

# Pipeline for Comparison of Connectivity Data using Binary Undirected graphs at Fixed Thresholds

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This tutorial shows how to perform a network analysis using *connectivity data* (see tutorial [Group of Subjects with Connectivity Data](#)), where one connectivity matrix per subject is available, as in diffusion weighted imaging or pre-calculated matrices obtained from functional MRI, MEG, or EEG. Step by step, this pipeline guides you to compare the data from two groups of subjects at fixed thresholds, which correspond, for example, to fixed levels of white matter integrity or of correlation between activation signals of pairs of brain areas. With this tutorial, you will be able to extract and plot differences between two groups. You will also be able to generate publication-quality figures.

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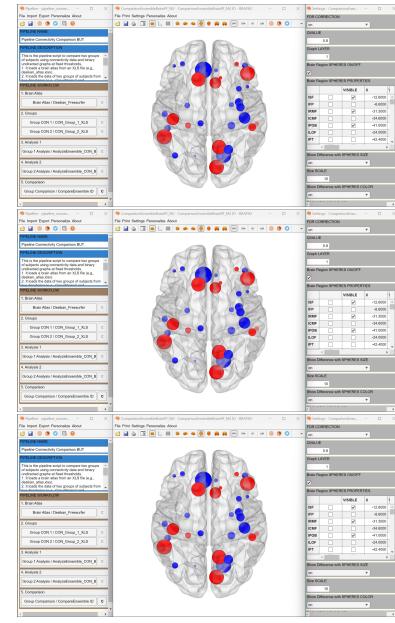


Figure 1: GUI for working with the pipeline to compare two groups of subjects with *connectivity data* at fixed thresholds. Example of the graphical user interface to perform group comparisons with *connectivity data* binarized at fixed thresholds.

## Generate Example Data

You can generate the example data by typing in the command line the instruction in Code 1.

**Code 1: Command to generate example data.** Command to generate the example data for connectivity analyses. They will be placed in the folder `./braph2/pipelines/connectivity/Example data CON XLS`, and include the brain atlas `atlas.xlsx`, two folders with the subject files `CON_Group_1_XLS` and `CON_Group_2_XLS`, and the associated covariates files `CON_Group_1_XLS.vois` and `CON_Group_2_XLS.vois`. The details about the format of these files can be found in the tutorials [Brain Atlas](#) and [Group of Subjects with Connectivity Data](#).

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<sup>1</sup> `test ImporterGroupSubjectCON_XLS`

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## Open the GUI

The general GUI of BRAPH 2.0 can be opened by typing `braph2` in MatLab's terminal. This GUI allows you to select a pipeline, in this case, *Pipeline Connectivity Comparison BUT*, as shown in Figure ??

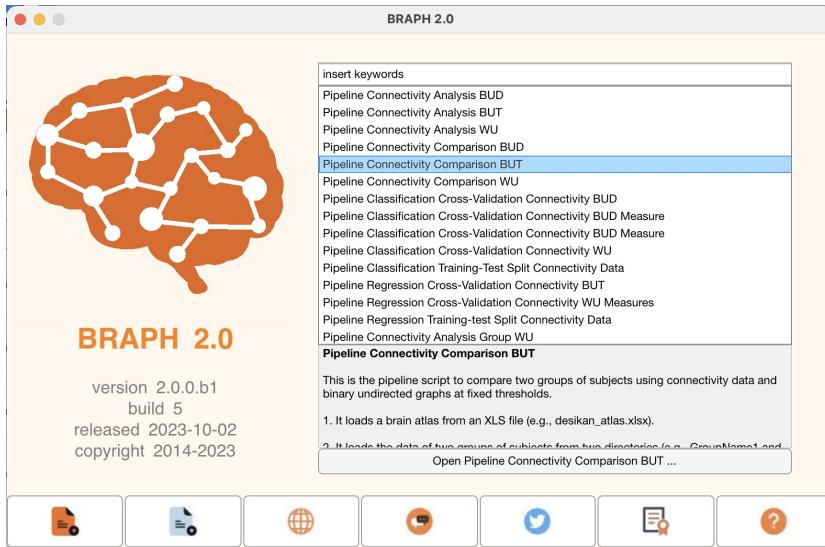


Figure 2: **BRAPH 2** main GUI. BRAPH 2 main GUI with the pipeline *Pipeline Connectivity Comparison BUT* selected.

### Pipeline launch from command line

To open the GUI and upload the connectivity comparison pipeline, you can also do it from the command line by typing the commands in Code 2.

**Code 2: Code to launch the GUI to upload a pipeline file to compare two groups of subjects.** This code can be used in the MatLab command line to launch the GUI to upload a pipeline file.

```

1 im = ImporterPipelineBGRAPH2( ...
2   'FILE', which('pipeline_connectivity_comparison_but.braph2') ...
3   );
4 pip = im.get('PIP');
5
6 gui = GUIElement('PE', pip, 'WAITBAR', true); gui.get('DRAW')
7 gui.get('SHOW')
```

Once the pipeline is uploaded, you can see a GUI that contains different steps to: upload a brain atlas, upload the connectivity data of two groups, analyze them, and finally, compare the groups (Figure 3).

