
MiTfAT

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CONTENTS:

1	Introduction	1
2	First Step	3
2.1	Installation	3
2.2	Compatibility	4
2.3	License	4
2.4	Citation	4
2.5	Authors	4
3	Basics	5
3.1	Loading the data	5
3.2	How to fill in the config file:	6
4	Basic Plots	7
5	Clustering	11
6	Hierarchical Clustering	15
7	Detrending	17
8	Experiments Including Trials	19
9	Altering the data after loading	23
10	mitfat package	25
10.1	Submodules	25
10.2	mitfat.bplots module	25
10.3	mitfat.clustering module	26
10.4	mitfat.collections module	28
10.5	mitfat.file_io module	28
10.6	mitfat.flags module	30
10.7	mitfat.fmri_dataset module	30
10.8	mitfat.mitfat_test_script module	33
10.9	Module contents	33
11	Indices and tables	35
Python Module Index		37
Index		39

CHAPTER ONE

INTRODUCTION

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License GPLv3

MiTfAT is a scikit-learn-friendly Python library to analyse fMRI data.

There are a few software packages that are commonly used by researchers to pre-process the fMRI time-series and then analyse them. But the decision to develop a new library which eventually led to *MiTfAT* library is motivated by a few reasons. The main reason is that all the commonly used fMRI analysis packages come with so many bells and whistles that it usually takes the user a long time to find out which parts of each software package is what he/she need. Another reason was that none of the commonly used software packages I could find was written in Python, which is my programming language of choice. And lastly, the analysis methods I needed for the problems I had in mind were not available in any of those software packages.

Hence the *MiTfAT* was developed. It is designed to be used for general fMRI time-series analysis, but in particular, signals obtained from molecular fMRI studies, i.e. the cases in which we measure the changes in concentration of molecules which might have been directly injected into the brain (which happens when the molecule is too big to pass through blood-brain-barrier).

The basic principle behind *MiTfAT* is that it imports all the relevant data of an fMRI experiment into a class object. The fMRI time-series are a member of this class and are stored as NumPy arrays. There are various functionalities available to analyse the data in a number of ways. They include:

- Clustering the time-series using K-means clustering. Clustering can be done based on values in all time-steps, or the mean value of each time-series or slope of a linear-regression passing through the time-series. And it can be applied to raw data or the normalised data. *MiTfAT* uses *scikit-learn* for all machine learning functions. Hence, K-means can be easily changed with any other clustering algorithm implemented in *scikit-learn*.
- Hierarchical clustering; which applies clustering in two stages. In the first step, the algorithm removes the time-series corresponding to voxels in which signal to noise ratio is not high enough. And in the second step, the time-series corresponding to the remaining voxels are clustered.
- Detrending. We can remove the general trends in time-series to make the transient changes more visible. As an example, if we cannot wait long enough until the concentration of our agent reaches steady-state level then transient variations in the signal caused by changes in experimental conditions, which is what we are interested in, might be obscured by such trends in the signal. *MiTfAT* can detrend the time series and give us a signal which looks like the one we might expect in steady-state. And then, transient changes due to experimental design would be quantifiable.
- Interpolation of time-series under varying conditions. Let's say we have an experiment in which the total recording time is divided into 3 segments. In the second segment, we record under a different condition compared to

the first and last segment. This can be, as an example, the occlusion of an artery which changes calcium concentration in the brain when the agent we have injected into the brain binds with calcium. Obviously, we want to quantify how the signal has changed in the second segment. In order to do so, we should interpolate the time-series in segment 2 based on values of segments 1 and 3, and then compare it with the actual measurements. *MiTfAT* provides such a feature for us.

- Averaging over many trials. If we repeat an experiment many times, then it is usually of interest to average the measurements over all the trials. This can be useful if each measurement is noisy and we want to attenuate the effects of noise. *MiTfAT* allows us to do so.

FIRST STEP

2.1 Installation

It is better to install *MiTfAT* in a new virtual environment. If you are using Anaconda Python, you can do the following:

```
conda create -n env_mitfat  
conda activate env_mitfat
```

Then in your command prompt or bash, simply type:

```
pip install mitfat
```

Or if you want to work with the latest beta-release, you can install directly from [this repository](#).

If you don't know anything about Python:

then you should not worry. In order to use this code, you do not need to know anything about python. You just need to install it and then follow the instructions in the Usage section to be able to run the code. But you need to install Python first. Python is just a programming language and unlike Matlab is not owned by a company or organization, hence you do not need to buy a license to use it. There are various ways to install Python, but the easiest is to go [here](#) and install Miniconda Python 3.x (3.7 at the time of writing). This will install Python and a minimal set of commonly used libraries (Libraries in Python are equivalent to toolboxes in Matlab). A little detail to keep in mind for Windows users is that you need to open an Anaconda Prompt (which you can find in your Start menu) and then type `pip install mitfat` to install the *MiTfAT* library. Typing it in a normal windows command prompt (which you can open by typing `cmd` in 'Search program or file' in the Start menu) might not work properly.

When Python is installed, then follow the instructions below to use this code to analyse your fMRI data. I should add though, that I sincerely hope using this code can motivate you to learn a bit about Python. I learned how to use Matlab 20 years ago and still use it to this day. But as I learn more about Python and what is available in this ecosystem, I use Matlab less and Python more and more everyday. Python provides powerful tools for you that you did not know you are missing when you were writing programs in Matlab. If you want to learn the basics of Python, I can suggest this [online book](#) to start with.

2.1.1 Requirements

```
"pandas",  
"numpy",  
"scipy",  
"matplotlib",  
"nibabel",  
"nilearn",
```

(continues on next page)

(continued from previous page)

```
"pathlib",  
"click",  
"seaborn",  
"openpyxl",
```

2.2 Compatibility

This code is tested under Python 3.7, and should work well for all current version of Python 3.

2.3 License

GNU General Public License (Version 3).

2.4 Citation

Please cite this code as follows:

Bokharaie VS (2019) “*MiTfAT*: A Python-based fMRI Analysis Tool”, Zenodo. <https://doi.org/10.5281/zenodo.3372365>.

This code was originally developed for a collaboration which led to the following publications:

Savić T. , Gambino G., Bokharaie V. S., Noori H. R., Logothetis N.K., Angelovski G., “Early detection and monitoring of cerebral ischemia using calcium-responsive MRI probes”, PNAS, 2019.

2.5 Authors

MiTfAT is maintained by Vahid Samadi Bokharaie.

BASICS

The *MiTfAT* library incorporates all the relevant data and information about an experiment into a Python class of type *fmri_dataset*, and then the user can perform various analysis and visualisatin steps. In order to load the fMRI data, currently, the required information about data files and details of the experiment should be written down in a specified format in a config file, details of which will be discussed shortly. But if you want to get started with some sample data and know some of the features of the library, you can download two sample scripts and corresponding datasets from [here](#). When up unzip the file, you can see a folder called `tests` in which you can see two python scrips. There are also two subfolder, each contains sample datasets that are used by each of the scripts. And you can also see three text files which are the config files used by scripts.

If you have installed *MiTfAT*, then you can run each of these scripts and the outputs they generate will be saved in new sub-folders inside the `tests` folder. Studying these two scripts can be quite informative and it is highly recommended for the users. If you want to use these samples scripts for your own data, you can simply edit the config files.

In the following chapters, main features of the code are explained. The figures you will see in the following chapter are generated using these two sample scripts.

3.1 Loading the data

All you need to do to load your dataset, including data file, mask file, time stamps, and optional descriptive parameters, is fill in a text file in a certain format (as explained below), to let *MiTfAT* know where and what your input data are. When this file is set up properly, and saved, for example as ‘`my_first_config_file.txt`’, then all you need to do to load the data is to run the following lines in Python:

```
from mitfat.file_io import read_data
list_of_datasets = read_data(info_file)
my_first_dataset = list_of_datasets[0]
```

If you have defined trials in your experiment and keep repeating the same stimulus and record the responses, then `list_of_datasets` would contain all of those datasets in a separate *fmri_dataset* format. If no trials are defined, the list would contain only one *fmri_dataset* object.

If you are new to Python, you should know that you can copy the above or any set of python commands, paste them to a file, save it with `.py` extension, and then in the command prompt, type

```
python my_first_python_file.py
```

These are just very basic issues that you know already if you have ever used python. But if you haven’t, you just need to spend half an hour learning them to be able to use this and a wealth of other libraries written in Python.

3.2 How to fill in the config file:

The config file has a specific format. Each line that starts with one of a number of keywords is assumed to be followed by the information. For example, the following line are what you can find in one of the config files that come with sample scripts:

```
# obligatory info:  
DATA_FILE: corr_FISP_UN1_s26.nii.gz  
MASK_FILE: UN1_scan26_1_00001_mask.nii.gz  
  
# optional: source and save folders  
DIR_SOURCE: datasets_trials  
DIR_SAVE: Output_Trials_Dataset  
  
# other optional info  
DS_NO: 26  
EXP_NAME: UN1  
  
SIGNAL_NAME: T1w  
MOL_NAME: PFCE_5_mM  
  
FIRST_TRIAL_TIME: 0.0  
TRIAL_LENGTH: 30.0  
TIME_STEP: 3  
EVENT_TIMES: 6.0, 12.0
```

The keywords are self-explanatory. They are not case-sensitive, but should always be followed by `: ' and then the data.

In order to have a copy of a sample config file with detailed description of the available options, saved as a text files in the current folder, enter the following two commands in python:

```
from mitfat.file_io import print_info  
print_info('sample_config_file.txt')
```

This sample file includes a full description of how the config file should be written and default values for optional parameters.

