

biacptype User Manual

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1 Overview

biacpye 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 further analysis. The main parts of biacpye contains:

- biac2bids: conversion from BIAC to BIDS
- ...

The structure of this repository is:

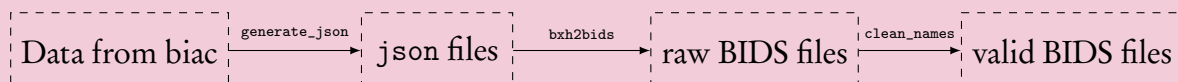
```
| -biacpye // serves as the library
|   |
|   | _biac2bids
|   | _ ...
|
| -scripts // scripts for running a variety of pipelines
|   |
|   | _convert_to_bids.py
|   | _ ...
|
| -docs    // documentation (under construction)
|   |
|   | _ ...
```

The following section will introduce main modules of biacpye, 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 bxx 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.txt
|   |   | -...
|   |
|   |-Anat
|   |   | -<[date_] subject >
|   |   |
|   |   |   | -<biac5_subject_task_run>.bxh
|   |   |   | -<biac5_subject_task_run>.nii.gz
|   |   |   | -...
|   |   |   | -series_order_note.txt
|   |   | -...
|
|-biac_id_mapping.csv

```

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.txt** 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.csv** 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.txt are as follows:

4	LOCALIZER
7	TRAIN1
...	...

Note:

- 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.csv` are as follows:

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

Note:

- 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