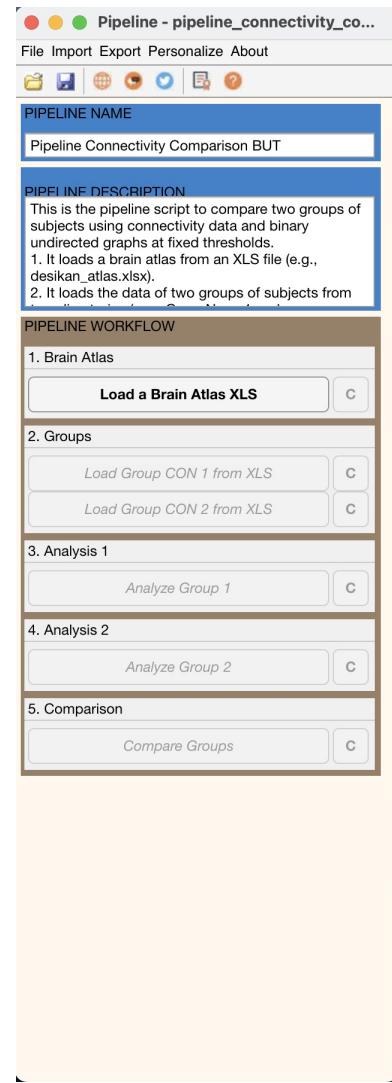


Figure 3: **Pipeline steps.** These are the steps of the pipeline. Only the first step is active when the pipeline is first opened. Subsequent steps will become active sequentially.

## Step 1: Load the Brain Atlas

Figure 4 shows how to upload and plot the brain atlas that you used to extract the *connectivity data* for your analysis. For more information on where to find different atlases or how to change plotting settings on the brain surface, check the tutorial [Brain Atlas](#).

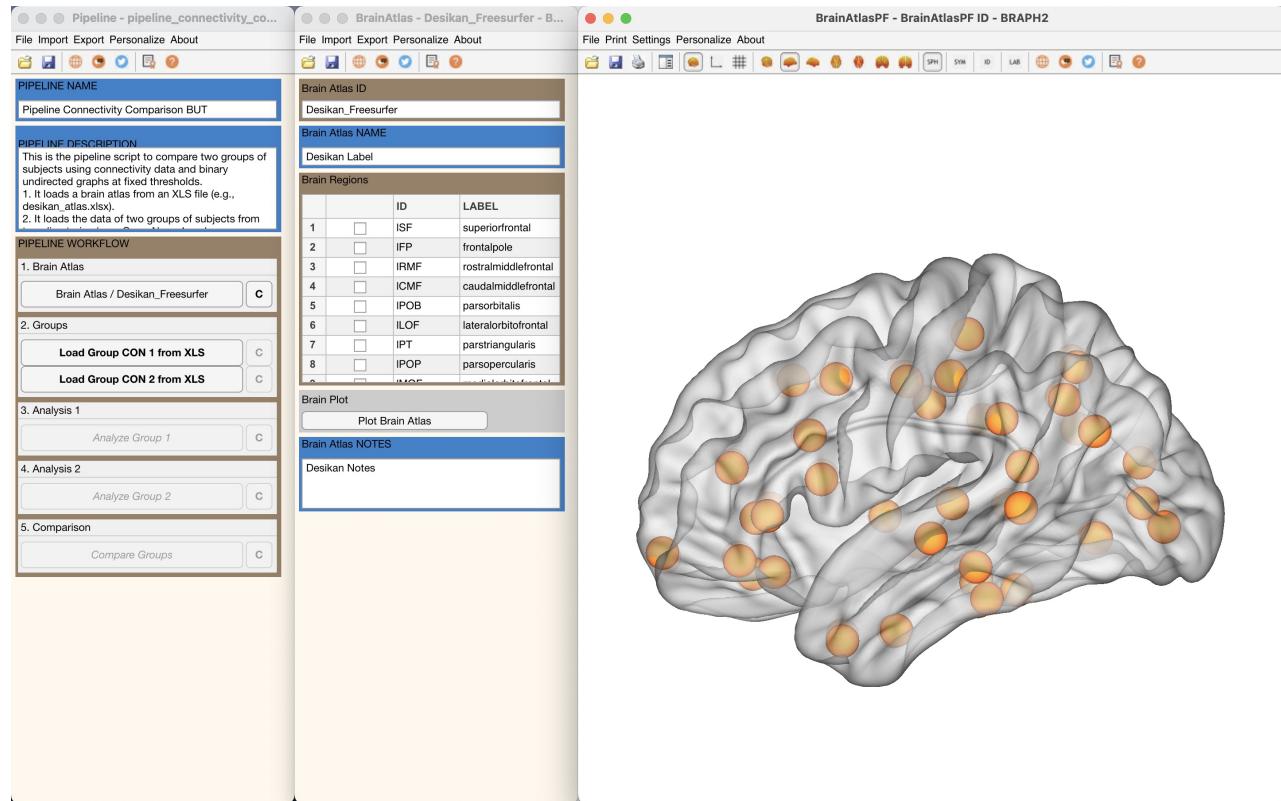


Figure 4: **Uploading the Brain Atlas.** Steps to upload the brain atlas: **a** Click on Load Atlas from the pipeline GUI. **b** Navigate to the BRAFP2 folder atlases and select one of the atlas files, in this example the *atlas.xlsx*. **c** You can visualize the brain atlas by pressing Plot Brain Atlas.

