BRANT Documentation

Release 3.36

Brainnetome

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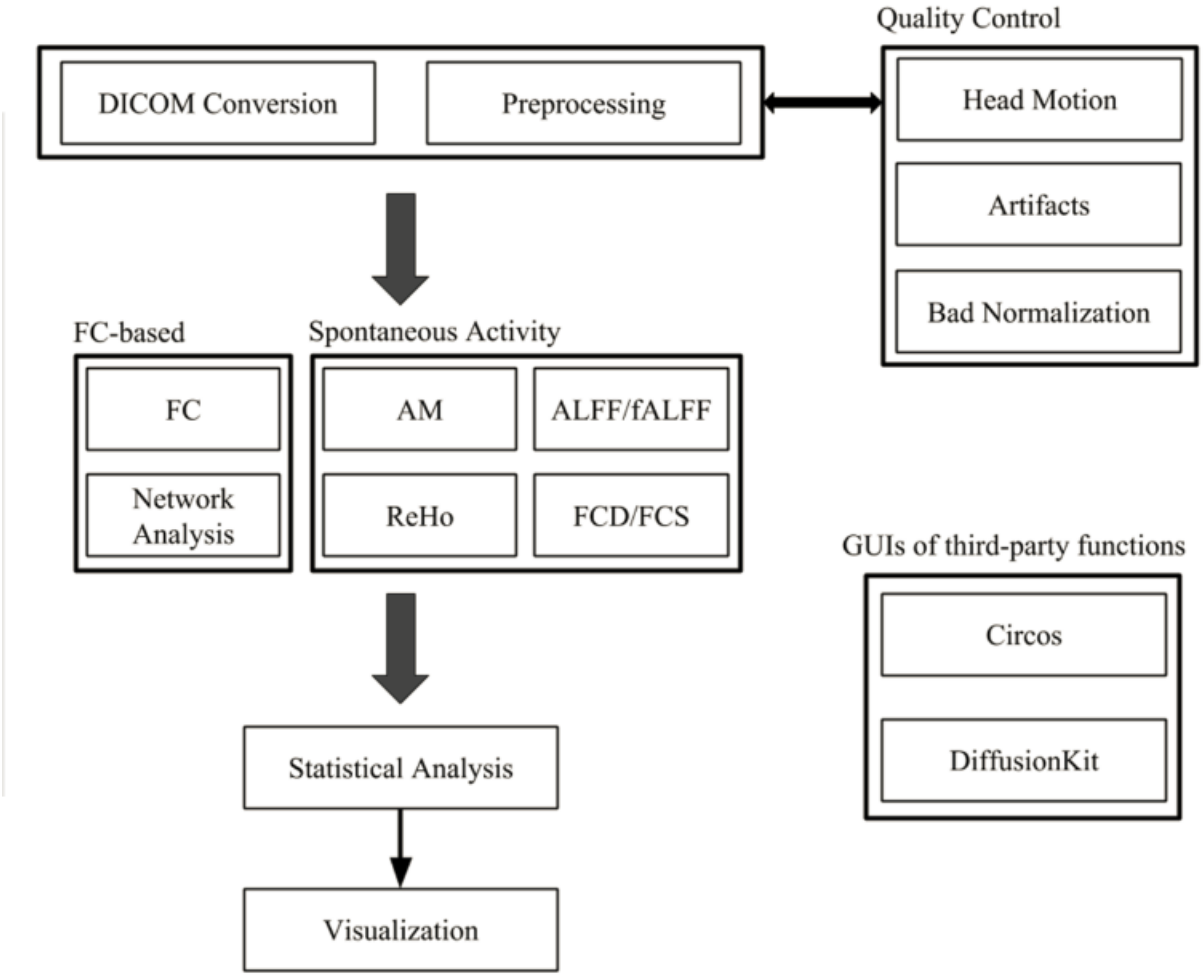
Contents

To facilitate data processing and deal with above listed issues, we've written an extendable MATLAB based toolbox BRANT (BRAinNetome Toolkit), which integrates fMRI data preprocessing, voxel-wise spontaneous activity analysis, functional connectivity analysis, complex network analysis, statistical analysis, data visualization as well as several useful utilities. We designed the toolbox using dynamically generated GUIs, with which other developers can generate their own GUIs by adding a few lines of MATLAB code. Also, to simplify the input process during using BRANT, most functions are initialized with default settings, users will only need to specify several necessary parameters, with free access to all.

Functions of BRANT are arranged into 7 modules, which are preprocessing, functional connectivity (FC), spontaneous activity (SPON), complex network analysis (NET), statistics (STAT), visualization (View) and utilities. More details on proper module can be found in its own part.

Please cite this work if you use the Brant.

Xu, K., Liu, Y., Zhan, Y., Ren, J., Jiang, T. (2018) BRANT: A Versatile and Extendable Resting-State fMRI Toolkit. Front Neuroinform, 12:52.


Quality Control
DICOM Conversion
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Artifacts
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Network Analysis
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CHAPTER 1

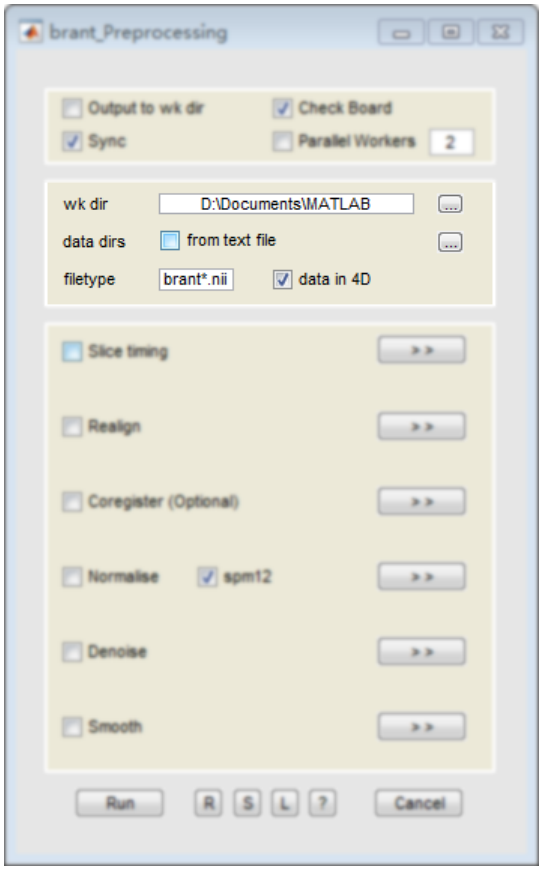
Preprocess

Raw data collected from MRI scanners are formatted as DICOM (Digital Imaging and Communications in Medicine) files, which are firstly converted to a single 4D NIfTI (Neuroimaging Informatics Technology Initiative) image for efficiently processing. For converted data, visual inspection is recommended to censor data with low quality (artifacts and distortions). Qualified data can be further processed in the preprocessing pipeline.

1.1 System Configuration

- **Output to wk dir**: Set to output results to wk (working) directory defined below. BRANT will create new directory for each subject and copy necessary files to the new directory, then start processing.
- **Check Board**: Open/Close CheckBoard.
- **Sync**: Synchronize parameters of TR in slice timing and denoise.
- **Parallel Workers**: The number of workers used during processing. e.g. when set to 2, BRANT will run 2 subjects in parallel. The processing speed depends on both CPU and Hard Drive speed, if there are a lot data IO with less computation task, set to more workers will slow down the entire process.

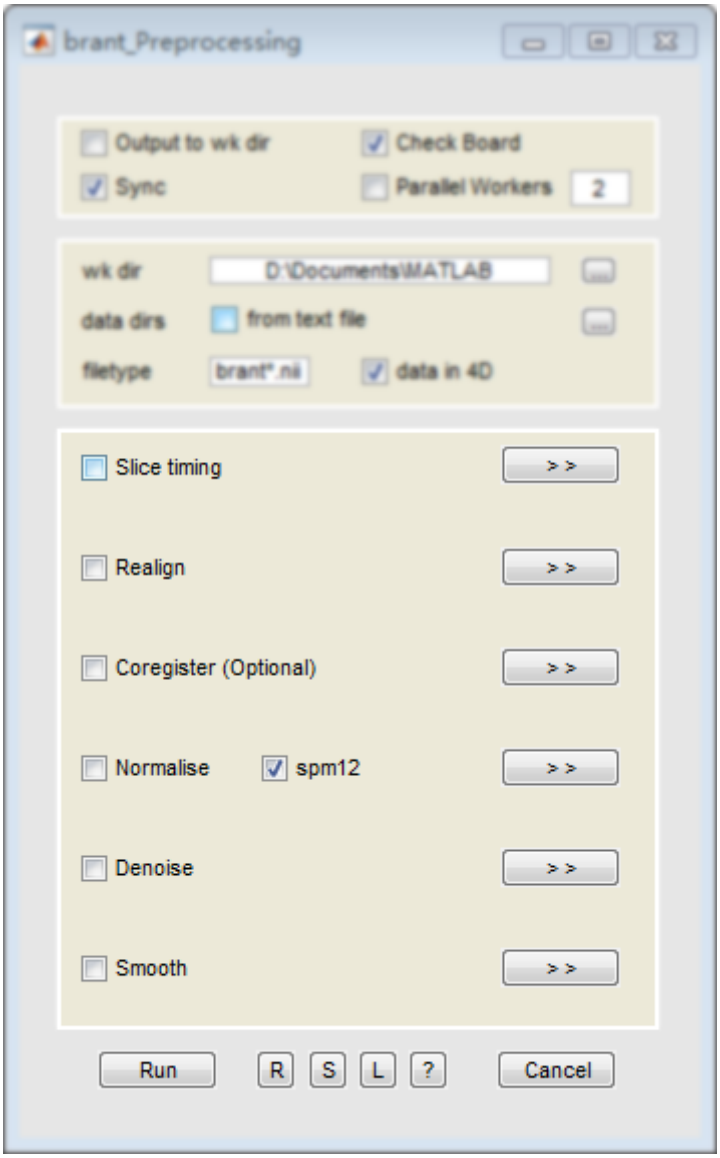
1.2 Directories



- **wk dir**: Working directory to save intermidiate files. By default is set to the current directory.
- **data dirs**: directories of each subject, can be input from an SPM input dialog of directories or from a `*.txt` file filled with one directory at a line.
- **filetype**: Initial filetype for processing, normally wildcard after DICOM conversion. The item can update itself after each process.
- **data in 4D**: Checked means input data is in 4D format, which is highly suggested. If 3D file format is used, each subjects directory will have up to thousands of files after process.

1.3 Preprocess Modules

For parameters, press help in each input dialog.



1.3.1 Slice Timing

Correct for timing information of each slice during one TR.

1.3.2 Realign

Correct and estimate spatially the head motion.

1.3.3 Coregister (optional)

Coregister structural image to mean functional images.

1.3.4 Normalize

Normalize functional images to standard space (both SPM12 and SPM8 methods is valid).

1.3.5 Denoise

Multi-variable regression and filter.

1.3.6 Smooth

3D spatial smooth with Gaussian kernal.

- **Buttons:**
  - **R**: Refresh (only checkboxes, parameters will remain untouched). Uncheck all selected items and recover the Run button when an error occurs.
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

CHAPTER 2

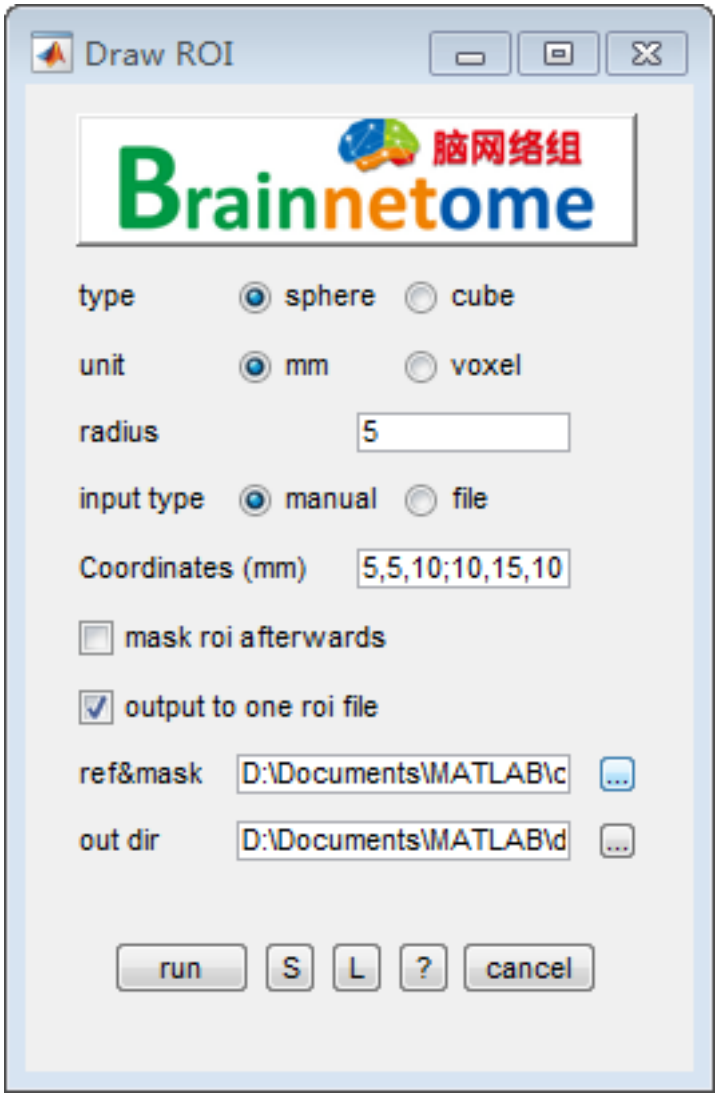
FC

Functional connectivity is calculated as the temporal correlation between pairs of time series extracted from ROIs or voxels.

In BRANT, three methods of preparing ROIs are provided, including drawing spheres/cubes from coordinates, extracting ROIs from an atlas and merging separate ROI files into one number-tagged template.

2.1 Draw ROI

Draw ROIs is implemented as automatically drawing spheres or cubes with ROI coordinates and a header reference 3D image. The ROI coordinages and labels are sorted in a `*.csv` table for output indexing purpose, while the header reference image is used to define the output image properties such as bounding box, originator, orientation, inclusive mask, and voxel size.



- **type**: draw roi as sphere or cube
- **unit**: unit of input radius
- **radius**: radius of sphere or 1/2 edge length for cubic
- **input type:**
  - manual: input coordinates seperated by ';'

    e.g:

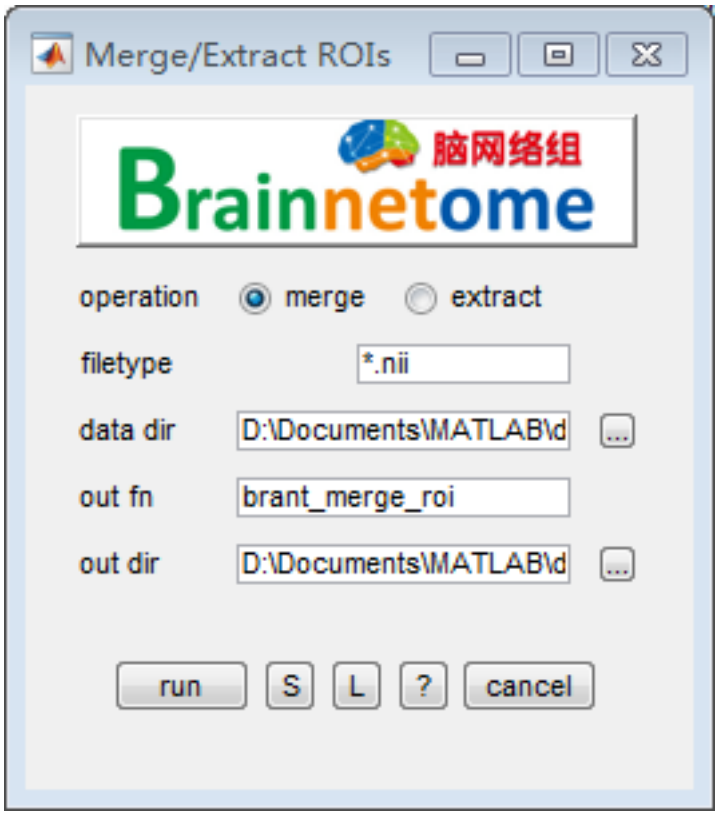
    ```
    25,5,10;10,15,10
    ```

  - file: input a csv file with 3 columns for x,y,z (the first line should be 'x', 'y' and 'z')
- **mask roi afterwards**: mask generated roi using input mask
- **output to one roi file**: instead of output one file for each roi, BRANT will generate one roi file with each roi labeled by number
- **ref&mask**: reference and mask file. for extracting information of origin, voxel size, bounding box, etc..
- **out dir**: directory for output

- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

2.2 Merge/Extract ROIs

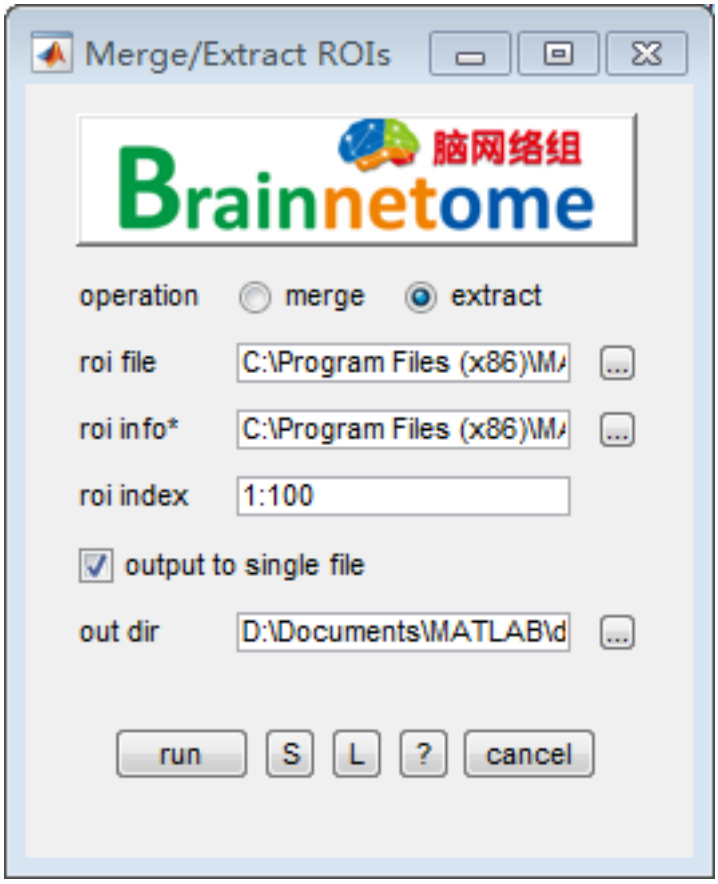
Given a number-tagged atlas, a subset of ROIs indexed by integers can be extracted and exported to one 3D image. At the opposite, given seperated ROI files, the current function can also merge them into one combined atlas-like ROI file, with ROI labels stored in a `*.csv` table.



- **Operation**: select to merge 3D rois into one, or extract ROIs from an atlas.
  - **Merge**:
  - **filetype**: files in the filetype will be searched in input directories.
  - **data dir**: directory in which stores 3D rois.
  - **out fn**: output filename
  - **out dir**: output directory
  - **Extract**:
  - **roi file**: ROIs in one nifti file
  - **roi info***: (* means optional) labels of tagged ROIs in a `*.csv` file. For example:

```
1,SFG
2,MFG
3,IFG
```

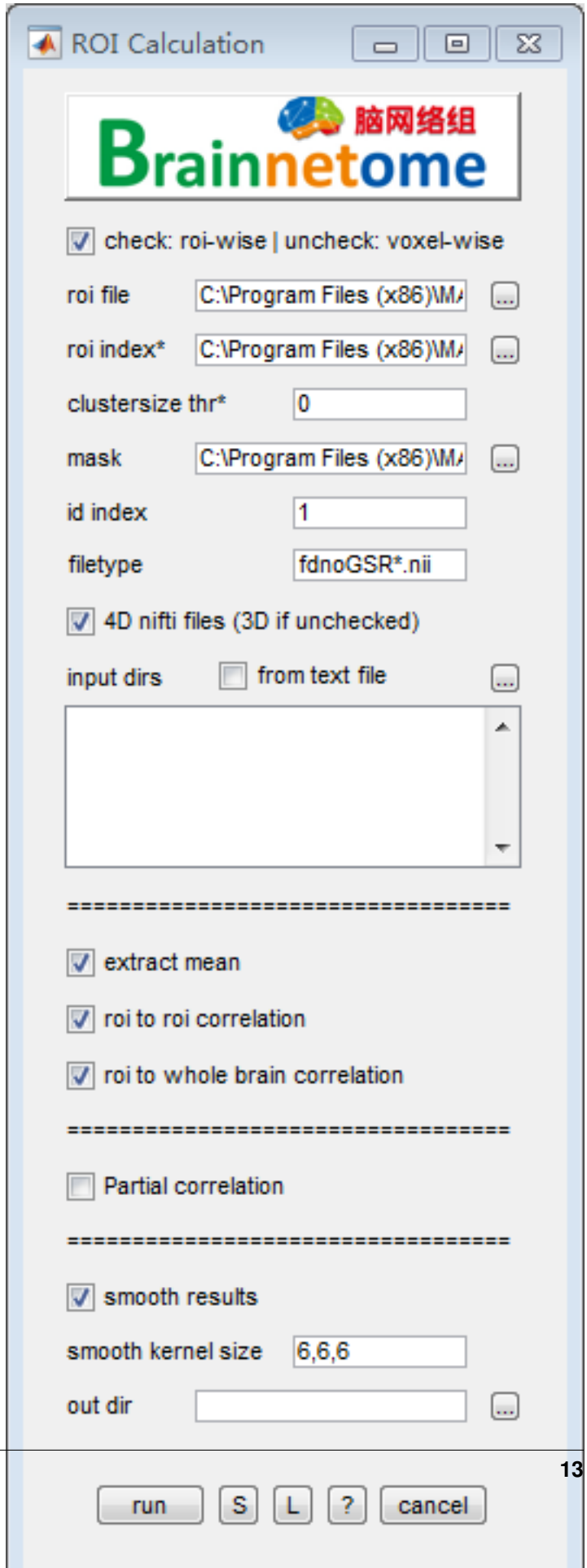
- **roi index**: a vector of integers. used for selecting wanted ROIs.
- **output to single file**: choose to output to only one file.
- **out dir**: output directory



- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

2.3 ROI Calculation

With a predefined atlas-like ROI file and a descriptive number-label table, the current function can extract mean time series from ROIs and voxels, and calculate Pearson's correlation as well as its Fisher-z transform. An option is provided to calculate partial correlation between each pair of ROIs, with mean signals of other ROIs as covariates.


ROI Calculation
脑网络组
Brainnetome
check: roi-wise | uncheck: voxel-wise
roi file
C:\Program Files (x86)\M
roi index*
C:\Program Files (x86)\M
clustersize thr*
0
mask
C:\Program Files (x86)\M
id index
1
filetype
fdnoGSR*.nii
4D nifti files (3D if unchecked)
input dirs
from text file
==========
extract mean
roi to roi correlation
roi to whole brain correlation
==========
Partial correlation
==========
smooth results
smooth kernel size
6,6,6
out dir
run
S
L
?
cancel

- **roi file**: ROIs in one nifti file
- **roi index(*)**: optional. labels of tagged ROIs in a `*.csv` file. For example:

```
1,SFG
2,MFG
3,IFG
```

- **clustersize thr**: threshold of cluster size.
- **mask**: could be whole brain mask or gray matter mask.
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **extract mean**: extract mean time series for each ROI
- **roi to roi correlation**: calculate correlation between pairs of ROI
- **roi to whole brain correlation**: calculate correlation between each ROI's mean time series and voxels in the mask.
- **Partial correlation**: (check to use Partial correlation, uncheck to use Pearson's correlation) when calculating correlation, between one roi mean time series and voxels/other time series, the rest of roi mean time serieses will be regressed out from the calculation.
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

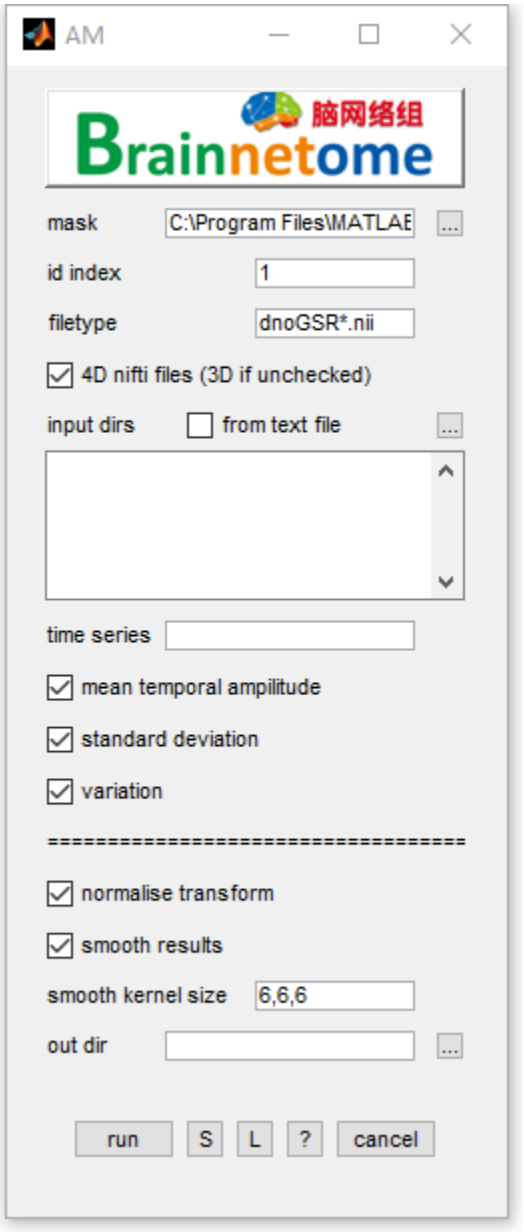
CHAPTER 3

SPON

Voxel-wise metrics of time series implemented in the current module include amplitude of time series (AM), (fractional) amplitude of low frequency fluctuation (ALFF/fALFF), regional homogeneity (ReHo), functional connectivity density (FCD) and functional connectivity strength (FCS).

3.1 AM

AM is calculated as the average amplitude and the standard deviation of the mean-subtracted time series. The AM represents the strength of time series' temporal fluctuation, which is similar to ALFF/fALFF.



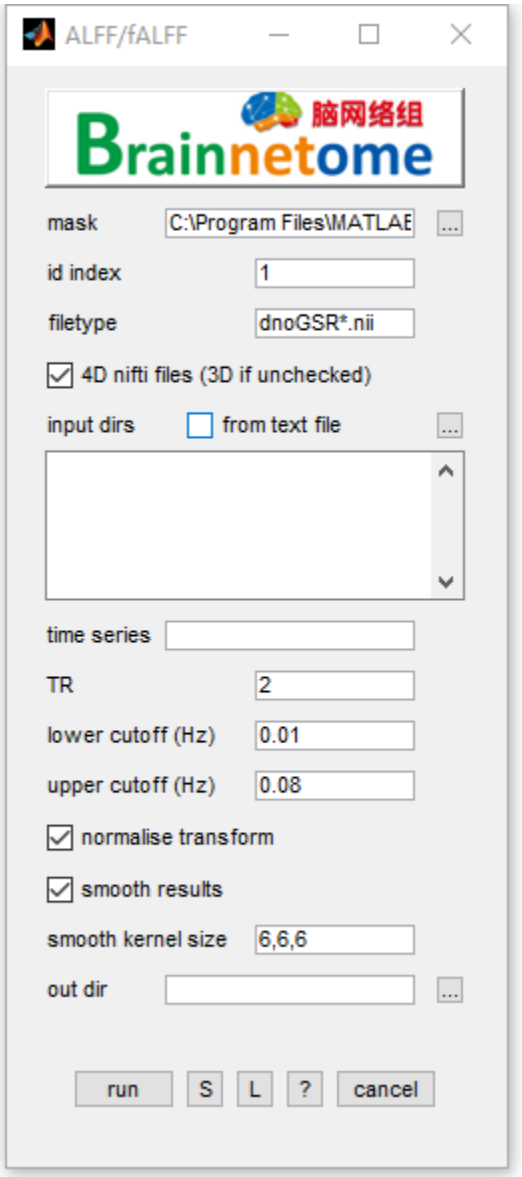
- **mask**: could be whole brain mask or gray matter mask.
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **time series**: choose the time series to calculate, seperated by ‘,’.
- **mean temporal ampilitude**: calculate absolute value of detrended and demeaned time series.
- **standard deviation**: calculate standard deviation of time series
- **variation**: calculate variation of time series

- **normalize transform**: in output file, a suffix of *_m* means the output is divided by mean intensity in the mask; a suffix of *_z* means the output is subtracted by mean intensity and divided by standard deviation.
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **Reference**:

1. Liu Y, Yu C, Zhang X, Liu J, Duan Y, Alexander-Bloch AF, et al. Impaired long distance functional connectivity and weighted network architecture in Alzheimer's disease. *Cereb Cortex 2014*; 24(6): 1422-35.

3.2 ALFF/fALFF

ALFF is calculated as the amplitude of the time series in a certain frequency band, which is the averaged square root of the power spectral density of the filtered time series. To increase the stability of ALFF across subjects, fALFF was proposed as calculating the fraction of a certain frequency band against the whole available frequency band.



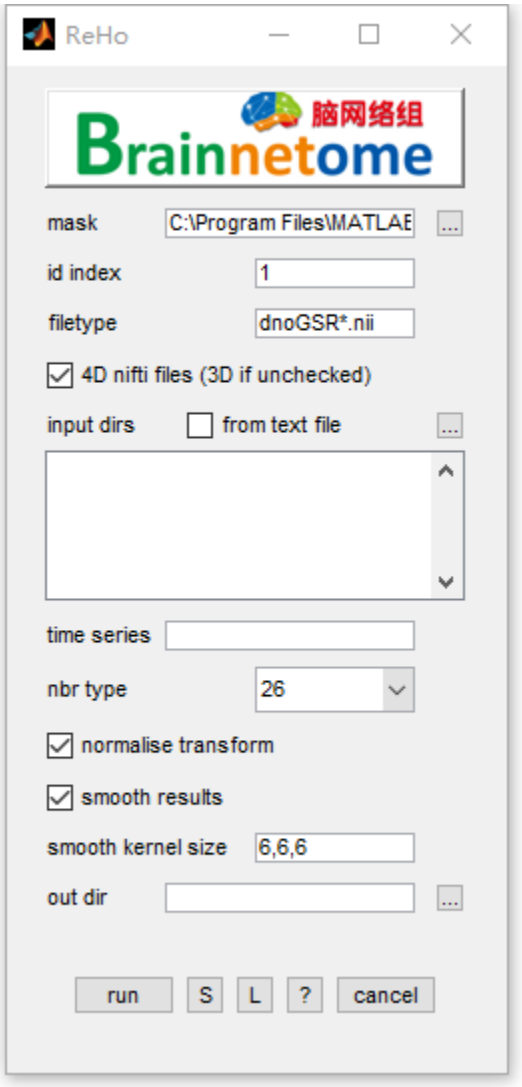
- **mask**: could be whole brain mask or gray matter mask.
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **time series**: choose the time series to calculate, seperated by ‘,’.
- **TR**: repetition time, used as sample frequency 1/TR to estimate width of frequency band.
- **lower cutoff (Hz)**: lower cutoff for band pass filter.
- **upper cutoff (Hz)**: upper cutoff for band pass filter.
- **normalize transform**: in output file, a suffix of *_m* means the output is divided by mean intensity in the mask; a suffix of *_z* means the output is subtracted by mean intensity and divided by standard deviation.

- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **References**:

1. Zang YF, He Y, Zhu CZ, Cao QJ, Sui MQ, Liang M, et al. Altered baseline brain activity in children with ADHD revealed by resting-state functional MRI. *Brain & development 2007*; 29(2): 83-91.
2. Zou QH, Zhu CZ, Yang Y, Zuo XN, Long XY, Cao QJ, et al. An improved approach to detection of amplitude of low-frequency fluctuation (ALFF) for resting-state fMRI: fractional ALFF. *J Neurosci Methods 2008*; 172(1): 137-41.

3.3 ReHo

ReHo is calculated as the Kendall's coefficient of concordance (KCC) among a seed voxel and its neighbor voxels, which indicates the degree of spontaneous activity in the seed voxel's vicinity. Voxels of higher intensity in ReHo maps indicate greater similarity among neighboring voxels' time series.



- **mask**: could be whole brain mask or gray matter mask.
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **time series**: choose the time series to calculate, seperated by ‘,’.
- **nbr type**: number of neighbor voxels, 6 face neighbor, 18 for edge neighbor and 26 for vertex neighbor.
- **normalize transform**: in output file, a suffix of *_m* means the output is divided by mean intensity in the mask.
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.

  - **?**: Help information.

- **Reference**:

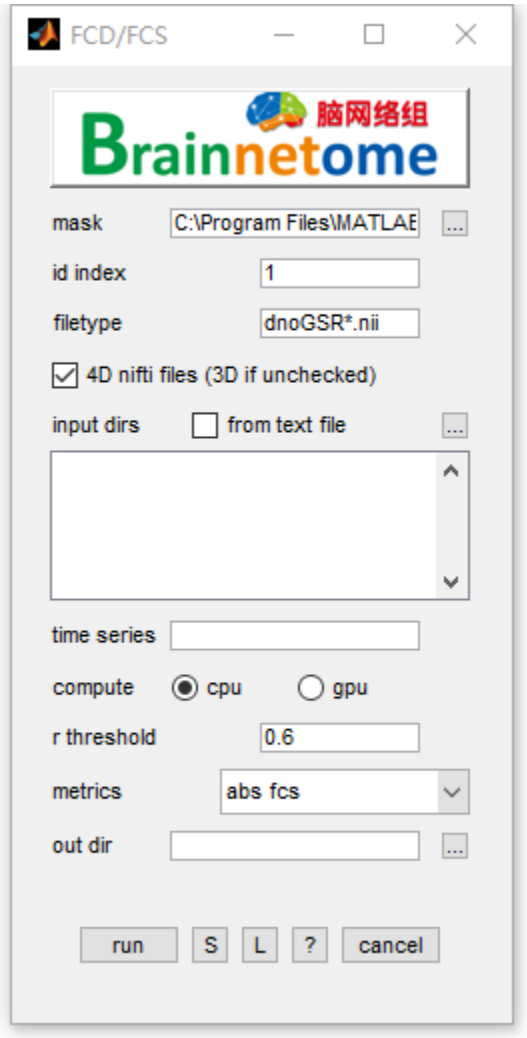
1. Zang Y, Jiang T, Lu Y, He Y, Tian L. Regional homogeneity approach to fMRI data analysis. *Neuroimage 2004*; 22(1): 394-400.

3.4 FCD/FCS

FCD is short for **Functional Connectivity Density** and **FCS** is short for **Functional Connectivity Strength**.

A region growing algorithm was carried out to measure the local degree of each voxel under a certain threshold of Pearson's correlation. FCD in BRANT has been implemented to calculate the local FCD (lFCD), the global FCD (gFCD) and the long-range FCD (lrFCD) at one time. The lFCD of each voxel represents the number of spatially connected voxels defined by the region growing algorithm, while the gFCD, which is also referred to as the voxel-wise degree centrality, represents the number of voxels that have higher-than-threshold correlation with the seed voxel. The lrFCD is calculated as the gFCD subtracted the lFCD.

Functional connectivity strength (FCS) measures the amount of information a node receives across whole graph or within a distance. Similar to FCD, the voxel-wise Pearson's correlation coefficients are firstly calculated in parallel and then Fisher-z transformed to improve normality. For each voxel, the FCS is calculated as the sum of connectivity that exceeds a given threshold divided by the number of voxels.



- **mask**: could be whole brain mask or gray matter mask.
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **time series**: choose the time series to calculate, seperated by ‘,’.
- **compute**: use OPENCL supported CPU or GPU to calculate FCD
- **r threshold**: threshold of correlation (to binarize functional connectivity and sum up)
- **metrics:**
    1. **fcd** - functional connectivity density, calculate global and region grow defined degree
    2. **fcs** - functional connectivity strength, calculate global-wise sum/mean of above threshold intensity
    3. **fcs abs** - absolute functional connectivity strength, firstly convert FC map to absolute value and calculate global-wise sum/mean of above threshold intensity
- **out dir**: output directory for saving results.

- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **Output files**:
  - **Raw:**
    - *gfcd(global fcd)*: count the number of voxels of voxel to whole brain correlation (rho > threshold)
    - *lfcd(local fcd)*: count the number of voxels of voxel to neighbour voxels' correlation (rho > threshold, with region grow method)
    - *lrfcd(long-range fcd)*: gfcd - lfcd
    - *fcs_sum*: sum of above threshold voxels' intensity
    - *fcs_ave*: mean of above threshold voxels' intensity
  - **Normalized:**
    - *gfcd*: gfcd(Raw) divided by mean value of gfcd(Raw)
    - *lfcd*: lfcd(Raw) divided by mean value of lfcd(Raw)
    - *lrfcd*: lrfcd(Raw) divided by mean value of lrfcd(Raw)
    - *fcs_sum_nor*: fcs_sum(Raw) divided by mean value of fcs_sum(Raw)
    - *fcs_ave_nor*: fcs_ave(Raw) divided by mean value of fcs_ave(Raw)
- **References**:

1. Tomasi, D., & Volkow, N. D. (2010). Functional connectivity density mapping. *Proceedings of the National Academy of Sciences of the United States of America*, 107(21), 9885-90.
2. Craddock R, Clark D. Optimized implementations of voxel-wise degree centrality and local functional connectivity density mapping in AFNI. *GigaScience 2016*; 5(suppl_1): 4-6.
3. Qin W, Xuan Y, Liu Y, Jiang T, Yu C. Functional Connectivity Density in Congenitally and Late Blind Subjects. *Cereb Cortex 2014*; 25(9): 2507-16.

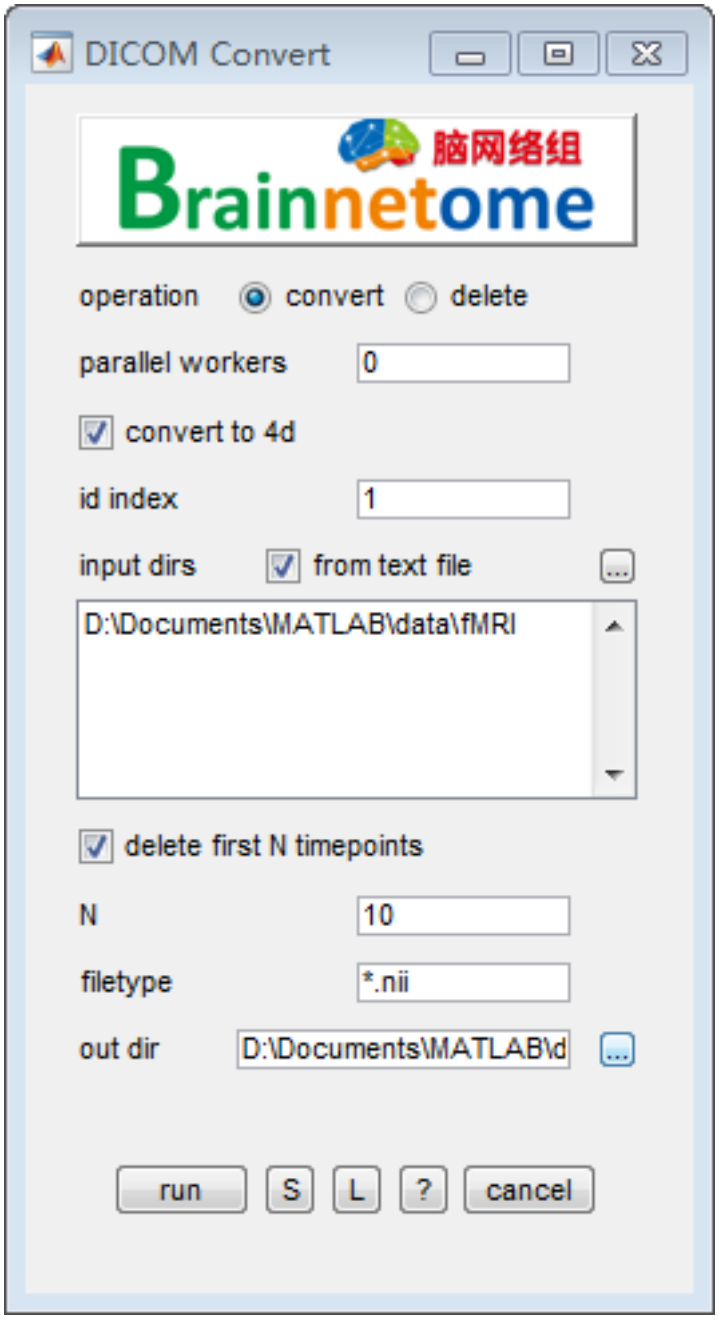
CHAPTER 4

Utilities

We have added several frequently used functions in this module to facilitate DICOM image conversion, the process of quality control, ROI coordinates extraction and 2D/3D signal extraction.

4.1 Dicom Convert

Since in practice raw MRI data exported from an MR scanner consists of a large number of DICOM images storing slices and volumes of different sequences, by convention we convert the DICOM images to packed 3D or 4D NIFTI images before all processing steps. In BRANT, we use the *dcm2nii* from MRIcron/MRIcro to convert DICOM files into 4D NIfTI images by default and use wildcard characters to locate rs-fMRI image files. For the matched images, the *First N timepoints removal* is used to remove the first N frames that could be influenced by large motion or the instability of magnetic field.



- **operation: convert**
  - **parallel workers**: select how many workers to start a parallel work. The default is 0.
  - **convert to 4d**: select to convert data to 4D format, otherwise to 3D.
  - **id index**: identifier to find unique string for each subject.
  - **input dirs**: directories can be input either using a *.txt* file or spm select window.
  - **delete first N timepoints**: delete heading fMRI volumes.
  - **N**: number of the heading timepoints to be deleted, the default is 10.
  - **filetype**: wildcard to search wanted fMRI data.

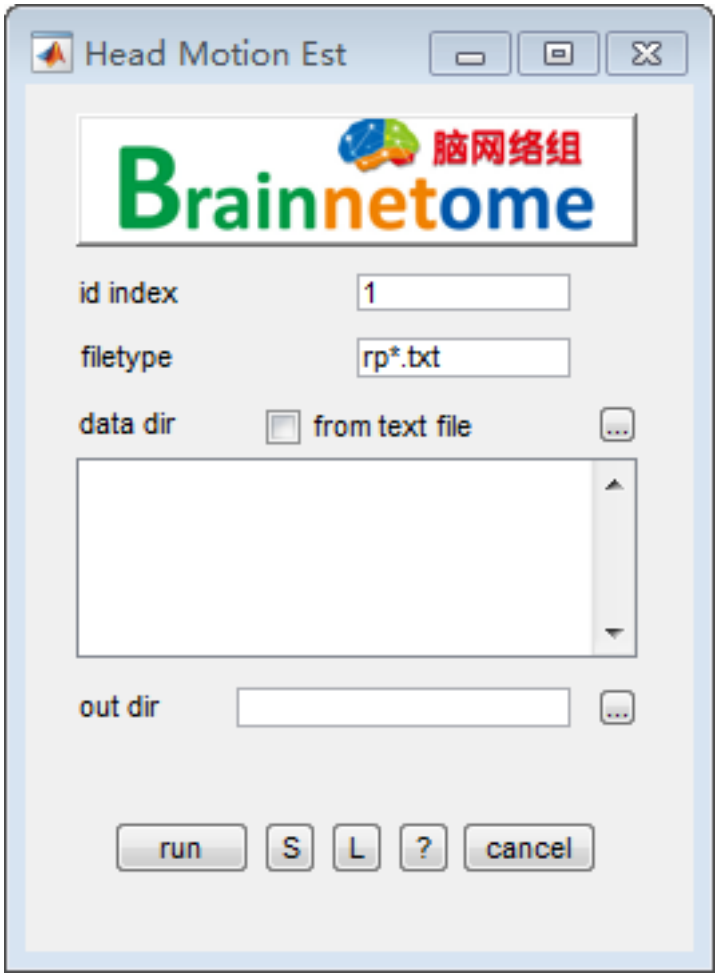
  - **out dir**: output directory for saving results.

- **operation: delete**
  - **id index**: identifier to find unique string for each subject
  - **filetype**: files in the filetype will be searched in input directories.
  - **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
  - **input dirs**: directories can be input either using a `*.txt` file or spm select window.
  - **delete first N timepoints**: delete heading fMRI volumes.
  - **output fn**: output filename.
  - **output to another directory**: output data to another directory
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **Reference**:

1. Rorden C, Brett M. Stereotaxic display of brain lesions. *Behav Neurol 2000*; 12(4): 191-200.

4.2 Head Motion Estimate

Head motion has been found having an impact on rs-fMRI signals. In preprocessing, six head motion parameters of (x-,y-,z-) translations and (pitch-,yaw-,roll-) rotations estimated during realignment are used as the inputs of the current function. By the default, the current function outputs the maximum absolute translation and rotation between frames as the exclusion criterion of large-motion subject. Additionally, the mean head displacement (the root-mean-square of translation parameters), the maximum head displacement, the number of micro displacement (>0.1mm), the mean absolute Euler angle of rotation, the framewise displacement (FD) and the number of frames with FD>0.5mm, are also exported to provide more subject exclusion criteria.



- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **input dirs**: directories can be input either using a `.txt` file or spm select window.
- **out dir**: output directory for saving results.
- **Meaning of results:**
  - **max-abstranslation(mm)**: maximum translation. Estimated as the max absolute value of the first 3 columns from `rp*.txt`
  - **max-absrotation(deg)**: maximum rotation. Estimated as the max absolute value of the last 3 columns from `rp*.txt` multiple by 180/pi.
  - **From van Dijk et al., Neuroimage 2012**
    - **max-motion-Dijk(mm)**: maximum root-mean-square of translation.
    - **mean-motion-Dijk(mm)**: mean root-mean-square of translation.
    - **num-movements-Dijk(>0.1mm)**: number of micro-movement. The number of root-mean-square of translation that is greater than 0.1mm
    - **mean-rotation-Dijk(deg)**: mean absolute Euler angle
  - **From Power et al., Neuroimage 2012**

* **mean-FD(mm)**: frame-wise displacement. Estimated using translation and rotation.
* **num-FD>0.5**: number of frame-wise displacement that is greater than 0.5mm.

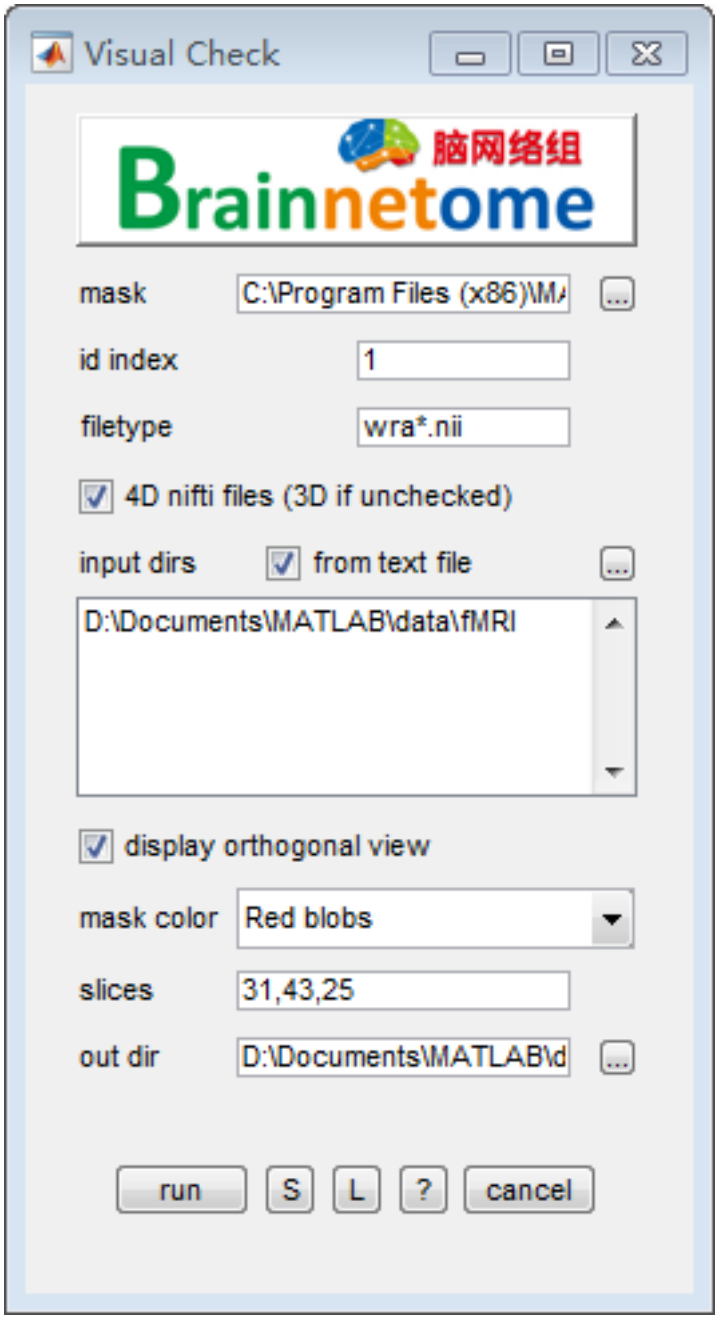
	A	B	C	D	E	F	G	H	I
1	subject-name	max-abstranslation(	max-absrotation	max-motion-Dijk(mm)	mean-motion-Dijk(mm)	num-movements-Dijk(>0.1mm)	mean-rotation-Dijk(deg)	mean-FD(mm)	num-FD>0.5
2	fMRI	0.7295	0.2714	0.56686	0.054145	18	0.024991	0.10875	3

- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **References**:

1. Van Dijk KR, Sabuncu MR, Buckner RL. The influence of head motion on intrinsic functional connectivity MRI. *Neuroimage 2012*; 59(1): 431-8.
2. Power JD, Barnes KA, Snyder AZ, Schlaggar BL, Petersen SE. Spurious but systematic correlations in functional connectivity MRI networks arise from subject motion. *Neuroimage 2012*; 59(3): 2142-54.

4.3 Visual Check

The current function provides batch operations to visually inspect artifacts and normalization quality, by calling *Display* from SPM. We've added keyboard operations to the *Display* figure that users can press up/down to switch fMRI volumes of one subject and press left/right to switch subjects. Before running the frame-by-frame inspection, the current function exports screenshots of selected slices overlaid by a semi-transparent brain mask for a glimpse of the overall image quality.



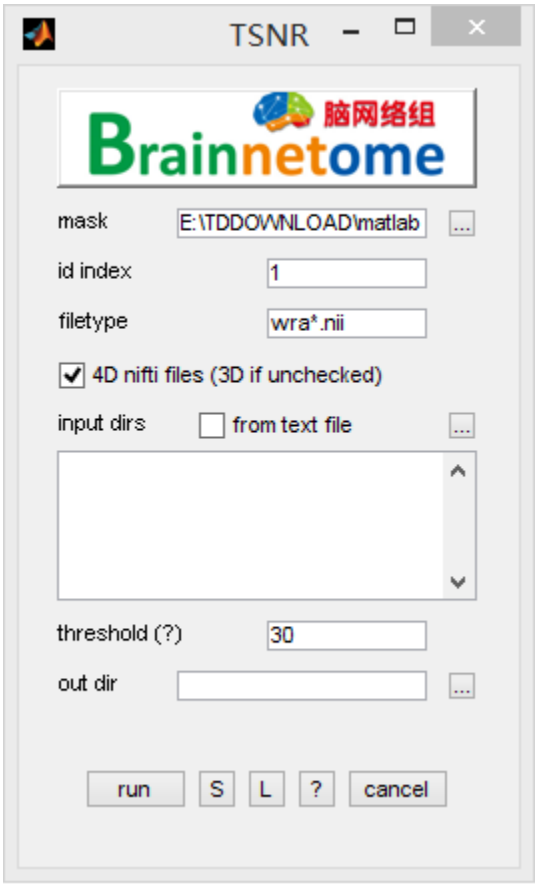
The function calls SPM Check Reg to visualize input volume, a keyboard callback is added to enable left/right and up/down to switch timepoint and subjects.

- **mask**: could be whole brain mask or gray matter mask.
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **display orthogonal view**: check to display orthogonal view of selected slices and save screenshots. uncheck will only save screenshots to out dir.

- **mask color**: color of the transparent overlaid mask.
- **slices**: modified image n-th slice of x,y,z to save.
- **out dir**: output directory for saving results.
- **Keyboard Operation:**
  - **Up/Down**: last/next timepoint of the same subject.
  - **Left/Right**: same timepoint of last/next subject.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

4.4 TSNR (Temporal Signal to Noise Ratio)

Influenced by the magnetic field inhomogeneity at air-tissue interfaces, rs-fMRI signals at orbitofrontal and temporal medial and polar areas suffer from a certain degree of distortions and signal loss. To exclude spurious voxels, we use the thresholded voxel-wise TSNR, which is calculated as the average intensity of time series divided ty the standard deviation, to generate subject-level or group-leval whole-brain mask.



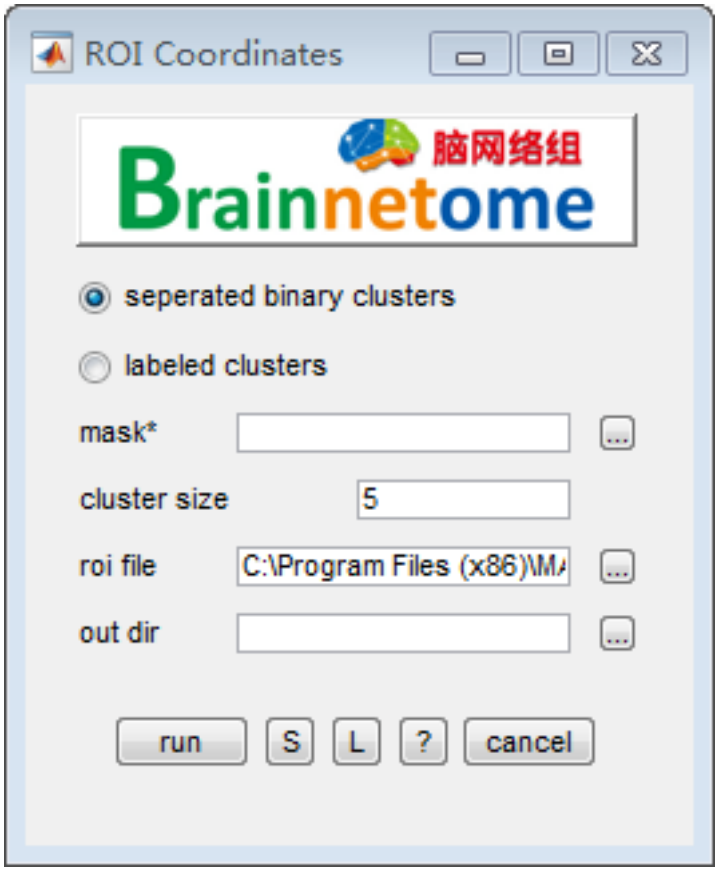
- **mask**: could be whole brain mask or gray matter mask.

- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **threshold**: intensity threshold for mean TSNR (to generate a binary mask).
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **References**:

1. Tomasi D, Volkow ND. Functional connectivity density mapping. *Proceedings of the National Academy of Sciences of the United States of America 2010*; 107(21): 9885-90.
2. Yeo BT, Krienen FM, Sepulcre J, Sabuncu MR, Lashkari D, Hollinshead M, et al. The organization of the human cerebral cortex estimated by intrinsic functional connectivity. *J Neurophysiol 2011*; 106(3): 1125-65.
3. Welvaert M, Rosseel Y. On the definition of signal-to-noise ratio and contrast-to-noise ratio for FMRI data. *PLoS One 2013*; 8(11): e77089.

4.5 ROI coordinates

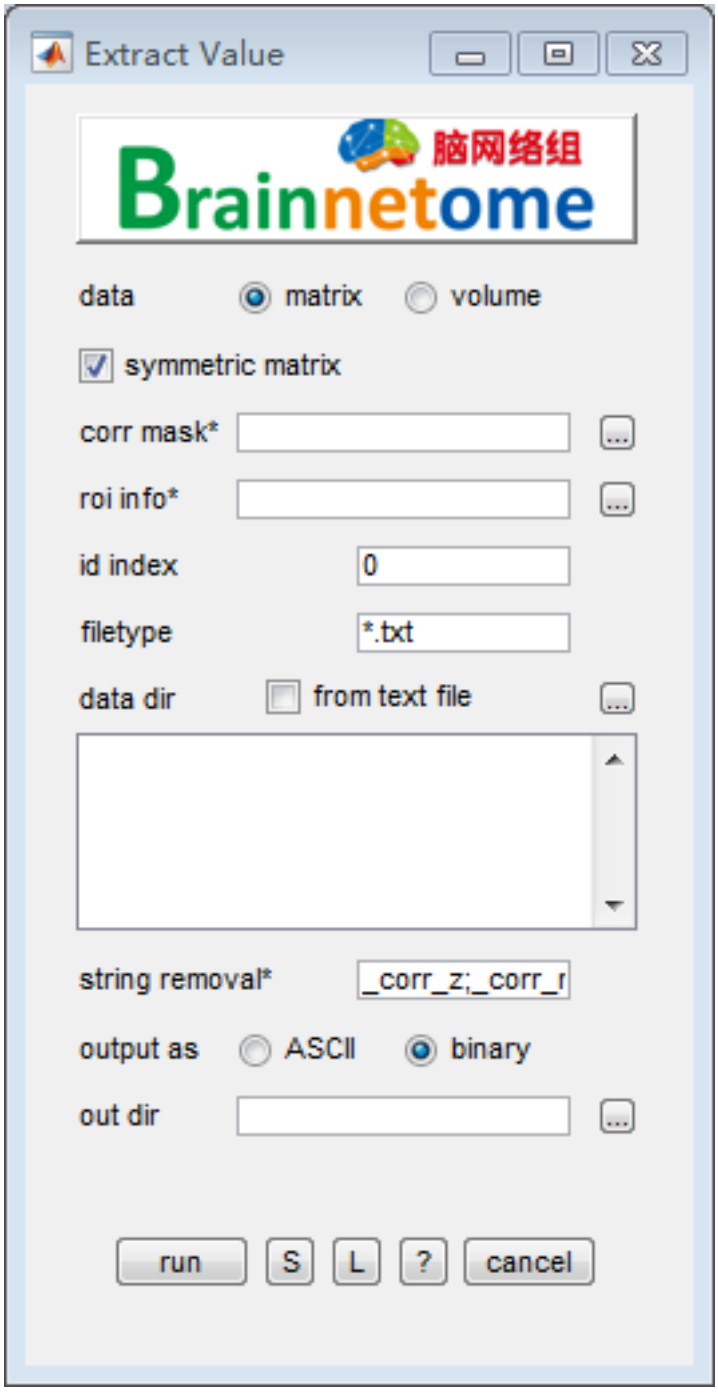
To visualize the topological strcture of network connections, ROI coordinates are expected as the centers of spheres. In the current function, coordinate of each number-tagged ROI is calculated as the center of mass with weights and then exported to a `*.csv` table.



The current function extracts coordinates for each cluster and output to a table.

- **input type**: seperated binary clusters or labeled clusters
- **mask***: optional. mask to do AND operation with.
- **cluster size**: threshold of cluster size.
- **roi file**: input ROI file
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

4.6 Extract Value



- **data: matrix**
  - **symmetric matrix**: check to extract the upper right matrix's elements, uncheck to extract all elements
  - **corr mask**: e.g. a matrix mask used to find significant links instead of all links
  - **roi info***: a `.csv` with at least one column start with "label"
  - **id index**: identifier to find unique string for each subject

  - **filetype**: filetype
  - **data dir**: Input directories of matrices.

