Prepare brain connectivity data

The BRAPH 2 Developers

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For *connectivity data*, a connectivity matrix per subject is already available and can be directly imported into the relative analysis pipeline. For example, the connectivity matrix could correspond to white matter tracts obtained from dMRI or pre-calculated coactivations maps obtained from fMRI data. This Tutorial explains how to prepare and work with this kind of data.

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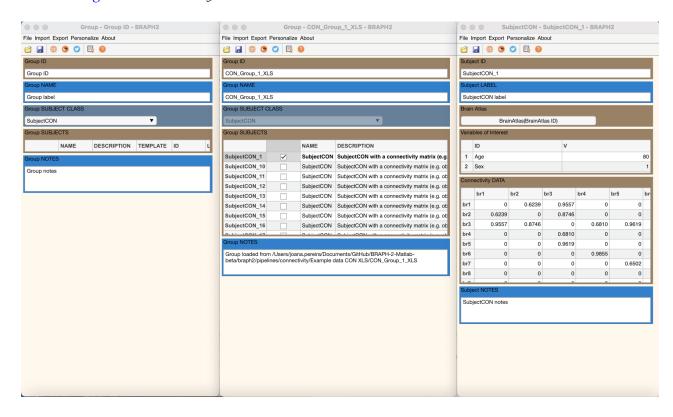


Figure 1: **Brain Connectivity Group GUI.** Full graphical user interface to work with brain connectivity group data in BRAPH 2.0.

Open the GUI

The group GUI is the second step in an analysis after you have selected a brain atlas. You can open it by typing braph2 in the MatLab's terminal, which allows you to select a pipeline containing the steps required to perform your analysis and upload a brain atlas. After these steps have been completed you can upload your group's data, as shown in Figure 2a.

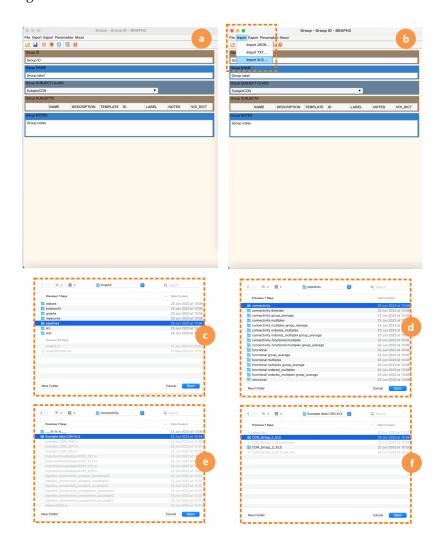


Figure 2: Upload a brain atlas. The different steps you need to follow to open brain connectivity data using the GUI and an example dataset: a Open the group GUI. **b** Import a folder containing the connectivity matrices in XLS or TXT format. c Navigate to the BRAPH 2.0 folder pipelines. d Navigate to the BRAPH 2.0 folder connectivity. e Navigate to the BRAPH 2.0 folder Example data CON XLS. f Select the folder containing the connectivity matrices of one group CON_Group_1_XLS.

To open the GUI and upload the brain connectivity data, you can also do it from the command line (i.e., without opening an analysis pipeline) by typing the commands in Code 1.

Code 1: Code to launch the Brain Connectivity Group GUI. This code can be used in the MatLab command line to launch the Brain

Connectivity Group without having to open a pipeline.

```
gr = Group('SUB_CLASS', 'SubjectCON'); (1)
 gui = GUIElement('PE', gr); (2)
4 gui.get('DRAW')(3)
 gui.get('SHOW') (4)
```

Visualize the Brain Connectivity Group Data

After launching the previous steps (Figure 2), you can visualize the data (Figure 3a), change the Group ID, name and notes (Figure 3b).



Finally, you can open a subject's connectivity matrix by selecting the subject, right click and select "Open selection" (Figure 4a), which will show the matrix values (Figure 4b). You can also change the ID, label, age, sex and even the values of your connectivity matrix.

- (1) creates a new object Group.
- (2) creates a GUI to upload the group
- \bigcirc draws the GUI.
- (4) shows the GUI.

Figure 3: Edit the Brain Connectivity Group data. Information that can be changed in the Brain Connectivity Group GUI: a The ID, name, and notes. **b** The values of the connectivity matrix.



Figure 4: **Individual Brain Connectivity Data GUI.** Visualising and editing a brain connectivity matrix of a single subject.

Preparation of the Data to be Imported

To be able to import connectivity data into BRAPH 2.0 you need to include the connectivity matrices for each subject in excel or text format inside a folder with the name of the group. Below you can see how your group directory should look like as well as an example of a brain connectivity matrix.

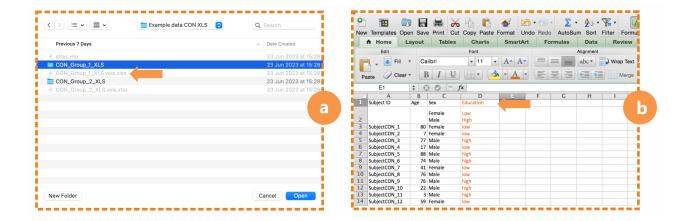


Adding Covariates

It is very common to have covariates in an analysis. In BRAPH 2.0 these covariates should be included in a separate excel file placed outside the group's folder and have the same name as the folder in addition to ".vois" as shown in Figure 6a), where "vois" stand for variables of interest. This covariates file should have a specific format, where the first two rows have the following information:

- Covariates names (row 1, column 1). For example: Subject ID, Age and Sex. In this example we have added a new covariate: Education.
- Covariates values (row 2, column 1). For example: Female and Male (Sex) or Low and High (Education).

Figure 5: Data preparation. The data should be organised in the following way: a The connectivity matrices from each subject should be included in one folder, for example: CON_group_1_XLS. b Each matrix should contain the connectivity values between each pair of brain regions denoted by the rows and columns. In this example, the values in the matrix correspond to the fractional anisotropy (white matter integrity) of anatomical connections derived from diffusion weighted imaging.



Then, from row 3, you should include the IDs of your subjects (1st column) and the values for the different covariates: age (2nd column), sex (3rd, 4th, and 5th columns), and educational level (6th column) Figure 5b).

Figure 6: Edit the Covariates. Information that can be changed in the Covariates file: a The names of the variables of interest (vois). b In case the vois are categorical, you can state which categories they have.