## Step 2: Load the Connectivity Group Data

After you loaded the brain atlas, you can upload the *connectivity data* for each group as shown in Figure 5. A new interface will be shown containing the data for the group you just selected. You can open each subject's connectivity matrices by selecting the subject, right click, and select “Open selection” (for more information check the tutorial [Group of Subjects with Connectivity Data](#)).

**Pipeline - pipeline\_connectivity\_co...**

**File Import Export Personalize About**

**PIPELINE NAME**  
Pipeline Connectivity Comparison BUT

**PIPELINE DESCRIPTION**  
This is the pipeline script to compare two groups of subjects. It loads connectivity data and binary undirected graphs at fixed thresholds.  
1. It loads a brain atlas from an XLS file (e.g., desikan\_atlas.xls).  
2. It loads the data of two groups of subjects from CON\_Group\_1\_XLS and CON\_Group\_2\_XLS.

**PIPELINE WORKFLOW**

1. Brain Atlas  
Brain Atlas / Desikan\_Freesurfer
2. Groups  
Group CON 1 / CON\_Group\_1\_XLS C  
Group CON 2 / CON\_Group\_2\_XLS C
3. Analysis 1  
Analyze Group 1 C
4. Analysis 2  
Analyze Group 2 C
5. Comparison  
Compare Groups C

**Group - CON\_Group\_2\_XLS - BRAPH2**

**File Import Export Personalize About**

**Group ID**  
CON\_Group\_2\_XLS

**Group NAME**  
CON\_Group\_2\_XLS

**Group SUBJECT CLASS**  
SubjectCON

**Group SUBJECTS**

	Subject ID	Subject LABEL
1	<input type="checkbox"/>	SubjectCON_100
2	<input checked="" type="checkbox"/>	SubjectCON_51
3	<input type="checkbox"/>	SubjectCON_52
4	<input type="checkbox"/>	SubjectCON_53
5	<input type="checkbox"/>	SubjectCON_54
6	<input type="checkbox"/>	SubjectCON_55
7	<input type="checkbox"/>	SubjectCON_56
8	<input type="checkbox"/>	SubjectCON_57
9	<input type="checkbox"/>	SubjectCON_58
10	<input type="checkbox"/>	SubjectCON_59

**SubjectCON - SubjectCON\_51 - BRAPH2**

**File Import Export Personalize About**

**Subject ID**  
SubjectCON\_51

**Subject LABEL**  
SubjectCON label

**Brain Atlas**  
BrainAtlas(Desikan\_Freesurfer)

**Variables of Interest**  
Age: 53  
Sex: Male

**Connectivity DATA**

	ISF	IFP	IRMF	ICMF	IPOB	ILOF	IPT	IPOP	IMOF	IRAC
ISF	0	0.7238	0	0	0	0	0	0	0	0
IFP	0.7238	0	0	0	0	0	0	0	0	0
IRMF	0	0	0	0	0	0	0	0	0	0
ICMF	0	0	0	0	0	0	0	0	0	0
IPOB	0	0	0	0	0	0	0	0	0	0
ILOF	0	0	0	0	0	0	0	0	0	0
IPT	0	0	0	0	0	0	0	0.7703	0	0
IPOP	0	0	0	0	0	0	0.7703	0	0	0
IMOF	0	0	0	0	0	0	0	0	0	0
IRAC	0	0	0	0	0	0	0	0	0	0

**Subject NOTES**  
SubjectCON notes

**Figure 5: Loading and visualizing the group data.** a From the pipeline GUI, click on Load Group CON 1 from XLS to load the data of group 1. b Once the data is uploaded, you can select a subject, right click and select Open selection. c This will open the connectivity matrix of the subject in addition to the age and sex of that subject (which are the variables of interest available for the example data). You can then repeat the same procedure for group 2.

### Step 3: Analyzing the Data of Group 1

Once you have loaded the data for both groups, you can begin analyzing the data for the first group by clicking on Analyze Group 1 (Figure ??a). This will open a new interface called **Analyze Ensemble**, which allows you to calculate and visualize graph measures for the first group. Before these network measures are calculated, it is important to ensure the following things:

1. The analysis parameters are set correctly (e.g., the thresholds).
2. The graph parameters are set correctly.
3. The measures are configured with the parameters you desire (note that not all measures have parameters).

Importantly, the parameters you select at the beginning will remain fixed for the rest of pipeline (including the analysis of the second group and the comparison between groups). We will now guide you through the process of preparing these parameters for both measures and graphs. It is important to keep in mind that the default parameters should work well for most cases.