CHAPTER
FOUR

BASIC PLOTS

There are already some basic operations done on the data. For example, the linear regression of the data in each time segment. Now you can plot raw, normalised, and linearly regressed time-series for each voxel as follows. Plots will be saved under the output folder which is created in the folder from which you are running the python.

```
# Basic plots of normalized time-series
dataset1.plot_basics()

# Plots of linearly regressed time-series.
# Linear regression is performed on each segment separately.
dataset1.plot_basics('lin_reg')

# plots of raw time-series
dataset1.plot_basics('raw')
```

Here is an example of the output plots:

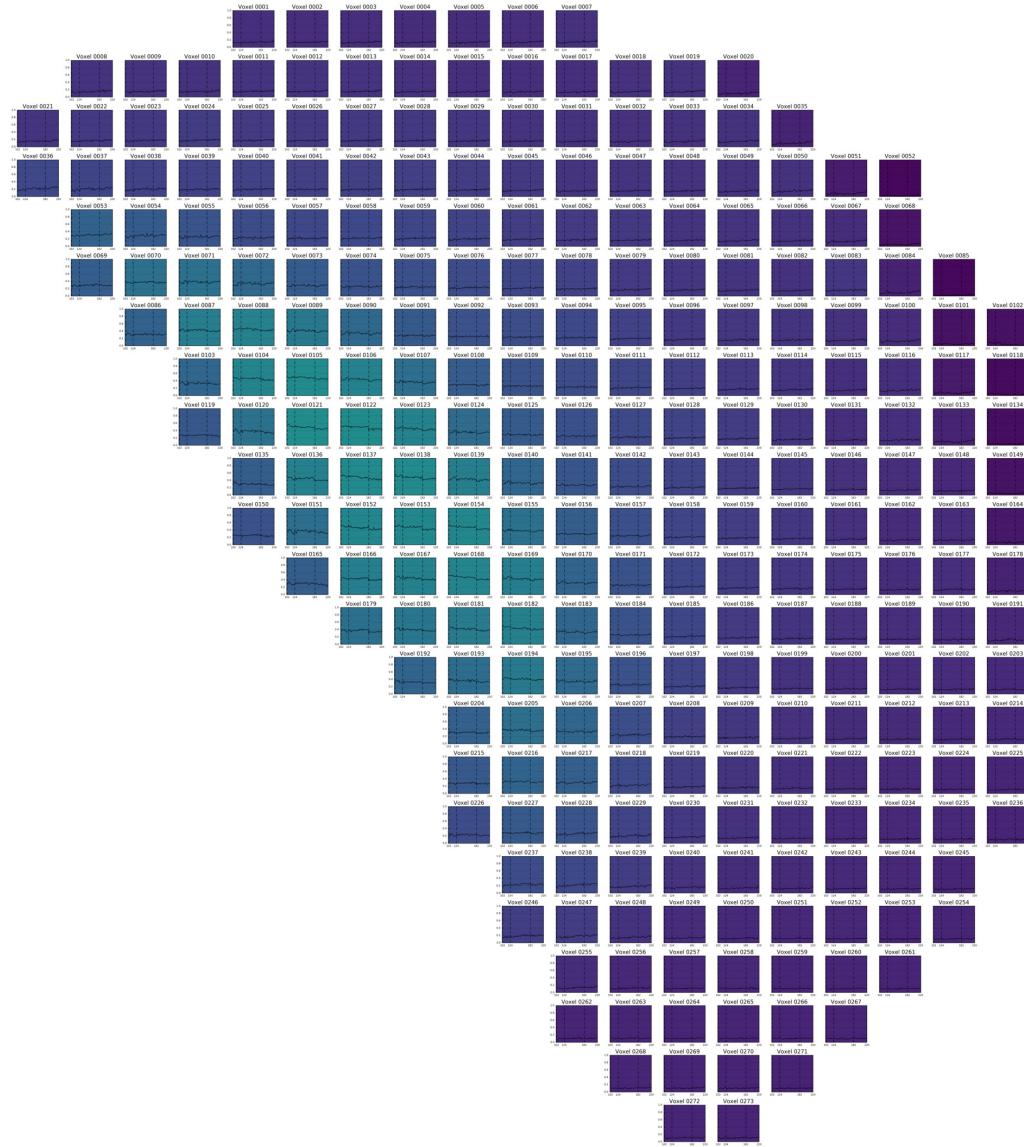


Fig. 1: Basic plots, layer 1 of the original mask.

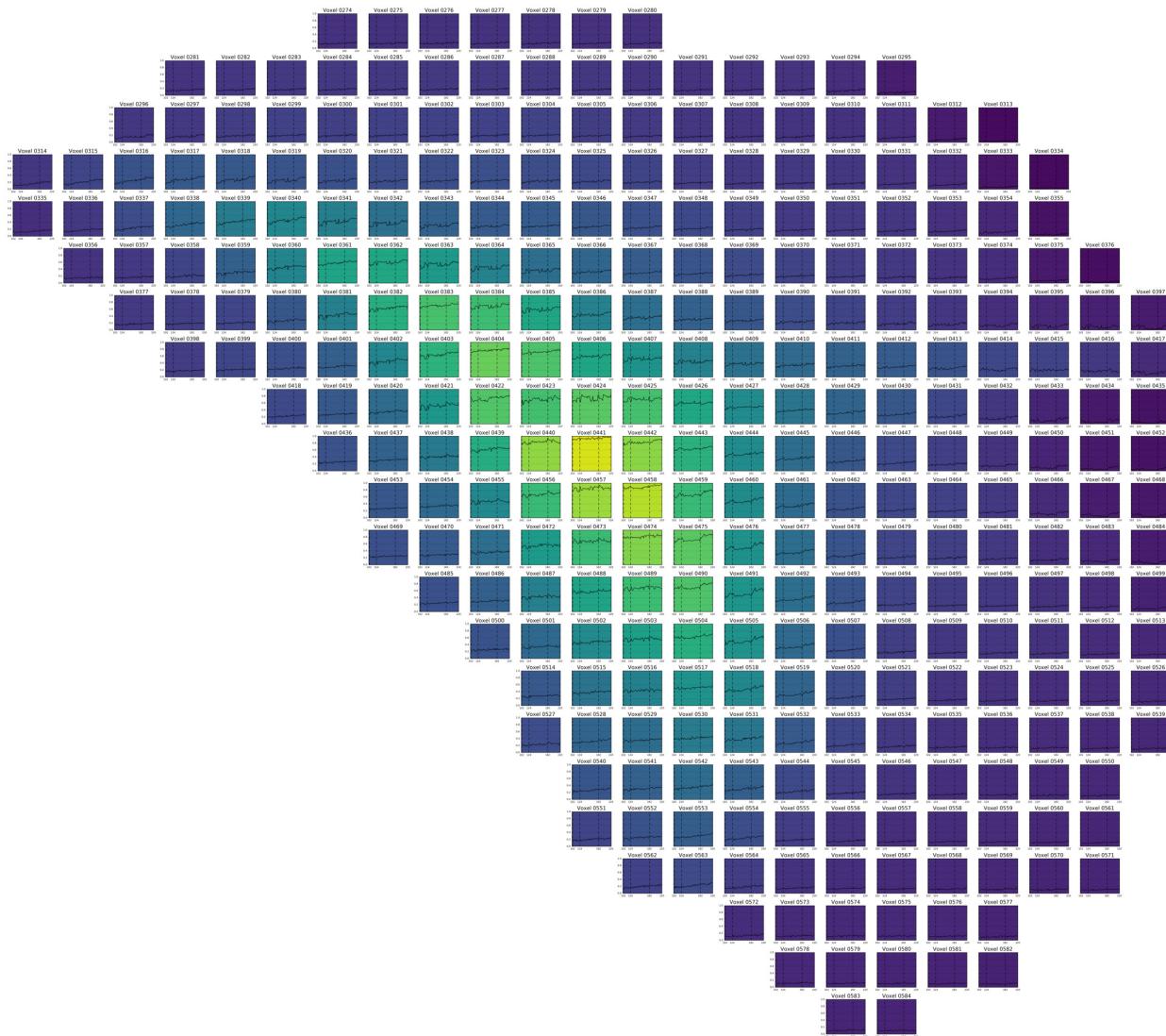


Fig. 2: Basic plots, layer 2 of the original mask.

