

# *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 % PDF: /tutorials/pipelines/tut_a_mp_st_bud/tut_a_mp_st_bud.pdf ③
11 % README: /tutorials/pipelines/tut_a_mp_st_bud/readme.md
12
13 %% Brain Atlas
14 ba = ImporterBrainAtlasXLS('WAITBAR', true).get('GET_FILE').get('BA'); ④
15
16 %% Groups
17 gr1 = ImporterGroupSubjectST_MP_XLS('BA', ba, 'WAITBAR', true).get('GET_DIR'
  ).get('GR'); ⑤
18 gr2 = ImporterGroupSubjectST_MP_XLS('BA', ba, 'WAITBAR', true).get('GET_DIR'
  ).get('GR'); ⑥
19 gr3 = ImporterGroupSubjectST_MP_XLS('BA', ba, 'WAITBAR', true).get('GET_DIR'
  ).get('GR'); ⑦
20
21 %% Analysis 1
22 a_BUD1 = AnalyzeGroup_ST_MP_BUD('GR', gr1, 'DENSITIES', [10 20 30 40 50]);
  ⑧
23
24 %% Analysis 2
25 a_BUD2 = AnalyzeGroup_ST_MP_BUD('GR', gr2, 'TEMPLATE', a_BUD1); ⑨
26
27 %% Analysis 3
28 a_BUD3 = AnalyzeGroup_ST_MP_BUD('GR', gr3, 'TEMPLATE', a_BUD1); ⑩
29
30 %% Comparison
31 c_BUD1 = CompareGroup('P', 1000, 'A1', a_BUD1, 'A2', a_BUD2, 'MEMORIZE',
  true); ⑪
32 c_BUD2 = CompareGroup('P', 1000, 'A1', a_BUD1, 'A3', a_BUD3, 'MEMORIZE',
  true); ⑫
33 c_BUD3 = CompareGroup('P', 1000, 'A2', a_BUD2, 'A3', a_BUD3, 'MEMORIZE',
  true); ⑬

```

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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 provides the relative file paths for this pipeline's tutorial, including both the PDF and README versions

④ loads the brain atlas.

⑤ loads group 1 from XLS.

⑥ loads group 2 from XLS.

⑦ loads group 3 from XLS. This is added.

⑧ performs the graph analysis for group 1. The default value of 'DENSITIES' is set to [10 20 30 40 50].

⑨ performs the graph analysis for group 2 with the same analysis template as with group 1.

⑩ performs the graph analysis for group 3 with the same analysis template as with group 1. This is added.

⑪ compares graph measures between groups 1 group 2. The default value of the number of permutations is 'P' set to 1000.

⑫ compares graph measures between groups 1 and 3. This is added.

⑬ compares graph measures between groups 2 and 3. This is added.