#### Setting Analysis Parameters

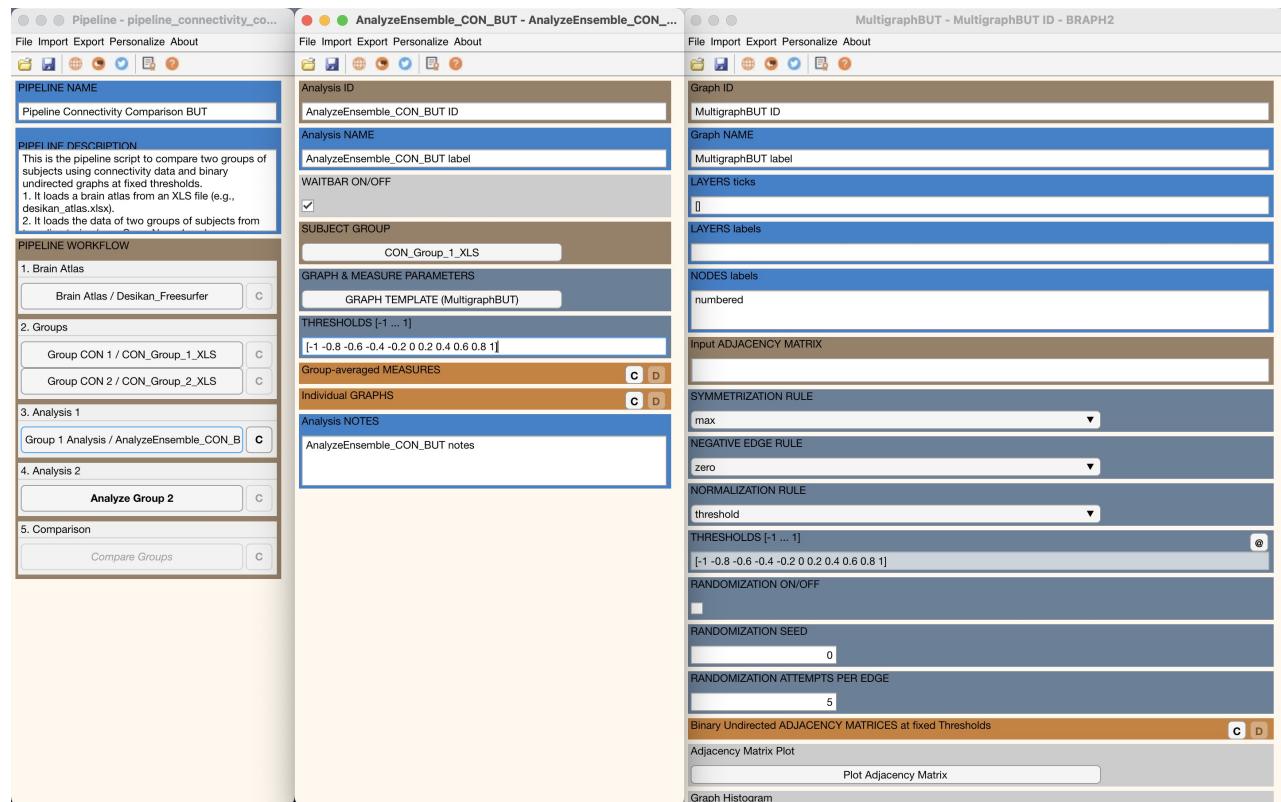
In the **Analyze Ensemble** interface (Figure 6), you can configure the analysis parameters. In the **THRESHOLDS** section, you can define the thresholds by entering values like `-1:1:1` (you can also use any other valid mathematical expression, such as `0 .25 .5 .75 1`, or `-1 0:.2:1`).

The figure displays two side-by-side screenshots of the **Analyze Ensemble** software interface. The left panel, titled "Pipeline - pipeline\_connectivity\_co...", shows a pipeline workflow with five main steps: 1. Brain Atlas, 2. Groups, 3. Analysis 1, 4. Analysis 2, and 5. Comparison. Step 1 loads a "Brain Atlas / Desikan\_FreeSurfer" file. Step 2 loads "Group CON 1 / CON\_Group\_1\_XLS" and "Group CON 2 / CON\_Group\_2\_XLS". Step 3 performs "Group 1 Analysis / AnalyzeEnsemble.CON\_B". Step 4 performs "Analyze Group 2". Step 5 compares the results. The right panel, titled "AnalyzeEnsemble\_CON\_BUT - AnalyzeEnsemble\_CON\_BUT ID - BRAPH2", is the detailed configuration interface. It includes sections for "Analysis ID" (set to "AnalyzeEnsemble.CON\_BUT ID"), "Analysis NAME" (set to "AnalyzeEnsemble.CON\_BUT label"), "WAITBAR ON/OFF" (checked), "SUBJECT GROUP" (set to "CON\_Group\_1\_XLS"), "GRAPH & MEASURE PARAMETERS" (set to "GRAPH TEMPLATE (MultigraphBUT)"), and "THRESHOLDS [-1 ... 1]" (set to "[ -1 -0.9 -0.8 -0.7 -0.6 -0.5 -0.4 -0.3 -0.2 -0.1 0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1 ]"). It also includes sections for "Group-averaged MEASURES" and "Individual GRAPHS", both currently empty. At the bottom, there is an "Analysis NOTES" field containing "AnalyzeEnsemble.CON\_BUT notes".

Figure 6: Configuring analysis parameters. a To initiate the analysis of data for group 1, click on Analyze Group 1. b You define the thresholds in the THRESHOLDS section.

## Setting Graph Parameters

To configure the graph parameters, you click on the section GRAPH & MEASURE PARAMETERS (Figure 7). This will open a new interface for graph template settings. In brain connectivity analysis, threshold values dictate the required connection strength between different brain regions for them to be considered “connected” in a binary undirected graph. Adjusting these thresholds allows you to explore varying levels of brain connectivity, providing insights into how regions communicate at different threshold settings.