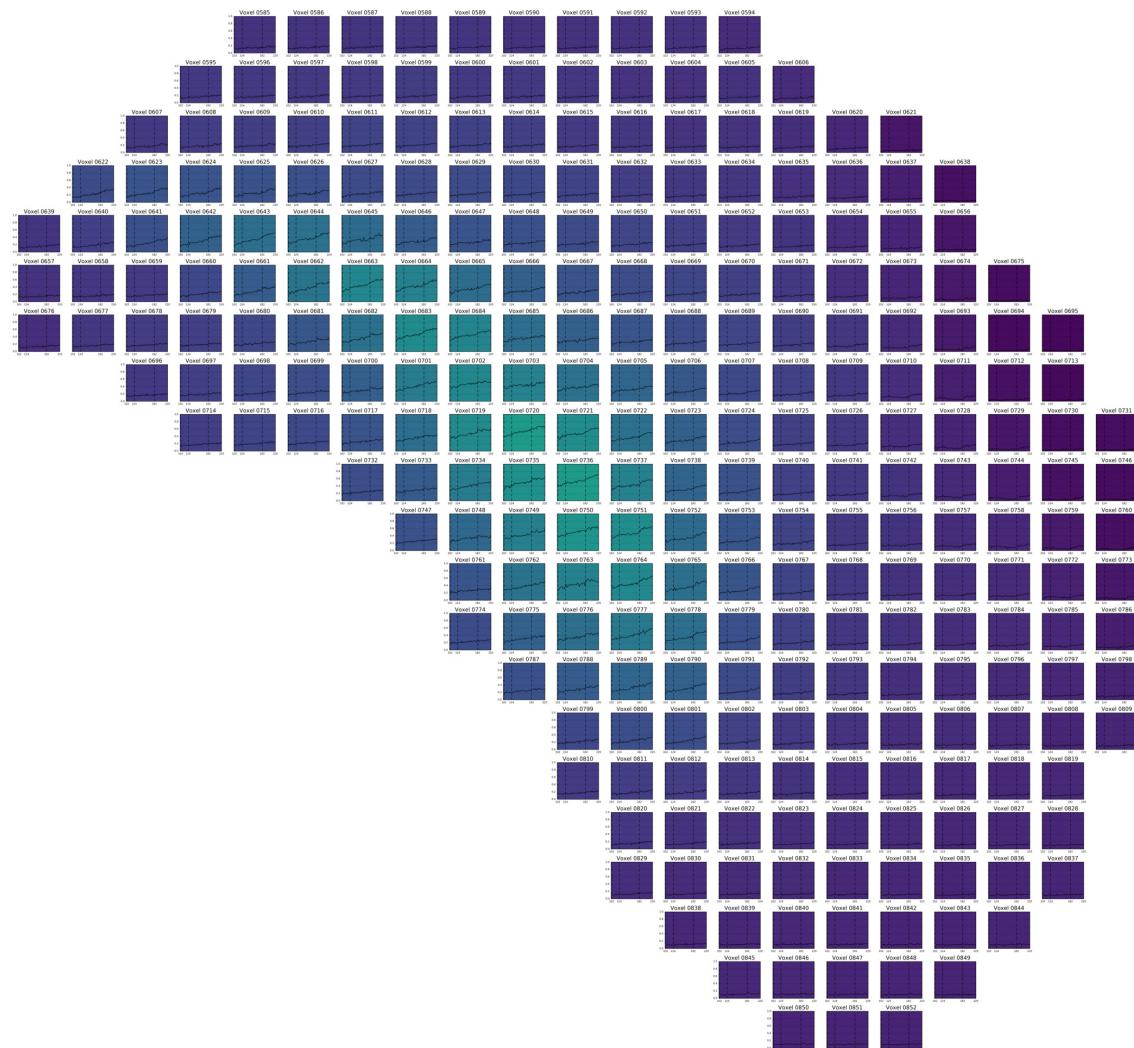


Fig. 3: Basic plots, layer 3 of the original mask.

**CHAPTER
FIVE**

CLUSTERING

You can also cluster the time-series (original or normalized versions), using Kmeans clustering from scikit-learn library:

```
X_train = dataset1.data
X_train_label = 'RAW_Normalised' # used in plot titles only
num_clusters = 5
cluster_labels, cluster_centroid = dataset1.cluster(X_train, num_clusters)
dataset1.save_clusters(X_train, X_train_label,
                      cluster_labels, cluster_centroid)
dataset1.plot_clusters(X_train, X_train_label,
                      cluster_labels, cluster_centroid)
```

which would lead to plots such as these, plus an excel file including the centroids of the clusters:

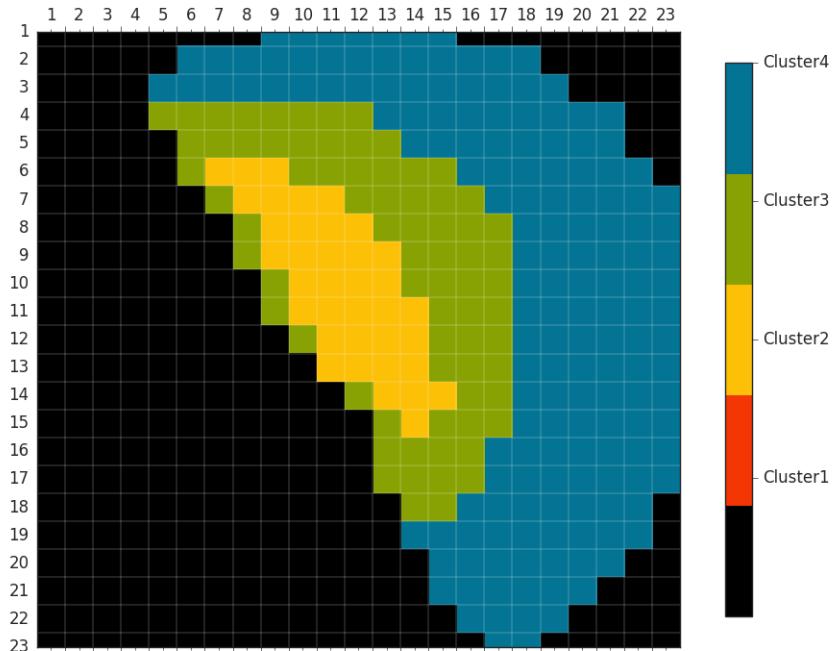


Fig. 1: Voxels color-coded based on their clusters, layer 3 of the mask.

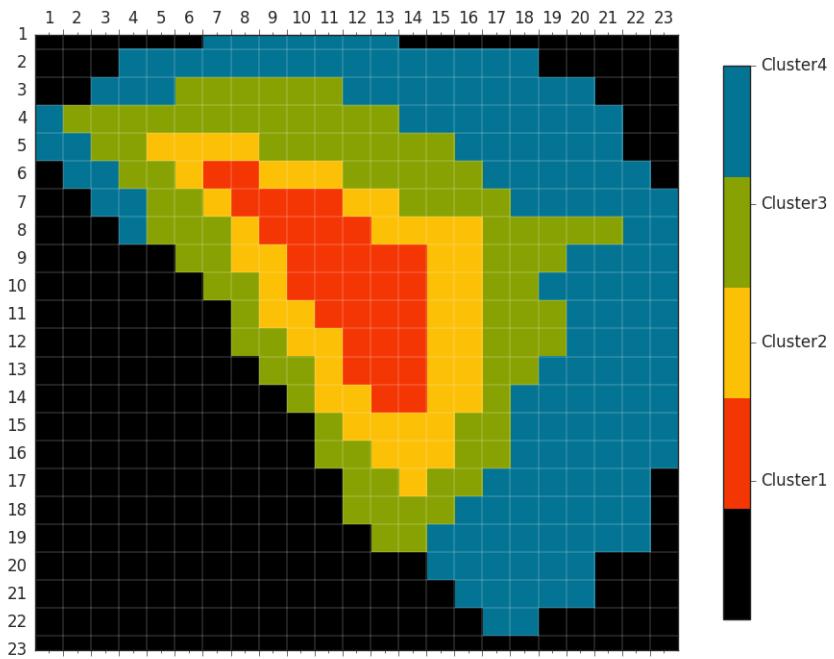


Fig. 2: Voxels color-coded based on their clusters, layer 3 of the mask.

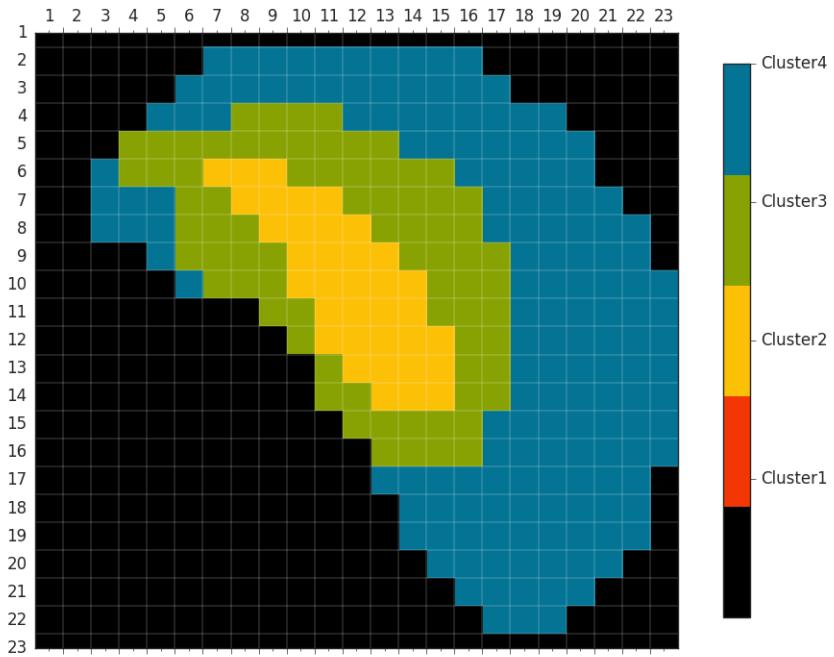


Fig. 3: Voxels color-coded based on their clusters, layer 3 of the mask.

