

fMRI IRM toolbox (fIT)

This toolbox runs the Infinite Relational Model (IRM) and other non-parametric Bayesian models [Mørup] on graphs derived from functional magnetic resonance imaging (fMRI) data.

Dependencies

The toolbox is implemented in MATLAB (<http://www.mathworks.com>). The toolbox uses functions from SPM, which is free and can be downloaded from (<http://www.fil.ion.ucl.ac.uk/spm/software/>). SPM must be in your Matlab path.

Install

Simply put the fIT folder somewhere in your Matlab path.

Running fIT

Type

```
>>fit <enter>
```

in the Matlab command window to start the toolbox. A GUI will appear.

Data

The toolbox includes two demo data sets, which consist of correlation matrices extracted from resting state fMRI data freely available from http://www.nitrc.org/projects/fcon_1000/. The Beijing data set consists of 42 of the subjects from the Beijing Zang release (Beijing_Zang_part2.tar). The Leipzig data set consists of 37 subjects.

Simply check the “Demo – Beijing data” or “Demo – Leipzig data” radiobuttons to run using the Beijing or Leipzig data. The mean time series was calculated in each of the AAL regions [Tzourio-Mazoyer] and the correlation matrix was formed by calculating Pearson correlation between each region.

If you want to run on your own data select “My own data” button. See below how the data should be organized.

Models to run

Select which of the model you want to run, please refer to [Mørup] for description of the models.

IRM – Infinite Relational Model

BCD – Bayesian Community Detection

IHW – Infinite Hofman-Wiggins

IDM – Infinite Diagonal Model

Assume same link probability matrix (eta) across subjects

By selecting 'Assume same link probability matrix (eta) across subjects' the models will use a shared link probability matrix across subjects [Andersen].

N iterations

Number of iterations used in the inference.

Graph density

The graph link density in percent.

Project Name

Only visible if 'My own data' is selected. Let you specify a name for the project. This is used in the output path to separate different projects.

File prefix

Only visible if 'My own data' is selected. Specify the prefix of your functional images (could be 'swf').

File extension

Specify the extension of you functional images (could be 'nii' or 'img'). [Only visible if 'My own data' is selected]

Data path

Only visible if 'My own data' is selected. The data path is the root directory for your data. In this directory you should have separate directories for your subjects. So it could for instance look like:

```
/pth/to/my/data/sub01/  
/pth/to/my/data/sub02  
...  
/pth/to/my/data/subN
```

It the subject directories the toolbox will look for files which match <prefix>*.<extension>

ROI path

Only visible if 'My own data' is selected. This is the path to the directory where the ROIs are located. In this directory the toolbox will look for images with the '.nii' extension (can be modified to something else). All matching images will be used as ROIs for the analysis. The AAL regions are provided in the the toolbox and can be found in the 'AAL_masks' folder.

Output path

Only visible if 'My own data' is selected. Specify the path to an output directory, where output from the toolbox will be stored.

Plot results

Check this box if you want the toolbox to make overlays of the resulting clusters. The toolbox will also make html-files, which will make it easy to browse the results.

RUN

Once you have specified all the necessary input click on the RUN button. The toolbox will then start running. If the correlation matrices have already been calculated (if you ran the model before with the same project name, file prefix, and output or if you run in demo mode) then the toolbox will use these correlation matrices. If not, the program will start by calculating all the correlation matrices and then start running the model inference. In the output directory there will be a directory with the correlation matrices, one for each subject. For each separate model inference there will be an output directory which have a .mat file with the output from the model inference. If 'plot results' was selected then there will be output directories with html files, plots and nifti images for each cluster.

Comments

If you have any comments or questions regarding this toolbox, please email: kwjo@dtu.dk

References

[Andersen] Andersen, K. W., Mørup, M., Siebner, H., Madsen, K. H., Hansen, L. K., 2012. Identifying modular relations in complex brain networks. In: Machine Learning for Signal Processing (MLSP), 2012 IEEE International Workshop on. pp. 1-6.

[Mørup] Mørup, M., Schmidt, M. N., Sep. 2012. Bayesian community detection. Neural computation 24 (9), 2434-56.

[Tzourio-Mazoyer] Tzourio-Mazoyer, N., Landeau, B., Papathanassiou, D., Crivello, F., Etard, O., Delcroix, N., Mazoyer, B., Joliot, M., Jan. 2002. Automated anatomical labeling of activations in SPM using a macroscopic anatomical parcellation of the MNI MRI single-subject brain. Neuroimage 15 (1), 273-89.