The available parameters are:

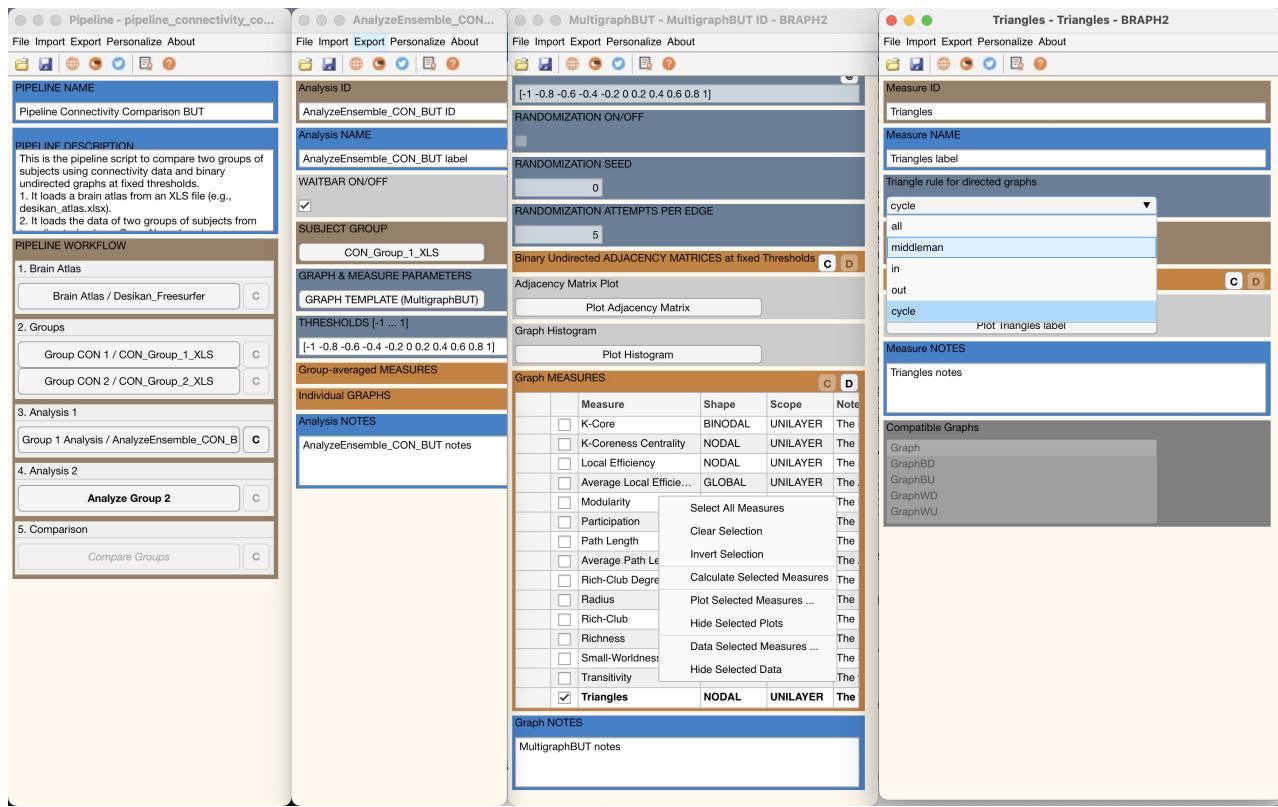
- SYMMETRIZATION RULE determines how to symmetrize the matrix.
- NEGATIVE EDGE RULE determines how to remove the negative edges.
- NORMALIZATION RULE determines how to normalize the weights between 0 and 1.
- THRESHOLDS determines the thresholds. *This cannot be set here. It is set in the previous step.*

Figure 7: Configuring Graph Parameters. a By clicking on the section GRAPH & MEASURE PARAMETERS, you open b a new interface that permits you to configure the graph parameters. c The available parameters shall be set at this point.

- RANDOMIZE ON/OFF determines whether to randomize the graph. *Typically not used*
- RANDOM SEED is the randomization seed. *Typically not used*
- RANDOMIZATION ATTEMPTS PER EDGE is the attempts to rewire each edge. *Typically not used*

