

INFOBAR is a GUI tool to implement [ICA-AROMA](#), especially useful for processing large datasets and performing quality checks on the data.

Note that the software currently implements the .feat processing functions of ICA-AROMA and cannot process raw NIFTI files.

Installation

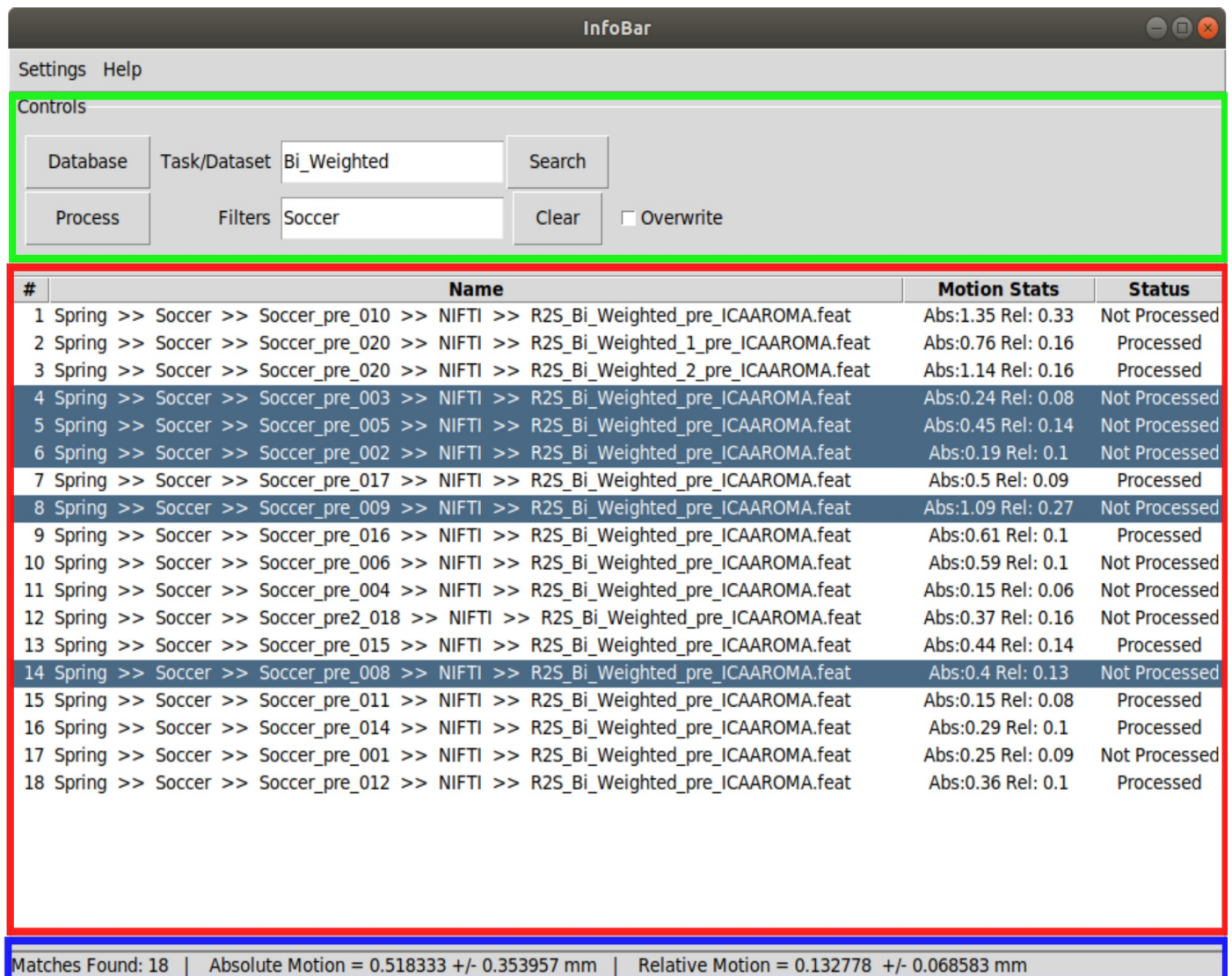
1. Extract contents of INFOBAR.zip to the local ICA-AROMA-master folder (The original ICA-AROMA program can be downloaded [here](#)).
2. Alternatively, extract the contents to any desired location. Upon first run, go to Settings and select the location to ICA_AROMA.py in the panel, then click save. This will save the default configuration.

Install Python modules dependencies using: `python3 -m pip install -r requirements.txt`

Usage

The software is written in Python 3 and can be launched from a bash prompt. To start the software, open up a terminal and type:

```
python3 <path_to_file>/INFOBAR.py
```



The screenshot shows the INFOBAR GUI window. At the top, there are 'Settings' and 'Help' buttons. Below them is a 'Controls' section with a 'Database' button, a 'Task/Dataset' input field containing 'Bi_Weighted', a 'Search' button, a 'Process' button, a 'Filters' input field containing 'Soccer', a 'Clear' button, and an 'Overwrite' checkbox. The main area is a table with 18 rows, each representing a match. The table has four columns: '#', 'Name', 'Motion Stats', and 'Status'. The 'Name' column contains a sequence of directory paths and file names. The 'Motion Stats' column shows absolute and relative motion values. The 'Status' column indicates whether the match has been processed or not.