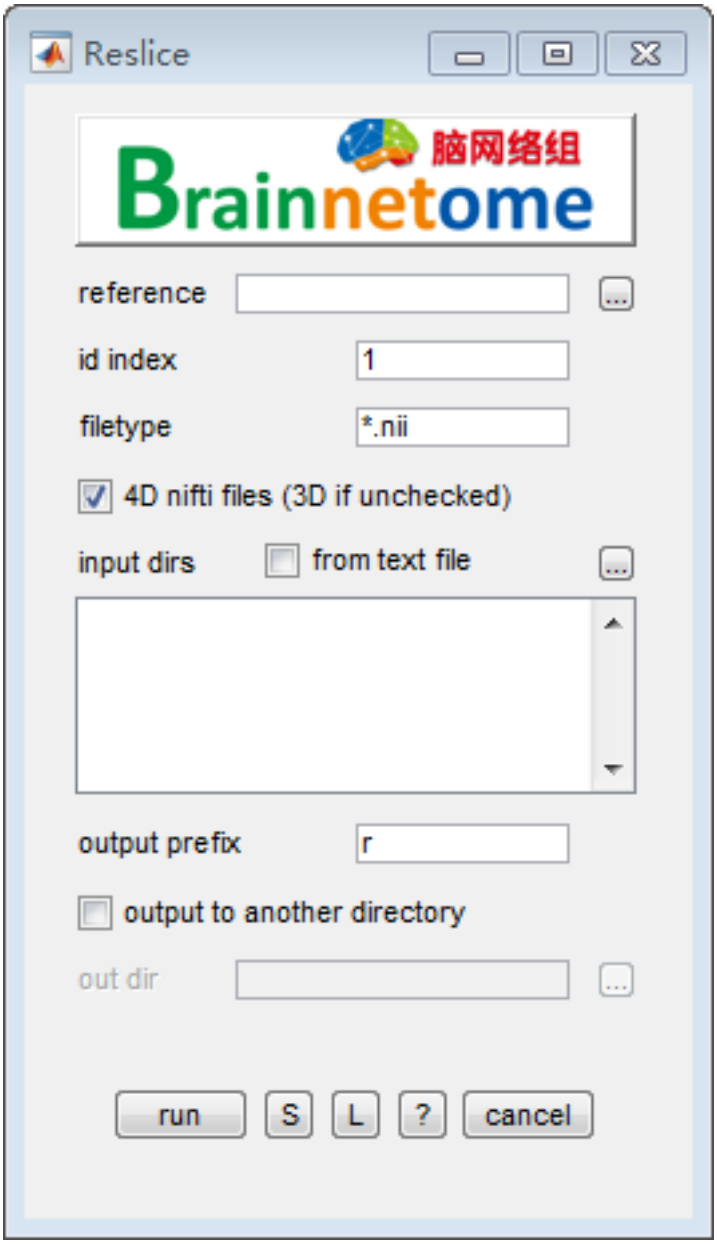
- **data: volume**
  - **roi file**: ROI file used for extracting mean intensity in each roi tagged by number.
  - **roi info**: labels of tagged ROIs. (optional)
  - **mask**: could be whole brain mask or gray matter mask.
  - **id index**: identifier to find unique string for each subject
  - **filetype**: files in the filetype will be searched in input directories.
  - **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
  - **input dirs**: directories can be input either using a `.txt` file or spm select window.

- **string removal***: optional. remove partial string from string parsed by id index.
- **output as**: (only works for data type 'matrix') choose to output data matrix as ASCII(can be edited with text reader) or binary(more hard drive friendly with large matrix). if binary is chosen, you need to handle the matrix by:

```
fid = fopen('brant_extract_links.txt', 'rt');
outmat = fread(fid, sizeofmat, 'single');
fclose(fid);
```

- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

4.7 Reslice



The current function reslice MRI images to a reference image (internally calls SPM-Coregister-Reslice).

- **reference**: reference image for header information.
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **output prefix**: prefix of output file, by default the program will output to the same directory as input file.
- **output to another directory**: check to output file to another directory.

- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

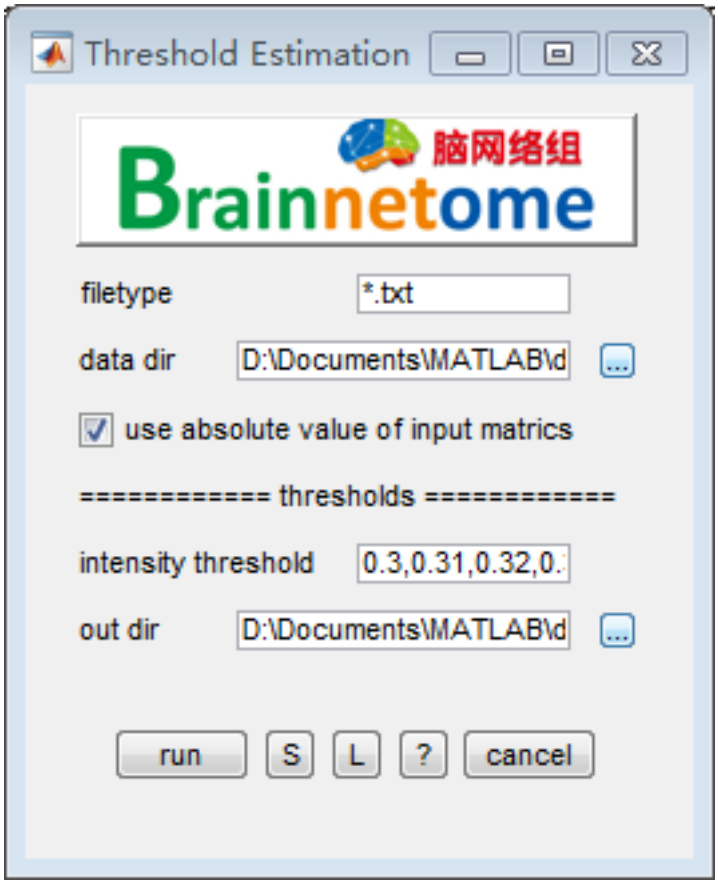
CHAPTER 5

NET

Network metrics depict the properties of information flow among predefined nodes. Regarding brain networks, ROIs are defined as nodes and the connections between pairs of ROIs are defined as edges. In the current module, connectivity matrices are firstly thresholded by intensity or sparsity to weighted or binary networks.For group comparisons under a vector of thresholds, Student's t-tests are provided.

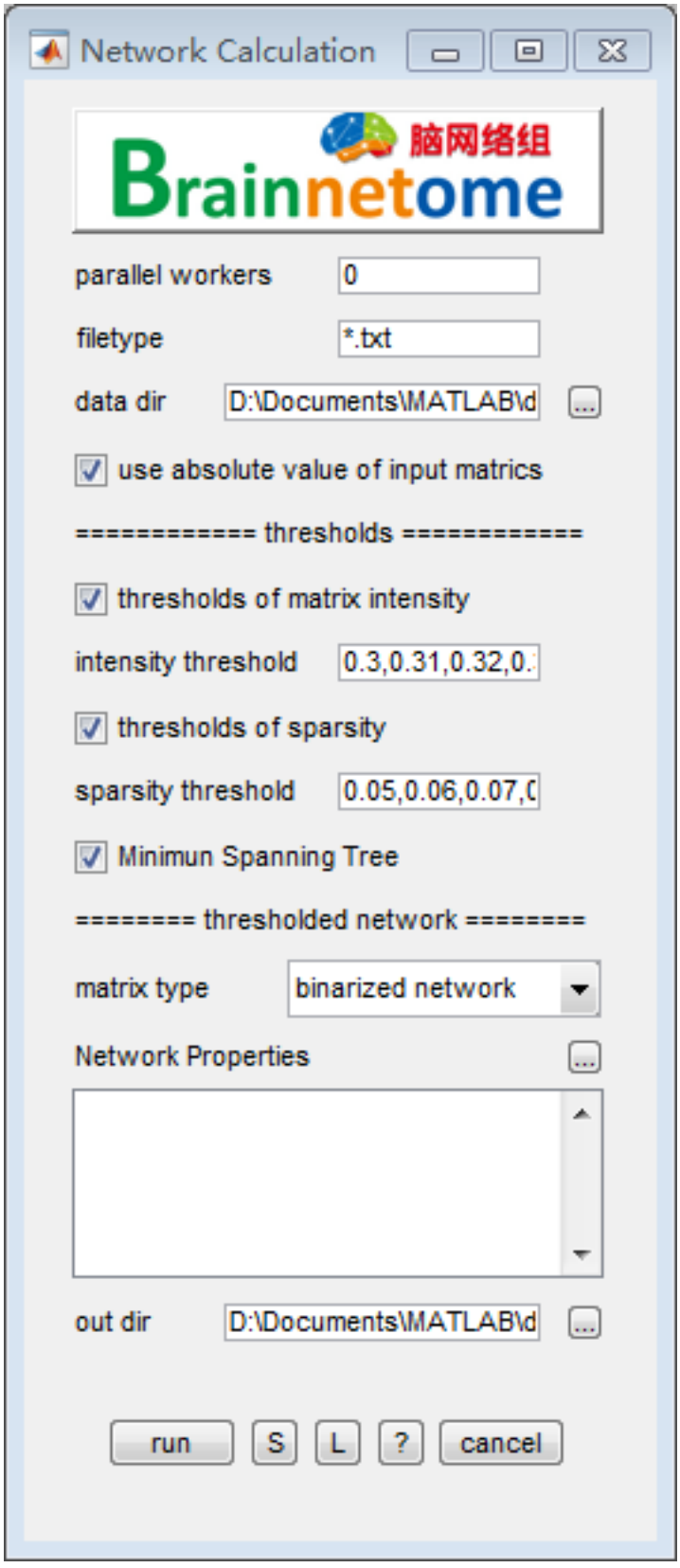
5.1 Threshold Estimation

Find out for each subject, the sparsity under each threshold of correlation



- **filetype**: files in the filetype will be searched in input directories.
- **data dir**: directory where all `*.txt` correlation matrix results are stored.
- **use absolute value of input matrics**: as it means
- **intensity threshold**: vector of thresholds for matrix intensity. e.g. correlation coefficient
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

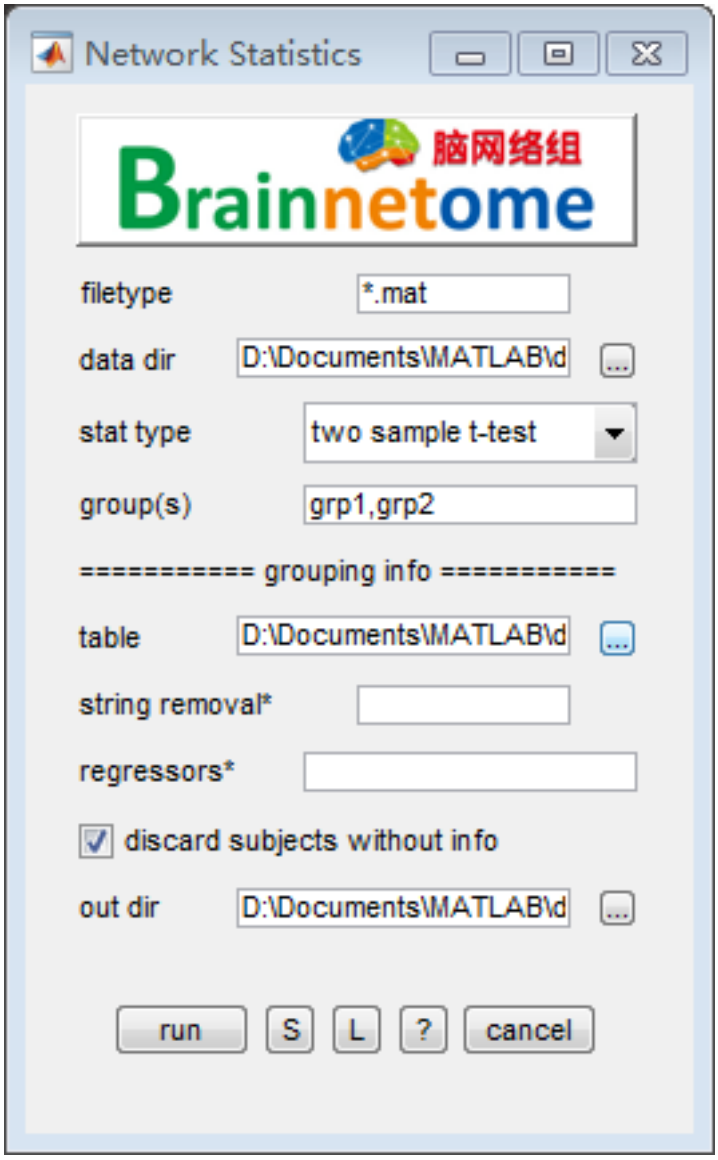
5.2 Network Calculation



- **parallel workers**: number of workers used for parallel computing.
- **filetype**: files in the filetype will be searched in input directories.
- **data dir**: directory where all `*.txt` correlation matrix results are stored.
- **use absolute value of input matrics:**
  - **raw value**: use raw value to construct binary matrix.
  - **absolute value**: use absolute value to construct binary matrix.
- **intensity threshold**: vector of thresholds for matrix intensity. e.g. correlation coefficient
- **sparsity threshold**: a vector of sparsity threshold, for each element, threshold the input matrix using the fraction of the matrix's largest number of connection n*(n+1)/2;
- **minimum spanning tree**: a process to avoid unconnected network. To label the backbone of the network's nodes.
- **matrix type**: binarized and weighted network. The binarized networks comes from thresholded input matrics, while the weighted network comes from a dot product operation of binarized network and the original network.
- **Network properies**: a panel to select network properties. In the option panel, (*) means the calculation of the property is slow.
- **out dir**: output directory for saving results.
- **zero value in clustering coefficient**: if the network is connected in a way (e.g. Hamilton path) that neighbour nodes are not connected; or the current node has only one neighbour node.
- **Inf in small worldness**: The small-worldness is calculated as real-network / random-network, and in real and random case, small-worldness is calculated as clustering coefficient/shortest-path length. If the mean clustering coefficient of the random-network is zero, then the small-worldness of random-network is zero, and it will cause the real-network / random-network to be Inf(any non-zero divided by 0). The solution is set smaller thresholds that avaliable for all subjects.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **Reference**:

1. Rubinov M, Sporns O. Complex network measures of brain connectivity: uses and interpretations. *Neuroimage 2010*; 52(3): 1059-69.

5.3 Network Statistics



- **filetype**: files in the filetype will be searched in input directories.
- **data dir**: directory where `*.mat` result of NETWORK CALCULATION is stored.
- **stat type**: one sample t-test, two sample t-test and paired t-test.
- **groups:**
  - for two sample t-test, e.g. SZ,NC -> will do two-sample t-test for SZ and NC
  - for paired t-test, e.g. SZ,NC -> will do paired t-test for SZ and NC
  - for one sample t-test, e.g. SZ;NC -> will do one-sample t-test for both SZ and NC group
- **grouping info:**
  - **table**: A comma-seperated values (csv) table, which is used for parsing subject names and covariates. The parsed names/ids will be matched to search results conducted with datadir and filetype. Before

matching, BRANT will remove specified strings.

– **For one and two sample t-tests:**

name	group	filter	age
subj1	SZ	center1	28
subj2	SZ	center1	27
subj3	NC	center1	30
subj4	NC	center2	25

– **For paired t-test, another column of paired_t_idx is required to specify paired subjects in each group:**

name	group	filter	age	paired_t_idx
subj1	stage1	center1	28	1
subj2	stage1	center1	27	2
subj3	stage2	center1	30	1
subj4	stage2	center2	25	2

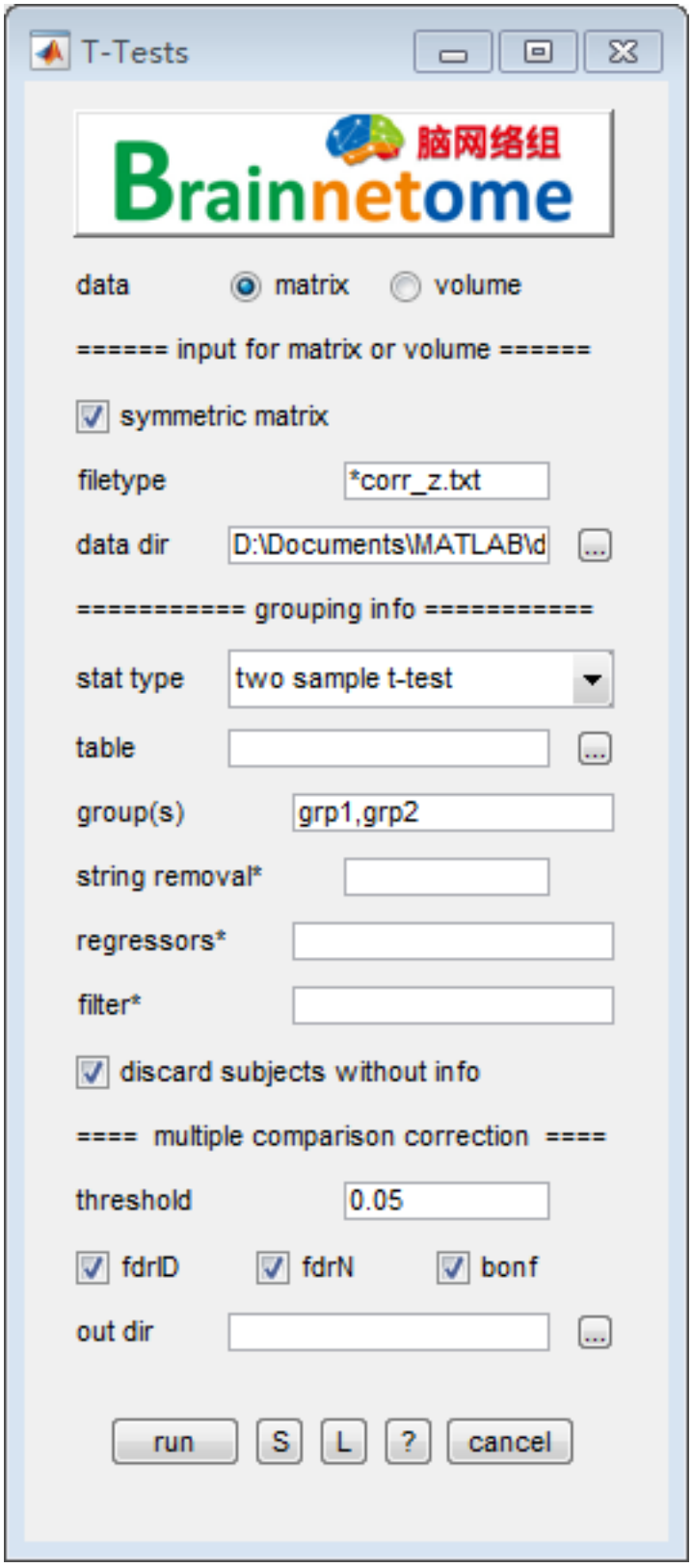
- **string removal***: optional. remove partial string from string parsed by id index.
- **regressors***: optional. title of regressors which will be regressed out before statistical analysis. e.g. age
- **filter***: optional. use the control for subject in different state or center, fill in center1 here and subject4 won't be included in the analysis.
- **discard subjects without info**: when checked, if subjects' information are not found in the table, a warning message will be shown; when unchecked, an error message will be shown.
- **out dir**: output directory for saving results.
- If the output figure is empty, check whether there is NaN or Inf in the output `*.csv` files, where the raw global network properties are extracted.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

CHAPTER 6

STAT

The current module provides Student's t-tests for sample mean comparisons and several methods for image-based meta-analysis (IBMA). For multi-comparison correction, we use the Benjamini-Hochberg and the Benjamini-Yekutieli procedures to control the false discovery rate (FDR) of dependent and independent cases, and the Bonferroni procedure to control the familywise error rate (FWER).

6.1 T-tests


T-Tests
Brainnetome
脑网络组
data
matrix
volume
====== input for matrix or volume ======
symmetric matrix
filetype
*corr_z.txt
data dir
D:\Documents\MATLAB\d
========== grouping info ==========
stat type
two sample t-test
table
group(s)
grp1,grp2
string removal*
regressors*
filter*
discard subjects without info
==== multiple comparison correction ====
threshold
0.05
fdrID
fdrN
bonf
out dir
run
S
L
?
cancel

- **data: matrix**
  - **symmetric matrix**: check to extract the upper right matrix's elements, uncheck to extract all elements
- **data: volume**
  - **mask**: could be whole brain mask or gray matter mask.
- **filetype**: filetype
- **data dir**: Input directories of matrices.
- **grouping info:**
  - **stat type**: one sample t-test, two sample t-test and paired t-test.
  - **groups:**
    - for two sample t-test, e.g. SZ,NC -> will do two-sample t-test for SZ and NC
    - for paired t-test, e.g. SZ,NC -> will do paired t-test for SZ and NC
    - for one sample t-test, e.g. SZ;NC -> will do one-sample t-test for both SZ and NC group
  - **table**: A comma-seperated values (csv) table, which is used for parsing subject names and covariates. The parsed names/ids will be matched to search results conducted with datadir and filetype. Before matching, BRANT will remove specified strings.
  - For one and two sample t-tests:

name	group	filter	age
subj1	SZ	center1	28
subj2	SZ	center1	27
subj3	NC	center1	30
subj4	NC	center2	25

  - For paired t-test, another column of paired_t_idx is required to specify paired subjects in each group:

name	group	filter	age	paired_t_idx
subj1	stage1	center1	28	1
subj2	stage1	center1	27	2
subj3	stage2	center1	30	1
subj4	stage2	center2	25	2

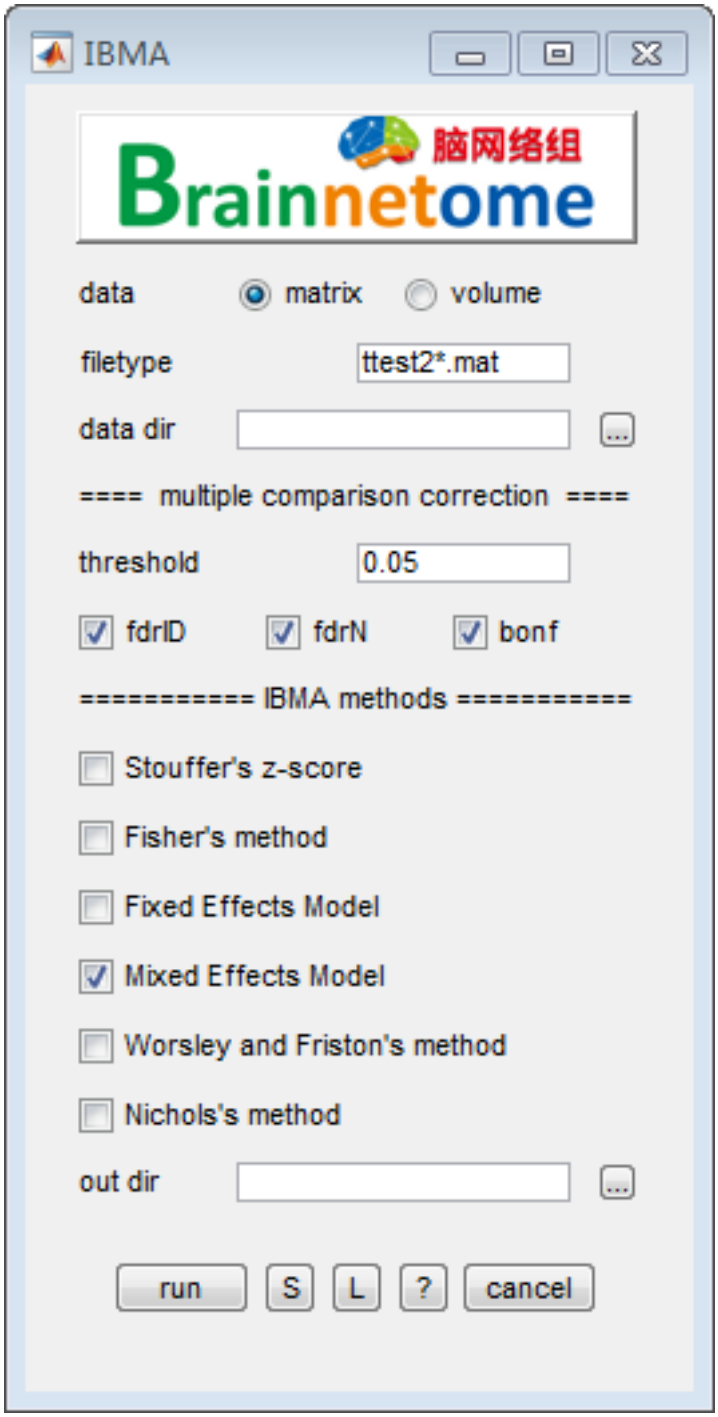
  - **string removal***: optional. remove strings from search results parsed by id index.
  - **regressors***: optional. title of regressors which will be regressed out before statistical analysis. e.g. age
  - **filter***: optional. use the control for subject in different state or center, fill in center1 here and subject4 won't be included in the analysis.
  - **discard subjects without info**: when checked, if subjects' information are not found in the table, a warning message will be shown; when unchecked, an error message will be shown.
- **Multiple comparison correction methods (voxel-wise)**
  - **threshold**: the level of MULCC
  - **fdrID**: false discovery rate (independent input)
  - **fdrN**: false discovery rate (inputs not independent)

  - **bonf**: Bonferroni correction for family wise error rate

- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

6.2 IBMA (Image-based meta-analysis)

With statistical maps of different datasets tested using same analysis pipeline, and the demography of each sample, users can perform meta-analysis to merge the multisite statistics using image-based or matrix-based meta-analysis. We have implemented Stouffer's z-score method, Fisher's method, fixed/mixed effects model, Worsley and Friston's method and Nichols' method.



- **data: matrix**
  - **filetype**: files in the filetype will be searched in input directories.
  - **data dir**: directory where all `ttest2*.mat` results are stored.
- **data: volume**
  - **center info: number of subjects for different centers. A csv format table is required. N1 and N2 is the number of**

center	N1	N2
ttest2_center1_a_vs_b	40	39
ttest2_center2_a_vs_b	38	37

  - **mask**: could be whole brain mask or gray matter mask.
  - **id index**: identifier to find unique string for each subject
  - **filetype**: files in the filetype will be searched in input directories.
  - **data dir**: directories can be input either using a `*.txt` file or spm select window.
- **Multiple comparison correction methods (voxel-wise)**
  - **threshold**: the level of MULCC
  - **fdrID**: false discovery rate (independent input)
  - **fdrN**: false discovery rate (inputs not independent)
  - **bonf**: Bonferroni correction for family wise error rate
- **IBMA Methods:**
  - Stouffer's z-score
  - Fisher's method
  - Fixed Effects Model
  - Mixed Effects Model
  - Friston's method
  - Nichols's method
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **References**:

1. **Stouffer's z-score** Stouffer, S.A., Suchman, E.A., DeVinney, L.C., Star, S.A. and Williams Jr, R.M., 1949. *The American soldier: Adjustment during army life.(Studies in social psychology in World War II), Vol. 1*. Princeton University Press, Princeton,.
2. **Fisher** Fisher, R.A. (1925). Statistical Methods for Research Workers. *Oliver and Boyd (Edinburgh)*. ISBN 0-05-002170-2.
3. **Fixed/mixed Effects Model** Hedges, L.V. (1992). Meta-Analysis. *Journal of Educational and Behavioral Statistics.* 17(4), 279-296. doi: 10.3102/10769986017004279.

   Konstantopoulos, S. (2006). Fixed and mixed effects models in meta-analysis. *Iza Discussion Papers*.
4. **Worsley and Friston's method** Worsley, K.J., and Friston, K.J. (2000). A test for a conjunction. *Statistics & Probability Letters.* 47(2), 135-140. doi: 10.1016/S0167-7152(99)00149-2.

5. **Nichols's method** Nichols, T., Brett, M., Andersson, J., Wager, T., and Poline, J.B. (2005). Valid conjunction inference with the minimum statistic. *Neuroimage.* 25(3), 653-660. doi: 10.1016/j.neuroimage.2004.12.005.

6. Salimi-Khorshidi G, Smith SM, Keltner JR, Wager TD, Nichols TE. Meta-analysis of neuroimaging data: a comparison of image-based and coordinate-based pooling of studies. *Neuroimage 2009*; 45(3): 810-23.

7. Benjamini Y, Hochberg Y. Controlling the False Discovery Rate - a Practical and Powerful Approach to Multiple Testing. J Roy Stat Soc B Met 1995; 57(1): 289-300.

8. Benjamini Y, Yekutieli D. The control of the false discovery rate in multiple testing under dependency. Ann Stat 2001; 29(4): 1165-88.