### Setting Measure Parameters

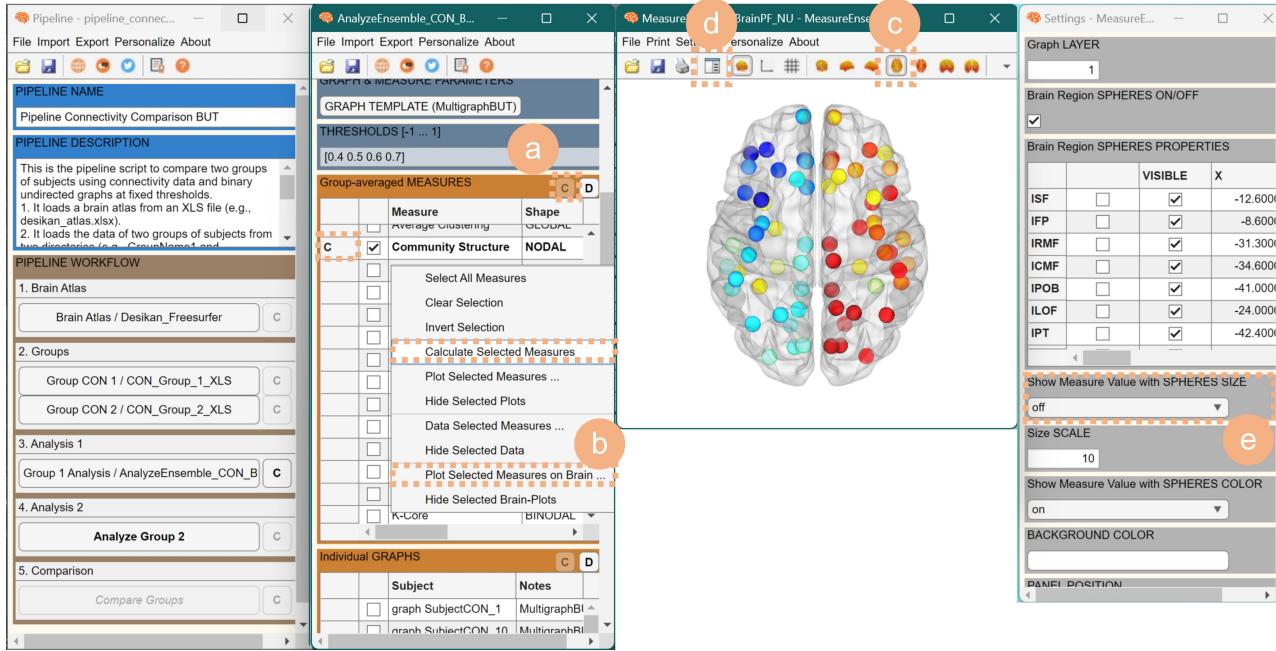
Now, if you scroll down to find the Graph MEASURES section, by clicking on the C button, all compatible measures will be displayed in a table. For example, you can select the Community Structure measure and then right-click at the top of the table (Figure 8a). In the right-click menu, choose Data Selected Measures. This will open the measure window, allowing you to specify the rules or parameters (Figure 8b).



**Figure 8: Configuring Measure Parameters.** **a** Expanding the Graph MEASURES panel, by clicking on the C button, reveals a table displaying all compatible measures. Select the Community Structure measure and then right-click at the top of the table. In the right-click menu, choose Data Selected Measures. **b** The measure window that opens allows you to define the parameters for the Community Structure measure. Select the louvain algorithm to calculate it.

### Calculate Measures

After configuring the parameters, you can proceed to calculate specific graph measures (Figure 9). To do this, return to the Analyze Ensemble interface (Figure 9a) and scroll down to locate the Group-averaged MEASURES panel. By clicking the 'C' button, you will see a table displaying all measures.



As an example, let us select the Community Structure measure, for which we previously set the rule to louvain. Right-click at the top of the table and choose Calculate Selected Measures. Once the calculation is complete, you will notice a C appearing in front of the Community Structure row, indicating that this measure has been calculated.

If you wish to visualize the results, right-click on the top of the table and select Plot Selected Measures on Brain within the Analyze Ensemble interface (Figure 9). This will open a brain surface with the Community Structure plotted on it.

Within the toolbar of the brain surface interface, you can explore various views. For instance, by clicking on the Axial dorsal button (Figure 9c), you will get the same view as shown in Figure 9d. Additionally, clicking on the Settings Panel Figure button (Figure 9e) in the same toolbar allows you to adjust different visualization settings.

For instance, within the settings menu (Figure 9e), you can disable the size effect, resulting in the same kind of figure as shown in Fig-