#	Name	Motion Stats	Status
1	Spring >> Soccer >> Soccer_pre_010 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:1.35 Rel: 0.33	Not Processed
2	Spring >> Soccer >> Soccer_pre_020 >> NIFTI >> R2S_Bi_Weighted_1_pre_ICAAROMA.feat	Abs:0.76 Rel: 0.16	Processed
3	Spring >> Soccer >> Soccer_pre_020 >> NIFTI >> R2S_Bi_Weighted_2_pre_ICAAROMA.feat	Abs:1.14 Rel: 0.16	Processed
4	Spring >> Soccer >> Soccer_pre_003 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.24 Rel: 0.08	Not Processed
5	Spring >> Soccer >> Soccer_pre_005 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.45 Rel: 0.14	Not Processed
6	Spring >> Soccer >> Soccer_pre_002 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.19 Rel: 0.1	Not Processed
7	Spring >> Soccer >> Soccer_pre_017 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.5 Rel: 0.09	Processed
8	Spring >> Soccer >> Soccer_pre_009 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:1.09 Rel: 0.27	Not Processed
9	Spring >> Soccer >> Soccer_pre_016 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.61 Rel: 0.1	Processed
10	Spring >> Soccer >> Soccer_pre_006 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.59 Rel: 0.1	Not Processed
11	Spring >> Soccer >> Soccer_pre_004 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.15 Rel: 0.06	Not Processed
12	Spring >> Soccer >> Soccer_pre2_018 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.37 Rel: 0.16	Not Processed
13	Spring >> Soccer >> Soccer_pre_015 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.44 Rel: 0.14	Processed
14	Spring >> Soccer >> Soccer_pre_008 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.4 Rel: 0.13	Not Processed
15	Spring >> Soccer >> Soccer_pre_011 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.15 Rel: 0.08	Processed
16	Spring >> Soccer >> Soccer_pre_014 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.29 Rel: 0.1	Processed
17	Spring >> Soccer >> Soccer_pre_001 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.25 Rel: 0.09	Not Processed
18	Spring >> Soccer >> Soccer_pre_012 >> NIFTI >> R2S_Bi_Weighted_pre_ICAAROMA.feat	Abs:0.36 Rel: 0.1	Processed

At the bottom of the window, there is a summary bar: 'Matches Found: 18 | Absolute Motion = 0.518333 +/- 0.353957 mm | Relative Motion = 0.132778 +/- 0.068583 mm'.

The software searches for .feat folders generated after pre-processing through FSL.

In the main window, there are options to select the Database location, Search using task/dataset names, and Filter using additional strings.

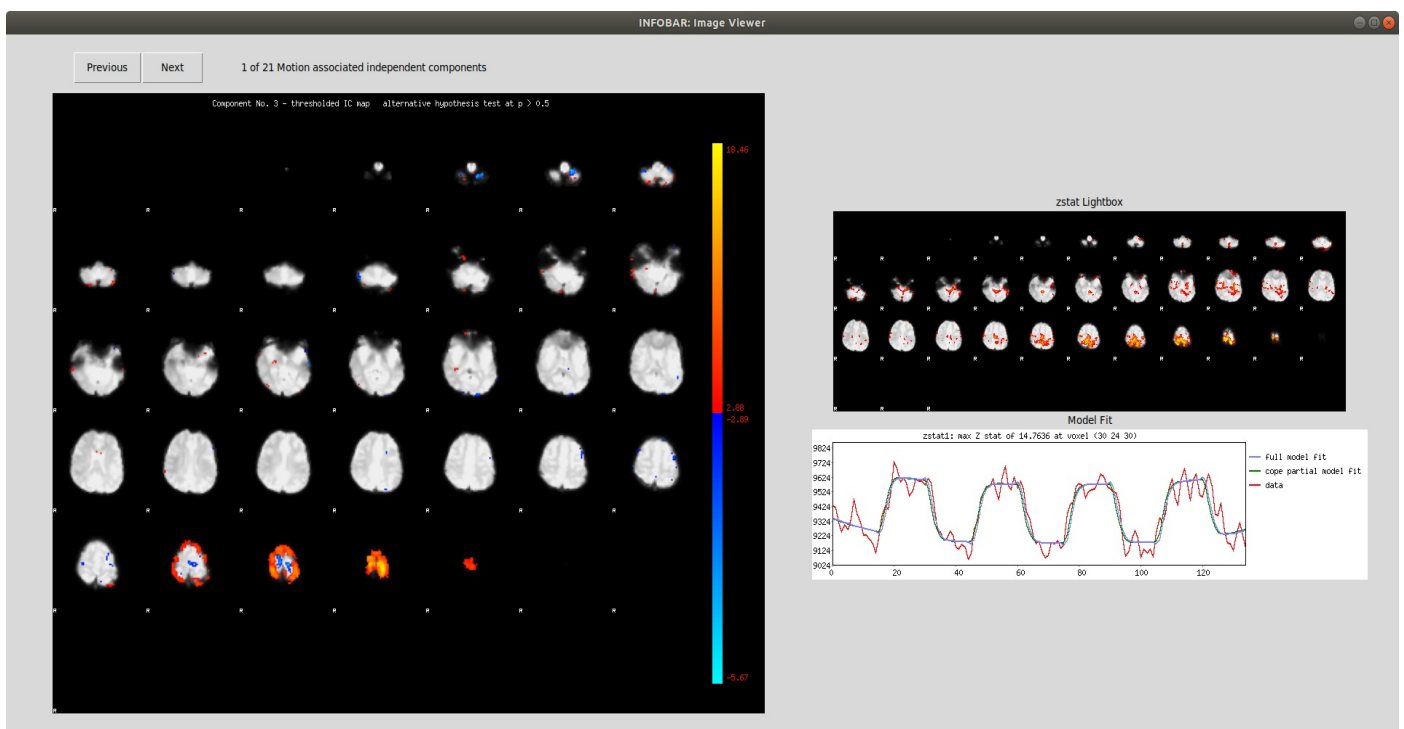
1. To start, click the Database button and selecting the root directory of your database.
2. Click Search to search for all .feat folders in the root directory.
3. Type in a task name and click Search to search for a specific task/dataset name.
4. Type in filters to narrow search based on subjects/ groups etc.
5. To delete a dataset from the queue, press d.
6. To process all subjects shown in the display panel, click Process.
7. Alternatively, select the datasets to be processed. Press ctrl to select multiple datasets. Click Process to process selected subjects. Click

