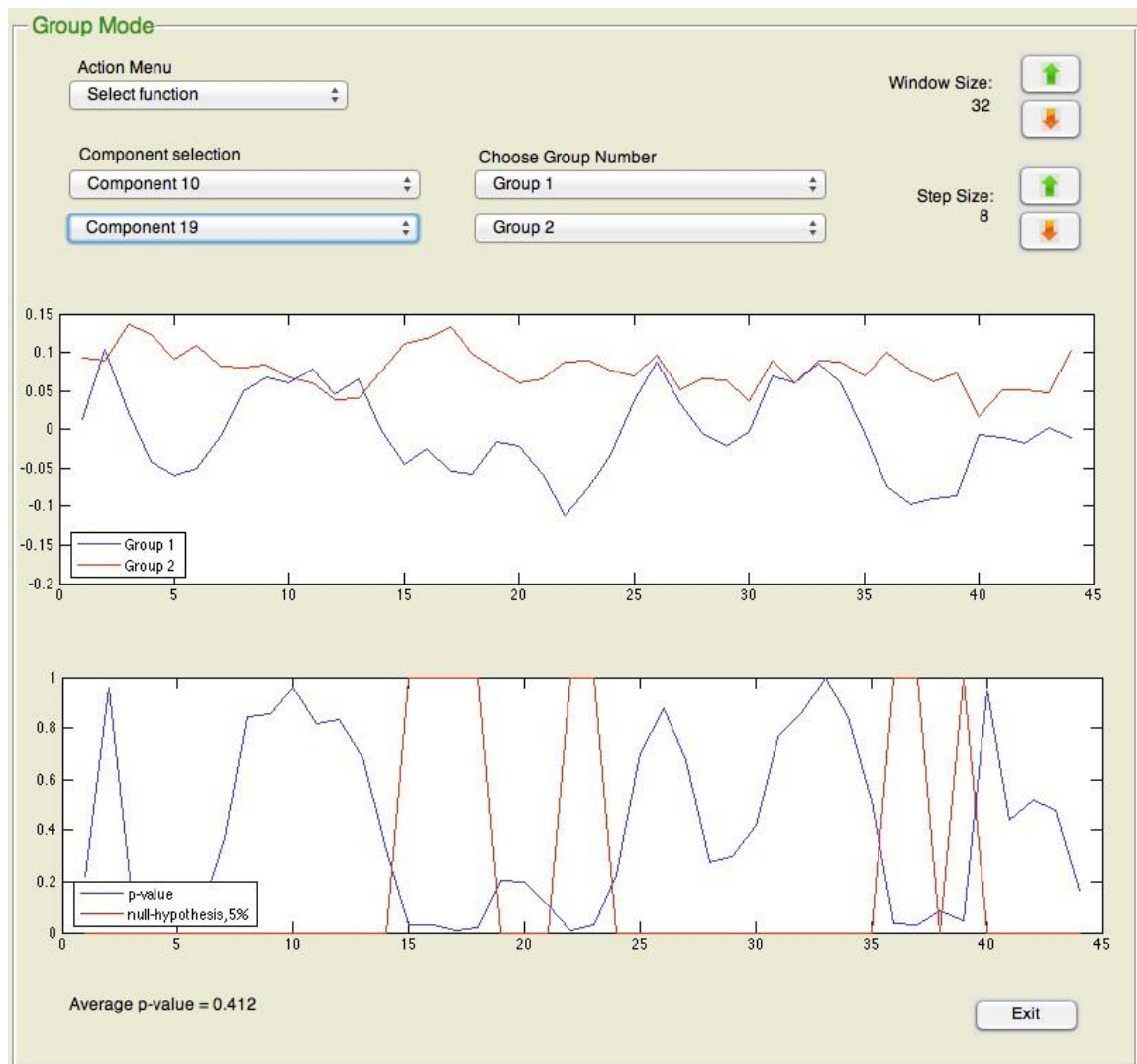

Figure 18. Main GUI in Group Mode.

Chapter 4 – Component Viewer GUI

4.1 – Component Display

The components that are currently selected in the Main window can be displayed in the component viewer by choosing *Show Regions* from the dropdown menu as shown in Figure 19.
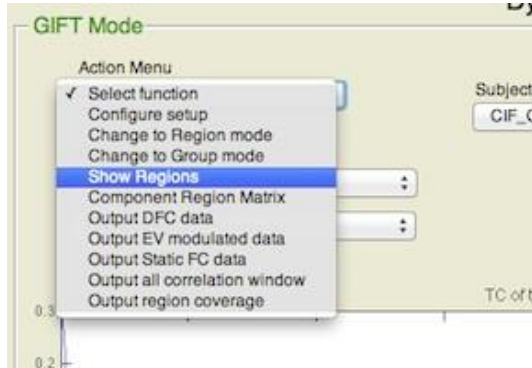

Figure 19. Selecting the component viewer.

At the top of the component display is a list of the anatomical regions that best overlap with the ICs that were selected.
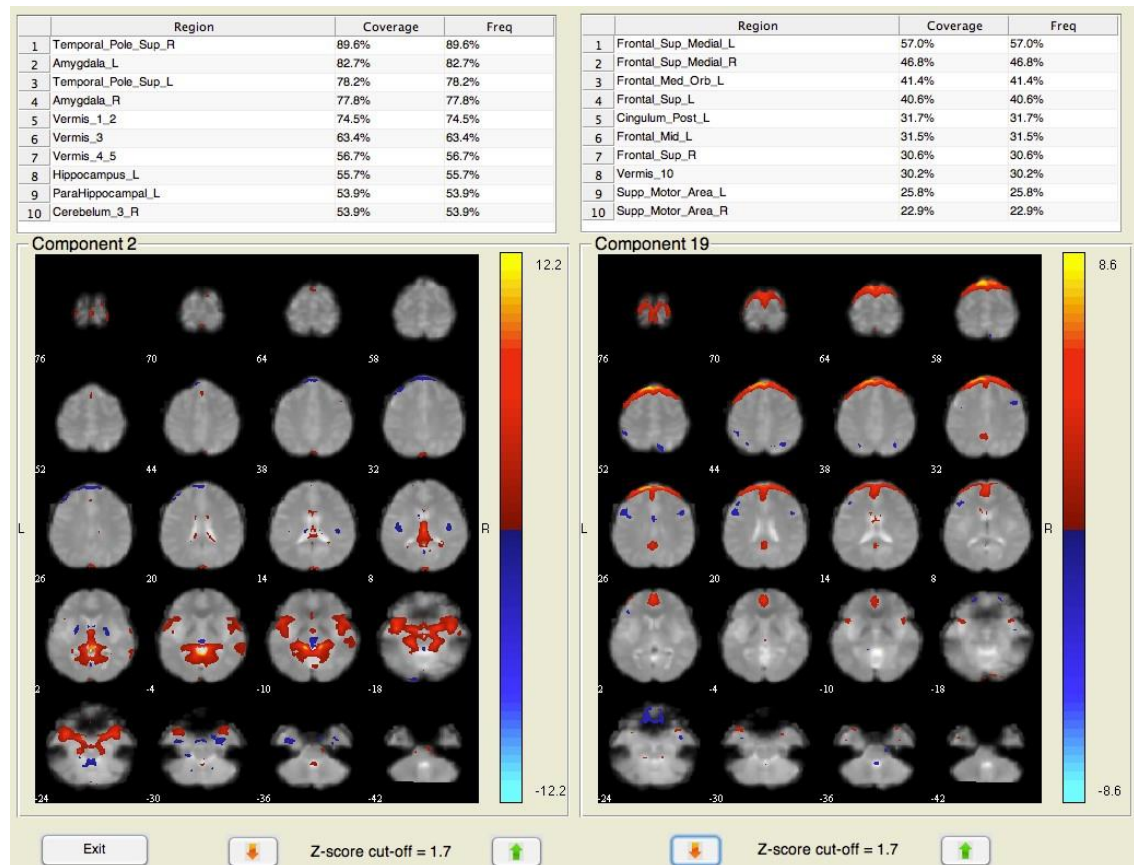
The Component Viewer, shown in **Figure 20**, provides a graphical representation

of the IC components that have been currently selected in the Main GUI.   The

view of the ICs is an axial view of both the positive and negative distribution tails

of ICA results. The results are converted to z-score before they are displayed.

The Component Viewer features a z-score cut-off function. The z-score cut-off

will hide the data that is from the middle of the IC data distribution. The higher

the z-score the more selective the filtering function becomes.

Figure 21 illustrates how the z---score cut---off function filters the middle distribution data. The benefit of using z---score is that the user can set a z---score cut---off and know the percentage of the population that is being hidden. For instance the default z--score cut---off is set to 1.7, which means 95% of population is being hidden. Furthermore, the 2.5% above the cut---off is displayed as red to yellow. The 2.5% below the lower cut---off is displayed as

blue to cyan. Because the IC data is converted to z---score we know that the standard deviation is 1.0; however, we don't know the upper limit and lower limit. Therefore the IC data limits are also displayed in the viewer.
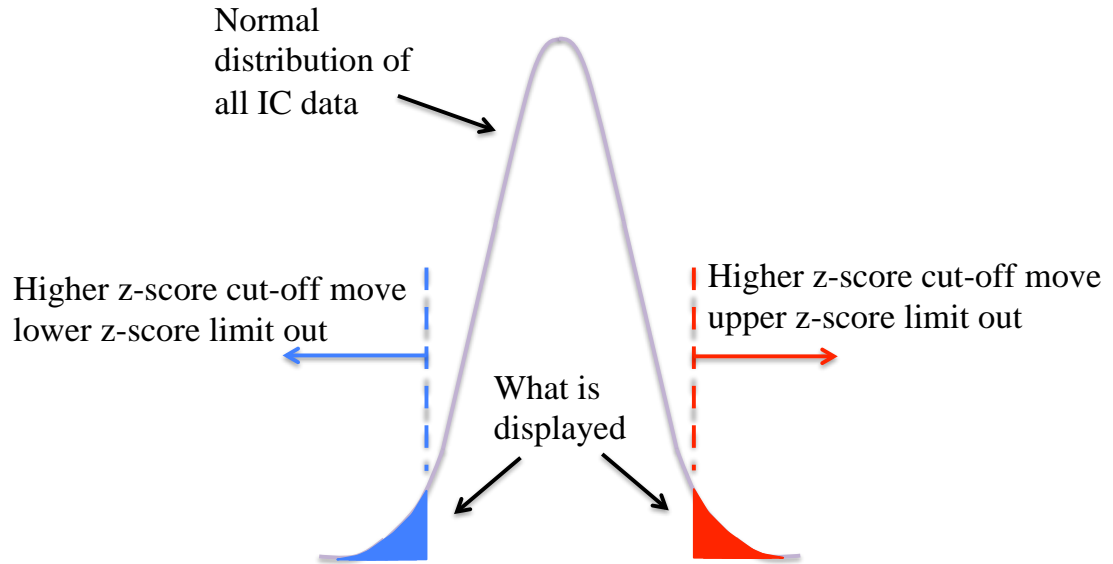

Figure 20. Component Viewer.

Figure 21. Z-score Cut-off Effect on Component Display.

Another aspect of the Component Viewer is the region coverage table. The purpose of the region coverage table is to provide identification of the anatomical brain regions that had the most coverage by the currently loaded IC. The method used to determine which regions had the most coverage was to identify the location of the voxels that are above the z---score cut---off. Once the locations are identified, each voxel can be associated with an anatomical region. The region with the most voxels has the highest frequency percentage. In the case of probability maps, the score for each voxel depends on the location. Therefore a percent coverage field is also displayed in the region coverage table. The difference between the coverage percentage and frequency percentage is that the coverage percentage takes into account the probability score of each voxel. The method used for calculating the region coverage score is shown in Code 6.

Code 6. Pseudo---code Snippet of Calculating Region Coverage Scores
IC3D = 3D spatial ICA map which has a z---score value at each IC---voxel.
AR3D = 3D spatial atlas which has a value K at each R---voxel.
// IC3D and AR3D have the same dimensions
// that we will call DimSize regionSum = regionTotal = 0
foreach xyz in DimSize
        regionTotal = regionTotal + AR3D[xyz]
        if abs(IC3D[xyz]) > 1.7
                regionSum = regionSum + AR3D[xyz] regionCoverage = regionSum /
regionTotal

