

# Group of Subjects with Connectivity Data

The BRAPH 2 Team

September 30, 2023

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.

## Contents

- Generation of Example Data 2
- Open the GUI 2
- Visualize the Group Data 3
- Visualize Each Subject's Data 3
- Preparation of the Data to be Imported 6
- Adding Covariates 6

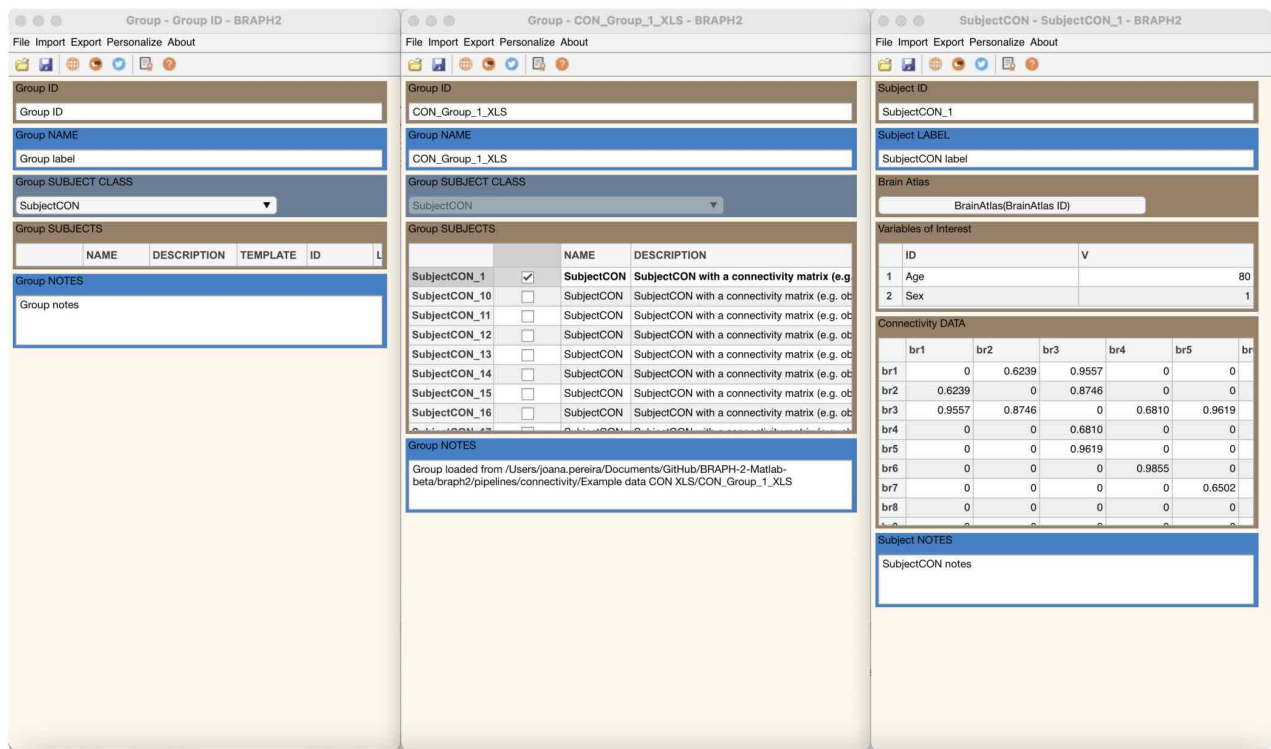


Figure 1: GUI for a group of subjects with connectivity data. Full graphical user interface to upload a group of subjects with connectivity data in BRAPH 2.0.

## Generation of Example Data

If you don't have the Example data CON XLS folder inside connectivity, then you can generate it by running the commands in Code 1.

**Code 1: Code to generate the example data folder.** This code can be used in the MatLab command line to generate the Example data CON XLS folder to the connectivity pipeline folder.