Clear to clear selection.

8. Left click on a dataset to view *MCFLIRT rotation, translation and displacement* plots.



1. Right/middle click or press w on a dataset to view the independent components associated with motion identified by the algorithm.
2. If the data has been post processed, these actions will also show *zstat1 lightbox image* and *peak voxel activation model fit*.



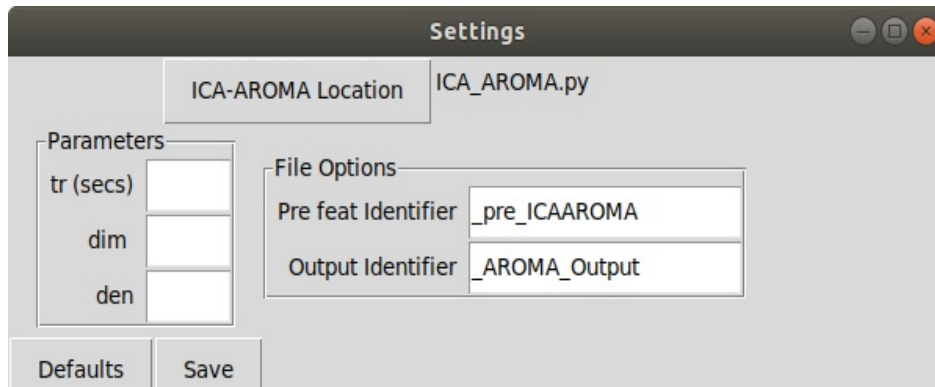
Preprocessing and Postprocessing steps

INFOBAR requires the data to be processed through FSL. Preprocessing involves: 1. Head movement correction by volume-realignment to the middle volume using MCFLIRT. 2. Global 4D mean intensity normalization. 3. Spatial smoothing (e.g. 6mm FWHM)

Importantly, no temporal filtering should be applied at this stage of processing.

Postprocessing includes nuisance regression: WM, CSF & linear trend and high-pass filtering

Settings



ICA-AROMA provides options to change the default TR, dimensionality reductions and de-noising techniques. The functionality is available here through a settings panel where the following user defined settings can be set.: 1. ICA-AROMA location: Select the location of the ICA_AROMA.py file from the original program. Default location is installation directory. 2. Parameters for ICA-AROMA: 1. tr (secs): TR in seconds. If this is not specified, the TR will be extracted from the header of the fMRI file using 'fslinfo'. In that case, make sure the TR in the header is correct! 2. dim: Dimensionality reduction into a defined number of dimensions when running MELODIC (default is 0; automatic estimation) 3. den: Type of denoising strategy (default is nonaggr:). Options include: 1. no: only classification, no denoising 2. nonaggr: non-aggressive denoising, i.e. partial component regression (default) 3. aggr: aggressive denoising, i.e. full component regression 4. both: both aggressive and non-aggressive denoising (two outputs)

1. File Options:

1. Pre feat Identifier: If the preprocessed files are stored with a unique keyword identifier for record keeping, this keyword can be specified here. This keyword will be replaced by the Output Identifier keyword. If the keyword is not found, the folder name will simply be augmented with the Output Identifier. Default value is '_pre_ICAAROMA'
2. Output Identifier: Keyword to replace Pre feat identifier. Default value is '_AROMA_Output'.

Settings tab also allows the user to select the location of the ICA-AROMA program file for function call. The settings are saved in a JSON file.

An example workflow is shown in the following video: