GRETNA

A Graph Theoretical Network Analysis Toolbox

Reference Manual for GRETNA (v2.0)

June 2017

National Key Laboratory of Cognitive Neuroscience and Learning
Beijing Key Laboratory of Brain Imaging and Connectomics
IDG/McGovern Institute for Brain Research

Beijing Normal University, Beijing, China

Table of Contents

1. Overview 4
2. License 5
3. Prerequisites 5
4. Installation 6
5. Network Construction 8
    - 5.1. R-fMRI Preprocessing 8
        - 5.1.1. DICOM to NIfTI 10
        - 5.1.2. Remove First Images 11
        - 5.1.3. Slice Timing 12
        - 5.1.4. Realign 13
        - 5.1.5. Normalize 14
        - 5.1.6. Spatially Smooth 17
        - 5.1.7. Regress Out Covariates 18
        - 5.1.8. Temporally Detrend 19
        - 5.1.9. Temporally Filter 20
        - 5.1.10. Scrubbing 21
        - 5.1.11. Results of R-fMRI Preprocessing 22
    - 5.2. Functional Connectivity Matrix Construction 25
        - 5.2.1. Static Correlation 26
        - 5.2.2. Dynamical Correlation 26
        - 5.2.3. Results of Functional Connectivity Matrix Construction 27
6. Network Analysis 28
    - 6.1. Global Network Metrics 31
        - 6.1.1. Small-World 32
        - 6.1.2. Efficiency 32
        - 6.1.3. Rich-Club 32
        - 6.1.4. Assortativity 33
        - 6.1.5. Synchronization 33
        - 6.1.6. Hierarchy 33
    - 6.2. Nodal and Modular Network Metrics 33
        - 6.2.1. Clustering Coefficient 34
        - 6.2.2. Shortest Path Length 34
        - 6.2.3. Efficiency 34
        - 6.2.4. Local Efficiency 34
        - 6.2.5. Degree Centrality 34
        - 6.2.6. Betweenness Centrality 35
        - 6.2.7. Community Index 35
        - 6.2.8. Participant Coefficient 36
        - 6.2.9. Modular Interaction 37
    - 6.3. Results of Network Analysis 37

    - 6.3.1. Global Network Metrics 38
    - 6.3.2. Nodal and Modular Network Metrics 41
- 7. Metric Comparison 47
  - 7.1. Network and Node 47
    - 7.1.1. One-Sample *t*-Test 49
    - 7.1.2. Two-Sample *t*-Test 50
    - 7.1.3. Paired *t*-Test 51
    - 7.1.4. One-Way ANCOVA 52
    - 7.1.5. One-Way ANCOVA (Repeated Measures) 53
    - 7.1.6. Correlation Analysis 54
  - 7.2. Connection 55
    - 7.2.1. Averaged (Functional) 56
    - 7.2.2. Backbone (Structural) 57
    - 7.2.3. One-Sample *t*-Test 58
    - 7.2.4. Two-Sample *t*-Test 59
  - 7.3. Results of Metric Comparison 60
    - 7.3.1. Network and Node 60
    - 7.3.2. Connection 62
- 8. Metric Plotting 64
  - 8.1. Bar 65
  - 8.2. Dot 66
  - 8.3. Violin 67
  - 8.4. Shade 68
- 9. GANNM 69
- Acknowledgements 70
- Reference 71

1. Overview

The GRETNA toolbox has been designed for the graph-theoretical network analysis of fMRI data. It is a suite of MATLAB functions and MATLAB-based interfaces for conventional fMRI preprocessing and for the calculation and statistical analysis of the most frequently used network metrics, such small-world parameters, efficiency, degree, betweenness, assortativity, hierarchy, synchronization and modularity.

Thank you for using GRETNA (v2.0.0). When using this package in your publicized work, **PLEASE CITE:**
Wang, J., Wang, X., Xia, M., Liao, X., Evans, A., & He, Y. (2015). GRETNA: a graph theoretical network analysis toolbox for imaging connectomics. Frontiers in human neuroscience, 9, 386.

Developed by Jinghui Wang and Xindi Wang
National Key Laboratory of Cognitive Neuroscience and Learning,
Beijing Normal University, China

Contact information:
Jinhui Wang: jinhui.wang.1982@gmail.com
Xindi Wang: sandywang.rest@gmail.com
Yong He: yong.he@bnu.edu.cn

2. License

GRETNA is distributed under the terms of the GNU General Public License as published by the Free Software Foundation (version 3). The details on ‘copyleft’ can be found at http://www.gnu.org/copyleft/.

3. Prerequisites

Getting started to run GRETNA on your computer:

- **MATLAB**: A high-level numerical mathematics environment developed by MathWorks, Inc. Natick, MA, USA. GRETNA requires MATLAB2010a or later version.
- **SPM8/SPM12**: SPM is freely available to the (neuro) imaging community andrepresents the implementation of the theoretical concepts of Statistical Parametric Mapping in a complete analysis package. Given that the names of certain functions in SPM8/SPM12 are the same as those in GRETNA or MATLAB, we recommend that you add only the path of the home folder of SPM8/SPM12 when you use GRETNA.
- **MatlabBGL**: MatlabBGL is a MATLAB package for working with graphs. It uses the Boost Graph Library to efficiently implement graph algorithms. GRETNA has included this package in its distribution. Thus, you do not need to download MatlabBGL again.
- **PSOM**: The pipeline system for GNU Octave and MATLAB (PSOM) is a lightweight library for managing complex multi-stage data processing. A pipeline is a collection of jobs, i.e. MATLAB or Octave codes, with a well identified set of options that use files for inputs and outputs. GRETNA has included this package in its distribution. Thus, you do not need to download PSOM again.