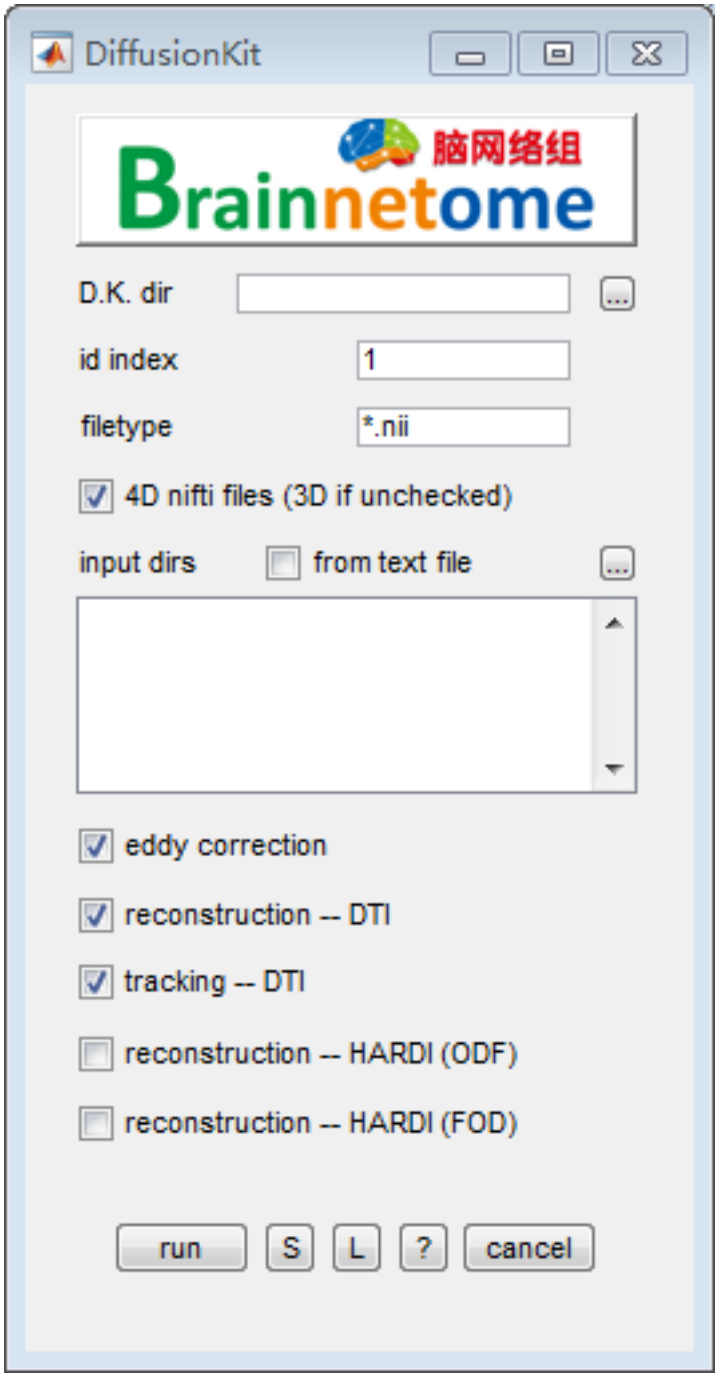
9. Lazar NA, Luna B, Sweeney JA, Eddy WF. Combining brains: a survey of methods for statistical pooling of information. *Neuroimage 2002*; 16(2): 538-50.

CHAPTER 7

Third Party

7.1 DiffusionKit

A batch processing GUI-interface for DiffusionKit



- **D.K. dir**: path of installed DiffusionKit, e.g. `C:/Program Files (x86)/DiffusionKit`
- **id index**: identifier to find unique string for each subject
- **filetype**: files in the filetype will be searched in input directories.
- **4D nifti files**: if the input data is 4D, check this item. Otherwise uncheck.
- **input dirs**: directories can be input either using a `*.txt` file or spm select window.
- **Choose below options to perform in each directory.**
  - eddy correction

  - reconstruction–DTI
  - tracking–DTI
  - reconstruction–HARDI(ODF)
  - reconstruction–HARDI(FOD)

Results will be saved in each input directory.

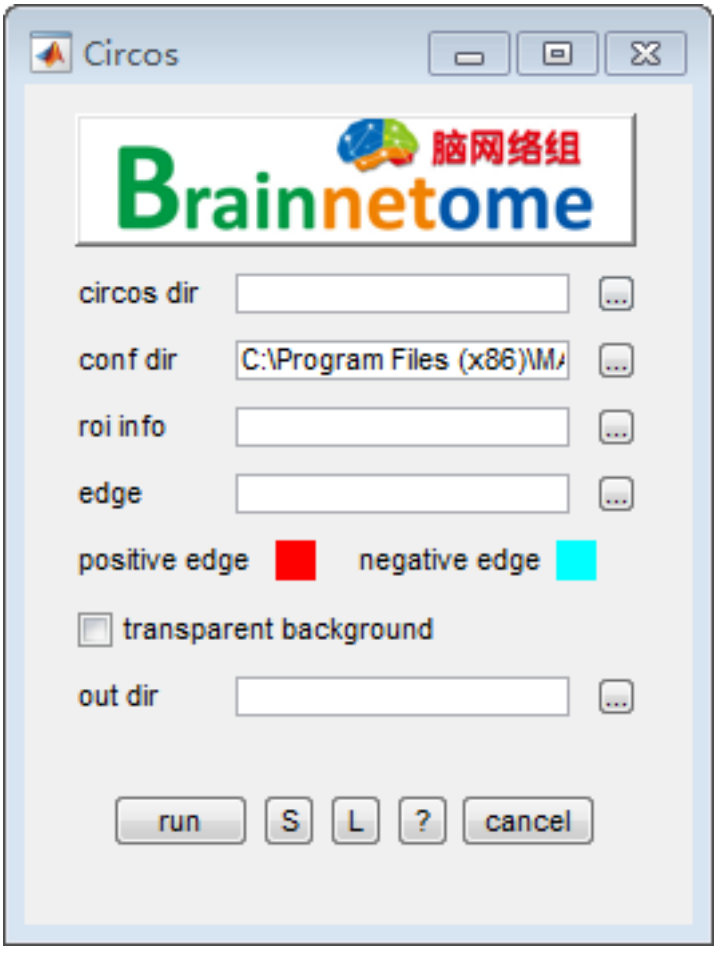
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

For more information, please visit http://diffusion.brainnetome.org/

- **Reference**:

1. Sangma Xie, Liangfu Chen, Nianming Zuo and Tianzi Jiang. DiffusionKit: A Light One-Stop Solution for Diffusion MRI Data Analysis. *Journal of Neuroscience Methods*. vol. 273, pp. 107-119, 2016.

7.2 Circos



- **circos dir**: Path of unzipped circos folder. `/circos_path/bin`
- **conf dir**: Path of circos configure file.
- **roi info**: CSV table which defines sub-areas and lobes, there is an example in `brant-master/circos/brant_circos_3mm_273.csv`
- **There should be at least four columns in the table:**
  - **label**: label of each sub-areas.
  - **module**: to which lobe/module does the sub-area belong.
  - **index_module**: order of the arranged module.
  - **index_node**: order of sub-areas within one module.

Before using the function, please download and install circos 0.69 or higher.

- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.
- **References**:

1. Krzywinski M, Schein J, Birol I, Connors J, Gascoyne R, Horsman D, et al. Circos: an information aesthetic for comparative genomics. *Genome Res 2009*; 19(9): 1639-45.
2. Irimia A, Chambers MC, Torgerson CM, Van Horn JD. Circular representation of human cortical networks for subject and population-level connectomic visualization. *Neuroimage 2012*; 60(2): 1340-51.
3. Fan L, Li H, Zhuo J, Zhang Y, Wang J, Chen L, et al. The Human Brainnetome Atlas: A New Brain Atlas Based on Connectional Architecture. *Cereb Cortex 2016*; 26(8): 3508-26.

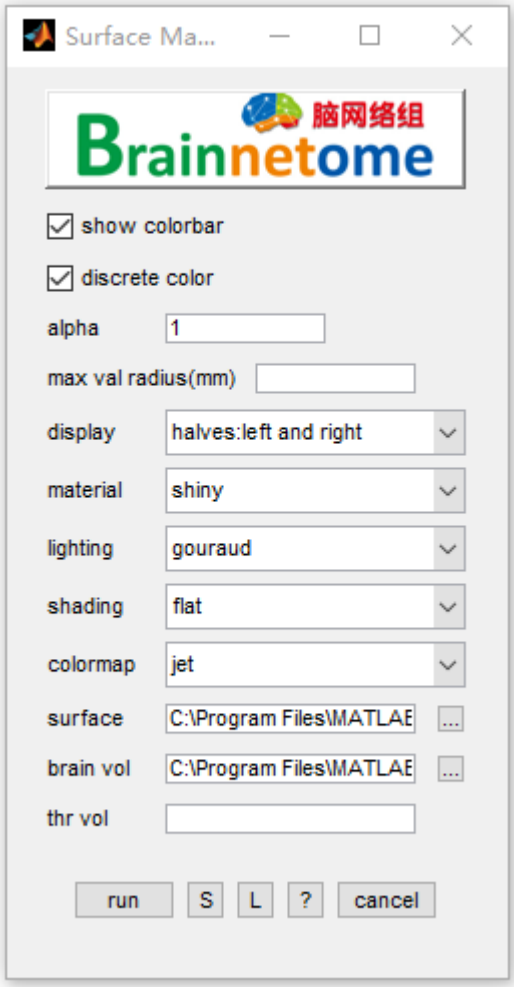
CHAPTER 8

VIEW

To visualize voxel intensities, we have implemented the *ROI Mapping* to extract and render the surface of 3D clusters, the *Surface Mapping* to project voxel intensity to vertices on a surface. To visualize ROI-ROI connectivity, *Network Visualization* is implemented to draw spheres and rods within a rendered brain surface, to present nodes and edges of the input network.

8.1 Surface Mapping

Besides shading each ROI/cluster, we can also project the voxel intensities to the surface. By the default, we use a rendered human brain surface constructed from vertices and triangular faces loaded from a pregenerated file. To draw another surface, users can input a binarized 3D mask, with which BRANT can extract the generate vertices and faces and render a new surface. When projecting a 3D volume to surface, the vertices on the surface are shaded as the intensity of the nearest voxel, while the material of the surface, the color maps of positive and negative intensities, the lighting and shading algorithm can be adjusted.



- **show colorbar**: display colorbar
- **discrete value**: the intensity of the input volume has float or integer datatype
- **alpha**: degree of opaque
- **max val radius(mm)**: radius for maximum neighbour interpolation. if the radius is greater than the size of a voxel, the program will search for maximum value within a sphere for each vertex, otherwise (leave empty or smaller than the size of a voxel) use the default 1-voxel interpolation.
- **display**: mode of display
- **material: sets the lighting characteristics of surface and patch objects**
  - **shiny**: sets the reflectance properties so that the object has a high specular reflectance relative to the diffuse and ambient light, and the color of the specular light depends only on the color of the light source
  - **dull**: sets the reflectance properties so that the object reflects more diffuse light and has no specular highlights, but the color of the reflected light depends only on the light source
  - **metal**: sets the reflectance properties so that the object has a very high specular reflectance, very low ambient and diffuse reflectance, and the color of the reflected light depends on both the color of the

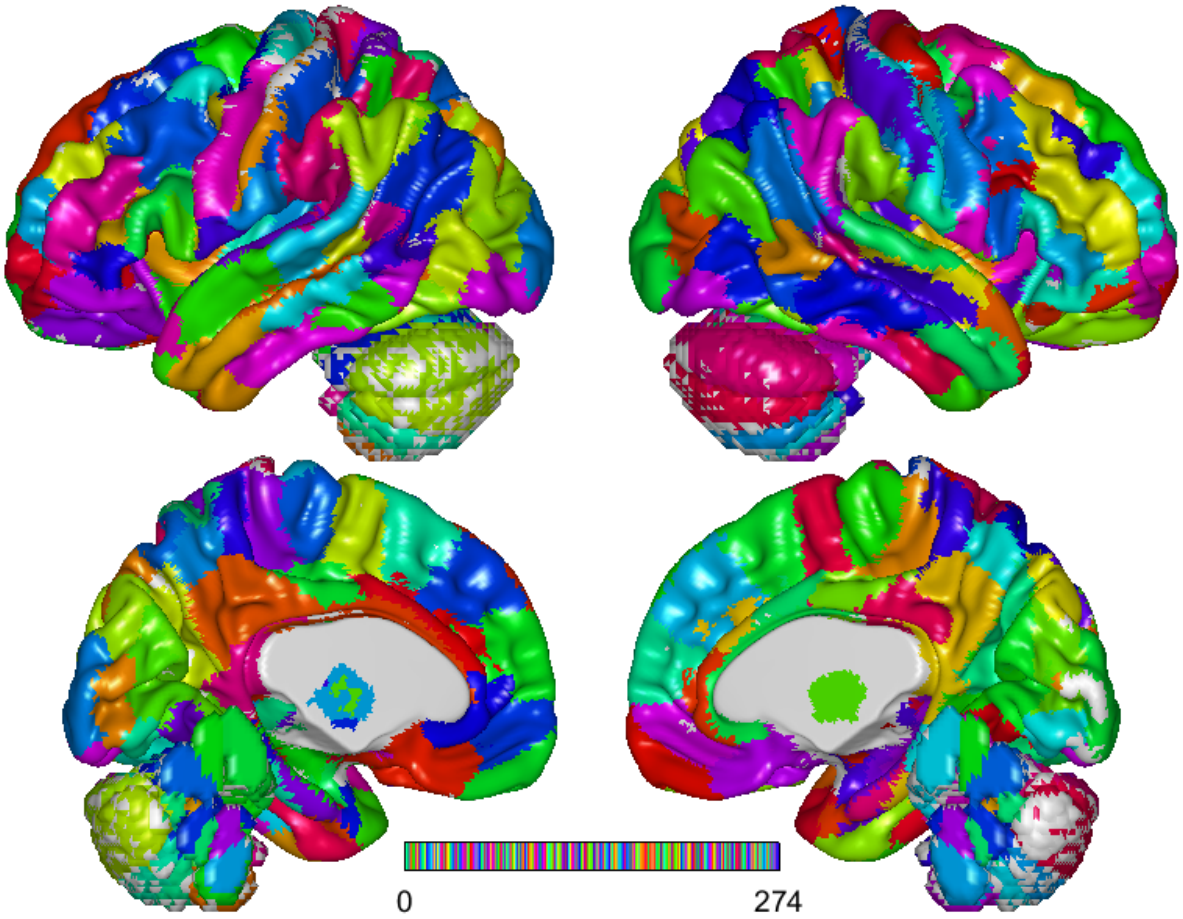
light source and the color of the object

- **lighting: selects the algorithm used to calculate the effects of light objects on all surface and patch objects in the current a**
  - **flat**: produces uniform lighting across each of the faces of the object. Select this method to view faceted objects
  - **gouraud**: calculates the vertex normals and interpolates linearly across the faces. Select this method to view curved surfaces
  - **phong**: sets the lighting to phong
  - **none**: turns off lighting
- **shading: controls the color shading of surface and patch graphics objects**
  - **flat**: each mesh line segment and face has a constant color determined by the color value at the endpoint of the segment or the corner of the face that has the smallest index or indices
  - **faceted**: flat shading with superimposed black mesh lines
  - **interp**: varies the color in each line segment and face by interpolating the colormap index or true color value across the line or face
- **colormap**: controls the colors used in displaying the surface
- **surface**: surface file
- **brain vol**: volume to map to the surface
- **thr vol**: set the range to generate a mask for input volume, seperated by ‘,’.

e.g:

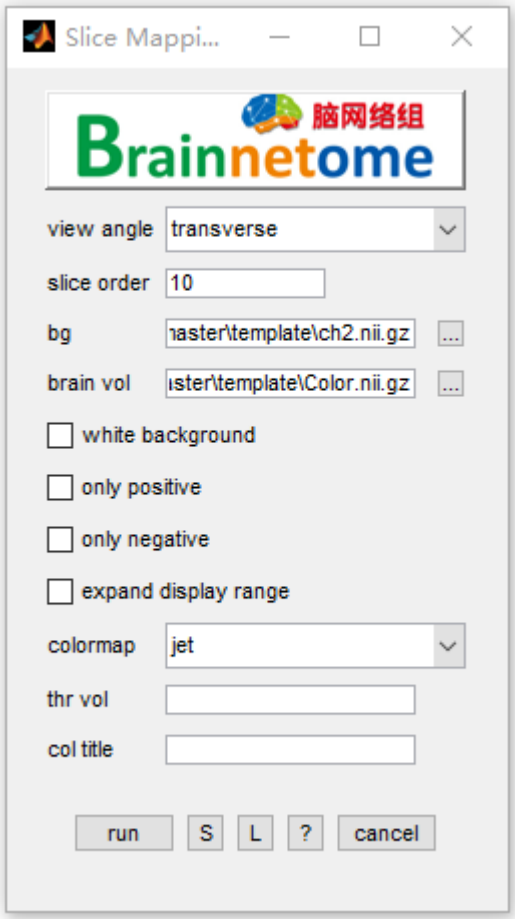
```
thr vol: 1, 5, 9, 15
```

- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.



8.2 Slice Mapping

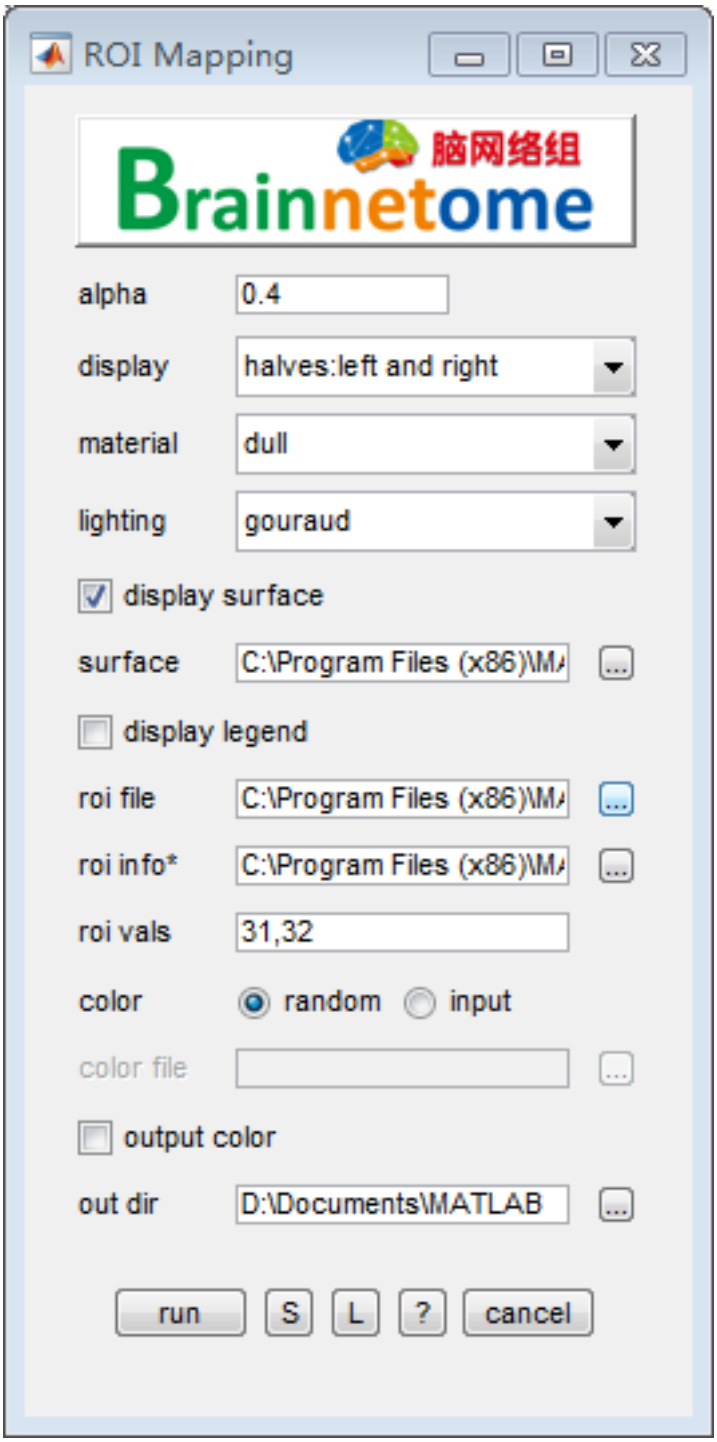
This function is used to visualize 3D volume by cut it into no more than 19 slices. All slices will be displayed in a single window, overlapped with the background volume. We can choose the range of displaying if necessary.



- **view angle**: direction of slice viewing
- **slice order**: choose which slice(s) to display
- **bg**: directory of backgroud volume file
- **brain vol**: directory of displayed volume file
- **white background**: the background of the display window will be white if checked, otherwise it will be black.
- **only positive**: only voxels with positive value will be displayed if checked
- **only negative**: only voxels with negetive value will be displayed if checked
- **expand display range**: if checked, the voxels with value out of range will be displayed as the threshold value
- **colormap**: choose the color map of slice viewing
- **thr vol**: set the range to generate a mask for input volume, seperated by ‘,’.
- **col title**: title of the colorbar
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

8.3 ROI Mapping

When visualizing ROIs from an atlas or clusters from a user-defined 3D volume (e.g., clusters with significant difference between sample means), we can use the current function to extract and shade the surface of each number-tagged ROI/cluster in random or user defined colors. The ROIs/clusters of the input 3D image should be tagged with positive-integers. With an additional input of a reference `*.csv` table containing number-label pairs (as described in Utilities -> DICOM Convert), we can further parse the labels of each shaded ROI/cluster and present them in a legend.



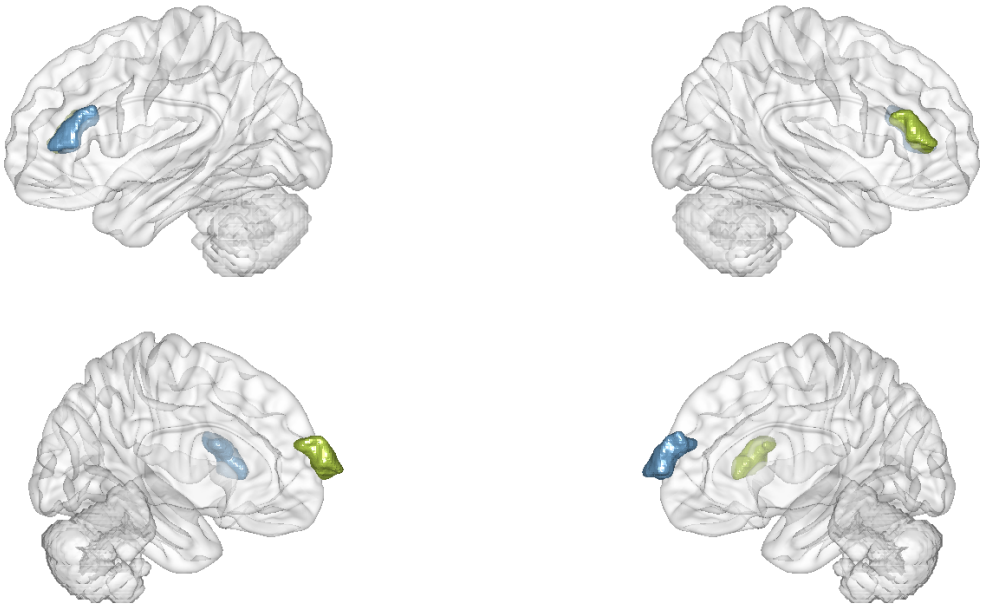
- **alpha**: degree of transparency.
- **display**: mode of display.
- **display surface**: show surface.
- **surface**: surface file.
- **display legend**: display legend.
- **roi file**: extract mean intensity in the roi tagged by numbers.
- **roi info***: optional. two columns of information for each labeled cluster in a `*.csv` file. For example:

```
1,SFG
2,MFG
3,IFG
```

- **roi vals**: select which roi to display.
- **color**: optional. use random color or input color file.
- **color file**: the input color could be (ROI tag, R, G, B):

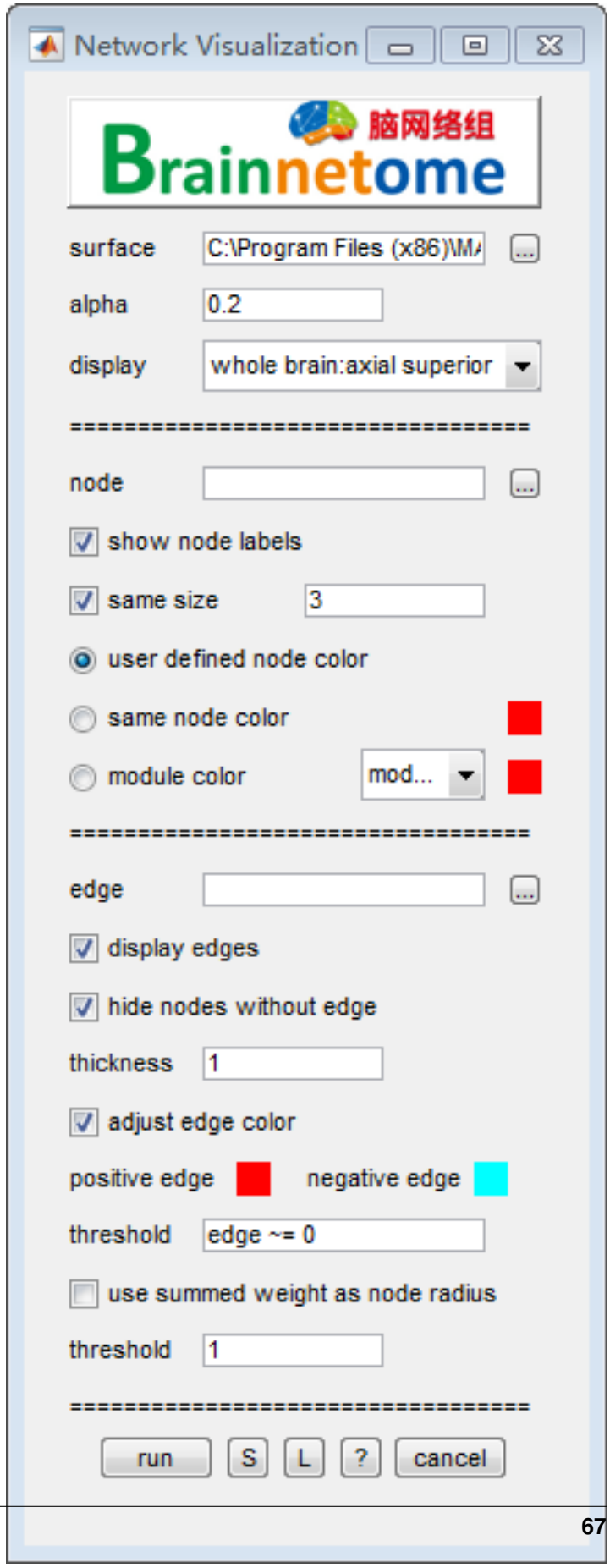
```
1,255,155,100
2,1,1,1
```

- **output color**: output color of current image.
- **out dir**: output directory for saving results.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.



8.4 Network Visualization

Using a `*.txt` file storing symmetric connectivity matrix and a `*.csv` table with nodal information (such as coordinate, label, module and color) as input, we can draw spheres and rods to visualize nodes and edges.


Network Visualization
脑网络组
Brainnetome
surface
C:\Program Files (x86)\M
alpha
0.2
display
whole brain:axial superior
node
show node labels
same size
3
user defined node color
same node color
module color
mod...
edge
display edges
hide nodes without edge
thickness
1
adjust edge color
positive edge
negative edge
threshold
edge ~= 0
use summed weight as node radius
threshold
1
run
S
L
?
cancel

- **surface**: surface file
- **alpha**: degree of opaque
- **display**: mode of display
- **node**: node file defined as csv table. All columns are optional except for 'x', 'y' and 'z'.

For example:

```
 x     y    z  size  module   r   g   b   label
 -1 , 20 , 20 , 4 , module1 , 5 , 5 , 5 , node1
-10 , 22 , 20 , 4 , module1 , 5 , 5 , 5 , node2
 12 , 20 , 20 , 4 , module2 , 5 , 5 , 5 , node3
```

- **show node labels**: check to show labels defined in input node file.
- **same size**: use same size for all node, uncheck to use user defined size in input node file.
- **user defined node color**: use color defined in input node file.
- **same node color**: use same color for all node.
- **module color**: use different color for each module. Modules are defined in input node file.
- **edge**: edge matrix for input file, the number of rows and columns should be the same as input file.
- **display edges**: display or not edges.
- **hide node without edge**: select not to show nodes without edge
- **thickness**: relative thickness for all edges
- **adjust edge color**: use different color for positive and negative edge.
- **threshold**: an expression that compatible with matlab syntax to filter out unwanted edges in edge matrix.
- **use summed weight as node radius**: sum up node's degree and define node size.
- **threshold**: nodes with degree smaller than the threshold will not be shown.
- **Buttons:**
  - **S**: Save parameters of the current panel to a `*.mat` file. The `*.mat` can be further loaded for the panel or be used in a script processing.
  - **L**: Load parameters from `*.mat` for the current panel.
  - **?**: Help information.

CHAPTER 9

Examples

9.1 STEP 1: DICOM Convert

- **Open Directories Selection GUI:** Click the *Utilities*, *DICOM Convert* and then select the input file by clicking the ... icon.
- **Input Directories of DICOM Files:** Directories can be navigated by operating folders in the left side panel or directories on the top. Folders matching the filter (*Filt*) are shown in the panel on the right and can be selected by clicking or dragging. Use the right mouse button if you would like to select all files. The panel at the bottom shows files that are already selected. Clicking a selected file will un-select it.
- **Usage of ID Index:** Using id index properly can help BRANT to find unique string for each subject. When id index is 1,it means the data folder contains subject string itself. 2 means subject information can be found in data folder's parent upper one. e.g. if your data are stored in `G:/TestData/1_NC001`, set id index to 1, if your data are stored in `G:/TestData/1_NC001/fMRI`, set id index to 2. Both output files will be put in the folder `out dir/1_NC001`.

9.2 STEP 2: Preprocessing

- **Input Directories for Preprocessing:** Click the *Preprocessing* button. Select the folders as data dirs where STEP 1 outputs. You can check the *from text file* and select a `brant_preprocess_paths.txt` file which has already automatically created.
- **Preprocessing Settings:** Check the checkboxes you need, remember to modify parameters. You donnot need to check the *Coregister* checkbox without structural images. Remember to change the *source* parameter in Normalise to `co*.nii` if you're preprocessing images with structural images.

Note: If an error occours during preprocessing, the *R* (refresh) button can recover the *run* button.

- Further information about preprocessing can be found in:

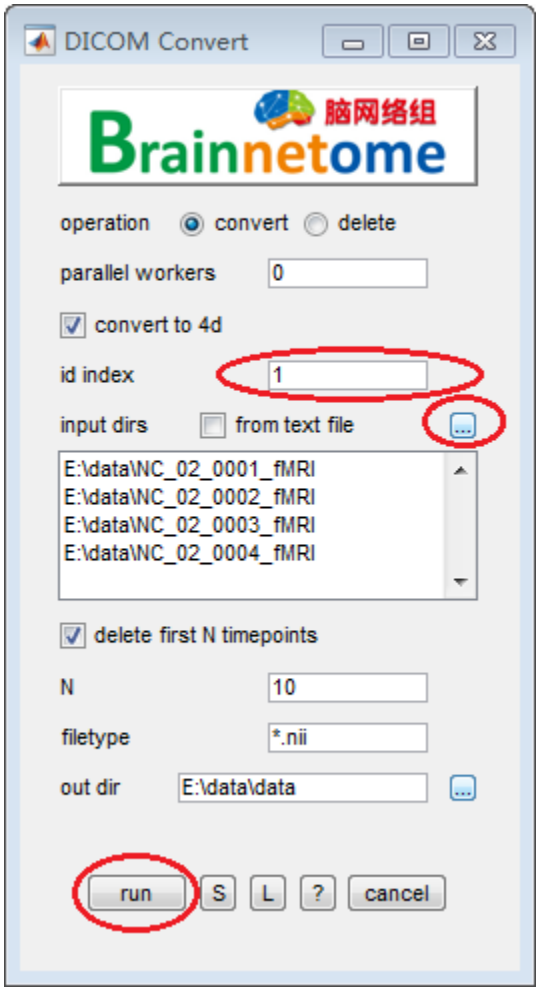


Fig. 1: fig.1 Utilities => DICOM Convert

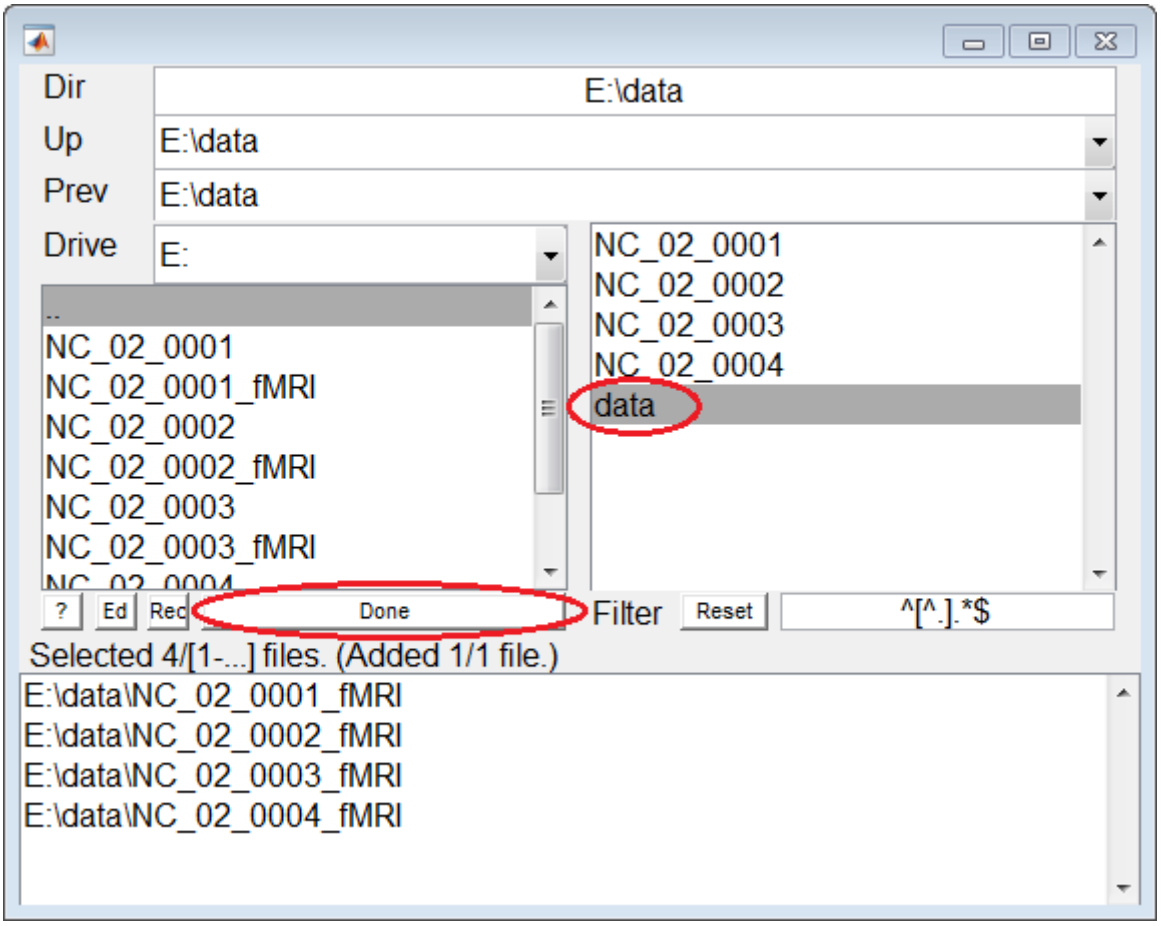
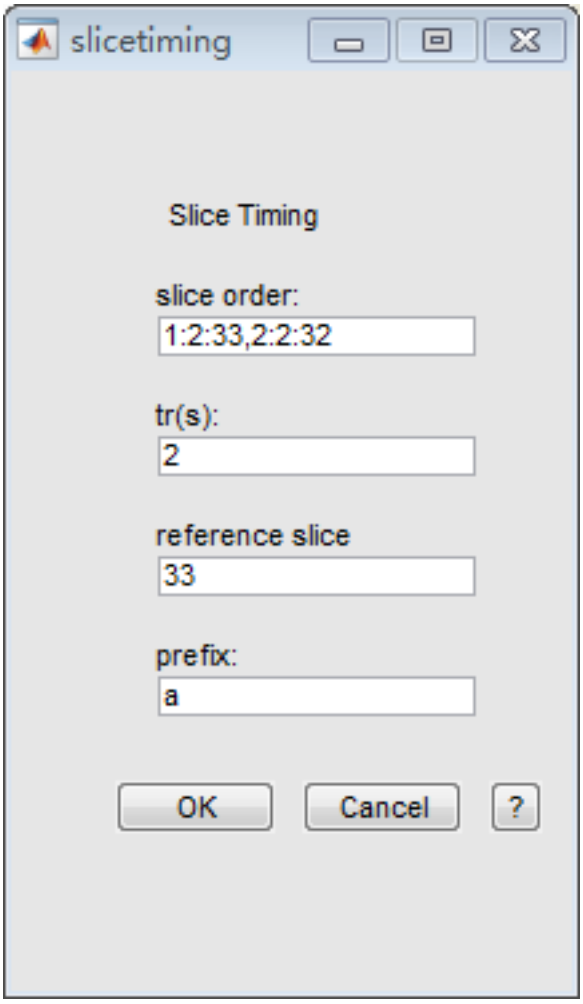


Fig. 2: fig.2 Selection GUI

9.2.1 Slice Timing

- **slice order**: the order of scans in one volume, seperated by comma or space.
- **TR(s)**: repetition time, cannot be 0.
- **reference slice**: normally be the number of scan in the middle of the order.(when dealing with task-fMRI, note that selecting the middle timepoint as reference will change the timing of task TR)
- **prefix**: output prefix.



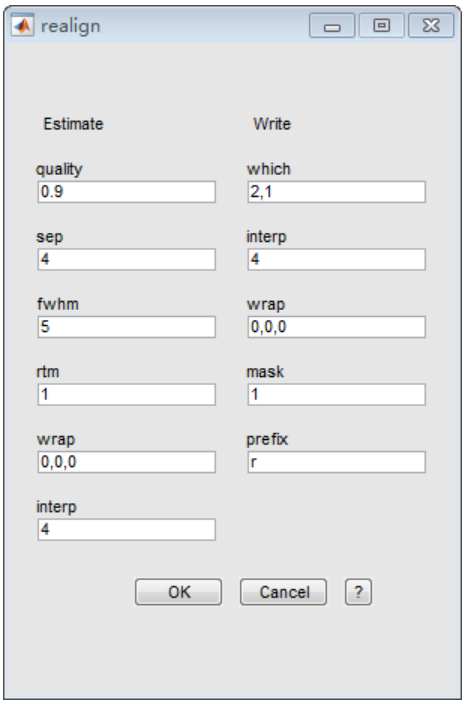
e.g:

```
slice order: 1:2:33,2:2:32
TR: 2
reference slice: 33
```

- **Preprocess Modules**
  - Slice Timing
  - Realign
  - Coregister (optional)
  - Normalize

    - SPM8
    - SPM12
  - Denoise
  - Smooth

9.2.2 Realign



- **Estimate: Estimate parameters for realignment.**
  - **quality**: Highest quality (1) gives most precise results, whereas lower qualities gives faster realignment.
  - **sep**: The separation (in mm) between the points sampled in the reference image. Smaller sampling distances gives more accurate results, but will be slower.
  - **fwhm**: Full width at half maximum of the Gauss smoothing kernel (mm).
  - **rtm**: 1 indicates images are registered to the mean image, while 0 indicates images are registered to the first image in each subject's folder.
  - **wrap**: 3 dimensions of wrapping, e.g. [1 1 1] for wrapping in X, Y and Z direction, [0 0 0] for no wrapping.
  - **interp**: Indexes of interpolation methods. (1 for Trilinear; 2-7 for 2nd-7th Degree B-Spline).
- **Write:**
  - **which**: The first parameter allows 0, 1 and 2 as input (0: create only a mean resliced image; 1: don't reslice the first image. 2: reslice all the image). The second parameter indicates whether to output a resliced mean image (0 for false and nonzero for true).
  - **interp**: Interpolation methods for write option. (0 for Nearest Neighbor; 1 for Trilinear; 2-7 for 2nd-7th Degree B-Spline; Inf for Fourier Interpolation).

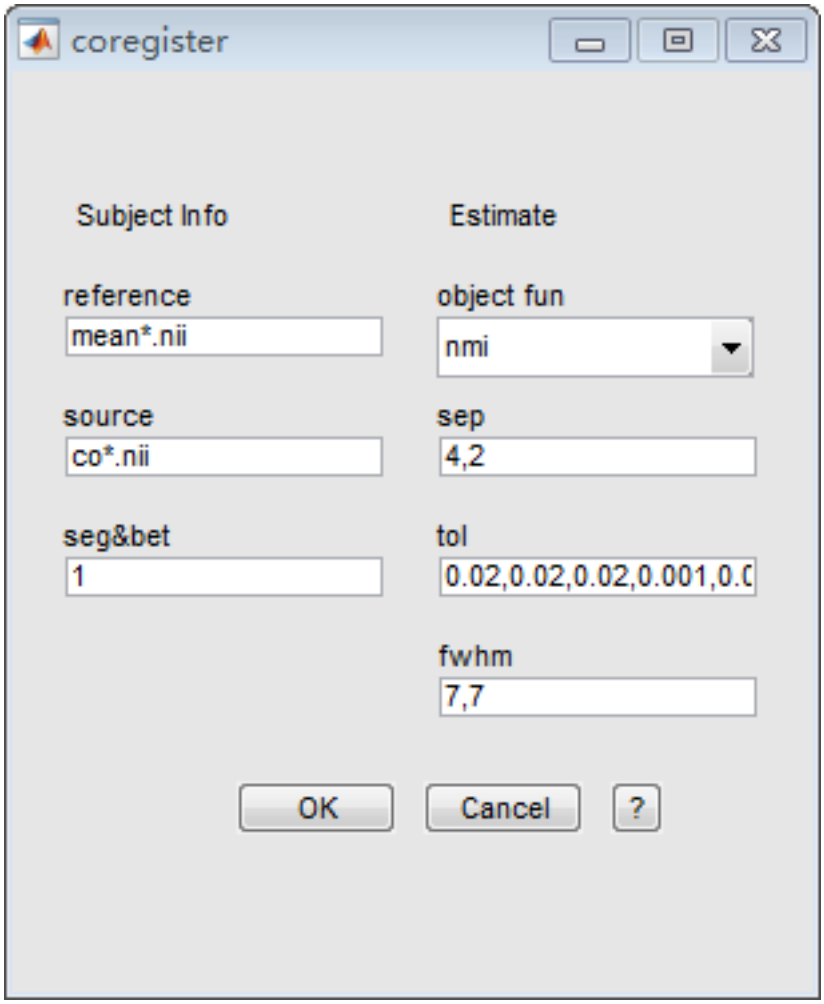
  - **mask**: Mask output images (true/false). If any image has a zero value at a voxel, then all images will have zero (or NaNs if allowed) values at that voxel.
  - **wrap**: 3 dimensions of wrapping, e.g. [1 1 1] for wrapping in X, Y and Z direction, [0 0 0] for no wrapping.
  - **prefix**: Output images will have a prefix of *r* by default.
- **Reference**: spm manual.
- **Preprocess Modules**
  - Slice Timing
  - Realign
  - Coregister (optional)
  - Normalize
    - SPM8
    - SPM12
  - Denoise
  - Smooth

9.2.3 Coregister

- **Subject info:**
  - **reference**: Filetype of reference image stored in each subject's folder to register.
  - **source**: Filetype of image to match the reference image stored in each subject's folder.
  - **seg & bet**: Segment and skull stripe structural T1/T2 image. Using skull striped T1/T2 image for coregistration is recommended.
    - **options:** 1: segment using new segment and bet based on tissue probability maps;

      2: bet only (there should be segmented `c1-c3*.nii` files in the directory);

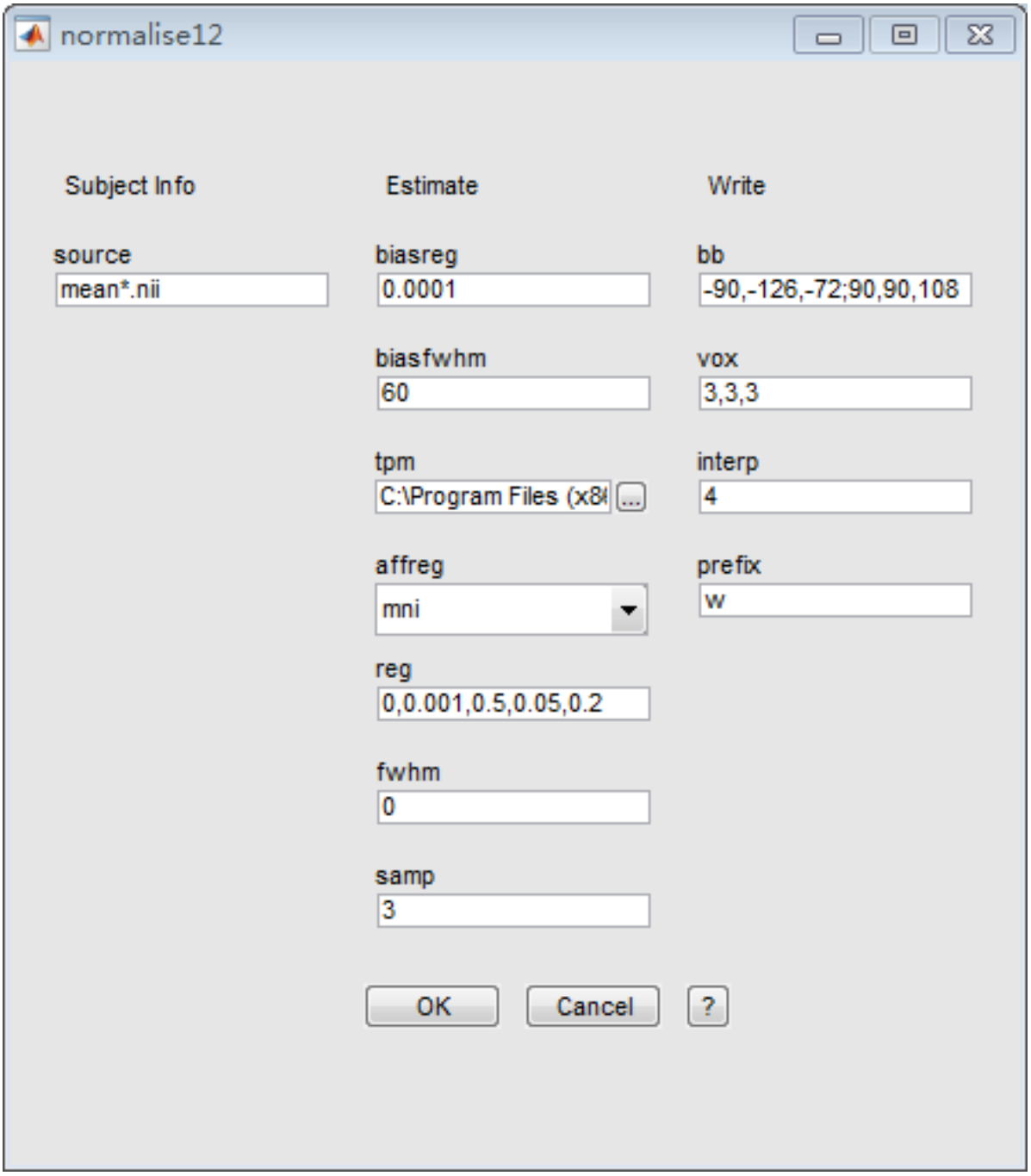
      other number: do not segment nor bet; we recommend using `co*.nii` instead of `bet*.nii` to normalise.



- **Estimate:**
  - **object fun**: Methods to maximise or minimise objective function.
  - **sep**: The average distance between sampled points (in mm).
  - **tol**: The accuacy for each paramters.
  - **fwhm**: Kernel of gaussian smooth to apply to the 256*256 joint histogram.
- **Reference**: spm manual.
- **Preprocess Modules**
  - Slice Timing
  - Realign
  - Coregister (optional)
  - Normalize
    - SPM8
    - SPM12
  - Denoise
  - Smooth

9.2.4 Normalise SPM12

- **Subject info:**
  - **source**: Filetype of images for normalization are stored. Default is the `mean*.nii` generated from realign. Users can also change it to T1/T2 structural image of each subject stored in each subject's folder. If Coregister is checked, remember to add prefix of Coregister to the source filetype and change to template to the same modality of source.

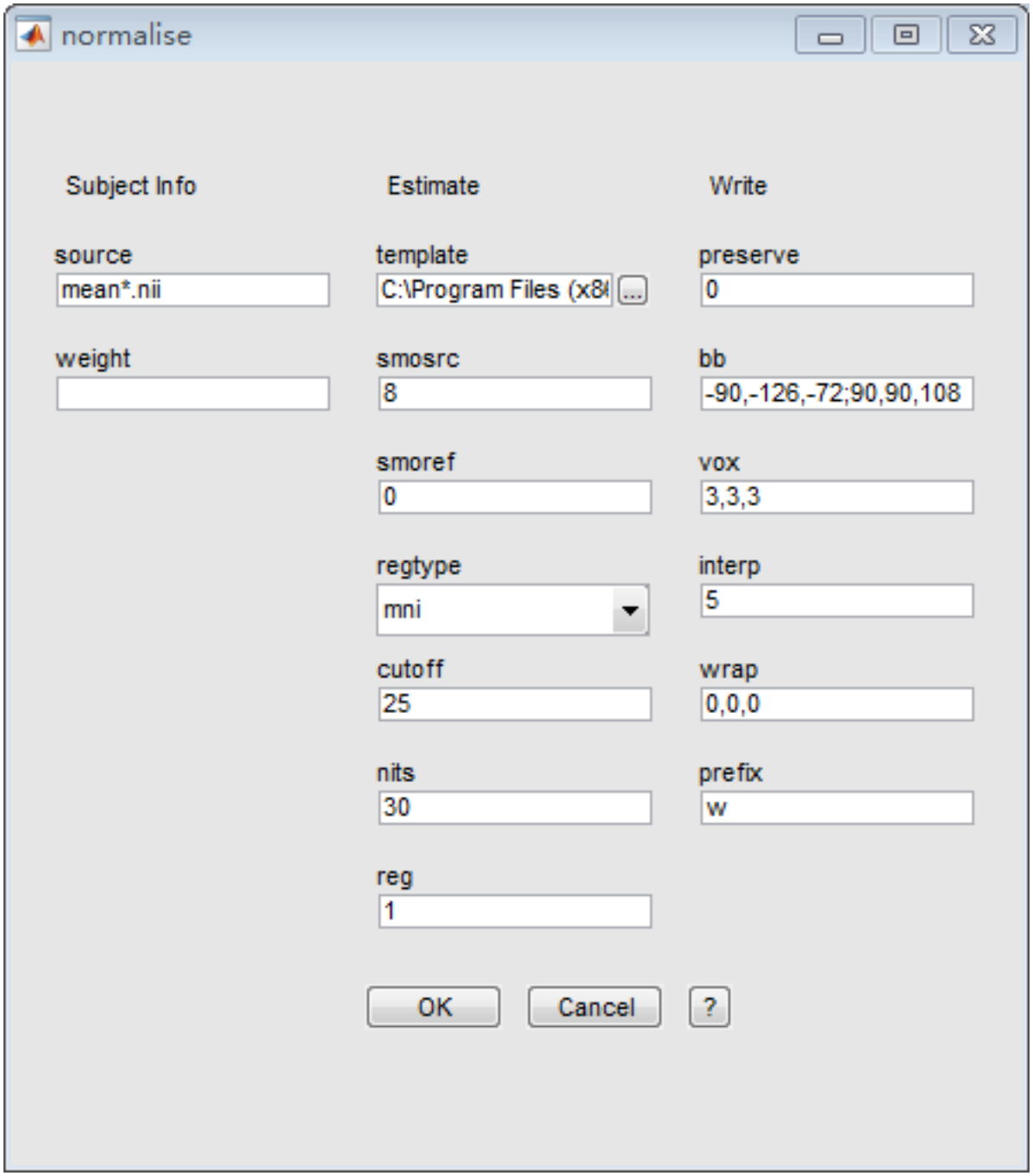


- **Estimate:**
  - **biasreg**: bias regularisation.

  - **biasfwhm**: FWHM of Gaussian smoothness of bias.
  - **tpm**: Tissue probability map which the source image will be registered to.
  - **affreg**: affine regularisation.
  - **reg**: the amount of regularization for the nonlinear part of the spatial normalization.
  - **fwhm**: option for smoothness.
  - **samp**: sampling distance.
- **Write:**
  - **bb**: Bounding box of the volume.
  - **vox**: The voxel sizes of the normalized images.
  - **interp**: Interpolation methods for write option. (0 for Nearest Neighbor; 1 for Trilinear; 2-7 for 2nd-7th Degree
  - **prefix**: Output images will have a prefix of *w* by default.
- **Reference**: spm manual.
- **Preprocess Modules**
  - Slice Timing
  - Realign
  - Coregister (optional)
  - Normalize
    - SPM8
    - SPM12
  - Denoise
  - Smooth

9.2.5 Normalize

- **Subject info:**
  - **source**: Filetype of images for normalization are stored. Default is the `mean*.nii` generated from realign. Users can also change it to T1/T2 structural image of each subject stored in each subject's folder. If Coregister is checked, remember to add prefix of Coregister to the source filetype and change to template to the same modality of source.
  - **weight**: weighting image of the template.

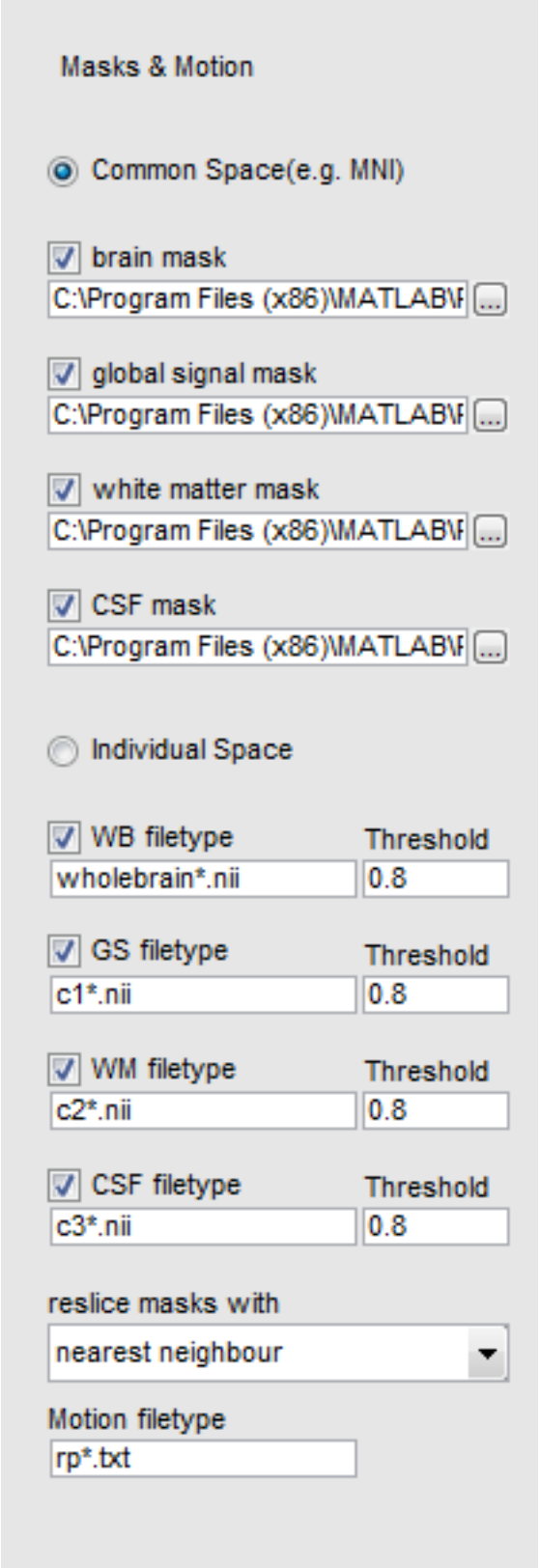


- **Estimate:**
  - **template**: A standard template image which the source image will be registered to.
  - **smosrc**: Smoothing to be applied to the copy of the source image. (Source image and the template should have the same smoothness)
  - **smoref**: Smoothing to be applied to the copy of the source image. (The default templates of spm already have been smoothed by 8mm)
  - **regtype**: mni (affine registration into MNI space), subj (Registering to an image that has an almost same size of the source image.) and none (No registration)

  - **cutoff**: Cutoff of DCT bases.
  - **nits**: Number of nonlinear wrapping iterations.
  - **reg**: The amount of regularization for the nonlinear part of the spatial normalization.

- **Write:**
  - **preserve**: 0 (The warped images preserve the intensities of the original images) and 1 (Spatially normalised images are "modulated" in order to preserve the total amount of signal in the images.)
  - **bb**: Bounding box of the volume.
  - **vox**: The voxel sizes of the normalized images.
  - **interp**: Interpolation methods for write option. (0 for Nearest Neighbor; 1 for Trilinear; 2-7 for 2nd-7th Degree B-Spline; Inf for Fourier Interpolation).
  - **wrap**: 3 dimensions of wrapping, e.g. [1 1 1] for wrapping in X, Y and Z direction, [0 0 0] for no wrapping.
  - **prefix**: Output images will have a prefix of *w* by default.
- **Reference**: spm manual.
- **Preprocess Modules**
  - Slice Timing
  - Realign
  - Coregister (optional)
  - Normalize
    - SPM8
    - SPM12
  - Denoise
  - Smooth

9.2.6 Denoise


Masks & Motion
Common Space(e.g. MNI)
brain mask
C:\Program Files (x86)\MATLAB\F
global signal mask
C:\Program Files (x86)\MATLAB\F
white matter mask
C:\Program Files (x86)\MATLAB\F
CSF mask
C:\Program Files (x86)\MATLAB\F
Individual Space
WB filetype
Threshold
wholebrain*.nii
0.8
GS filetype
Threshold
c1*.nii
0.8
WM filetype
Threshold
c2*.nii
0.8
CSF filetype
Threshold
c3*.nii
0.8
reslice masks with
nearest neighbour
Motion filetype
rp*.txt

- **Masks & Motion** Input mask files for whole brain, global mean signal, white matter signal and CSF signal;

  If common space is selected, one mask file for each mask type should be input.

  If indivisual space is selected, wildcard for individual mask should be input, BRANT will search the mask within each subject's directory.

  The threshold for common space mask is 0.5 by default, while for individual space the threshold can be altered.

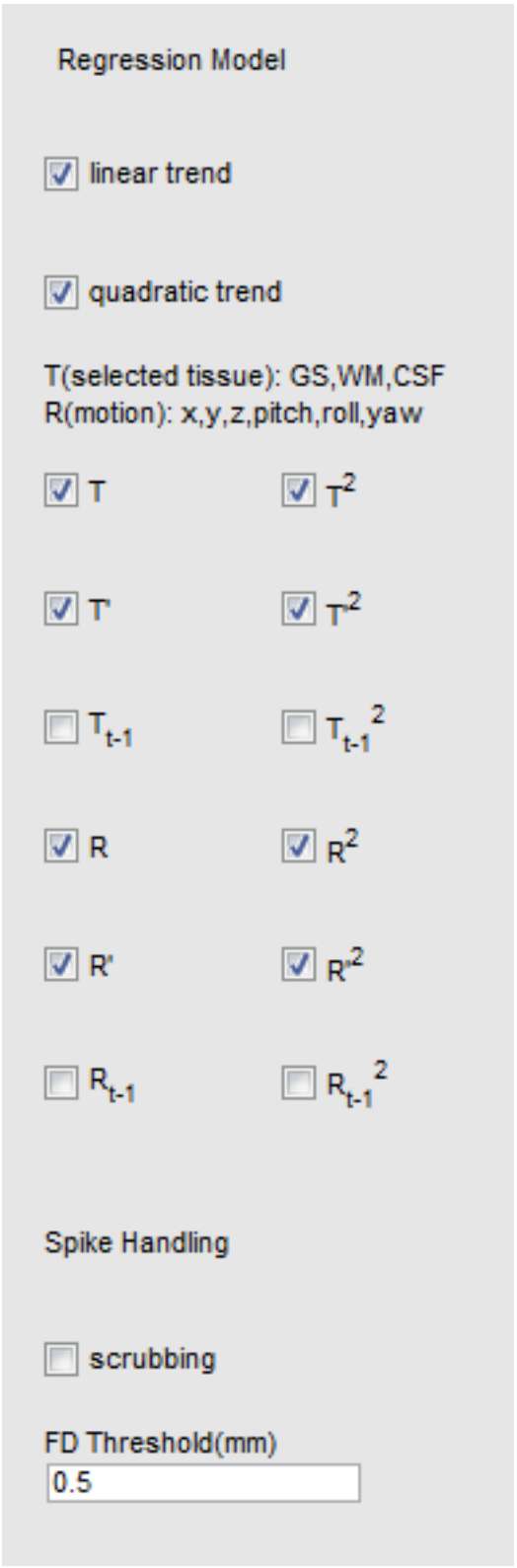
  (common space masks normally are binarized, however in individual space are probability)

  - **reslice masks with**: if the header information (size, FOV, originator, orientation and etc.) is different between data and mask, BRANT will: in common space reslice masks to the first input data

    in individual space reslice masks to the each subject's input data accordingly

    If the masks are stored as binarized value, the suggested method for reslice is nearest neighbour, otherwise 4th degree B-spline.

  - **motion filetype**: BRANT will search estimated headmotion file in each subject's folder, normally by spm the file is `rp*.txt`



- **Regerssion Model**
  - **linear trend**: regressor of 1:T
  - **quadratic trend**: regressor of [1,2^2,3^2:T^2]

- **T**: a gross regressors for selected global signal, white matter signal and CSF signal
- $\mathbf{T}^2$: element-wise square of T
- **T'**: temporal derivatives of T, zero padded
- $\mathbf{T'}^2$: element-wise square of T'
- $\mathbf{T}_{t-1}$: 1-frame lagged T, zero padded
- $\mathbf{T}_{t-1}{}^2$: element-wise square of T_{t-1}
- **R**: a gross matrix for motion, should be 6 columns, loaded from *rp*.txt*
- $\mathbf{R}^2$: element-wise square of R
- **R'**: temporal derivatives of R, zero padded
- $\mathbf{R'}^2$: element-wise square of R'
- $\mathbf{R}_{t-1}$: 1-frame lagged R, zero padded
- $\mathbf{R}_{t-1}{}^2$: element-wise square of R_{t-1}
- **Spike Handling**:

As suggested in *1.* , spikes are censored with a threshold of FD.

FD is calculated as:

```
motion_diff = diff(R);
FD = [0; sum([abs(motion_diff(:, 1:3)), 50 * abs(motion_diff(:, 4:6))], 2)];
```

The scrubbing will take place before the regression model. For example, if order of denoise is selected as Filter first and Regression, the scrubbing will not affect Filter.

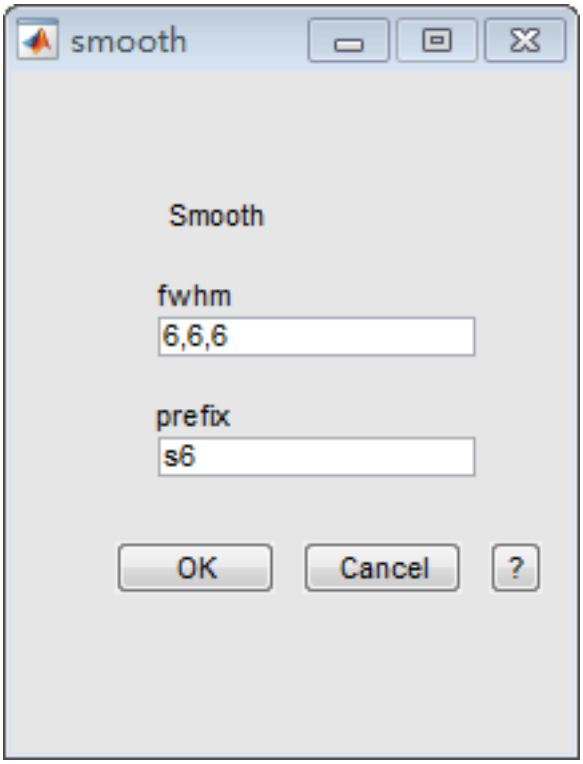

Filter
tr(s)
0
Lower cutoff(Hz)
0.01
Upper cutoff(Hz)
0.08
Output Options
Regression + Filter
Filter + Regression
Regression only
Filter only
Run with and without GSR
Save only last results
Output to *.gz format
multi-regression prefix
d
filter prefix
f

- **Filter:**
  - **tr**: repetition time.
  - **lower cutoff (Hz)**: lower cutoff for band pass filter.
  - **upper cutoff (Hz)**: upper cutoff for band pass filter.
- **Output Options:**
  - **Regression + Filter**: do regression first and then filter
  - **Filter + Regression**: do filter first and then regression
  - **Regression only**: do only regression
  - **Filter only**: do only filter
  - **Run with and without GSR**: if checked and mask of global signal is specified, BRANT will run selected process twice with and without global signal as regressor in T, and output to different file in the current and following processes.
  - **Save only last results**: if checked, no middle files will be saved.
  - **Output to *.gz format**: check to output to `*.gz` files (note that the following smooth process from SPM would require uncompressed files, if it's checked, an error will occur in smooth); choolse if smooth is done beforehand or not required.
  - **multi-regression prefix**: prefix for output of GLM
  - **filter prefix**: prefix for output of filter
- **References**:

1. Power, J. D., Mitra, A., Laumann, T. O., Snyder, A. Z., Schlaggar, B. L., & Petersen, S. E. (2014). Methods to detect, characterize, and remove motion artifact in resting state fMRI. *Neuroimage*, 84(1), 320-341.

- **Preprocess Modules**
  - Slice Timing
  - Realign
  - Coregister (optional)
  - Normalize
    - SPM8
    - SPM12
  - Denoise
  - Smooth

9.2.7 Smooth



- **fwhm**: full width half maximum for gauss kernel.
- **prefix**: output prefix.
- **Preprocess Modules**
  - Slice Timing
  - Realign
  - Coregister (optional)
  - Normalize
    - SPM8
    - SPM12
  - Denoise
  - Smooth
- Further information about output files can be found in the Filename part.

9.3 STEP 3: Visual Check and Head Motion Estimation

- **Input Directories for Visual Check:** Click the *Utilities* button, then *Visual Check*. Select the folders as input directories where STEP 2 outputs.
- **Visual Check:** Check the output. Arrow keys can switch the images among different timepoints or subjects during Visual Check. The images will be saved automatically.

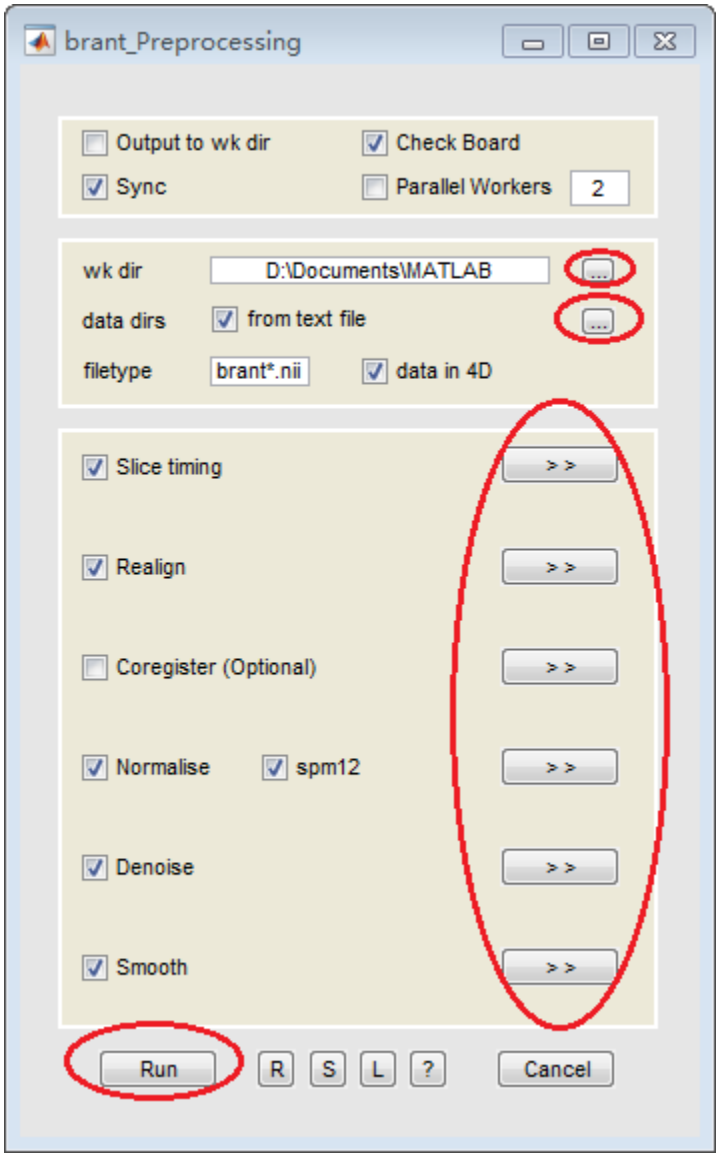


Fig. 3: fig.1 Preprocessing

- **Head Motion Estimation:** Click the *Utilities* button, then *Head Motion Est*. Select the folders as input directories where STEP 2 outputs. The results will be saved as `brant_headmotion_result.csv` and `brant_headmotion_exclusions.txt` automatically.

Fig. 5: fig.2 Visual Check Output

9.4 STEP 4: Functional Connectivity

- **Input Coordinates for ROI Drawing:** Click *FC*, *Draw ROI*. Both making a `*.csv` with coordinates (input type: file) or input coordinates divided with ";"(input type: manual) are admitted in BRANT. *Fig.2* shows the format of the csv file.
- **Choose Ref&mask:** Choose a `*.nii` file as an example. The output files will follow its extracting information of origin, voxel size, bounding box, etc..
- **Extract ROI:** Click *Merge/extract ROIs* in *FC* GUI, switch the operation to *extract*. Input *roi index* to choose which part you need in the roi file.
- **Input Directories for ROI Calculation:** Click *ROI Calculation* in *FC* GUI. Select the folders as input directories where STEP 2 outputs.
- **ROI Calculation:** Change filetype to `fdnoGSR*.nii`, input roi file and roi index or just use the default settings. Select output directories.

9.5 STEP 5: SPON

- **AM:** Click *SPON* button, then *AM*. Select the folders as input directories where STEP 2 outputs. Change filetype to `dnoGSR*.nii`.

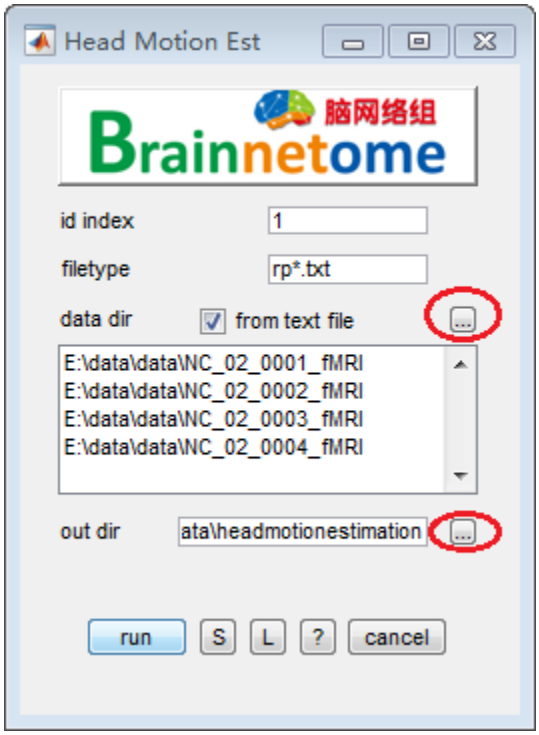


Fig. 6: fig.3 Utilities => Head Motion Estimation

A	B	C	D	E	F	G	H	I
subject-na	max-abstr	max-absrc	max-motic	mean-mot	num-move	mean-rota	mean-FD(r	num-FD>0.5
NC_02_000	0.45371	0.33263	0.52459	0.10025	94	0.04269	0.1946	2
NC_02_000	0.7295	0.2714	0.56686	0.054145	18	0.024991	0.10875	3
NC_02_000	0.45358	0.30468	0.4489	0.080279	62	0.02583	0.13536	4
NC_02_000	0.90152	0.94765	0.47257	0.12587	140	0.053862	0.24202	9

Fig. 7: fig.4 brant_headmotion_result.csv

```
Subjects excluded for threshold 5.0 mm or 5.0 degree

Subjects excluded for threshold 4.5 mm or 4.5 degree

Subjects excluded for threshold 4.0 mm or 4.0 degree

Subjects excluded for threshold 3.5 mm or 3.5 degree

Subjects excluded for threshold 3.0 mm or 3.0 degree

Subjects excluded for threshold 2.5 mm or 2.5 degree

Subjects excluded for threshold 2.0 mm or 2.0 degree

Subjects excluded for threshold 1.5 mm or 1.5 degree

Subjects excluded for threshold 1.0 mm or 1.0 degree

Subjects excluded for threshold 0.5 mm or 0.5 degree
NC_02_0002_fMRI
NC_02_0004_fMRI
```

Fig. 8: fig.5 brant_headmotion_exclusions.txt

x	y	z	label
40	-16	50	ROI1
-40	-16	50	ROI2

Fig. 10: fig.2 example for csv format input

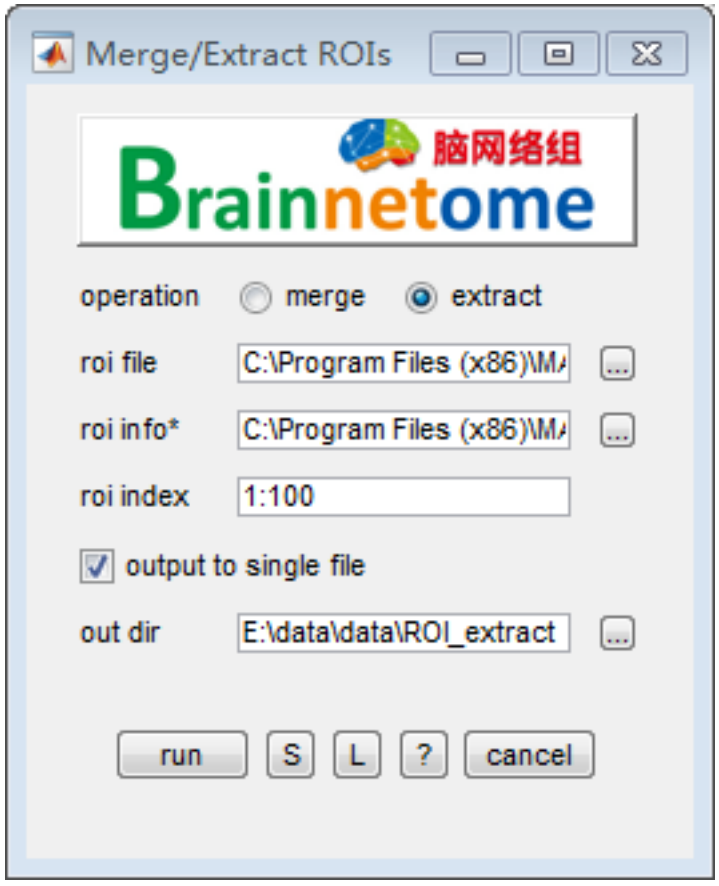


Fig. 11: fig.3 FC => Merge/extract ROIs

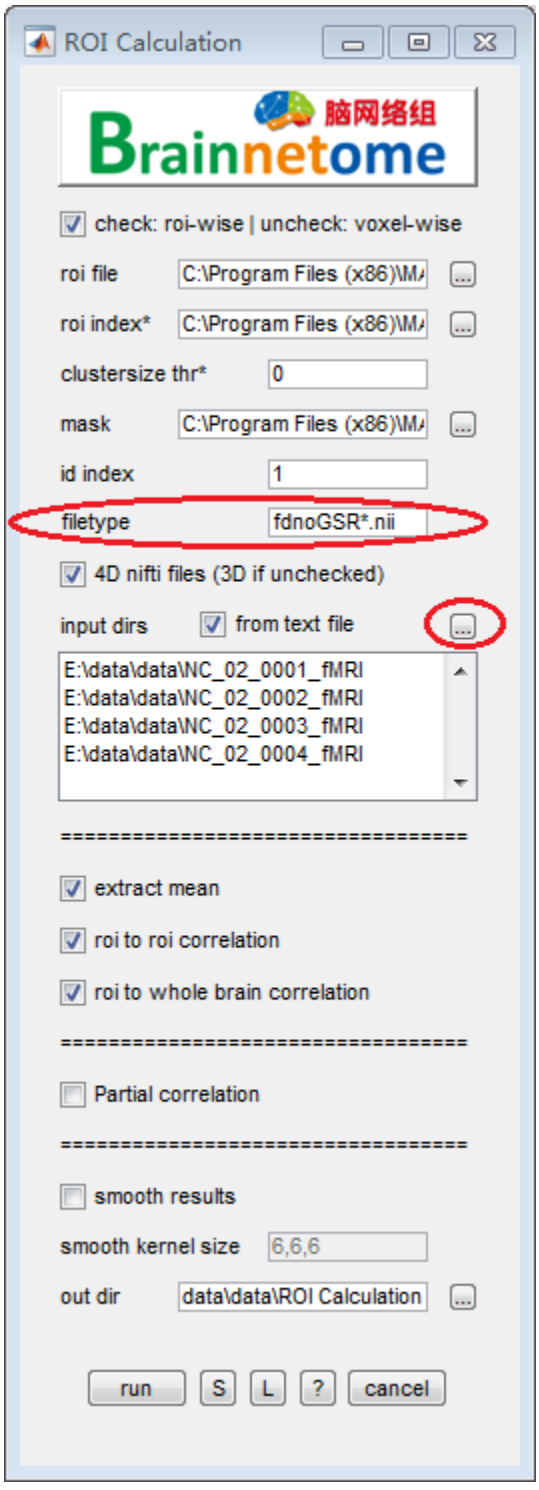


Fig. 12: fig.4 FC => ROI Calculation

Select output directories.

- **ALFF/fALFF:** Click *ALFF/fALFF* button in *SPON* GUI. Select the folders as input directories where STEP 2 outputs. Change filetype to `dnoGSR*.nii`. Remember that TR cannot be 0. Select output directories.
- **ReHo:** Click *ReHo* button in *SPON* GUI. Select the folders as input directories where STEP 2 outputs. Change filetype to `dnoGSR*.nii`. Change nbr type to 6 (face neighbor), 18 (edge neighbor) or 26 (vertex neighbor) if necessary. Select output directories.
- **FCD/FCS:** Click *FCD/FCS* button in *SPON* GUI. Select the folders as input directories where STEP 2 outputs. Change filetype to `dnoGSR*.nii`. The computation can use either OpenCL supported CPU or GPU. Select output directories. You can also calculate FCS with absolute value if necessary by selecting the *abs fcs* in *metrics*.

Important: Make sure your graphics drivers are up-to-date before using FCD/FCS function.

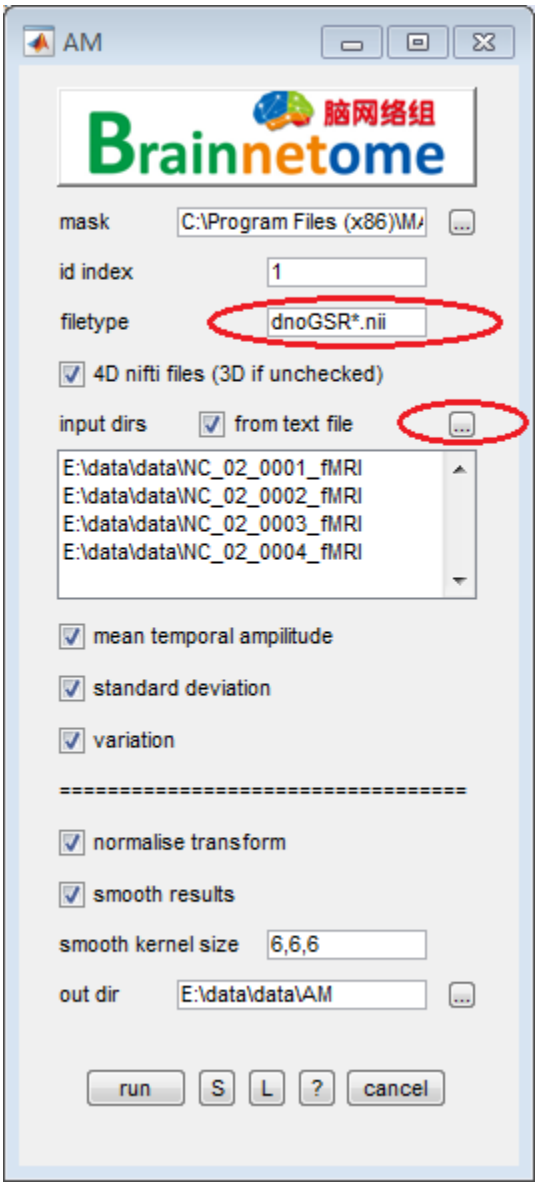


Fig. 13: fig.1 AM

9.6 STEP 6: Statistics for Differences among Groups

- **Input Directories of T-Tests:** Click the *STAT* button, then *T-Tests*. Open the directories selection GUI and find the folder where *ROI Calculation* in STEP 4 outputs, then select the `roi2roi_z_pearson_correlation` folder as input directories. Remove strings from search results parsed by id index by typing the strings into the *string removal*.
- **Group Table:** Create a `*.csv` file, input filenames without extensions, group strings, covariates as *fig 2*. Select this file for *table*.

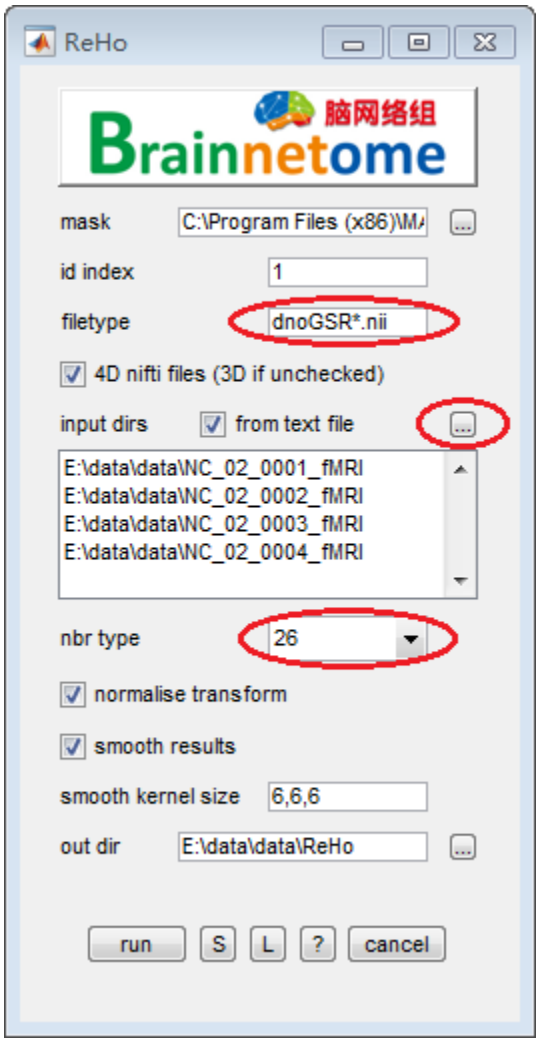


Fig. 15: fig.3 ReHo

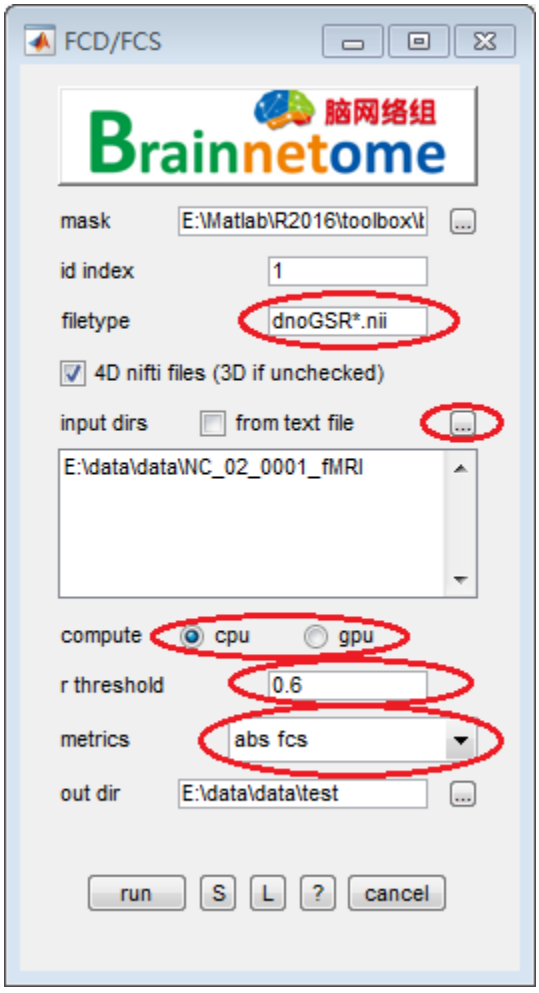


Fig. 16: fig.4 FCD/FCS

If your table file contains other information such as age or sex, you can input those titles in the *regressors*.

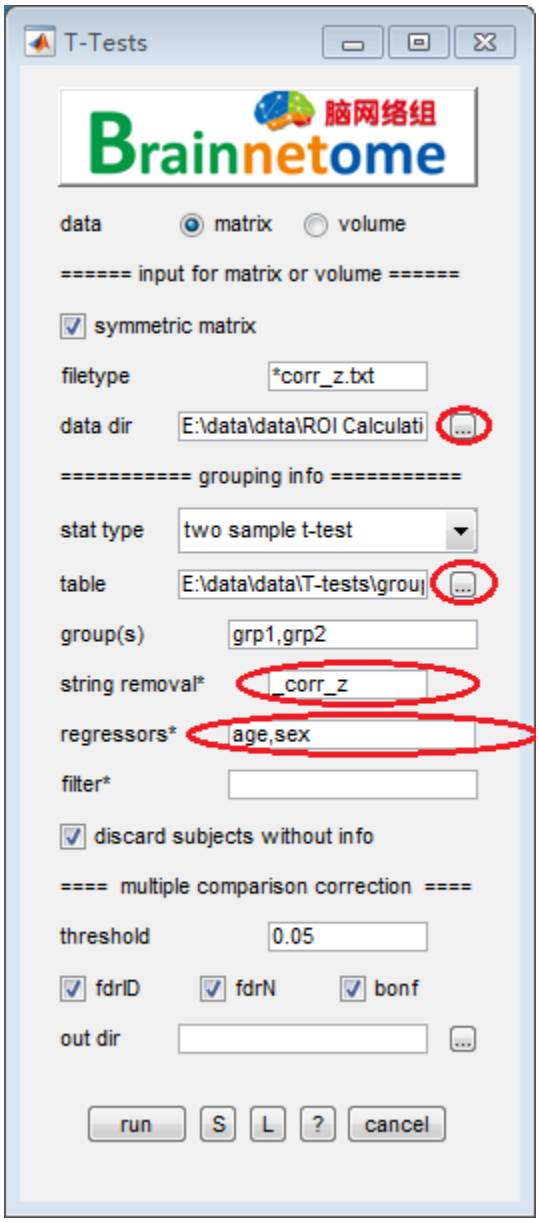


Fig. 17: fig.1 STAT => T-Tests

9.7 STEP 7: Network Properties

- **Input Directories of Network Calculation:** Click the *NET* button, then *Network Calculation*. Open the data directories selection GUI and find the folder where *ROI Calculation* in STEP 4 outputs.
- **Network Calculation:** Click the ... button of *Network Properties*,

name	group	age	sex
NC_02_000	grp1	31	0
NC_02_000	grp2	27	0
NC_02_000	grp1	36	0
NC_02_000	grp2	37	1

Fig. 18: fig.2 Tabel input

select those you need in the *Brant Net Measure Options* GUI. Those options with (*) will slow down the speed of calculation.

- **Input Directories of Network Statistics:** Click *Network Statistics* button in *NET* GUI. Open the directories selection GUI and find the folder where *Network Calculation* above outputs.
- **Network Statistics** Remove strings from search results parsed by id index such as `_corr_z_network` by typing the strings into the *string removal*. Select the `*.csv` file created in STEP 6 as input of *table*. If your table file contains other information such as age or sex, you can input those titles in the *regressors* to ignore them.

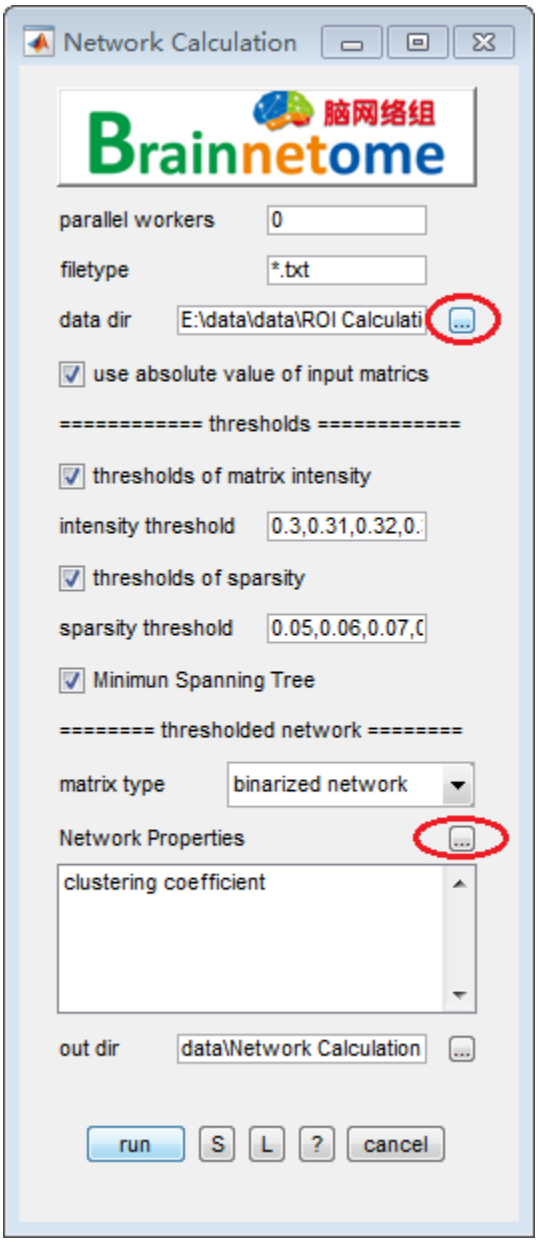


Fig. 19: fig.1 NET => Network Calculation

9.8 STEP 8: Visualization

- **Surface Mapping** Click the *VIEW* button, then *Surface Mapping*. Select material, lighting and shading if necessary.
- **ROI Mapping** Click *ROI Mapping* button in *VIEW* GUI. Select material, lighting and shading if necessary.
- **Network Visualization** Click *Network Visualization* button in *VIEW* GUI. Open the *node* directories selection GUI and find the `brant_roi_info.csv` file where *ROI Calculation* in STEP

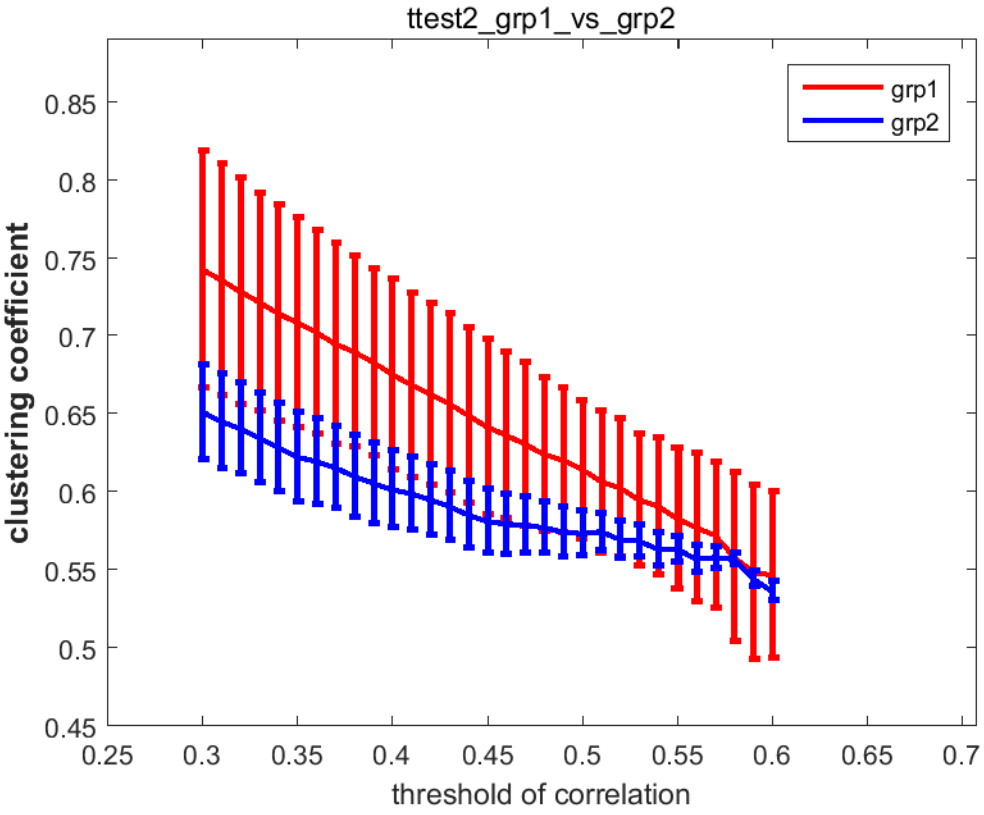


Fig. 21: fig.3 Network Statistics Result 1

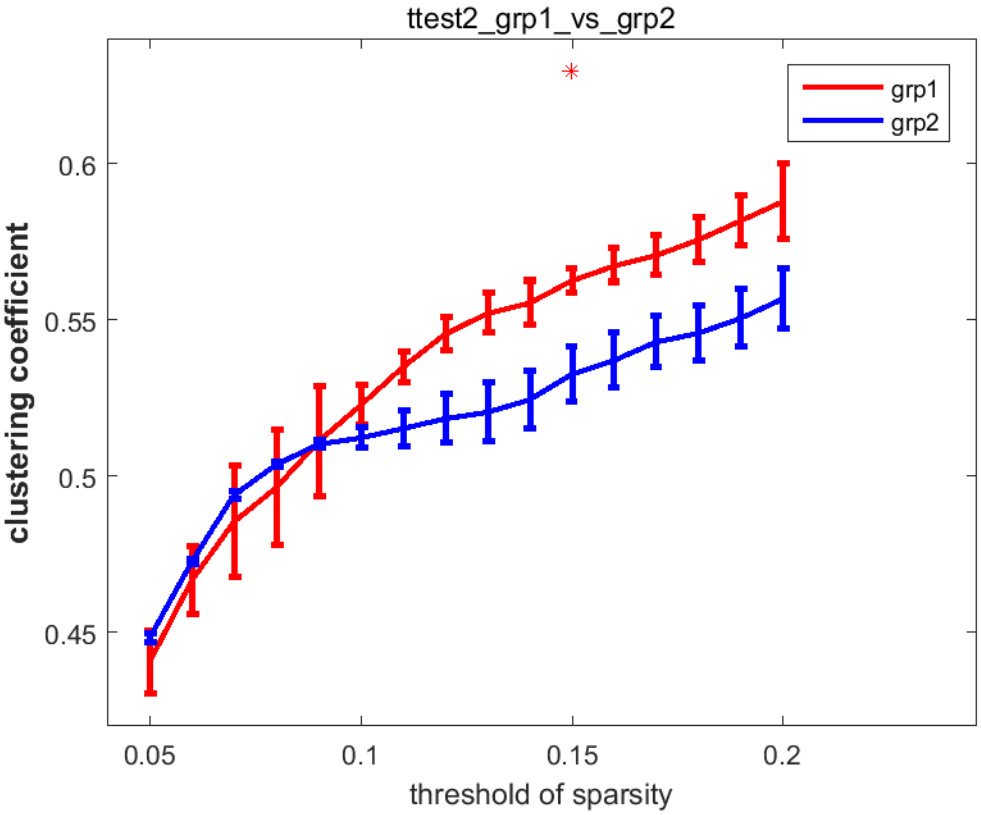


Fig. 22: fig.4 Network Statistics Result 2

4 outputs. Open the *edge* directories selection GUI and find the `ttest2_grp1_vs_grp2_h_unc.txt` file where *T-Tests* in STEP 6 outputs.

- **Circos** Click the *Embedded* button, then *Circos*. Select the circos' directories as input or *circos dir*, e.g. `D:/circos-0.69-5/bin`. ROI info can use the example `brant_circos_3mm_273.csv` file in `*/Matlab/toolbox/brant-master/circos`.
  Open the *edge* directories selection GUI and find the `ttest2_grp1_vs_grp2_h_unc.txt` file where *T-Tests* in STEP 6 outputs.

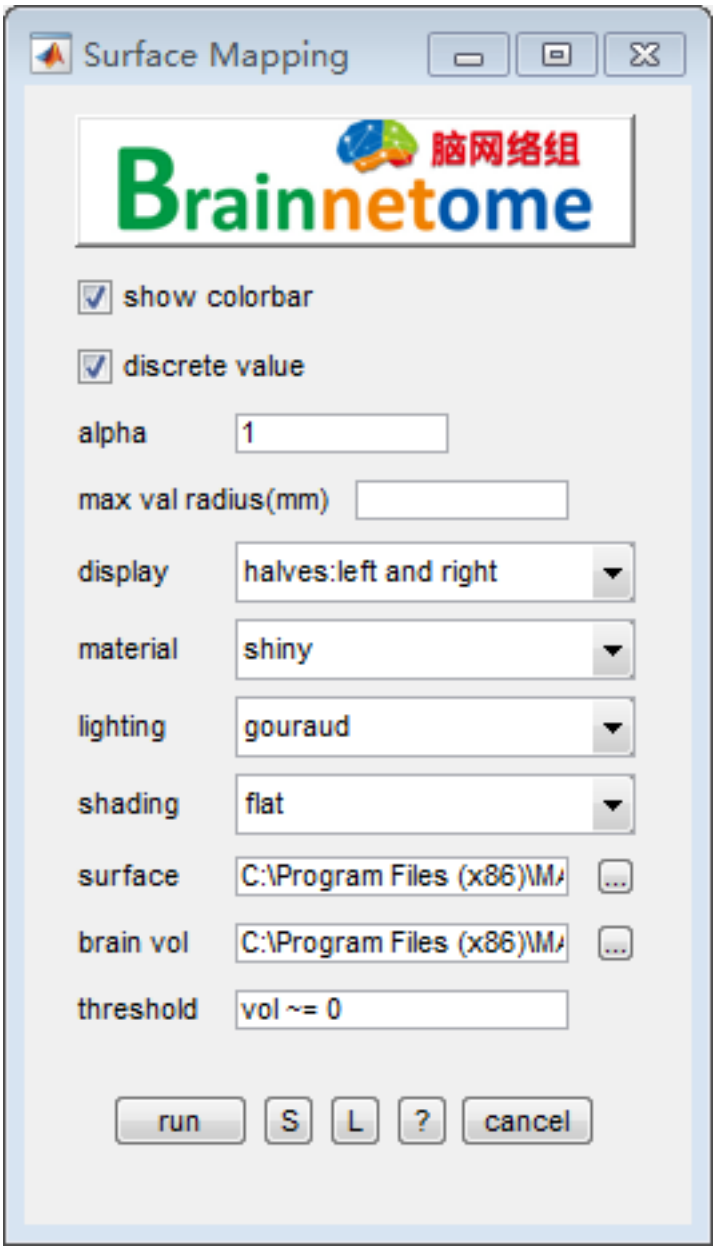


Fig. 23: fig.1 VIEW => Surface Mapping

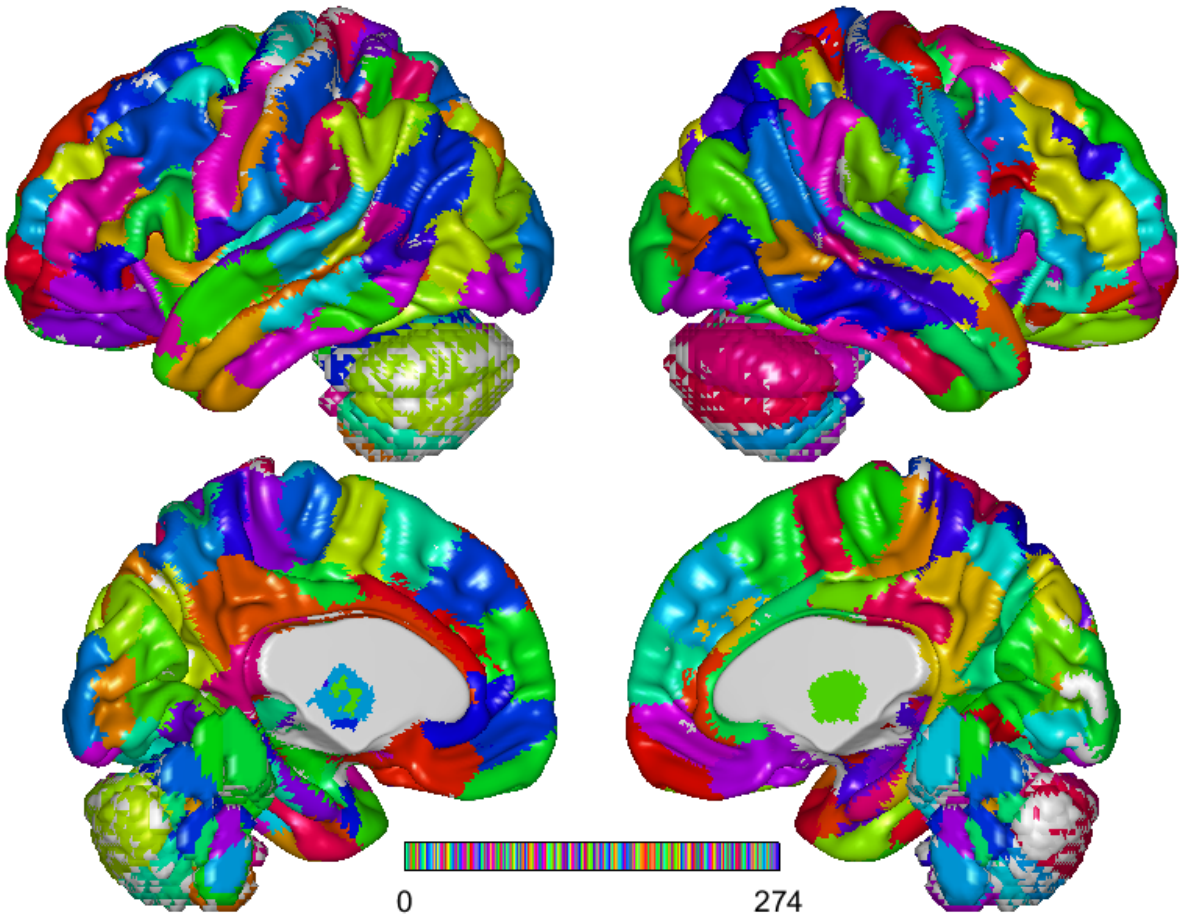


Fig. 25: fig.3 Result of Surface Mapping

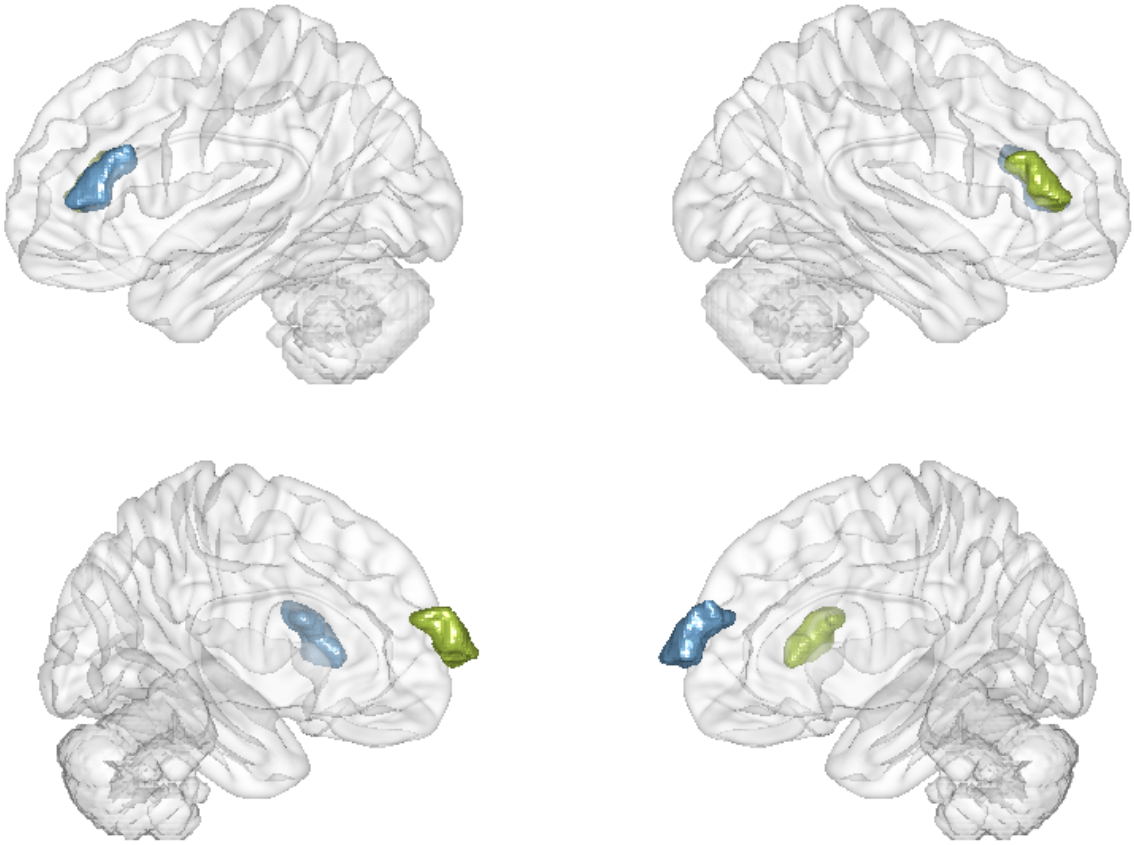


Fig. 26: fig.4 Result of ROI Mapping

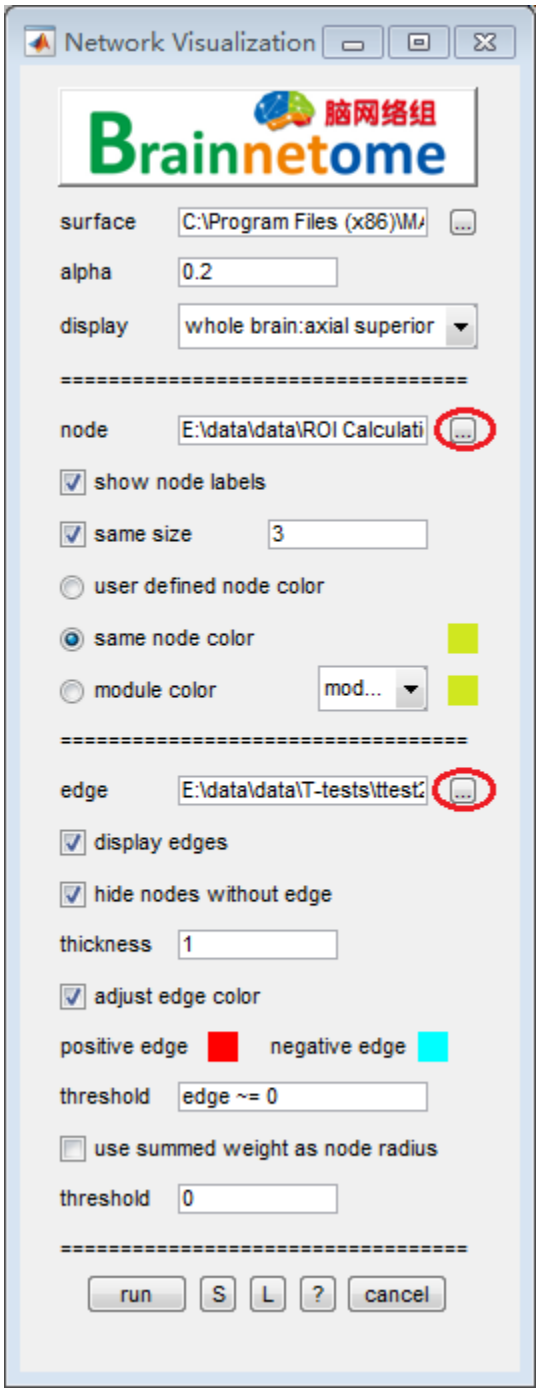


Fig. 27: fig.5 VIEW => Network Visualization

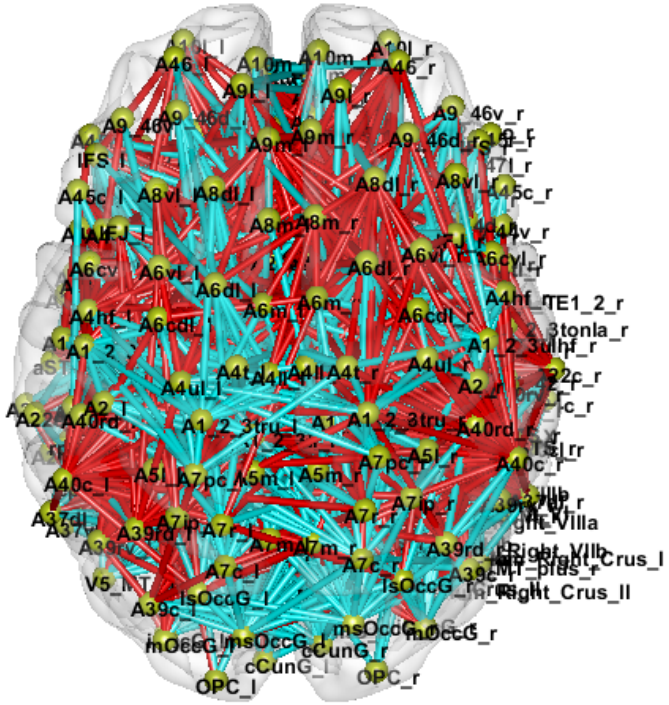


Fig. 28: fig.6 Result of Network Visualization

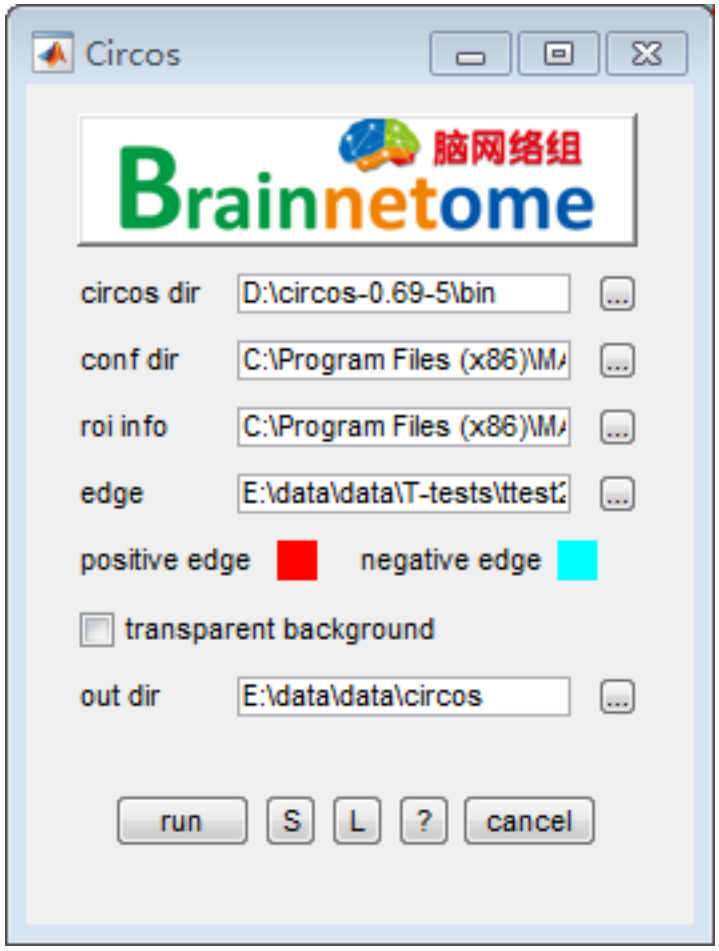


Fig. 29: fig.7 Embedded => Circos

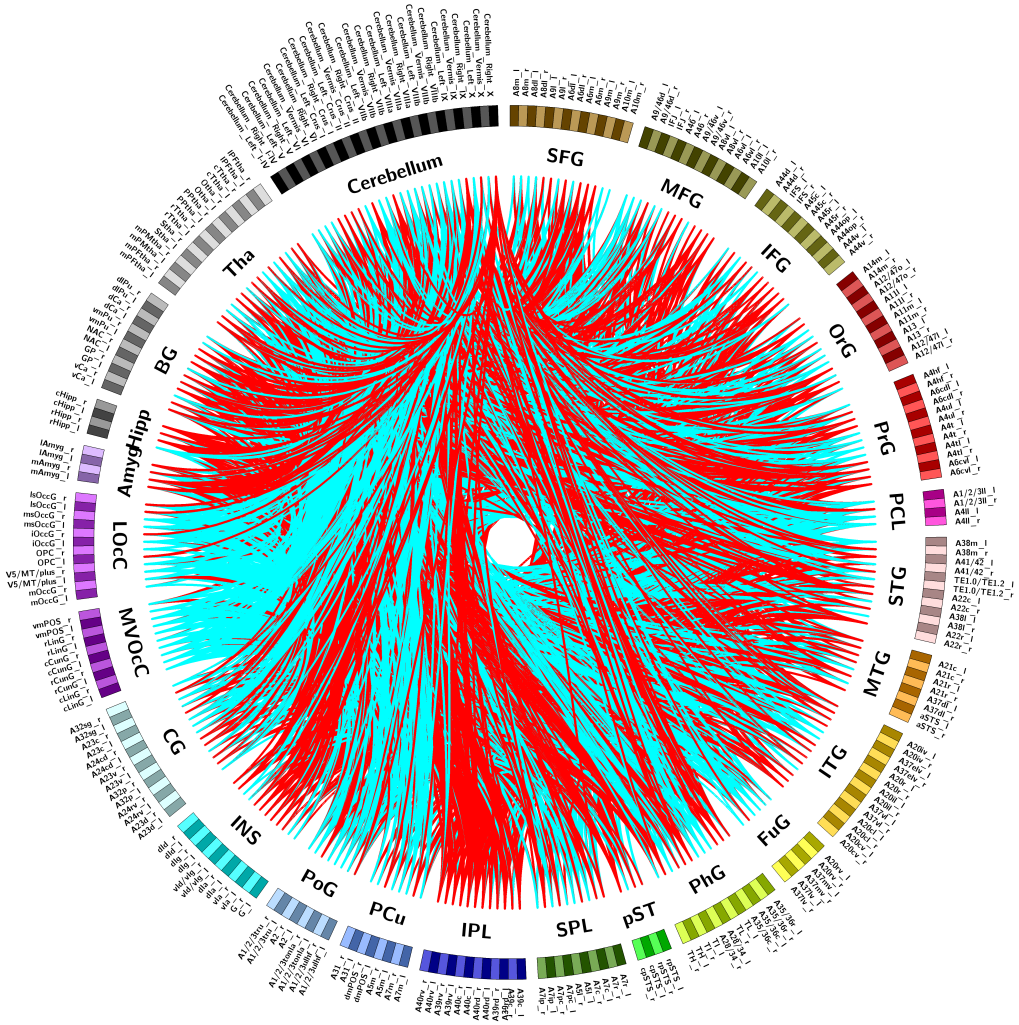


Fig. 30: fig.8 Result of Circos

9.9 File Name

Operation Name	File/Folder Name
DICOM Convert	brant_4D.nii
slice timing	abrant_4D.nii
	abrant_4D.mat
realign	rabrant_4D.nii
	meanabrant_4D.nii
	rp_abrant_4D.txt
coregister	wholebrain.nii
	betStruchImg.nii
normalise	wrabrant_4D.nii
denoise	dGSRwrabrant_4D.nii
	dnoGSRwrabrant_4D.nii
	fdGSRwrabrant_4D.nii
	fdnoGSRwrabrant_4D.nii
smooth	s6fdGSRwrabrant_4D.nii
	s6fdnoGSRwrabrant_4D.nii
Visual Check	axial (folder)
	coronal (folder)
	ortho (folder)
	sagital (folder)
Head Motion Est	brant_headmotion_exclusions.txt
	brant_headmotion_result.csv
Draw ROI	brant_2_sphere_rois.nii/brant_2_cube_rois.nii
	roi_info_sphere_2_rois.csv/roi_info_cube_2_rois.csv
ROI Calculation	mean_ts(folder)
	roi2roi_r_pearson_correlation (folder)
	roi2roi_z_pearson_correlation (folder)
	roi2wb_r_pearson_correlation (folder)
	roi2wb_z_pearson_correlation (folder)
	brant_roi_info.csv
	roi_history.txt
T-Tests	grp1_grp2_group_info.csv
	group_info.mat
	ttest2_diary.txt
	ttest2_grp1_vs_grp2.mat
	ttest2_grp1_vs_grp2_h_unc.txt
	ttest2_grp1_vs_grp2_pval_left_unc.txt
	ttest2_grp1_vs_grp2_pval_right_unc.txt
	ttest2_grp1_vs_grp2_tval.txt
Network Calculation	*_corr_z_network.mat
Network Statistics	clustering_coeffecient_corr_ttest2_grp1_vs_grp2.png
	clustering_coeffecient_spar_ttest2_grp1_vs_grp2.png
	network_clustering_coeffecient.csv
	network_clustering_coeffecient_ttest2_grp1_vs_grp2_stat.csv
	readme.txt

9.10 Result of rs-fMRI data analysis

To validate the efficacy of our toolkit, we used the same preprocessing pipelines provided by BRANT and DPABI v2.3, to compare ReHo, fALFF and FCs using a rs-fMRI dataset consists of 18 patients with mild cognitive impairment (MCI), 17 patients with mild Alzheimer's disease (mAD), 18 patients with severe Alzheimer's disease (sAD) and 21 normal controls (NC). This dataset is available online.

AD subjects were diagnosed using standard operationalized criteria (Diagnostic and Statistical Manual of Mental Disorders, Fourth Edition (DSM-IV); American Psychiatric Association 1994 and National Institute of Neurological and Communicative Disorders and Stroke - Alzheimer's Disease and Related Disorders Association (NINCDS-ADRDA)). The severity of dementia was assessed using the Clinical Dementia Rating (CDR) scale. Patients with a diagnosis of AD and CDR score of 1 were classified as mild AD and those with a CDR score of 2 or 3 were diagnosed as severe AD. MCI was diagnosed according to standard criteria, which included subjective memory loss with objective evidence of memory impairment in the context of normal or near-normal performance on other domains of cognitive functioning; minimal impairment of activities of daily living with a CDR score of 0.5. Normal volunteers have a CDR score of 0.