Figure 22 shows the Component Viewer in region mode.   During Region Mode, the Component Viewer will only show the regions that are selected in the Main GUI. Since the definition of the regions are determined by the brain atlas, there is no need for z---score cut---off in region mode so it is hidden. Similarly, since a single region is being displayed in region mode, there is no need for the region coverage table, so it is also hidden in this mode.
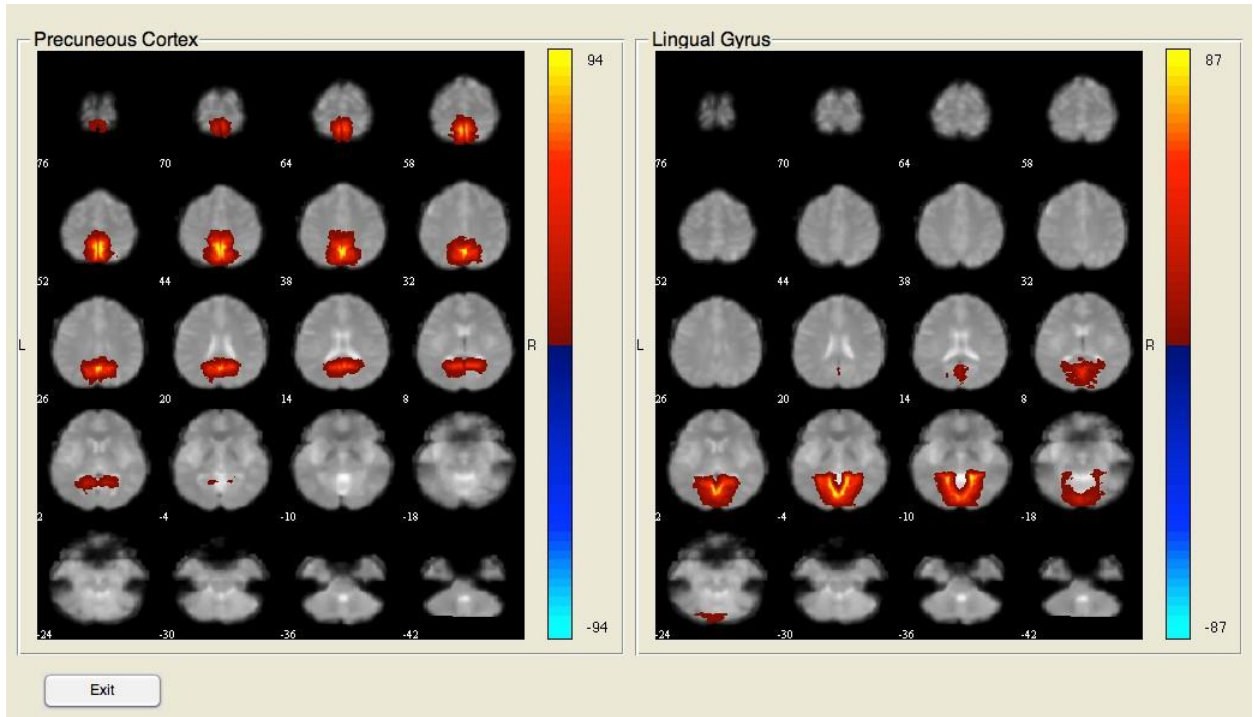
Figure 22. Component Viewer in Region Mode.

4.2 – Region Display

After the setup has been configure

Chapter 5 – DFC Matrix Display GUI

5.1 – Selecting a result

The DFC Matrix Display, as shown in *Figure 23*, provides a method to view the DFC results for all of the subject and component or region combinations. Each cell in the matrix is an average of all the ccs from the DFC correlation. The result will always be positive since