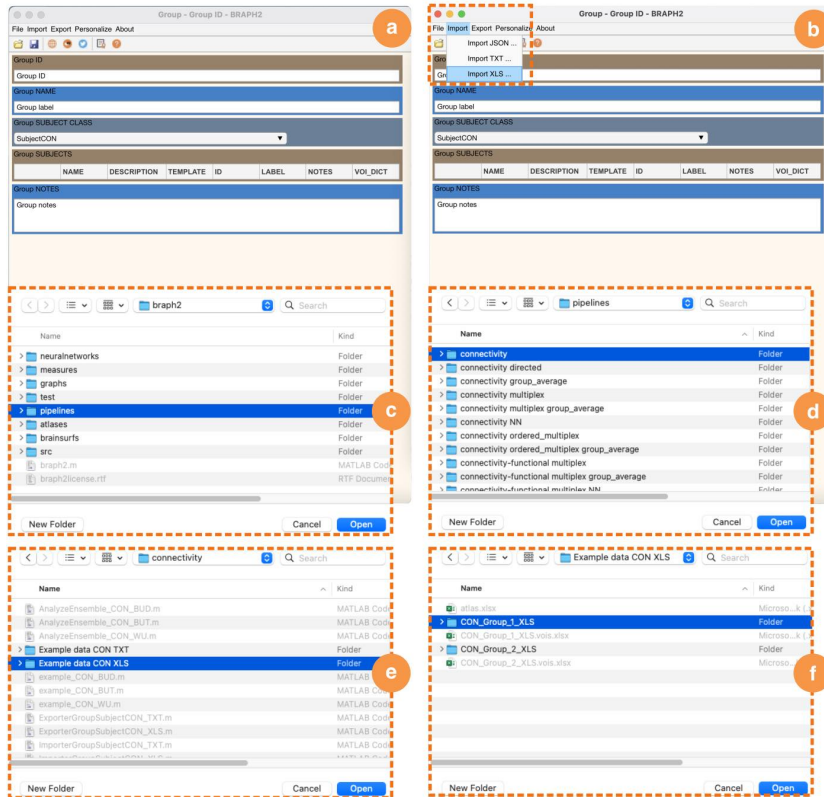
```
1 test_ImporterGroupSubjectCON_XLS ①
2 test_ImporterGroupSubjectCON_TXT ②
```

① generates the example connectivity XLS data folder.

② generates the example connectivity TXT data folder.

## Open the GUI

In most analyses, the group GUI is the second step 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 directly (Figure 2c-f) after clicking "Load Group".



**Figure 2: Upload the data of a group of subjects.** Steps to upload a group of subjects with 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 (see below for details on their format). To upload the test connectivity data: **c-f** navigate to the BRAPH 2.0 folder pipelines, **d** connectivity, **e** Example data CON XLS, and **f** select the folder containing the connectivity matrices of one group `CON_Group_1_XLS`.

### GUI launch from command line

You can also open the GUI and upload the brain connectivity data using the command line (i.e., without opening an analysis pipeline) by typing the commands in Code 2. In this case, you can upload the data as shown in Figure 2a-f.

**Code 2: Code to launch the GUI to upload a group of subjects with connectivity data.** This code can be used in the MatLab command line to launch the GUI to upload a group of subjects with connectivity data without having to open a pipeline.

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

### *Visualize the Group Data*

After completing the steps described in Figure 2, you can see the data (Figure 3a), and change the Group ID, name, and notes (Figure 3b).

### *Visualize Each Subject's Data*

Finally, you can open each subject's connectivity matrix by selecting the subject, right click, and select "Open selection" (Figure 4a), which shows the matrix values (Figure 4b). Here, you can also change the subject's metadata (ID, label, notes), its variables of interest, and the values of its connectivity matrix.

Group - CON\_Group\_1\_XLS - BRAPH2

File Import Export Personalize About

Group ID  
CON\_Group\_1\_XLS

Group NAME  
CON\_Group\_1\_XLS

Group SUBJECT CLASS  
SubjectCON

Group SUBJECTS

	Subject ID	Subject LABEL	Brain Atlas	Variables of Interest	Connectivity DATA	Subject NOTES
1	<input type="checkbox"/>	SubjectCON_1	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
2	<input type="checkbox"/>	SubjectCON_10	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
3	<input type="checkbox"/>	SubjectCON_11	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
4	<input type="checkbox"/>	SubjectCON_12	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
5	<input type="checkbox"/>	SubjectCON_13	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
6	<input type="checkbox"/>	SubjectCON_14	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
7	<input type="checkbox"/>	SubjectCON_15	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
8	<input type="checkbox"/>	SubjectCON_16	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes

Group NOTES  
Group loaded from /Users/anna.canal.garcia/Documents/GitHub/BRAPH-2-Matlab-beta/braph2/pipelines/connectivity/Example data CON XLS/CON\_Group\_1\_XLS

---

Group - CON\_Group\_1\_XLS - BRAPH2

File Import Export Personalize About

Group ID  
CTR

Group NAME  
Controls

Group SUBJECT CLASS  
SubjectCON

Group SUBJECTS

	Subject ID	Subject LABEL	Brain Atlas	Variables of Interest	Connectivity DATA	Subject NOTES
1	<input type="checkbox"/>	SubjectCON_1	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
2	<input type="checkbox"/>	SubjectCON_10	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
3	<input type="checkbox"/>	SubjectCON_11	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
4	<input type="checkbox"/>	SubjectCON_12	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
5	<input type="checkbox"/>	SubjectCON_13	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
6	<input type="checkbox"/>	SubjectCON_14	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
7	<input type="checkbox"/>	SubjectCON_15	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes
8	<input type="checkbox"/>	SubjectCON_16	SubjectCON label	BrainAtlas(BrainAtlas ID)	IndexedDictionary with 2 VOI [68 x 68]	SubjectCON notes

Group NOTES  
Control group for the analysis of DWI connectivity matrices

Figure 3: **Edit the group metadata.** **a** The GUI of the group's connectivity data. **b** The information you see on this GUI that can be changed. In this example, we have edited the ID, name, and notes of the group but can also change the subject's specific information.

