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.

```
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 unidrected 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)
```

(1) specifies the name of the piepline.

(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.