

# *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, we will explain how to edit a \*.braph2 file to change the steps of a pipeline in braph2genesis. Here, we will use as an example the pipeline Pipeline Structural Multiplex Comparison BUD (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.

## *Contents*

## Adaption of the pipeline

### Pipeline Structural Multiplex Comparison BUD

We will start by adapting in detail Pipeline Structural Multiplex Comparison BUD.

Code 1: The pipeline for comparing two 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
30 c_BUD2 = CompareGroup('P', 1000, 'A1', a_BUD1, 'A3', a_BUD3, 'MEMORIZE',
  true); (11)
31
32 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.

(2) The descriptions for each step are annotated.

(3) loads the brain atlas.

(4) loads group 1 from XLS.

(5) loads group 2 from XLS.

(6) loads group 3 from XLS.

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

(8) performs the graph analysis for group 2 while maintaining the same template 'TEMPLATE' with group 1 'a\_BUD1'.

(9) performs the graph analysis for group 3 while maintaining the same template 'TEMPLATE' with group 1 'a\_BUD1'.

(10) compares graph measures between the group 1 and group 2. The default value of the number of permutation test 'P' is 1000.

(11) compares graph measures between the group 1 and group 3.

(12) compares graph measures between the group 2 and group 3.