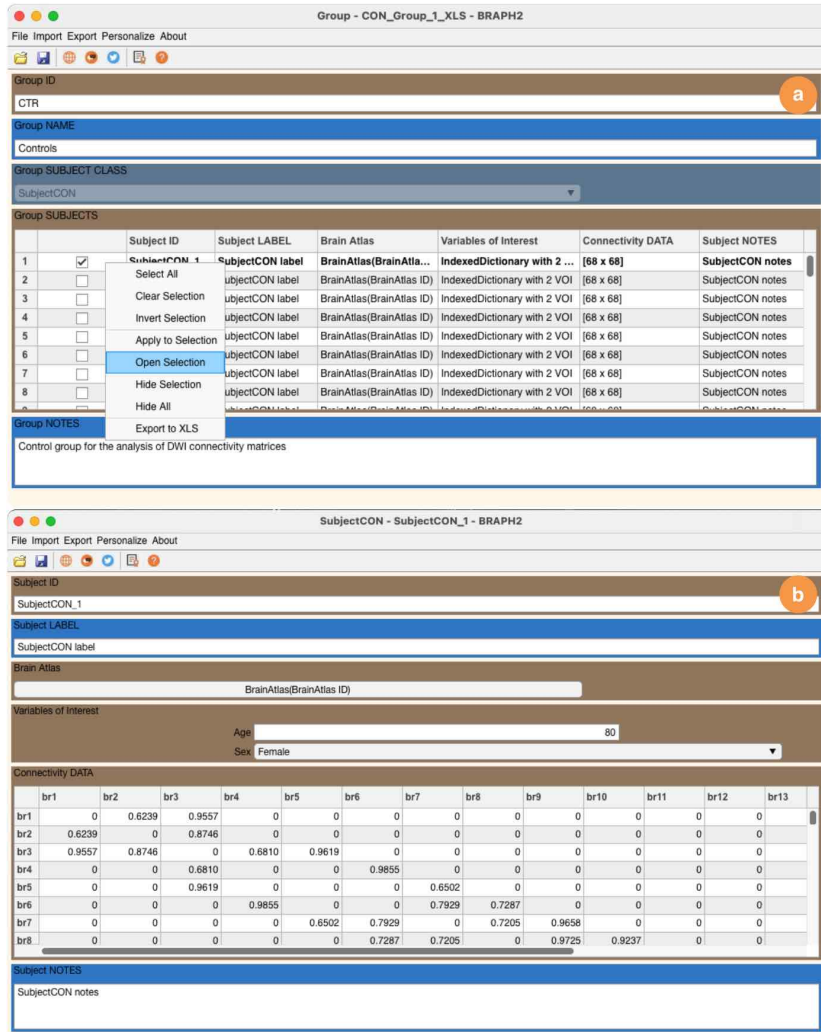
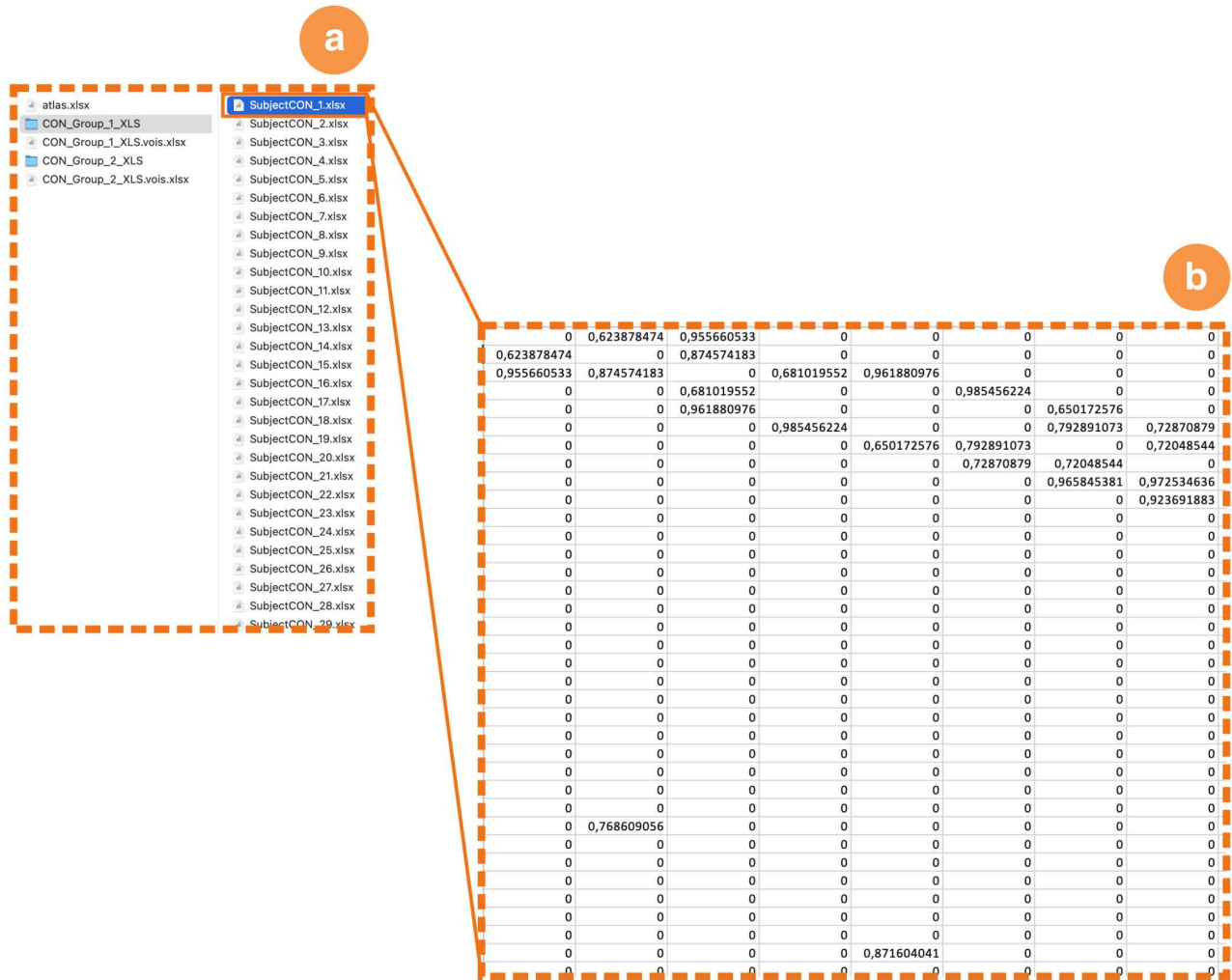


