**Team 5**

**Install Dependency**

The required dependencies to use the software are:

1. Python >= 3.5,
2. setuptools
3. Numpy >= 1.11
4. SciPy >= 0.19
5. Scikit-learn >= 0.19
6. Joblib >= 0.12
7. Nibabel >= 2.0.2
8. matplotlib >= 1.5.1

**Data Fetching**

**You have to fetch the data using Nilearn built in function**

If you want to run the tests, you need pytest >= 3.9 and pytest-cov for coverage reporting.

nilearn.datasets.fetch\_abide\_pcp(*data\_dir=None, n\_subjects=None, pipeline='cpac', band\_pass\_filtering=False, global\_signal\_regression=False, derivatives=['func\_preproc'], quality\_checked=True, url=None, verbose=1, \*\*kwargs*)

**Fetch ABIDE dataset**

Fetch the Autism Brain Imaging Data Exchange (ABIDE) dataset wrt criteria that can be passed as parameter. Note that this is the preprocessed version of ABIDE provided by the preprocess connectome projects (PCP).

**Parameters/Arguments**

**data\_dir: string, optional**

Path of the data directory. Used to force data storage in a specified location. Default: None

**n\_subjects: int, optional**

The number of subjects to load. If None is given, all available subjects are used (this number depends on the preprocessing pipeline used).

**pipeline: string, optional**

Possible pipelines are “ccs”, “cpac”, “dparsf” and “niak”

**band\_pass\_filtering: boolean, optional**

Due to controversies in the literature, band pass filtering is optional. If true, signal is band filtered between 0.01Hz and 0.1Hz.

**global\_signal\_regression: boolean optional**

Indicates if global signal regression should be applied on the signals.

**derivatives: string list, optional**

Types of downloaded files. Possible values are: alff, degree\_binarize, degree\_weighted, dual\_regression, eigenvector\_binarize, eigenvector\_weighted, falff, func\_mask, func\_mean, func\_preproc, lfcd, reho, rois\_aal, rois\_cc200, rois\_cc400, rois\_dosenbach160, rois\_ez, rois\_ho, rois\_tt, and vmhc. Please refer to the PCP site for more details.

**quality\_checked: boolean, optional**

if true (default), restrict the list of the subjects to the one that passed quality assessment for all raters.

**kwargs: parameter list, optional**

Any extra keyword argument will be used to filter downloaded subjects according to the CSV phenotypic file. Some examples of filters are indicated below.

**SUB\_ID: list of integers in [50001, 50607], optional**

Ids of the subjects to be loaded.

**DX\_GROUP: integer in {1, 2}, optional**

1 is autism, 2 is control

**DSM\_IV\_TR: integer in [0, 4], optional**

O is control, 1 is autism, 2 is Asperger, 3 is PPD-NOS, 4 is Asperger or PPD-NOS

**AGE\_AT\_SCAN: float in [6.47, 64], optional**

Age of the subject

**SEX: integer in {1, 2}, optional**

1 is male, 2 is female

**HANDEDNESS\_CATEGORY: string in {‘R’, ‘L’, ‘Mixed’, ‘Ambi’}, optional**

R = Right, L = Left, Ambi = Ambidextrous

**HANDEDNESS\_SCORE: integer in [-100, 100], optional**

Positive = Right, Negative = Left, 0 = Ambidextrous

Notes

Code and description of preprocessing pipelines are provided on the *PCP website <http://preprocessed-connectomes-project.github.io/>*.

**References**

Nielsen, Jared A., et al. “Multisite functional connectivity MRI classification of autism: ABIDE results.” Frontiers in human neuroscience 7 (2013).