And also the centroids:

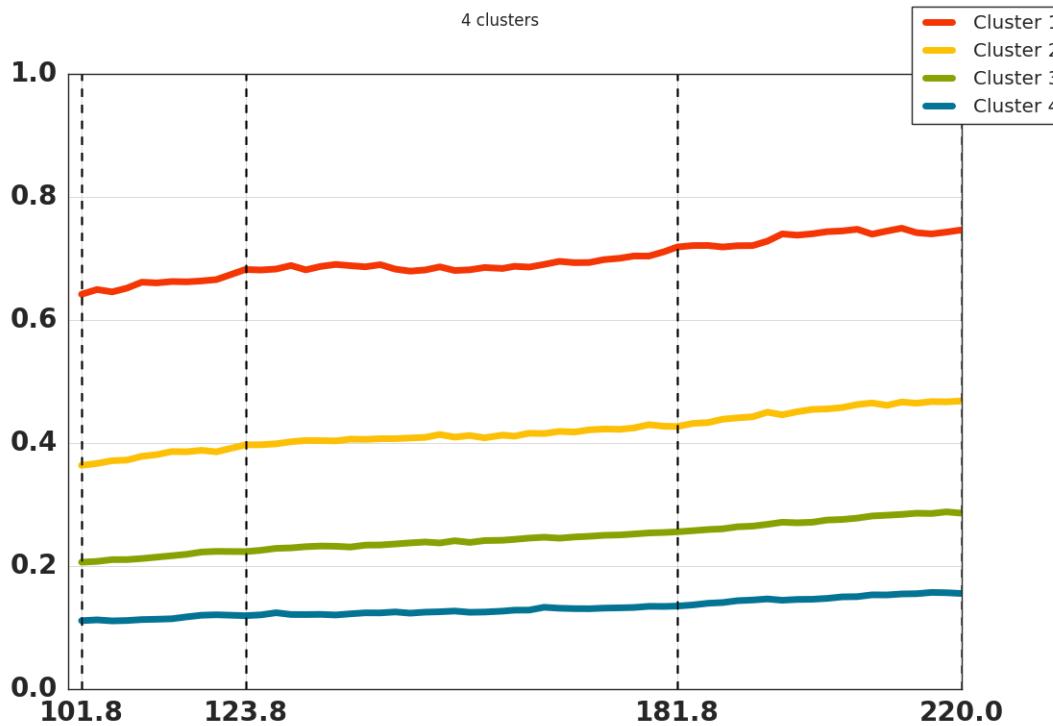


Fig. 4: Centroids.

or cluster voxels based on their mean value:

```
X_train = dataset1.data_mean
X_train_label = 'Mean_Normalised'
num_clusters = 4
cluster_labels, cluster_centroid = dataset1.cluster(X_train, num_clusters)
dataset1.save_clusters(X_train, X_train_label,
                      cluster_labels, cluster_centroid)
dataset1.plot_clusters(X_train, X_train_label,
                      cluster_labels, cluster_centroid)
```

or you can cluster your voxels based on the slope of your three segments.

```
X_train = dataset1.line_reg_slopes
X_train_label = 'Lin_regression_slopes_per_segments'
num_clusters = 4
cluster_labels, cluster_centroid = dataset1.cluster(X_train, num_clusters)
dataset1.save_clusters(X_train, X_train_label,
                      cluster_labels, cluster_centroid)
dataset1.plot_clusters(X_train, X_train_label,
                      cluster_labels, cluster_centroid, if_slopes=True)
```

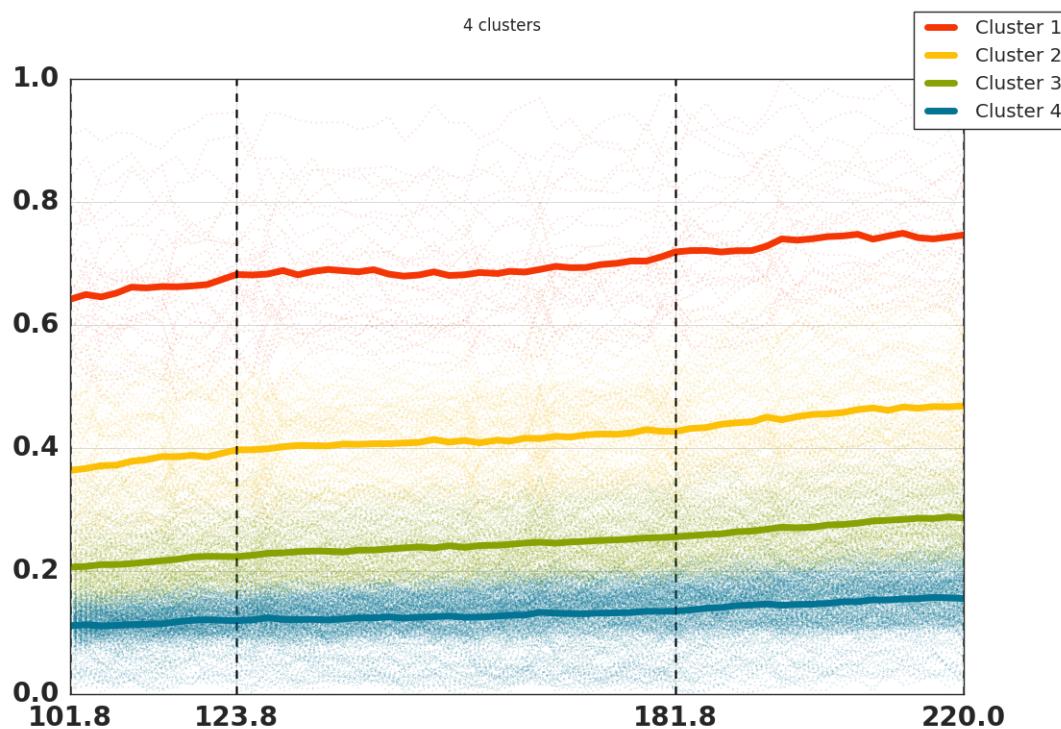


Fig. 5: Centroids with original data.

**CHAPTER
SIX**

HIERARCHICAL CLUSTERING

You can also do hierarchical clustering. This technique is quite useful when you are not sure about the size of your original mask. You might have included some voxels in the mask which are too noisy and including them in clustering might lead to redundant results. Hierarchical clustering works in two steps. In the first step, a Kmeans clustering with 2 clusters is performed. This will separate voxels based on their signal-to-noise ratio. The algorithm selects voxels corresponding with the centroid which has a higher absolute mean value. Then another Kmeans with two clusters is performed over these voxels, and the result is saved and plotted. You can do all that by simply typing:

```
# signal can be 'raw', 'mean', 'slope', 'slope_of_segments', 'mean_segments'  
signal = 'raw'  
dataset1.cluster_hierarchial(signal, if_save_plot=True)
```

This leads to a decrease in the total number of considered voxels, which can be seen in the following figure.

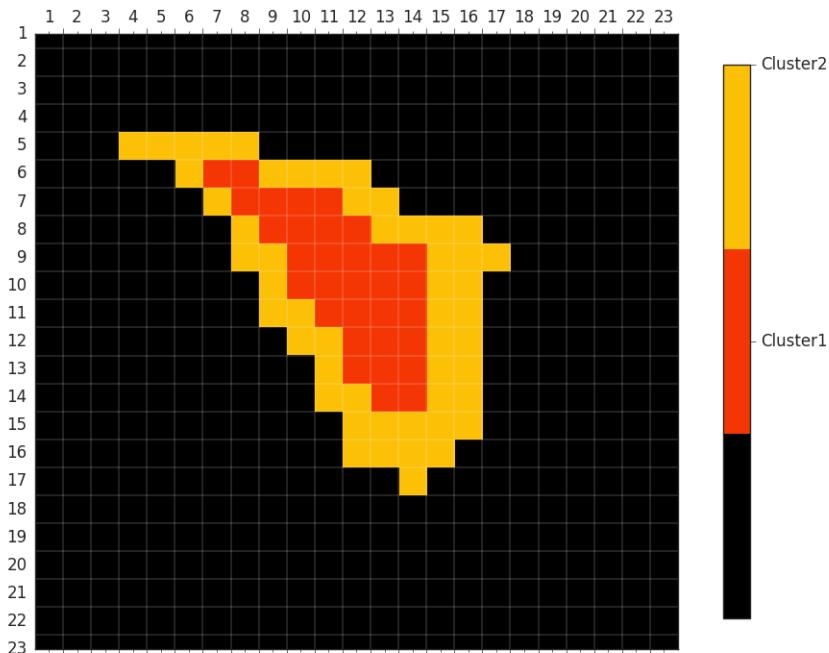


Fig. 1: Voxels color-coded based on their clusters, layer 2 of the mask.

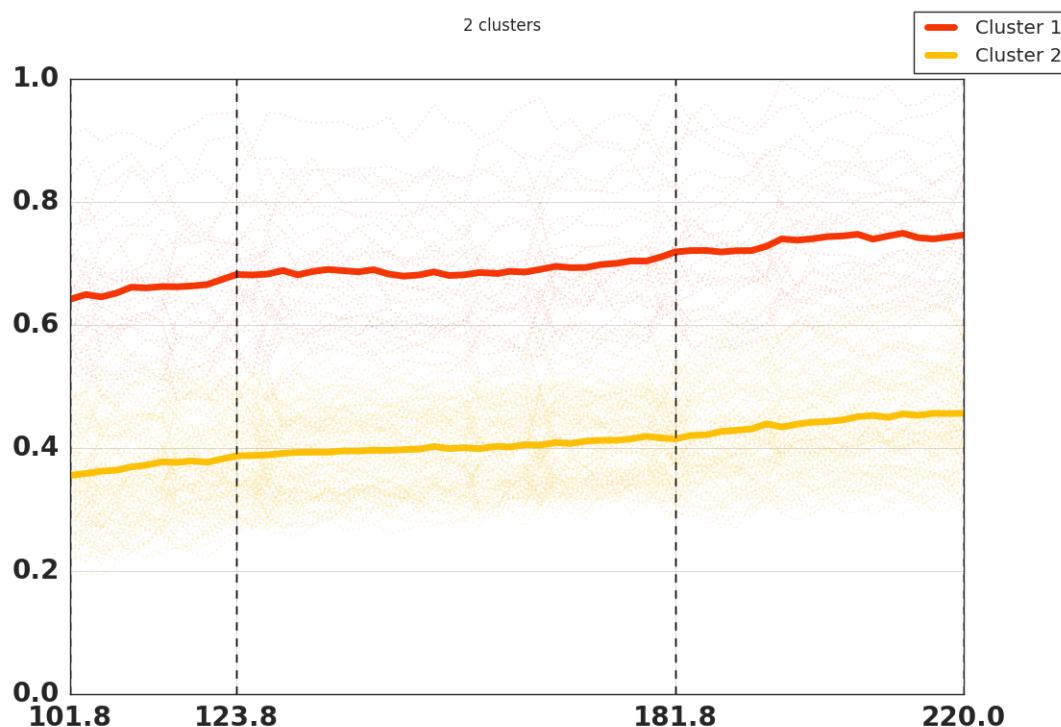


Fig. 2: Centroids.

