

# *Adapt a Pipeline Script*

*The BRAPH 2 Developers*

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This is the developer tutorial for adapting a pipeline script. In this tutorial, you will learn how to edit a \*.braph2 file to change the steps of a pipeline. Here, you will use as an example the pipeline Pipeline Structural Multiplex Comparison BUD in the file pipeline\_structural\_multiplex\_comparison\_bud.braph2 (the pipeline for comparing two groups of subjects using structural multiplex data and binary undirected graphs at fixed densities) and adapt it in order to add a third group for structural multiplex.

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## Adaption of the pipeline

You will adapt in Pipeline Structural Multiplex Comparison BUD in the file `pipeline_structural_multiplex_comparison_bud.braph2` as shown in Code 1. The changes are highlighted in the comments.

Code 1: Adapted pipeline to compare three groups of subjects using structural multiplex data and binary undirected graphs at fixed densities.

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1 %% Pipeline Structural Multiplex Comparison BUD (1)
2
3 % This is the pipeline script to compare two groups of subjects using
  structural multiplex data and binary undirected graphs at fixed
  densities. (2)
4 % 1. It loads a brain atlas from an XLS file (e.g., desikan_atlas.xlsx).
5 % 2. It loads the data of two groups of subjects from two directories (e.g.,
  ST_MP_group_1_XLS and ST_MP_group_2_XLS).
6 % 3. It analyzes the first group using structural multiplex analyses (ST_MP)
  based on binary undirected graphs at fixed densities (BUD).
7 % 4. It analyzes the second group using the same parameters selected for the
  first group.
8 % 5. It compares the results of the two analyses.
9
10 %% Brain Atlas
11 ba = ImporterBrainAtlasXLS('WAITBAR', true).get('GET_FILE').get('BA'); (3)
12
13 %% Groups
14 gr1 = ImporterGroupSubjectST_MP_XLS('BA', ba, 'WAITBAR', true).get('GET_DIR'
  ).get('GR'); (4)
15 gr2 = ImporterGroupSubjectST_MP_XLS('BA', ba, 'WAITBAR', true).get('GET_DIR'
  ).get('GR'); (5)
16 gr3 = ImporterGroupSubjectST_MP_XLS('BA', ba, 'WAITBAR', true).get('GET_DIR'
  ).get('GR'); (6)
17
18 %% Analysis 1
19 a_BUD1 = AnalyzeGroup_ST_MP_BUD('GR', gr1, 'DENSITIES', [10 20 30 40 50]);
  (7)
20
21 %% Analysis 2
22 a_BUD2 = AnalyzeGroup_ST_MP_BUD('GR', gr2, 'TEMPLATE', a_BUD1); (8)
23
24 %% Analysis 3
25 a_BUD3 = AnalyzeGroup_ST_MP_BUD('GR', gr3, 'TEMPLATE', a_BUD1); (9)
26
27 %% Comparison
28 c_BUD1 = CompareGroup('P', 1000, 'A1', a_BUD1, 'A2', a_BUD2, 'MEMORIZE',
  true); (10)
29 c_BUD2 = CompareGroup('P', 1000, 'A1', a_BUD1, 'A3', a_BUD3, 'MEMORIZE',
  true); (11)
30 c_BUD3 = CompareGroup('P', 1000, 'A2', a_BUD2, 'A3', a_BUD3, 'MEMORIZE',
  true); (12)

```

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(1) specifies the name of the pipeline. **The name is changed to avoid conflicts.**

(2) provides descriptions for the overall pipeline as well as for each step. **This is updated to reflect the updated pipeline.**

(3) loads the brain atlas.

(4) loads group 1 from XLS.

(5) loads group 2 from XLS.

(6) loads group 3 from XLS. **This is added.**

(7) performs the graph analysis for group 1. The default value of 'DENSITIES' is set to [10 20 30 40 50].

(8) performs the graph analysis for group 2 with the same analysis template as with group 1.

(9) performs the graph analysis for group 3 with the same analysis template as with group 1. **This is added.**

(10) compares graph measures between groups 1 group 2. The default value of the number of permutations is 'P' set to 1000.

(11) compares graph measures between groups 1 and 3. **This is added.**

(12) compares graph measures between groups 2 and 3. **This is added.**