Figure 4: **Edit the individual subject data.** **a** Each subject's connectivity matrix can be opened by selecting the subject, right click, and select "Open selection" **b** In this subject GUI, it is possible to view and edit the metadata of the subject (ID, label, notes), its variables of interest (in this case, age and sex), and the values of the connectivity matrix.

## 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 *variables of interest* (i.e., *covariates* and *correlates*) in an analysis. In BRAPH 2.0, these variables of interest should be included in a separate excel file placed just outside the group's folder and with the same name as the folder followed by .vois (Figure 6a).

Figure 5: **Data preparation.** The data should be organised in the following format: **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 example, the (simulated) values in the matrix correspond to the fractional anisotropy (white matter integrity) of anatomical connections derived from diffusion weighted imaging.

**a**

**b**

	A	B	C	D	E
1	Subject ID	Age	Sex	Education	
2			Female		
3	SubjectCON_1	80	Female	low	
4	SubjectCON_2	7	Female	low	
5	SubjectCON_3	77	Male	high	
6	SubjectCON_4	17	Male	high	
7	SubjectCON_5	88	Male	high	
8	SubjectCON_6	74	Male	high	
9	SubjectCON_7	41	Female	low	
10	SubjectCON_8	76	Male	low	
11	SubjectCON_9	76	Male	high	
12	SubjectCON_10	22	Male	high	
13	SubjectCON_11	3	Male	high	
14	SubjectCON_12	59	Female	low	

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.

This file should have a specific format (Figure 6b):

Subject IDs (column A). Column A should contain the subject IDs starting from row 3.

Variables of interest (column B and subsequent columns). Column B (and subsequent columns) should contain the variables of interest (one per column). In this example we have “Age” and “Sex”, as in the example file, as well as the additional “Education”. In each column, row 1 should contain the name of the variable of interest, row 2 should contain the categories separated by a return (only for categorical variables of interest, like “Sex” and “Education”), and the subsequent rows the values of the variable of interest for each subject.