CHAPTER SEVEN

DETRENDING

You can detrend the data in *MiTfAT*. This is done in two different ways, based on the nature of the data. If there is no ‘events’ entry defined for the data, then detrending includes Spline smoothing of the data. If there are two events, which means the time range is split into three time-segments, then a spline is fit to the first and third segments, and then this smoothed curve is used to interpolate the values of the second segment and then compared with the actual data. The underlying assumption has been that the recording conditions have changed in the second time-segment, and we want to extract the changes only due to that change from the information in the first and third segments. Detrending currently works only for data with zero or two ‘events’ (one or three time-segments) but will be extended to the general case in future releases.

As an example, assume the average of a number of voxels of interests looks like the black line in the following image:

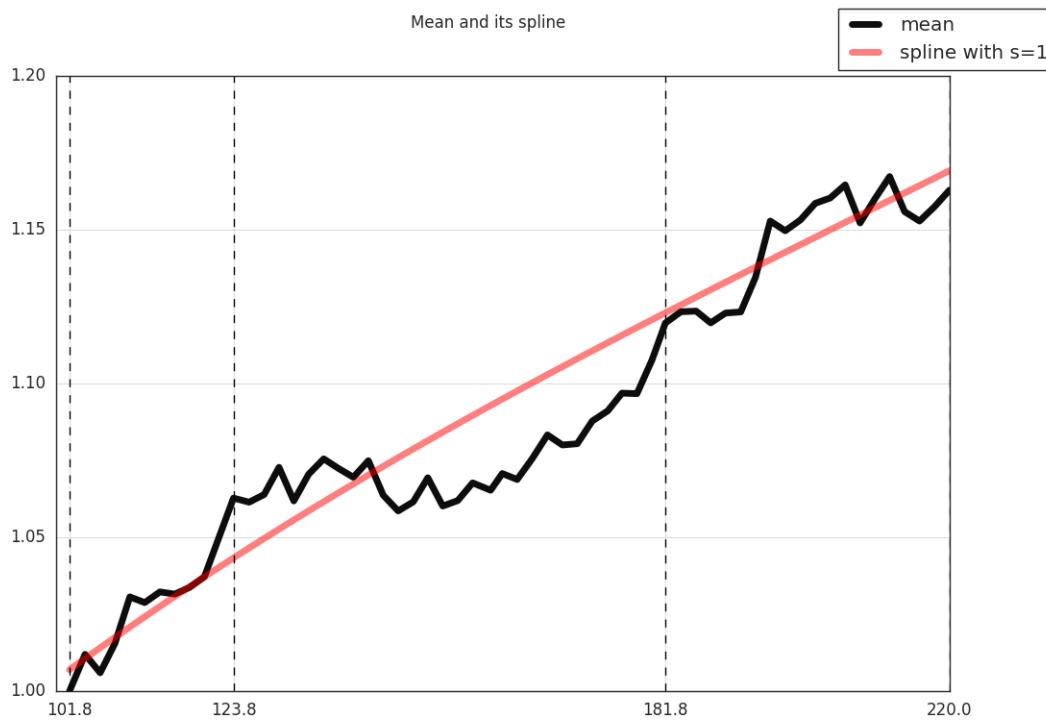


Fig. 1: The signal of interest (black), and the spline calculated only based on segments 1 and 3 (red).

The red signal is a spline that is fit only to the first and the last segment of the original signal. The part of the red curve in segment 2 represents the interpolation of segment 2 based on this spline curve. The difference between red and black lines in segment 2 represents the changes in the signal trend in segment 2.

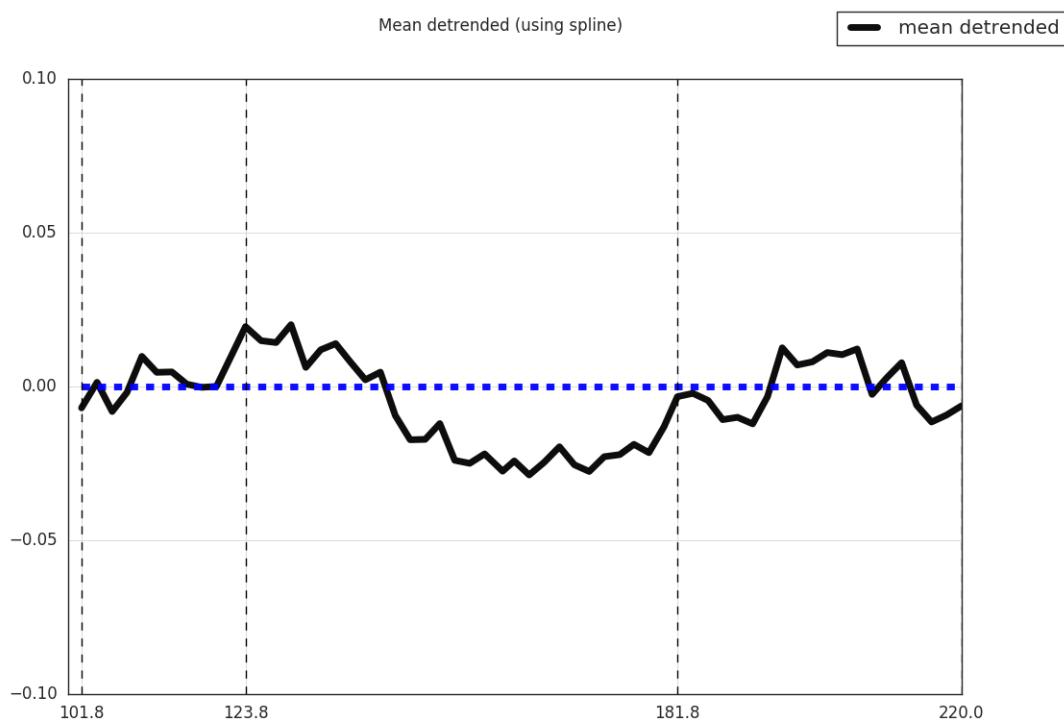


Fig. 2: The detrended signal.

**CHAPTER
EIGHT**

EXPERIMENTS INCLUDING TRIALS

If you run an experiment, which includes trials of a fixed length, you can use *MiTfAT* to analyze such data. Let's say each 10 time-steps in your fMRI recording represent one trial. To tell *MiTfAT* that it should divide the fMRI time-series into a number of trials, you should have the following lines in the info file:

```
FIRST_TRIAL_TIME: 0.0
TIME_STEP: 3
TRIAL_LENGTH: 30.0
EVENT_TIMES: 6.0, 12.0
```

`FIRST_TRIAL_TIME` specifies the time for the first step of the first trial. `TIME_STEP` specifies the time between each two samples. If you don't care about the actual time, just set this to 1. `TRIAL_LENGTH` specifies how long (in units of time) is each trial. `EVENT_TIMES` specifies possible event times of interest in each trial.

Looking at `script_trails.py` you can see what kinds of analysis you can perform on the data. For example, you can choose top N voxels (in terms of amplitude) in the overall time-series of the fMRI signal, and then average these N voxels, and cluster the average over all the trials. You can then plot the centroids of these clusters and also a heat-map indicating to which cluster each trial belongs. This will be quite useful in checking possible patterns in the data.

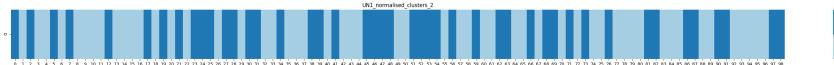


Fig. 1: Sequence of Cluster labels for each trial in an experiment with 99 trials.

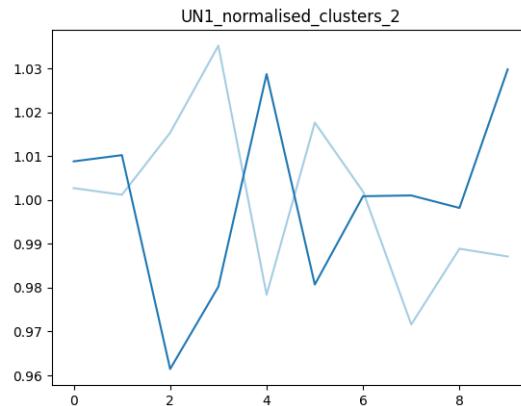


Fig. 2: Centroids of two clusters of the average signals for each trial

As a reminder, to make the above plots, we calculated the mean for N voxels in each trial. And clustered these signals to see if and how the trials differ. It is also worth averaging all these signals to see the average response over all the

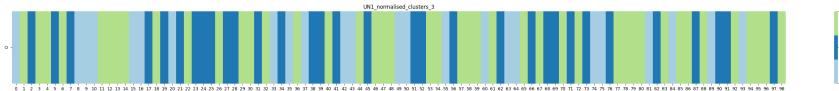


Fig. 3: Sequence of Cluster labels for each trial in an experiment with 99 trials.

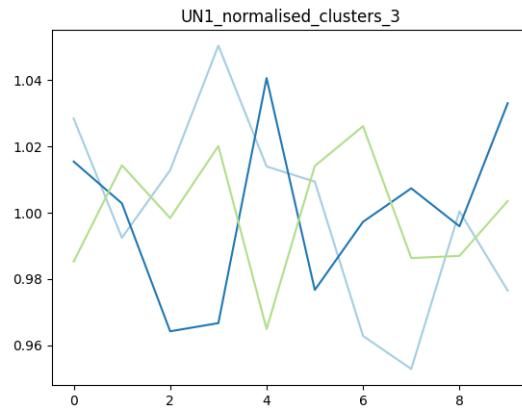


Fig. 4: Centroids of three clusters, time-series being the average signals of each trial

trials. This is possible in two ways: either averaging the raw signals or normalising the signal for each trial first, then averaging them.

We can also group trials and cluster these groups. This is useful when there might be a delay in the fMRI response with respect to the onset of the stimulus. Below, you can see cluster over signals obtained over every two consecutive trials. It means the first set of the signals obtained by concatenating trials 1 and 2, then 2 and 3, and so on.

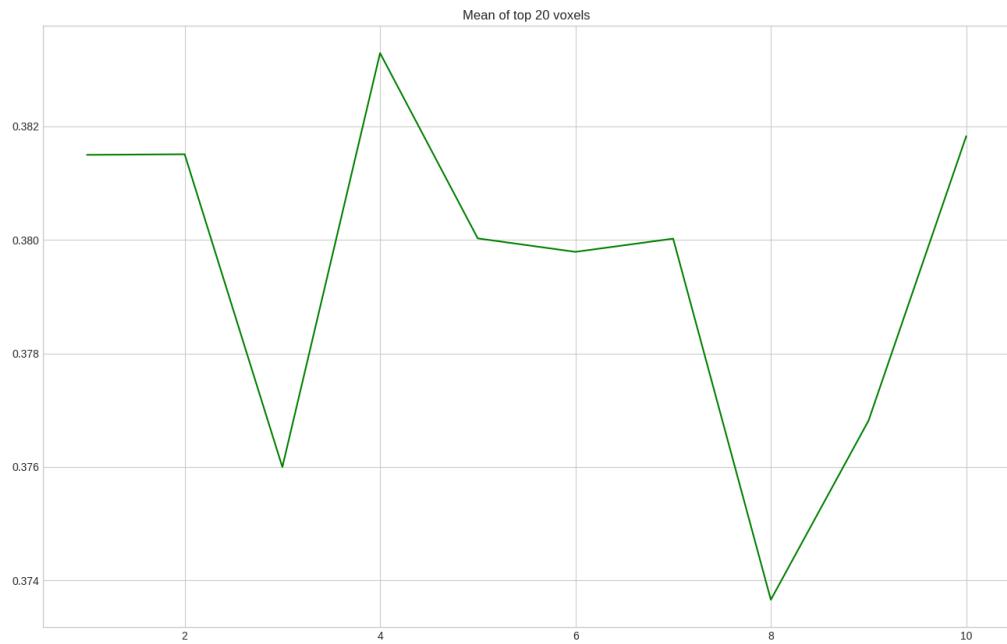


Fig. 5: Average of all 99 trials.

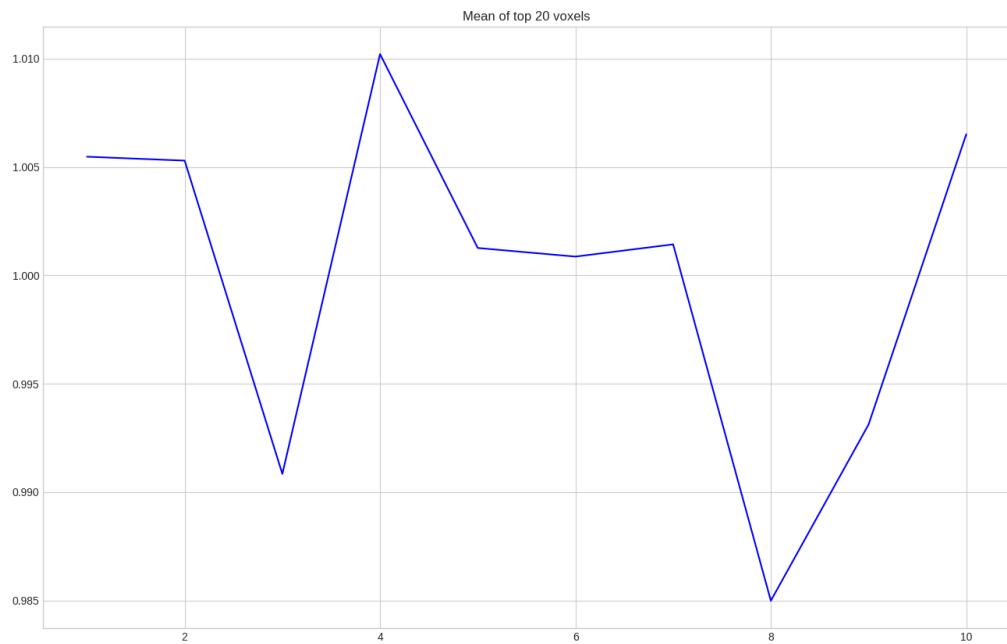


Fig. 6: Average of all 99 trials, each trial signal is normalised before averaging.



Fig. 7: Sequence of Cluster labels for each two consecutive trial in an experiment with 99 trials.

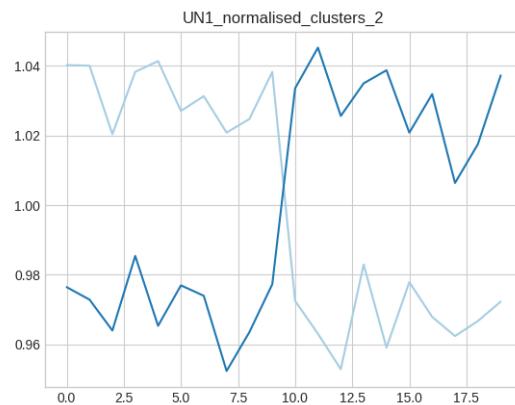


Fig. 8: Centroids of two clusters of the average signals for each two consecutive trial

ALTERING THE DATA AFTER LOADING

If you want to change a property (attribute in Python-speak) of the dataset, different than what was written in the config file when you loaded the data, you can do so easily. For example, the example dataset is set to save the output plots and excel files into a subfolder called ‘output’ under the current python working directory. If you want to change it, you can simply do the following:

```
dataset1.dir_save = 'COPY_FOLDER_PATH_HERE'
```

You can change various other properties of the dataset. There are some of these attributes which are read directly from the input data-files:

```
data_raw    # raw data
data        # normalized data.
data_mean   # mean value of time-series for each voxel
mask        # the fMRI mask. Number of 1s in it should match data.shape[1]
num_voxels  # generated from data
num_time_steps # generated from data
time_steps  # (OPTIONAL) a float array of time-steps.
            # Their length should match sdata.shape[0].
            # If there is no such data available, time-steps would be
            # consecutive integers to match data shape.
indices_cutoff # (OPTIONAL) indices of 'events'.
                # If dataset has for example 59 time-steps,
                # it should be a list of integers in [0,58] range.
                # something like [11, 42].
dir_source  # (OPTIONAL) from which folder the data was loaded?
            # default is 'dataset' subfolder in the folder containing
            # the config file (config file explained below)
dir_save    # (OPTIONAL) from which folder the data was loaded?
            # default is 'output' subfolder in the current folder in python
```

When the dataset1 object is created, linear regression is automatically performed on the normalised data. If indices_cutoff is not empty, linear regression is performed on each segment separately. Results of linear regression are stored in the following attributes:

```
line_reg    # the same shape as data, but linearised version of the data
line_reg_slopes # slopes. If there are for example 2 cutoff indices,
                # it will of [3, N_voxels] shape. Otherwise [1, N_voxels]
line_reg_biases # offsets for each linear regression.
                 # Same dimensions as line_reg_slopes.
```

And then there are some which merely hold miscellaneous information and can be changed at will:

```
signal_name # a string, can be 'T1w', 'T2*', 'FISP'  
          # or any other signal you have recorded  
experiment_name # a string  
dataset_no # an integer.  
mol_name # Molecule name. Useful for molecular fMRI studies.  
description # a short description
```

MITFAT PACKAGE

10.1 Submodules

10.2 mitfat.bplots module

Created on Mon Feb 24 17:38:15 2020

@author: vbokharaie

```
mitfat.bplots.plot_and_save_bbox_continuous(my_bbox,      dir_save_bb,      sup_title=[],  
                                             v_min=0.0, v_max=1.0)
```

Plot the continuous bbox.

when elemnts are continuous values (such as mean) default color pallete is default (virdis), 0 will be navy and 1 will be yellow.

my_bbox [numpy.ndarray] Those voxels that we want to plot..

dir_save_bb [str or pathlib.Path] where to save.

sup_title [str, optional] main title. The default is [].

v_min [float, optional] Minimum value for coloarbar. The default is 0.0.

v_max [TYPE, optional] Maximum value for coloarbar. The default is 1.0.

None.

```
mitfat.bplots.plot_and_save_bbox_discrete(my_bbox, dir_save_bb, sup_title=[], limits=[],  
                                         colours=[])
```

Plot the continuous bbox.

when elemnts are continuous values (such as mean) default color pallete is default (virdis), 0 will be navy and 1 will be yellow.

my_bbox [numpy.ndarray] Those voxels that we want to plot..

dir_save_bb [str or pathlib.Path] where to save.

sup_title [str, optional] main title. The default is [].

limits [list of floats, optional] y-axis limits. The default is [].

colours [list of matplotlib colors, optional] colours for the plot. The default is [].

None.

```
mitfat.bplots.plot_line(data_array,  time_array,  figsize=(16, 10),  title_str="",  label_str="",  
                        vert_line_times=[], color='black')
```

Plot line-plot for centroids.

data_array [NumPy array.] original data.

time_array [NumPy array.] time-stamps for each entry of data_array.

figsize [set of (int, int), optional] Figure size. The default is (16, 10).

title_str [str, optional] plot title. The default is “”.

label_str [str, optional] Label. The default is “”.

vert_line_times [list of float, optional] Times to be marked with a vertical red line. The default is [].

color [valid matplotlib color, optional] color in plot. The default is ‘black’.

fig [matplotlib Figure] matplotlib Figure.

my_ax [matplotlib axes] matplotlib axes.

```
mitfat.bplots.plot_trial_cluster_seq(centroid_to_plot,           labels_to_plot,           my_title,
                                      dir_save='./clusters_one_trial', Cluster_num=2)
```

Plot a heatmap of cluster labels for each trial in a sequence of trials.

centroid_to_plot [NumPy array.] centroids.

labels_to_plot [int] numeral lables for each centroid.

my_title [str] plot title.

dir_save [str or pathlib.Path, optional] where to save the plots. The default is ‘./clusters_one_trial’.

Cluster_num [int, optional] Number of clusters. The default is 2.

None.

```
mitfat.bplots.save_fig(fig, dir_save, filename_in, figsize=(16, 12))
```

Save the matplotlib Figure.

fig [matplotlib Figure] Figure to be saved to disk.

dir_save [str or pathlib.Path] where to save..

filename_in [str or pathlib.Path] filename.

figsize [set of (int, int), optional] OBSOLETE, becasue it has gone obsolete in matplotlib.

None.

10.3 mitfat.clustering module

Created on Tue Jul 23 18:54:26 2019

@author: vbokharaie

This module includes methods of fmri_dataset class used for clustering.

```
mitfat.clustering.cluster_raw(X_train, no_clusters)
```

K-means clustering of time-series data.

Sorts the cluster such that cluser 1 always corresponds with the one with highest absolute mean.

X_train [numpy.ndarray] data to be clustered. Shape is (N=1, N_voxels).

no_clusters [int] Number of clusters.

cluster_labels_sorted [numpy.ndarray] Cluster label for each data-entry. Shape is (N voxel, 1).

cluster_centroids_sorted [numpy.ndarray] Centroids for each cluster. Shape is (N_time_steps, N voxels)

mitfat.clustering.**cluster_scalar**(X_train, no_clusters)

K-means clustering of scalar data. Scikit-learn implementation.

Sorts the cluster such that cluser 1 always corresponds with the one with highest absolute mean.

X_train [numpy.ndarray] data to be clustered. Shape is (N=1, N voxels).

no_clusters [int] Number of clusters.

cluster_labels_sorted [numpy.ndarray] Cluster label for each data-entry. Shape (N voxel, 1).

cluster_centroids_sorted [numpy.ndarray] Centroids for each cluster.

mitfat.clustering.**kmean_it**(self, cluster_no)

To function as a wrapper for sklearn.cluster.KMeans.

Sorts the clusters, assigns cluster labels to bbox non-zero cells

cluster_no [int] cluster number..

bbox_cat [numpy array] mask for voxels to consider. shape (e1, e2, e3).

cluster_labels_sorted [list of int] Sorted list of cluster labels.

cluster_centroids_sorted [numpy array] Centroids, sorted.

mitfat.clustering.**kmeans_missing**(xx, no_clusters, max_iter=30)

Perform K-Means clustering on data with missing values.

Found it in stackoverflow

xx [Numpy array] An [n_samples, n_features] array of data to cluster.

no_clusters [int] Number of clusters to form..

max_iter [int, optional] Maximum number of EM iterations to perform.. The default is 30.

labels [list of int] An [n_samples] vector of integer labels.

centroids [Numpy array] An [n_clusters, n_features] array of cluster centroids..

x_hat [Numpy arra] Copy of xx with the missing values filled in..

mitfat.clustering.**sort_cluster**(cluster_labels, cluster_centroids)

Sort the cluster numbers.

Sorted such that cluster 1 always correspond with centroid with highest mean absolute value.

cluster_labels [list of int] cluster labels.

cluster_centroids : cluster centroids.

cluster_labels_out [list of int] sorted lable list.

clusters_centroids_out [Numpy array] sorted centroids.

10.4 mitfat.collections module

Created on Fri Nov 22 12:58:00 2019

@author: vbokharaie

This module includes functions which will operate on a list of fmri_datasets, such as calculating the average of a list of datasets.

mitfat.collections.**calc_mean_dataset** (*list_of_fmri_datasets*)

Reads a list of fmri_datasets, returns an fmri_dataset which contains the average of the data in all of them.

Parameters

- **list_of_fmri_datasets** – list of fmri_datasets to be averaged
- **first_trial_time** – the beginning time of the first trial, default 0.0

Raises Happiness level, and checks if input is a list and a list of fmri_dataset

Returns fmri_dataset, average of input list data

Return type ‘fmri_dataset’ type

10.5 mitfat.file_io module

Created on Thu Aug 13 14:55:19 2018

@author: vbokharaie

This module includes methods of fmri_dataset class used for I/O operations.

mitfat.file_io.**convert_real_time_to_index** (*time_steps*, *cutoff_times_to_convert*)

Return index values for first time steps bigger than input time-values.

times_files: ‘str’ path to file including values of time-steps

cutoff_times_to_convert: ‘list’ of ‘float’

output_list: ‘list’ if ‘int’ indices for time values

mitfat.file_io.**main_get_data** (*info_file_name*)

Read actual data based on info_file_name.

uses read_info_file to read the config file and then loads the data. A ‘sample_info_file.txt’ accompanying the library includes standard format. Run mitfat.file_io.print_info() to see how config files should be organised.

info_file_name [‘str’ or pathlib.Path] config file.

data_nii_masked: ‘numpy.ndarray’, (N_time_steps, N_voxels)

mask_roi_numpy: ‘numpy.ndarray’, (d1, d2, d3)

time_steps: ‘list’ of ‘float’ time steps

signal_name: ‘str’ signal name

indices_cutoff: ‘list’ if ‘int’ times in which experimental conditions changed.

experiment_name: ‘str’ name

dataset_no: ‘int’ dataset number

mol_name: ‘str’ name of molecule

dir_source: source folder
dir_save: ‘str’ or `pathlib.Path` where to save
mask_roi_numpy: `Numpy.ndarray` maks for voxels to consider
description: ‘str’ descriptions for dataset

`mitfat.file_io.make_list_of_trial_times(time_steps, first_trial_time=0.0, trial_length=None)`

Read time-steps, first trial time and trial length.

calculates ands returns the indices and time-steps of consecutive trials

Parameters

- **time_steps** (*list of floats*) – time-steps of the fMRI recording
- **first_trial_time** (*float, optional*) – the beginning time of the first trial, default 0.0
- **first_trial_time** – length of each trial, default None (would be set to `max(time_steps)`)

Returns `list_of_trial_times, list_of_trial_times_indices`

Return type list of floats, list of integers

`mitfat.file_io.print_info(filename_info=None)`

Print info text.

filename_info [str or `pathlib.Path`, optional] If given, info is written to file otherwise to standard output. The default is None.

None.

`mitfat.file_io.read_data(info_file_name)`

Read the input dataset info from a file.

returns a `fmri_dataset` object including all those files.

info_file_name: str an `os.path` filename object

`fmri_dataset: obj`

`mitfat.file_io.read_info_file(info_file_name)`

Read the config file.

assigns default values to `fmri_dataset` object if not defined in config file. A ‘sample_info_file.txt’ accompanying the library includes standard format.

info_file_name: ‘str’ or `pathlib.Path` path to config file

data_file_name: ‘str’ or `pathlib.Path` `data_file_name`

mask_file_name: ‘str’ or `pathlib.Path` `mask_file_name`

time_file_name: ‘str’ or `pathlib.Path` `time_file_name`

dir_source: ‘str’ or `pathlib.Path` `dir_source`

dir_save: ‘str’ or `pathlib.Path` `dir_save`

mol_name: ‘str’ molecule name

exp_name: ‘str’ Experiment name

dataset_no: ‘int’ number assigned to dataset.

cutoff_times: ‘list’ of ‘float’ Times in which experimental conditions changed.

description: ‘str’ general descriptions.

signal_name: ‘str’ name of signal. ‘T1’, ‘T2’, ‘T1*’, ‘FISP’, etc.

`mitfat.file_io.save_clusters(self, X_train, data_label, cluster_labels, cluster_centroids, subfolder_c=“)`
Save cluster to excel file.

X_train [Numpy array.] Data to cluster. N_clustered_data can be N_time_steps, 1, or N_segments. Shape is (N_clustered_data, N_voxels)

data_label [str] used in establishing save folders

cluster_labels [list of int] labels for clusters.

cluster_centroids [Numpy array] centroids.

subfolder_c [str, optional] adding an optional subfolder. The default is “.”.

None.

`mitfat.file_io.test_script(filename=None)`
Return back the name of test script.

filename [str or pathlib.Path, optional] Either a user-defined test file, or the default that already exists in mitfat.
The default is None.

None.

10.6 mitfat.flags module

Created on Tue Jul 23 18:21:14 2019

@author: vbokharaie

10.7 mitfat.fmri_dataset module

Created on Thu Jul 26 10:55:19 2018

@author: vbokharaie

`class mitfat.fmri_dataset.fmri_dataset(data_masked, mask_numpy, time_steps, signal_name, indices_cutoff, experiment_name, dataset_no, mol_name, dir_source, dir_save, description, first_trial_time, trial_length, trial_no=0)`

Bases: object

A class as a container for all relevant data of an fMRI recording.

class method are distributed in different modules whose names start with ‘_’

`calc_lin_reg()`

Calculate linear regression for the time-series.