The MR images were acquired on a 3.0-T MR scanner (Magnetom Trio, Siemens, Germany). Functional MRI data were acquired using an echo planar imaging (EPI) sequence sensitive to BOLD contrast: Repetition time (TR) = 2000 ms, echo time (TE) = 30 ms, flip angle (FA) = 90°, matrix = 64 × 64, field of view (FOV) = 220 mm × 220 mm, slice thickness = 3 mm with inter-slice gap = 1 mm. Each brain volume comprised 32 axial slices, and each scanning session lasted for 360 s. Sagittal T1-weighted MR images were acquired by a magnetization-prepared rapid gradient-echo sequence (TR/TE = 2000/2.6 ms, FA = 9°, matrix = 256 × 224, FOV = 256 mm × 224 mm, 176 continuous sagittal slices with 1 mm thickness).

No significant differences (P>0.05) of age (two-tailed two sample t-test), gender (chi-squared

test) and education (two-tailed two sample t-test) were found between each patient group and NC group. T-statistic maps of fALFF, ReHo and results of FCs (P<0.001, uncorrected) based on different toolkits have quite similar patterns, which suggest BRANT is another optimal toolkit for rs-fMRI research community. In the results, the minor differences can be induced by 489 different implementations of trends removal, covariance regression and band-pass filter. For the results, we didn't draw a strong conclusion, since the interpretation requires multiple comparison corrections and is not the main point of the current study.

We have listed the differences among BRANT and other Matlab-based toolboxes in FAQs. We can also find that t-statistic maps of fALFF, ReHo and results of FCs (P<0.001, uncorrected) based on different toolkits have quite similar patterns, which suggest BRANT is another optimal toolkit for rs-fMRI research community.

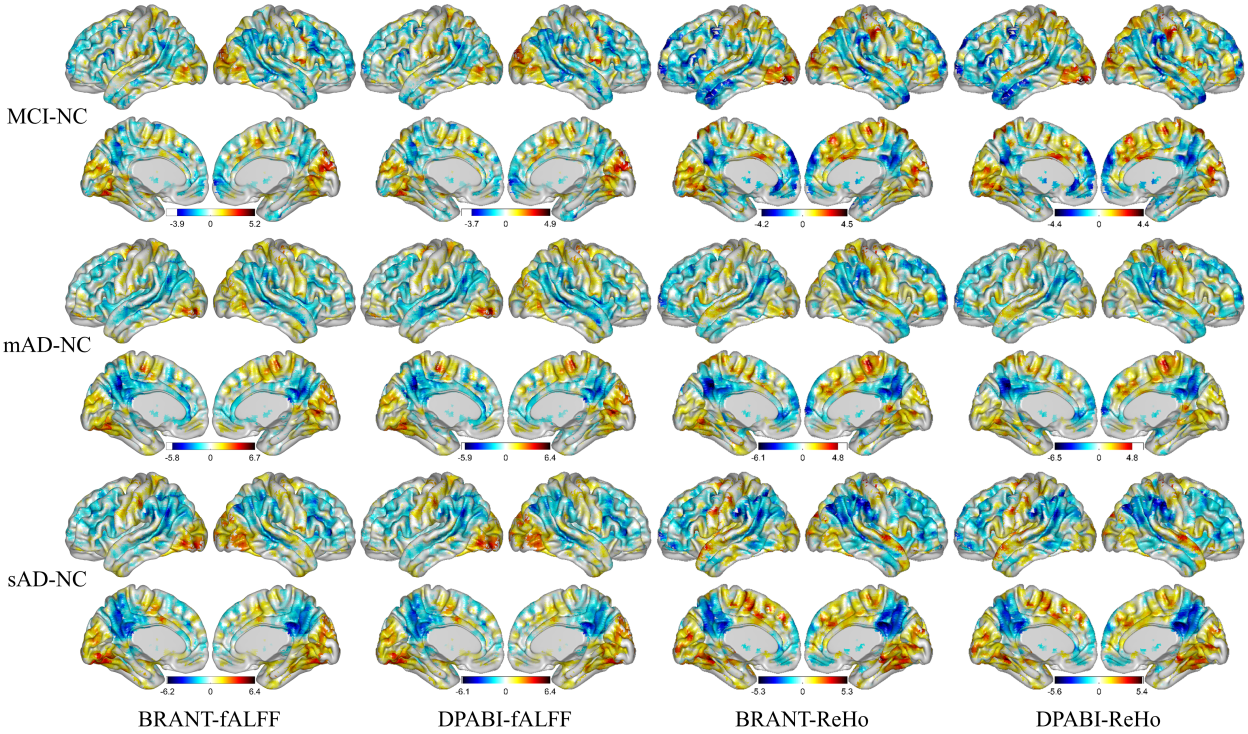


Fig. 31: fig.1 T-statistic maps of fALFF and ReHo based on different toolkits

- **References**:

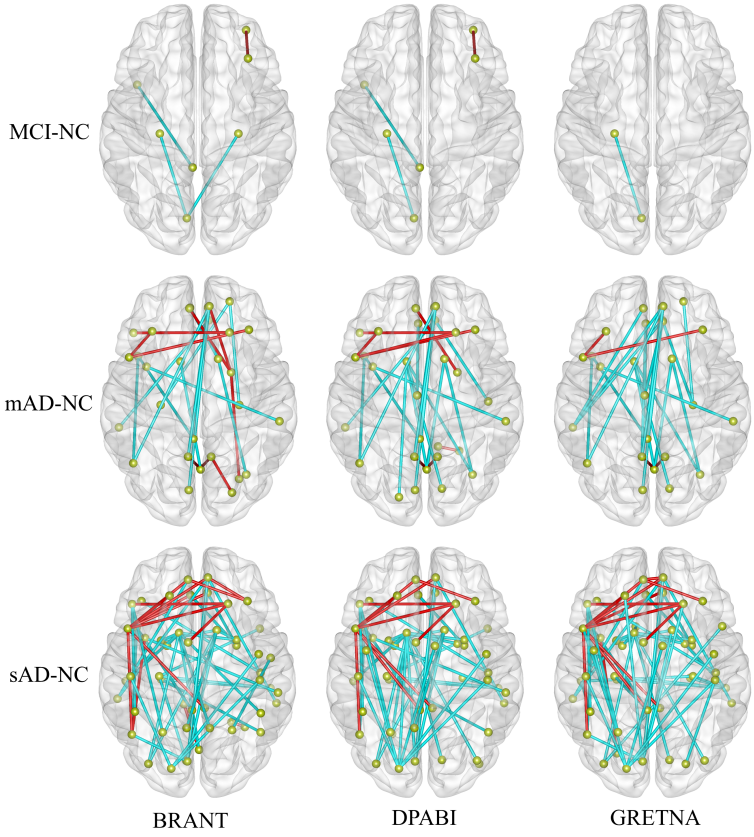


Fig. 32: fig.2 results of FCs based on different toolkits

1. Yan CG, Wang XD, Zuo XN, Zang YF. DPABI: Data Processing & Analysis for (Resting-State) Brain Imaging. *Neuroinformatics 2016*; 14(3): 339-51.

2. Wang J, Wang X, Xia M, Liao X, Evans A, He Y. GRETNA: a graph theoretical network analysis toolbox for imaging connectomics. *Front Hum Neurosci 2015*; 9: 386.

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5. Liu Y, Yu C, Zhang X, Liu J, Duan Y, Alexander-Bloch AF, et al. Impaired long distance functional connectivity and weighted network architecture in Alzheimer's disease. *Cereb Cortex 2014*; 24(6): 1422-35.

6. He X, Qin W, Liu Y, Zhang X, Duan Y, Song J, et al. Abnormal salience network in normal aging and in amnestic mild cognitive impairment and Alzheimer's disease. *Human brain mapping 2014*; 35(7): 3446-64.

7. Liu J, Zhang X, Yu C, Duan Y, Zhuo J, Cui Y, et al. Impaired Parahippocampus Connectivity in Mild Cognitive Impairment and Alzheimer's Disease. *J Alzheimers Dis 2016*; 49(4): 1051-64.

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9. Morris JC. The Clinical Dementia Rating (CDR): current version and scoring rules. *Neurology 1993*; 43(11): 2412-4.

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11. Petersen RC, Doody R, Kurz A, Mohs RC, Morris JC, Rabins PV, et al. Current concepts in

mild cognitive impairment. *Arch Neurol 2001*; 58(12): 1985-92.

12. Choo IH, Lee DY, Youn JC, Jhoo JH, Kim KW, Lee DS, et al. Topographic patterns of brain functional impairment progression according to clinical severity staging in 116 Alzheimer disease patients: FDG-PET study. *Alzheimer Dis Assoc Disord 2007*; 21(2): 77-84.

CHAPTER 10

Download

- **You can get the latest version of BRANT from** https://github.com/YongLiuLab/brant-stable/archive/master.zip
- **Some functions are based on SPM, you can get it from** http://www.fil.ion.ucl.ac.uk/spm/software/spm12
- **Circos in STEP 8 can be downloaded from** http://circos.ca/distribution/circos-0.69-5.tgz
- Unzip the *brant-master.zip* file and move both brant and spm12 folders to `/path/of/toolbox`. (The path can be anywhere in your computer as long as it's in English)
- Configure SPM paths:
  1. Click *Set Path* in MATLAB
  2. Click *add folder*
  3. Select SPM's root folder
  4. Run `spm fmri` in MATLAB's Command Window to let spm add its subfolders. (Note that some SPM's subfolders are called internally in SPM and should not be added in MATLAB's search path. Scripts in those folders are conflicting with MATLAB functions, and could cause untraceable errors)
- Configure BRANT paths:
  1. Click *Set Path* in MATLAB
  2. Click *Add with subfolders*
  3. Select the unzipped BRANT folder
  4. Click *Save*.

Tip:

- **An alternative way to configure both SPM and BRANT Paths:**
  - **Run in MATLAB's Command Window:**
    - `cd('/path/of/unzipped/brant/');` % to set current working directory to the unzipped brant

* `brant_configure_paths;` % to add BRANT paths (same as *add with subfolders*)
* `brant_configure_paths('/path/of/spm12/');` % to add SPM paths

CHAPTER 11

FAQs

11.1 How can I Download and Install BRANT

- **You can get the latest version of BRANT from** https://github.com/YongLiuLab/brant-stable/archive/master.zip
- **Some functions are based on SPM, you can get it from** http://www.fil.ion.ucl.ac.uk/spm/software/spm12
- **Circos in STEP 8 can be downloaded from** http://circos.ca/distribution/circos-0.69-5.tgz
- Unzip the *brant-master.zip* file and move both brant and spm12 folders to `/path/of/toolbox`. (The path can be anywhere in your computer as long as it's in English)
- Configure SPM paths:
  1. Click *Set Path* in MATLAB
  2. Click *add folder*
  3. Select SPM's root folder
  4. Run `spm fmri` in MATLAB's Command Window to let spm add its subfolders. (Note that some SPM's subfolders are called internally in SPM and should not be added in MATLAB's search path. Scripts in those folders are conflicting with MATLAB functions, and could cause untraceable errors)
- Configure BRANT paths:
  1. Click *Set Path* in MATLAB
  2. Click *Add with subfolders*
  3. Select the unzipped BRANT folder
  4. Click *Save*.

Tip:

- **An alternative way to configure both SPM and BRANT Paths:**

- **Run in MATLAB's Command Window:**
  - `cd('/path/of/unzipped/brant/');` % to set current working directory to the unzipped brant
  - `brant_configure_paths;` % to add BRANT paths (same as *add with subfolders*)
  - `brant_configure_paths('/path/of/spm12/');` % to add SPM paths

11.2 What is BRANT's Advantage Compared with Other Matlab-based Toolboxes

Compared with DPABI v2.3, GRETNA v2.0.0 and CONN v17.f, the differences are listed in the table below.

In conclusion, BRANT can directly support `*.gz` for most postprocessing functions, use OPENCL-based parallel computing for time consuming FCD/FCS calculation to save time. Other than focusing on several specific types of rs-fMRI data processing, functions of BRANT cover a wide range of rs-fMRI data processing methods. Also, GUIs are created automatically with a few lines of MATLAB code instead of drawn manually.

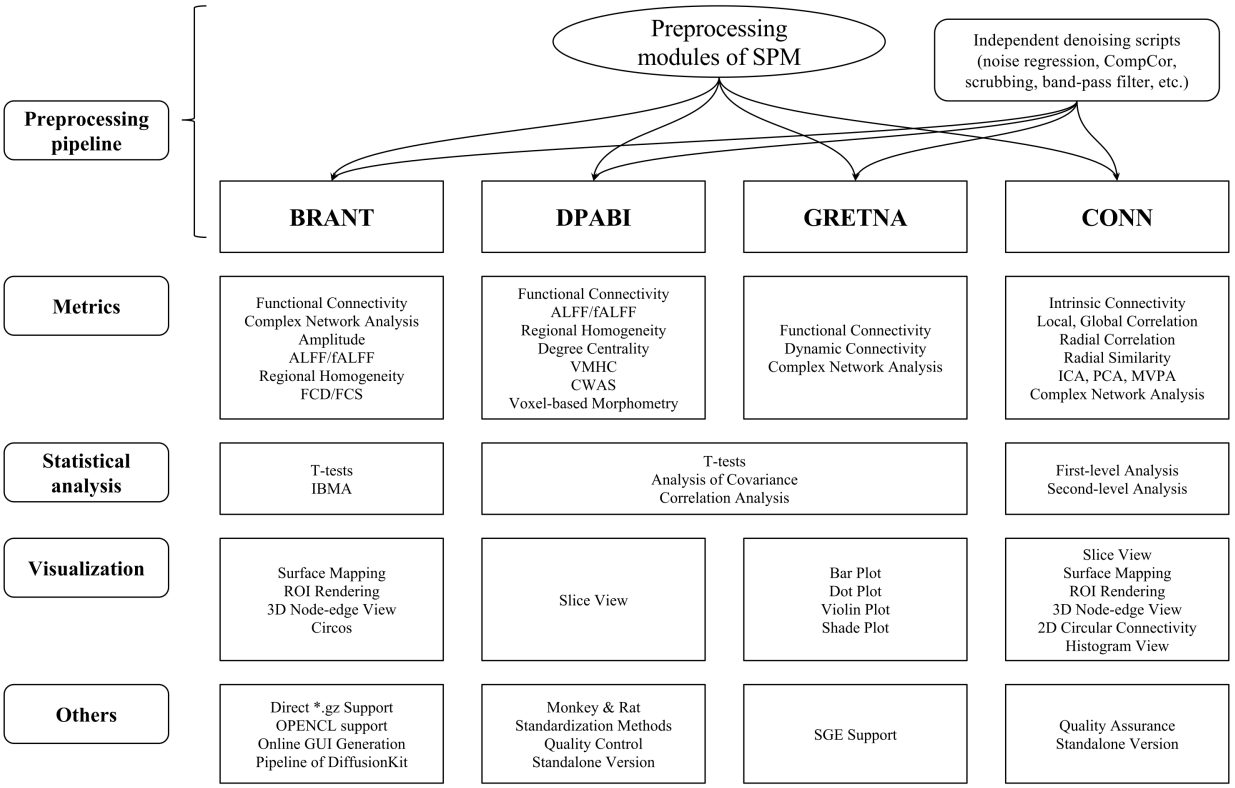

Fig. 1: fig.1 differences among four Matlab-based toolboxes

11.3 How to Format Tables Correctly

- In some fuctions, you may have to use some `*.csv` files to input data. If you cannot find any proper existed `*.csv` files, you can create a `*.csv` file by Excel or Notepad. e.g.

– **STEP 4 => FC => Draw ROI => Coordinates in txt or csv file (input type: file)**

x	y	z	label
40	-16	50	ROI1
-40	-16	50	ROI2

– **STEP 6 => STAT => T-Tests => table**

name	group	age	sex
NC_02_0001_fMRI	grp1	31	0
NC_02_0002_fMRI	grp2	27	0
NC_02_0003_fMRI	grp1	36	0
NC_02_0004_fMRI	grp2	37	1

If you select *paired t-test*, the table should contain an additional column of paired_t_idx

name	group	filter	age	paired_t_idx
subj1	stage1	center1	28	1
subj2	stage1	center1	27	2
subj3	stage2	center1	30	1
subj4	stage2	center2	25	2

– **STEP 8 => VIEW => Network Visualization => node**

x	y	z	label	vox_num	index
-4.6213	15.6	53.2468	A8m_l	235	1
…	…	…	…	…	…

This `brant_roi_info.csv` file can be found in the folder as the *out dir* of *ROI Calculation* in STEP 4.

– **STEP 8 => Embedded => Circos => roi info**

x	y	z	label_old	label	vox_num	index	module	index_module	index_node
-4.6213	15.6	53.2468	SFG_L_7_1	A8m_l	235	1	SFG	1	1
…	…	…	…	…	…	…	…	…	…

This `brant_circos_3mm_273.csv` file can be found in the `*/Matlab/toolbox/brant-master/circos`.

11.4 What can I Do When an Error Occurs

- Here are some common errors with their reasons and solutions below. You can also modify parameters with the help of examples and rerun former steps. If these all cannot work, please contact us.

1.

- Reason: Misuse id index.

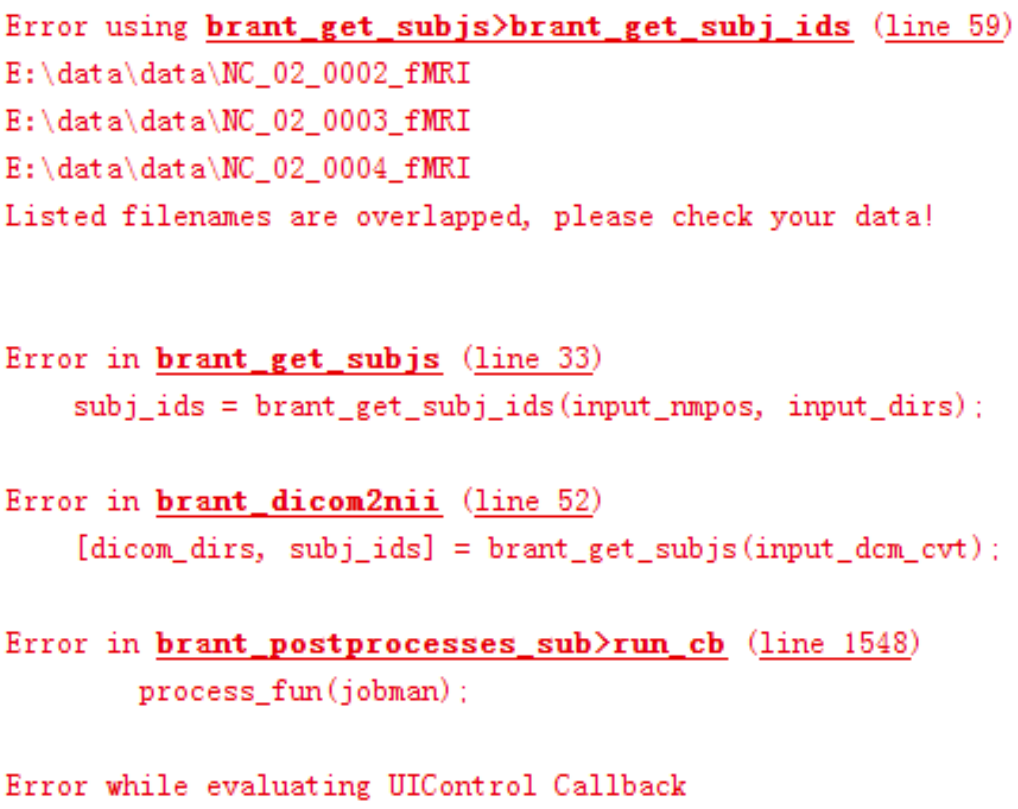

Fig. 2: fig.2 error during DICOM Convert

- Solution: Delete files created before the error occurs. Read example to use id index properly.

2.

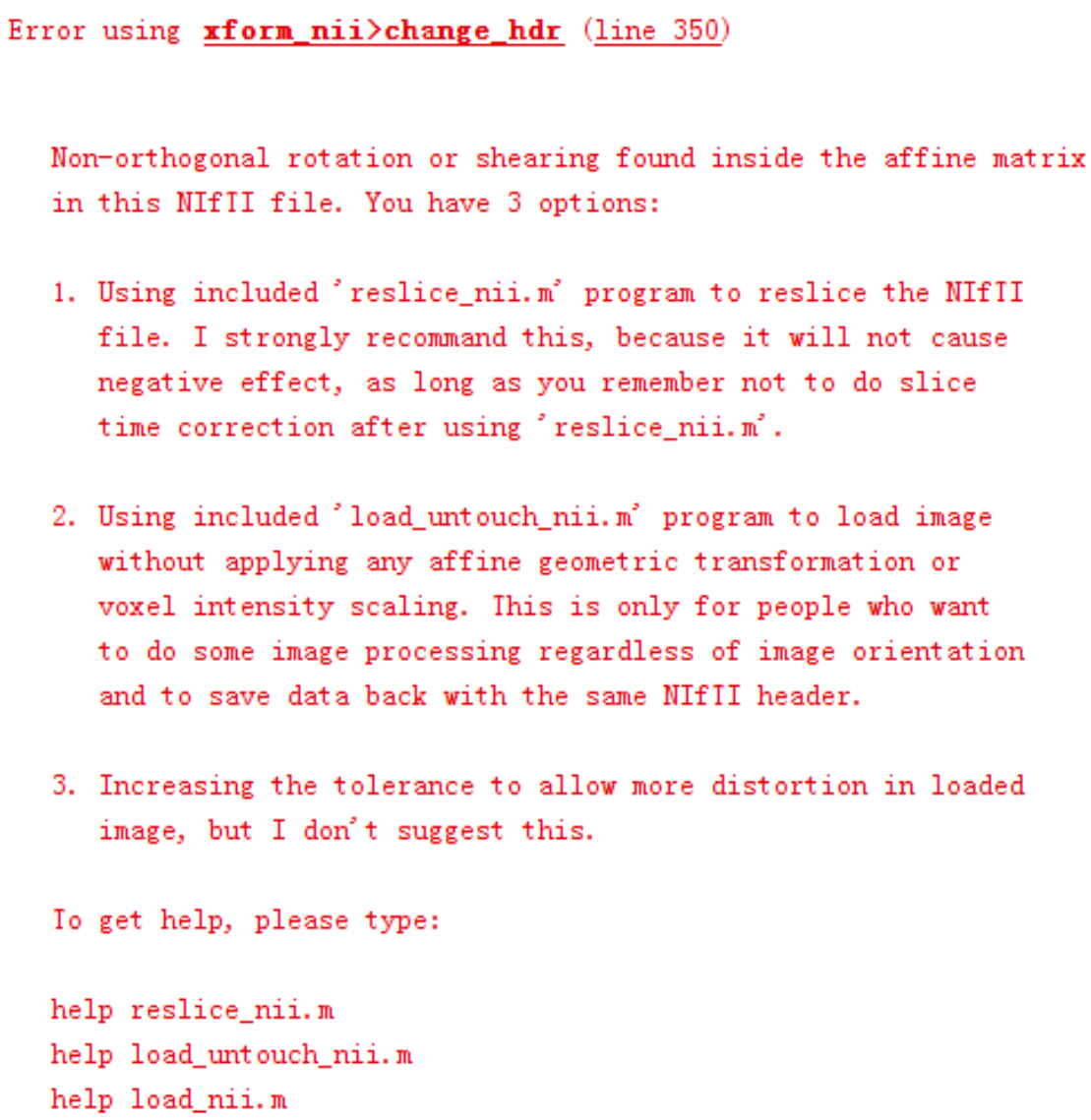

Fig. 3: fig.3 error after preprocessing

- Reason: The preprocessing may be interrupted and create wrong `*.nii` files.
- Solution: Delete files created during preprocessing, examine your preprocessing settings and run preprocessing again.

3.

- Reason: TR(s) in Preprocessing is zero.
- Solution: Set tr(s) in *Silce Timing* to a legal value.

4.

- Reason: The table file is incorrect.

```
Error using spm_realign>error_message (line 471)
Insufficient image overlap.

Error in spm_realign>realign_series (line 301)
        if length(msk)<32, error_message(P(i)); end

Error in spm_realign (line 136)
    P{1} = realign_series(P{1}, flags);

Error in spm_run_realign (line 31)
    spm_realign(P, flags);

Error in brant_run_realign>loop_realign (line 31)
    spm_run_realign(rea_infos);

Error in brant_run_realign (line 10)
        loop_realign(data_tmp(m), rea_infos);

Error in brant_preprocess_jobman (line 225)
                    end_prefix = feval(['brant_run_', processes_curr{m}], run_data.(processes_curr{m}),
                    run_data.subjs.files, data_input.is4d, par_on);

Error in brant_preprocess>run_cb (line 343)
brant_preprocess_jobman(jobman, gcf);

Error while evaluating UIControl Callback
```

Fig. 4: fig.4 error during preprocessing

```
Error using brant_chk_tbl_cols (line 7)
None or more than one column of name!

Error in brant_parse_subj_info2 (line 14)
[tbl_fns, fns_good] = brant_chk_tbl_cols(tbl_data, tbl_title, {'name'}, 'str');

Error in brant_stat (line 124)
        [data_infos, subj_ind, fil_inds, reg_good_subj, paired_t_idx] = brant_parse_subj_info2(regressors_tbl,
        subj_ids_org, group_est, filter_est, reg_est, score_est, discard_bad_ind);

Error in brant_postprocesses_sub>run_cb (line 1548)
        process_fun(jobman);

Error while evaluating UIControl Callback
```

Fig. 5: fig.5 error during STAT

- Solution: Confirm that the table file contains a row with group information and contains only one row. Open it with notepad to check if the data in this file is divided by comma.

5.

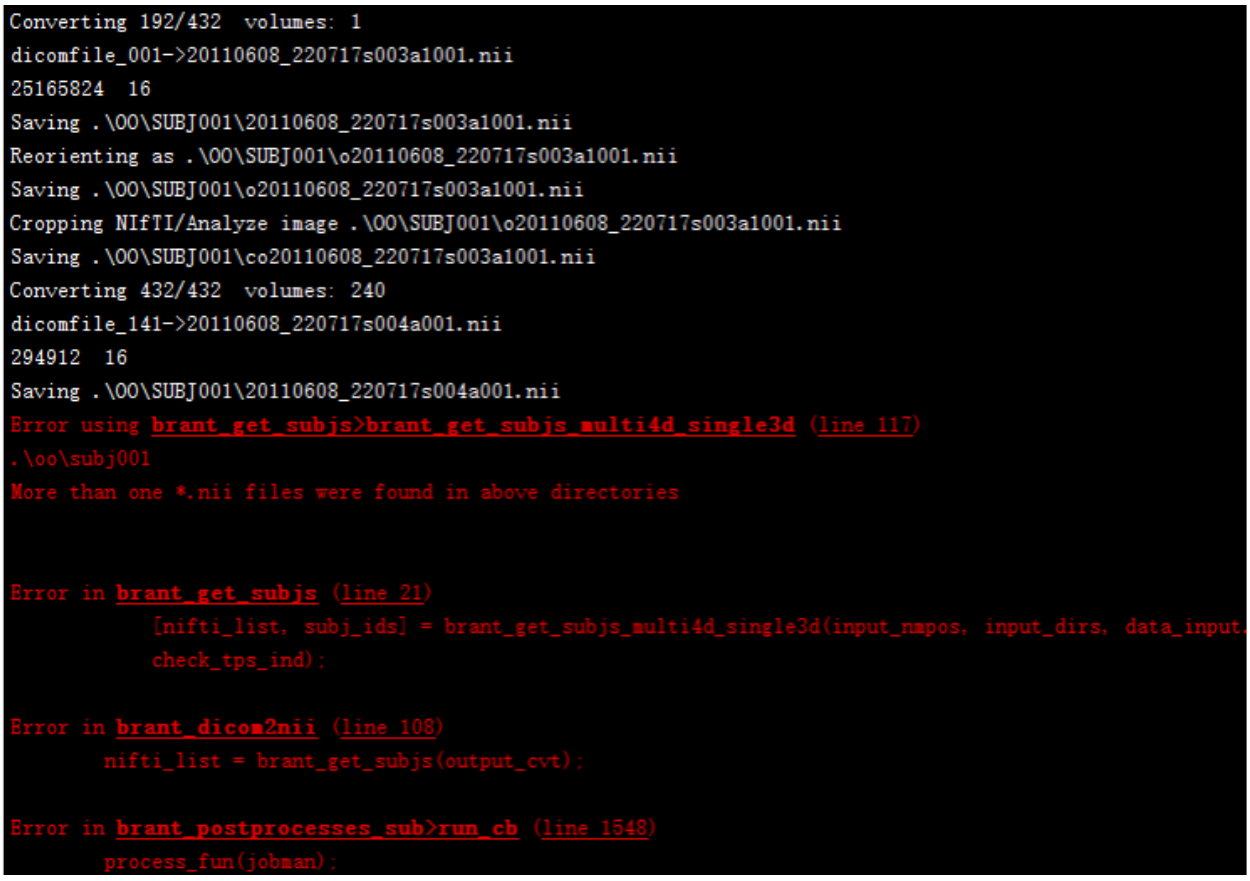

Fig. 6: fig.6 error after DICOM Convert

- Reason: More than one `*.nii` files were found in above directories.
- Solution: Uncheck the *delete first N timepoints* or convert just one set of data per time.

CHAPTER 12

Publications using Brant

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[5] Y. Zhang, X. Liu, K. Zhao, L. Li, and Y. Ding, "Study of altered functional connectivity in individuals at risk for Alzheimer's Disease.," *Technol Health Care*, vol. 26, no. S1, pp. 103–111, 2018.

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[3] M. Xiao et al., "Attention Performance Measured by Attention Network Test Is Correlated with Global and Regional Efficiency of Structural Brain Networks," *Front. Behav. Neurosci.*, vol. 10, 2016.

[2] S. Yang et al., "Altered Intranetwork and Internetwork Functional Connectivity in Type 2 Diabetes Mellitus With and Without Cognitive Impairment," *Sci Rep*, vol. 6, no. 1, p. 32980, Dec. 2016.

[1] Y. Wang et al., "Using Regional Homogeneity to Reveal Altered Spontaneous Activity in Patients with Mild Cognitive Impairment," *BioMed Research International*, vol. 2015, pp. 1–8, 2015.