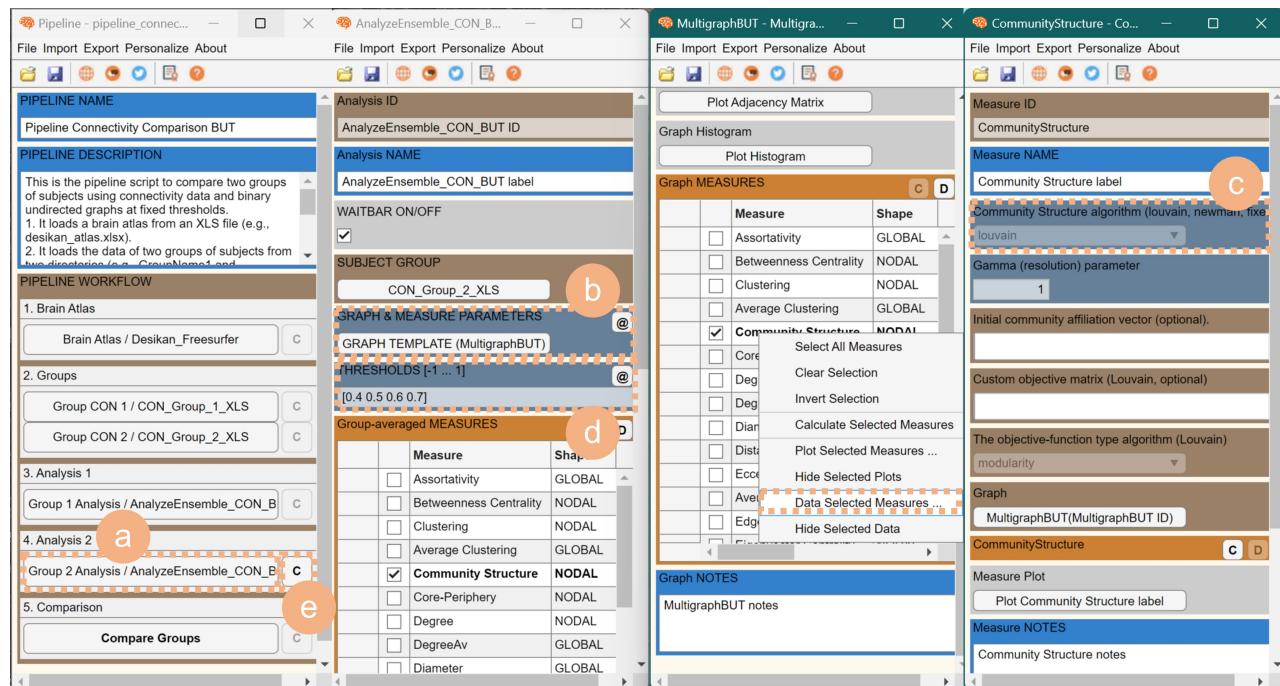
**Figure 9: Analyzing the Group Data.**  
**a** Locate the Group-averaged MEASURES panel and click the C button to see all available measures. Choose the Community Structure measure, right-click it, and select Calculate Selected Measures to perform the calculation. **b** To visualize the results, right-click on the top of the table and choose Plot Selected Measures on Brain in the Analyze Ensemble interface. This action opens a brain surface with the Community Structure plotted. **c** Explore different views such as the Axial dorsal button in the brain surface toolbar. **d** Adjust visualization settings by clicking on the Settings Panel Figure button in the same toolbar. **e** Customize and save plot visualizations within the settings menu. Here, we turned off the option to show the spheres corresponding to the nodes of each community with different sizes.

ure 9d. Within the settings menu, you can customize the visualization of the plots and save them for reference.

Finally, when you right-click in the Group-averaged MEASURES panel, you will find other options to explore, such as Plot Selected Measures (which generates a line plot for the selected measure at different thresholds and/or different nodes) and Data Selected Measure (providing the calculated values of the selected measures). These options can also be saved for further analyses outside BRAPH 2.0.

#### Step 4: Analyzing the Data of Group 2

After completing the analysis of the first group, you can analyze the second group by simply clicking on Analyze Group 2 (Figure 10a). You will notice that in the new GUI (Figure 10b-d), the parameters you previously selected for the first group are already preselected and fixed for this analysis.



If you want to change some of the parameters you previously selected, you can reset the analysis parameters by clicking on the cancel button marked with a C (Figure 10e) near the analysis of the first group.

Figure 10: Parameters blocked in the Analysis of Group 2. a Click on Analysis 2 in the pipeline's GUI. b In this new window, you can see that the measure parameters, such as the b GRAPH TEMPLATE and c rule for Community Structure, as well as the graph property d THRESHOLDS, are blocked since they should be the same as the ones set in the analysis of group 1. You can reset the analysis parameters for Group 1 by clicking on the checkbox marked with a 'C' next to the settings of Group 1 e.

## Step 5: Comparing Groups

After exploring the network measures for each group, you can proceed to their statistical comparison by clicking on **Compare Groups** (Figure 11a).

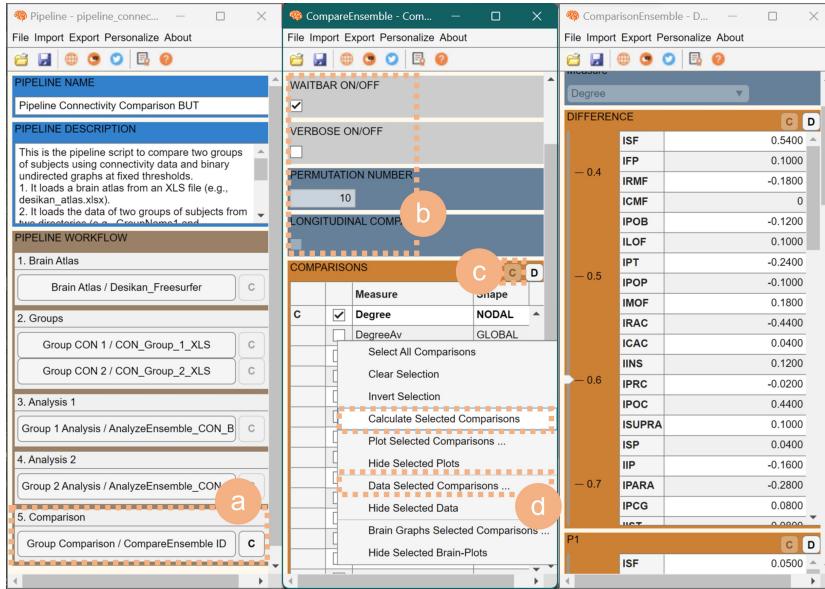


Figure 11: **Compare the groups.** **a** Click on **Compare Groups** in the pipeline's GUI. **b** In this new window, you can select to turn ON/OFF the wait bar and verbose functions, you can change the number of permutations, and whether to perform a longitudinal group comparison. We set the number of permutations to 10 for this tutorial **c**. Finally, you can calculate the comparisons of some graph measures between groups **d**.