the higher of the positive and negative correlation is used. Part of the objective of the DFC Matrix
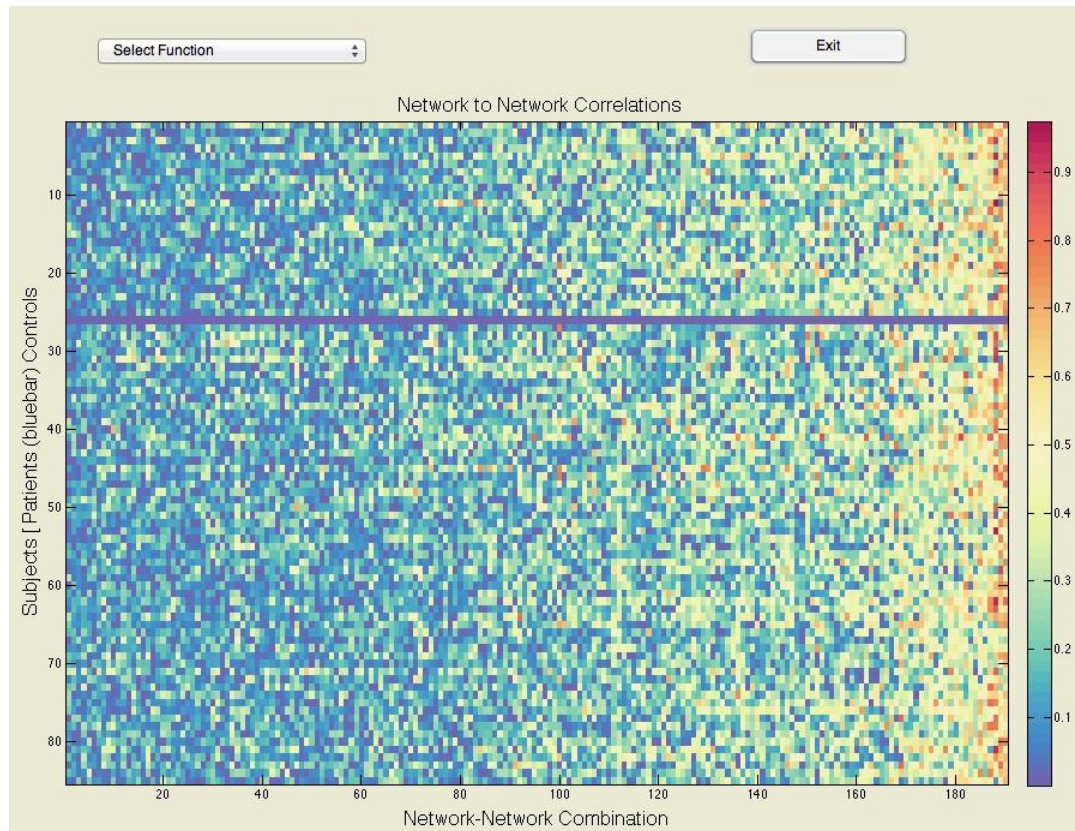
Figure 23. DFC Matrix Display.

Display is to illustrate any differences in the DFC results between groups. The arrangement to support this objective is to place all of the subjects from a group together. Then all IC or region combinations are sorted based on the average from the first group. Therefore, if there is a difference between the first group and any other group, then it may be observable in the matrix plot. The first group is at the top of the plot and the second larger group is below the purple separating line. In the figure there are only two groups, but DynaConn can support any number of groups. Each group will be separated with a purple line.

The DFC Matrix Display has two supporting functions. The first function allows the user to select any of the points on the plot. Once the user clicks on one of the data points, the display will close and will update the Main GUI with the subject and component or region combination that was selected. The EV file will also change to the selected subject. If the Component Viewer is open, it will close and reopen with the user selected subject components. This function gives the user the ability to navigate through a possibly large amount of data to find a data point of higher significance. If the dataset is large, seeing and especially being able to select the data points can be difficult. Therefore this GUI was designed to allow the user to expand and maximize the window. In addition, a user can use

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the magnifier in the MATLAB toolbar to zoom in on a group of data points before selecting a single data point. These features add to improving the clarity and usability of the GUI.

The second supporting function can change the color map used to display the correlation matrix. The default color map in MATLAB is the Jet color map, which is synonymous with the rainbow color map in other plotting and mapping tools. The issue with using the rainbow color map is that the hues in the color map match well to the electromagnetic spectrum but not well with human perceptual order (Borland & Taylor, 2007). In fact our visual comprehension tends to interpret the rainbow color map as several bands of constant hues. Humans can perceive small changes in luminance much better than changes in hue; therefore, gray---scale is the best representation of numerical data.   However, Cynthia Brewer (2006) created a tool called Color Brewer that creates color maps that have better perceptual order than the rainbow map. Jonathan Lansey (2013) built a MATLAB function to utilize the Color Brewer map called linspecer, which is implemented in DynaConn. **Error! Reference source not found.** illustrates the difference in smoothness of the rainbow, gray---scale, and the Color Brewer color maps by displaying a linear variable from 0.0 to 100.0. The DFC Matrix Display allows changing the color map to gray--scale, copper, rainbow, or Color Brewer. DynaConn will recall the previously used color map if the setup has been saved.