Uses numpy.linalg.lstsq.

line_reg : ‘numpy.ndarray’, data.shape line_reg_slopes: ‘numpy.ndarray’, (num_voxels, num_segments)
line_reg_biases: ‘numpy.ndarray’, (num_voxels, num_segments)

```

calc_mean_segments()
    Mean value of each time-segment in the time-series.

    Time-segments are automatically defined based on specified values of cutoff indices of times. If they are not defined, there would be only one time-segment including all time-steps.

    mean_segments : ‘numpy.ndarray’, (len_segments-1, num_voxels)

cluster(X_train, num_clusters)
    A wrapper for clustering methods. calls cluster_scalar if input data is 1 dimensional, otherwise calls cluster_raw.

    X_train: ‘numpy.ndarray’, (N=1, N_voxels) no_clusters: ‘int’

    cluster_labels_sorted: ‘numpy.ndarray’, (N_voxel, 1) cluster_centroids_sorted:’numpy.ndarray’,
    cluster_scalar, cluster_raw

cluster_TopN(signal='raw', n_top=20, if_save_plot=True, subfolder_c='Cluster_TopN')
    Just plotting Top N voxels, in term of signal amplitude.

    signal: {‘raw’, ‘mean’, ‘slope’, ‘slope’Segments’, ‘mean_segments’} num_clusters: int
    default=2

if_save_plot: ‘bool’ default=False

    cluster_labels2: ‘list’ of ‘int’ cluster_centroid2: ‘numpy.ndarray’

    Incomplete for ‘mean’, ‘slope’, ‘slope’Segments’, ‘mean_segments’

cluster_hierarchical(signal='raw', num_clusters=2, if_save_plot=False, sub-
    folder_c='Cluster_Hierarchical')
    Hierarchical clustering.

    First 2 cluster over all data, choose all voxels corresponding to bigger centroid Then 2 clusters over these voxels.

    signal: {‘raw’, ‘mean’, ‘slope’, ‘slope’Segments’, ‘mean_segments’} num_clusters: int
    default=2

if_save_plot: ‘bool’ default=False

    cluster_labels2: ‘list’ of ‘int’ cluster_centroid2: ‘numpy.ndarray’

    Incomplete for ‘mean’, ‘slope’, ‘slope’Segments’, ‘mean_segments’

data = None
    normalised, unless flags.if_normalise=False

data_mean = None
    mean of each voxels

data_raw = None
    raw data, always

detrend()
    Detrending the time-series. When cutoff times are set merely to begining and end times:
    spline-smooth the time-series, and subtract it from the original signal.

```

For three segments: Fits a spline to first and third time-segments. Interpolates the second segment, and subtract it from the original time-series values. In doing so, chnages in the signal trend in segment 2 becomes evident.

Saves detrended plots, saved in png and optionaly eps format. Saves bar plots of detrended time segments, saved in png and optionaly eps format Saves an .xlsx file including values of detrended signals

```
fix_anomalies()
    Fix overshoot and undershoots occasioanlly recorded by the fMRI scanners.

    Replaces any value outside +3 SD range of signal MEAN with np.nan.

    my_data : 'numpy.ndarray', np.shape(self.data)

impute()
    Interpolates nan values in the time series.

    uses sklearn.impute.SimpleImputer

    data: 'numpy.ndarray'

mask = None
    3d mask

normalise()
    Normalise the time-series. Divides all voxel time-series to their collective maximum value.

    data_normalised : 'numpy.ndarray' data: 'numpy.ndarray' bbox_data_mean: 'numpy.ndarray' data_mean: 'numpy.ndarray' mean_segments : 'numpy.ndarray'

num_time_steps = None
    int

num_voxels = None
    int

plot_basics(data_type='normalised', figsize=None)
    Plots the time-series corresponsing to each voxel. The plots are arranged in a layout which follows the mask. Each layer is saved in a separeta file. Parameters ——— data_type : { 'normalised', 'raw', 'lin_reg' }

    'normalised' (default): plot normalised time-series. 'raw': plot raw signal 'lin_reg': plot linear regression of time-series

figsize [set of float, (fig_w, fig_h)] fig dimensions in inches

NameError If data is not normalised and user tries to plot normalised data.

plot_clusters(original_data, data_label, cluster_labels, cluster_centroids, if_slopes=False, if_hierarchical=False, subfolder_c=')
    Plots the cluster, saves cntroid values. Including bbox plots, centroid plots. centroids are saved in .xlsx file in the same folder as plots.

    The plots are arranged in a layout which follows the mask. Each layer is saved in a separeta file.

    original_data: 'numpy.ndarray', (N_clustered_data, N_voxels) N_clustered_data can be N_time_steps, 1, or N_segments

    data_label: 'str' used in establishing save folders

    cluster_labels: 'numpy.ndarray', (N_voxels, 1) cluster_centroids: 'numpy.ndarray', (N_clusters, N_clustered_data) subfolder_c: str,
```

name of subfolder inside main dir_save to save the plots

NameError If data is not normalised and user tries to plot normalised data.

```
plot_voxel(data_type='normalised', voxel_num=1, list_voxel_num=None, figsize=(16, 10),
            dir_save=None, filename_pre="")
```

Plots the time-series corresponding to each voxel. The plots are arranged in a layout which follows the mask. Each layer is saved in a separate file. Parameters ————— data_type : {‘normalised’, ‘raw’, ‘lin_reg’}

‘normalised’ (default): plot normalised time-series. ‘raw’: plot raw signal ‘lin_reg’: plot linear regression of time-series

figsize [set of float, (fig_w, fig_h)] fig dimensions in inches

voxel_num: int voxels number to be plotted. Should be in (1, self.voxel_no) range

NameError If data is not normalised and user tries to plot normalised data.

```
save_clusters(X_train, data_label, cluster_labels, cluster_centroids, subfolder_c="")
```

Save cluster to excel file.

X_train [Numpy array.] Data to cluster. N_clustered_data can be N_time_steps, 1, or N_segments. Shape is (N_clustered_data, N_voxels)

data_label [str] used in establishing save folders

cluster_labels [list of int] labels for clusters.

cluster_centroids [Numpy array] centroids.

subfolder_c [str, optional] adding an optional subfolder. The default is “”.

None.

```
time_steps = None
```

flow list

```
total_created_objects = 0
```

keeps track of total number of objects

10.8 mitfat.mitfat_test_script module

10.9 Module contents

MiTfAT - python-based fMRI Analysis Tool.

CHAPTER
ELEVEN

INDICES AND TABLES

- genindex
- modindex
- search

PYTHON MODULE INDEX

m

mitfat, 33
mitfat.bplots, 25
mitfat.clustering, 26
mitfat.collections, 28
mitfat.file_io, 28
mitfat.flags, 30
mitfat.fmri_dataset, 30

INDEX

C

calc_lin_reg() (*mitfat.fmri_dataset.fmri_dataset method*), 30
calc_mean_dataset() (*in module mitfat.collections*), 28
calc_mean_segments() (*mitfat.fmri_dataset.fmri_dataset method*), 30
cluster() (*mitfat.fmri_dataset.fmri_dataset method*), 31
cluster_hierarchial() (*mitfat.fmri_dataset.fmri_dataset method*), 31
cluster_raw() (*in module mitfat.clustering*), 26
cluster_scalar() (*in module mitfat.clustering*), 27
cluster_TopN() (*mitfat.fmri_dataset.fmri_dataset method*), 31
convert_real_time_to_index() (*in module mitfat.file_io*), 28

D

data (*mitfat.fmri_dataset.fmri_dataset attribute*), 31
data_mean (*mitfat.fmri_dataset.fmri_dataset attribute*), 31
data_raw (*mitfat.fmri_dataset.fmri_dataset attribute*), 31
detrend() (*mitfat.fmri_dataset.fmri_dataset method*), 31

F

fix_anomalies() (*mitfat.fmri_dataset.fmri_dataset method*), 32
fmri_dataset (*class in mitfat.fmri_dataset*), 30

I

impute() (*mitfat.fmri_dataset.fmri_dataset method*), 32

K

kmean_it() (*in module mitfat.clustering*), 27
kmeans_missing() (*in module mitfat.clustering*), 27

M

main_get_data() (*in module mitfat.file_io*), 28

make_list_of_trial_times() (*in module mitfat.file_io*), 29
mask (*mitfat.fmri_dataset.fmri_dataset attribute*), 32
mitfat (*module*), 33
mitfat.bplots (*module*), 25
mitfat.clustering (*module*), 26
mitfat.collections (*module*), 28
mitfat.file_io (*module*), 28
mitfat.flags (*module*), 30
mitfat.fmri_dataset (*module*), 30

N

normalise() (*mitfat.fmri_dataset.fmri_dataset method*), 32
num_time_steps (*mitfat.fmri_dataset.fmri_dataset attribute*), 32
num_voxels (*mitfat.fmri_dataset.fmri_dataset attribute*), 32

P

plot_and_save_bbox_continuous() (*in module mitfat.bplots*), 25
plot_and_save_bbox_discrete() (*in module mitfat.bplots*), 25
plot_basics() (*mitfat.fmri_dataset.fmri_dataset method*), 32
plot_clusters() (*mitfat.fmri_dataset.fmri_dataset method*), 32
plot_line() (*in module mitfat.bplots*), 25
plot_trial_cluster_seq() (*in module mitfat.bplots*), 26
plot_voxel() (*mitfat.fmri_dataset.fmri_dataset method*), 33
print_info() (*in module mitfat.file_io*), 29

R

read_data() (*in module mitfat.file_io*), 29
read_info_file() (*in module mitfat.file_io*), 29

S

save_clusters() (*in module mitfat.file_io*), 30

save_clusters() (*mitfat.fmri_dataset.fmri_dataset method*), 33
save_fig() (*in module mitfat.bplots*), 26
sort_cluster() (*in module mitfat.clustering*), 27

T

test_script() (*in module mitfat.file_io*), 30
time_steps (*mitfat.fmri_dataset.fmri_dataset attribute*), 33
total_created_objects (*mitfat.fmri_dataset.fmri_dataset attribute*),
33