`biacpype` User Manual

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Contents

1 Overview

`biacpype` serves as a pipeline for converting raw fMRI data from Brain Imaging & Analysis Center (BIAC) at Duke University to the new standard Brain Imaging Data Structure (BIDS) format, and supporting furthur analysis. The main parts of `biacpype` contains:

- `biac2bids`: conversion from BIAC to BIDS

- ...

The structure of this repository is:

```
|-biacpype // serves as the library
|     |
|     |_biac2bids
|     |_ ...
|
|-scripts  // scripts for running a variety of pipelines
|     |
|     |_convert_to_bids.py
|     |_ ...
|
|-docs     // documentation (under construction)
    |
    |_ ...
```

The following section will introduce main modules of `biacpype`, and the corresponding scripts for using the pipelines.

If you have any questions, please email Preston Jiang at linxing.jiang@duke.edu or prestonj@cs.washington.edu

2 `biac2bids`

`biac2bids` module is the pipeline for converting raw data from BIAC in forms of `bxh` and `nifti` to BIDS format. The workflow is as follows:
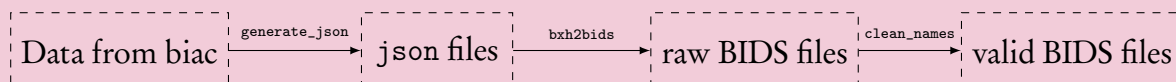
2.1 Prerequisites

`biac2bids` makes the following assumptions on the format of your raw data from BIAC:

```
|-Data
|      |
|      |-Func
|      |  |
|      |  |-<[date_]subject>
|      |  |         |
|      |  |         |-<biac5_subject_task_run>.bxh
|      |  |         |-<biac5_subject_task_run>.nii.gz
|      |  |         |-...
|      |  |         |-series_order_note.tsv
|      |  |-...
|      |
|      |-Anat
|         |-<[date_]subject>
|         |         |
|         |         |-<biac5_subject_task_run>.bxh
|         |         |-<biac5_subject_task_run>.nii.gz
|         |         |-...
|         |         |-series_order_note.tsv
|         |-...
|
|-biac_id_mapping.tsv
```

Explanations:

- Data folder has to contain Func and Anat, and they must have the exact same folders

- Subfolders in Func and Anat are in format [date_]subject where [date_] is optional. E.g. 19354 and 20140101_19354 are both acceptable.

- Each file in Func and Anat must in format biac5_subject_task_run. Usually, task is a single digit number, run is two-digit. E.g. biac5_19354_4_01.bxh

- Each subfolder in Func and Anat **must contain** a series_order_note.tsv to tell the pipeline what each task number stands for. E.g. 4 stands for "TRAIN". Requirements for this file are later explained.

- In the same folder containing Data, there **must contain** a biac_id_mapping.tsv which tells the pipeline the mapping from BIAC_ID (e.g. 19354) to the session name (e.g. Session-1) and the Real_ID used by your lab (e.g. 101). Requirements for this file are later explained.

Requirements on series_order_note.tsv are as follows:

4	LOCALIZER
7	TRAIN1
...	...

Note:

- The values must be **tab** separated.

3

- Task numbers in the first column *must* match that in the imaging files. For example, a "4" in `translation_file` and a "004" in the imaging file will result in an error.

- The first column must be task code, and the second column must be the task name. There can only be two columns

Requirements on `biac_id_mapping.tsv` are as follows:

BIAC_ID	Session	Real_ID
19354	SRM	101
19338	SPM	102
19368	SPM	101
...	...	...

Note:

- The values must be **tab** separated.

- The headers must follow the rules (watch letter cases)!

- If your experiment does not multiple sessions, use only the first and last column.

2.2   Scripts

The script associated with this module is `scripts/convert_to_bids.py`. There are four parameters the user has to toggle. They are:

- `STUDY_PATH`: the path to your study file (which contains `Data` and `bids_id_mapping.csv`)

- `JSON_OUTPUT_PATH`: the path where the user wants the json files to be saved

- `BIDS_PATH`: the path where the user wants the new BIDS format data to be saved

- `LOG_PATH`: the path where the user wants the logs to be saved