In the new window, you have several options to configure the analysis. First, you can choose whether to enable a progress bar and verbose functions while the analysis is running, which can help you monitor the progress of the analysis. You can also specify how many permutations you want to use to assess differences between groups (Figure 11b).

If your groups are not independent and represent the same subjects assessed in different points in time, you can select the longitudinal comparison option. This option will permute the values within each subject, considering their temporal relationship (Figure 11b).

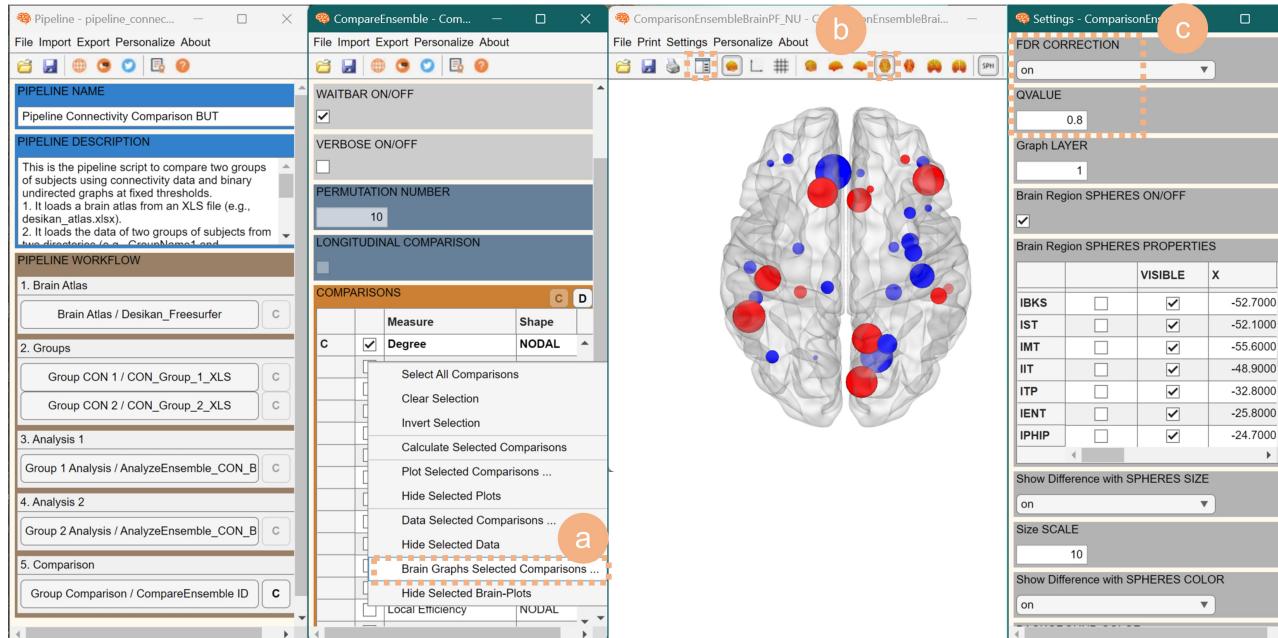
For computational efficiency, in this tutorial we have set the number of permutations to 10. However, for your research analysis, we recommend using a higher number, such as 1000 or 10000 permutations, to ensure the results are robust.

Next, you can select the specific graph measures you wish to compare between the groups. To do this, click on **C** in the **COMPARISONS** section (Figure 11c). Once you have chosen all the measures of interest, right-click and select **Calculate Selected Comparisons**.

If you have enabled the progress bar and verbose functions, two

additional windows will appear to display the progress of the comparison calculations. Finally, there is an option in this GUI to save intermediate results during the permutations, which can be helpful for further analysis.

To obtain the results from the comparisons, select the measures in the COMPARISONS panel and press Data Selected Comparisons (Figure 11d), and a new window will open where we can check the value of the difference between groups, the p-values (1-tailed and 2-tailed), as well as the confidence intervals.



If you wish to visualize the results, right-click at the top of the table and select Brain Graph Selected Comparison within the Compare Ensemble interface (Figure 12a). This action will open a brain surface displaying the difference between these two groups in terms of the Degree data or any other nodal measure you have calculated.

Within the brain surface interface's toolbar, you have various options to explore. For example, by clicking on the "Axial dorsal" button (Figure 12b), you can access the same view depicted in Figure 12. Additionally, the "Settings Panel Figure" button in the same toolbar allows you to fine-tune different visualization settings.

For further customization, within the settings menu (Figure 12c), you can activate the FDR CORRECTION feature to control for multiple comparisons and reduce the chance of false positive results when as-

Figure 12: Visualize the group comparison results on a brain surface. **a** Click on Brain Graph Selected Comparison in the Comparisons panel. **b** In this new window, you will see the comparison results, with positive values in red and negative values in blue on the brain surface. **c** You can customize this visualization using the settings menu.

sessing the significance of connectivity measures across multiple brain regions. You can also use the settings menu to personalize the visualization of your plots and save them.