4. Installation

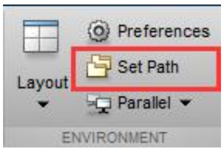
Run MATLAB. You can add the GRETNA path to the MATLAB search path in one of two ways: Command-line or Interface.

- **Command-line**

Type the following command in the MATLAB command window.

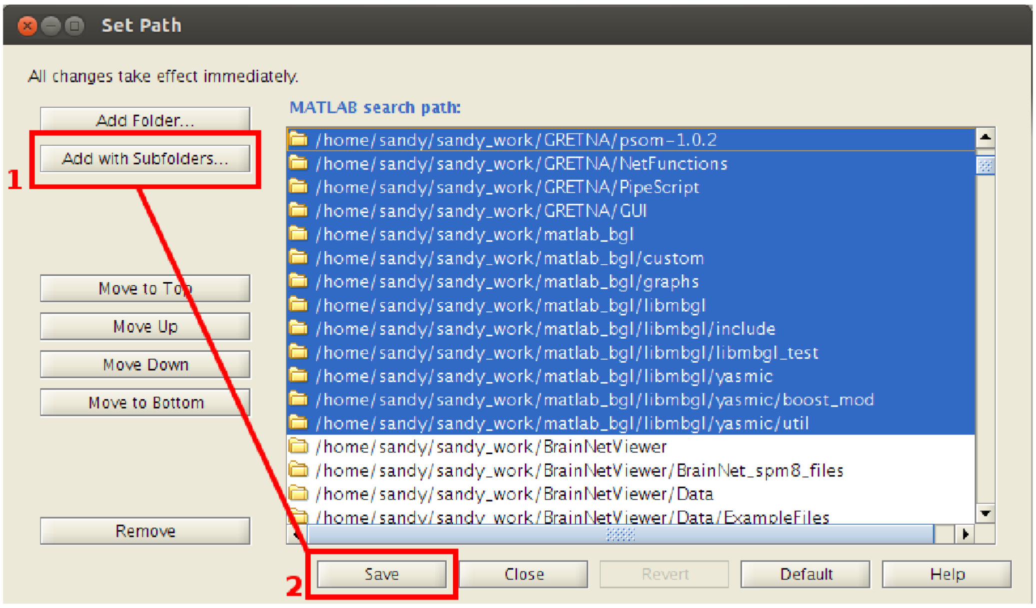
```
>>addpath(genpath('D:\...\GRETNA'));
```

where 'D:\...\GRETNA' is the path of GRETNA on your computer.



- **Interface**

Click '**Set Path**' on the MATLAB panel, or type 'pathtool' in the MATLAB command window. Click '**Add with Subfolders...**' button, and select your GRETNA path, i.e. '`D:\...\GRETNA`'.



All changes take effect immediately.

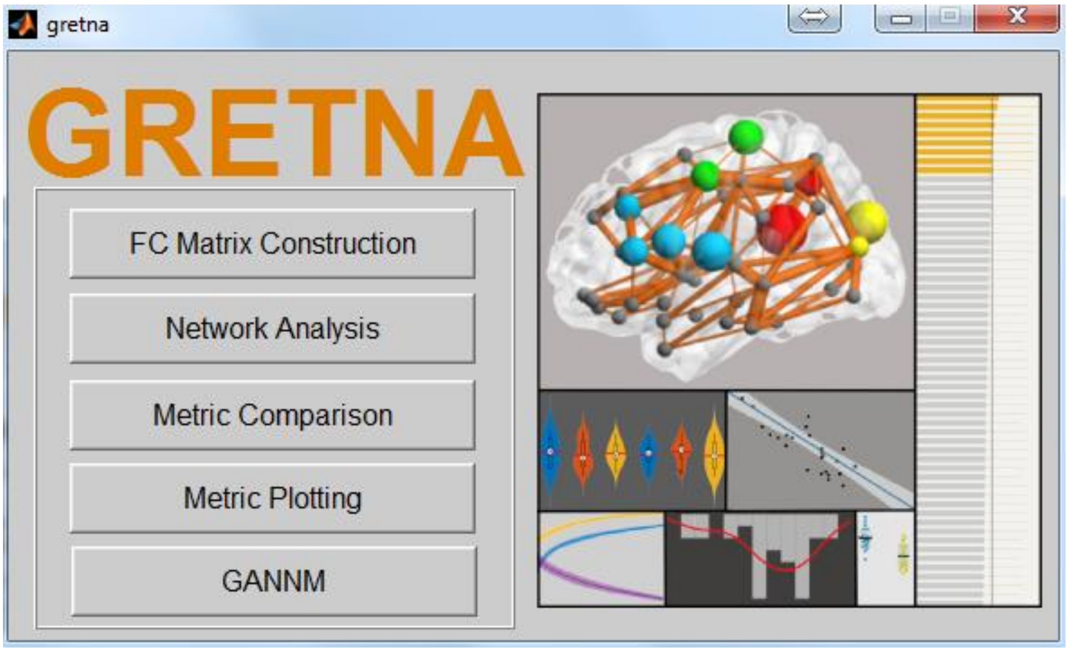
```
/home/sandy/sandy_work/GRETNA/psom-1.0.2
/home/sandy/sandy_work/GRETNA/NetFunctions
/home/sandy/sandy_work/GRETNA/PipeScript
/home/sandy/sandy_work/GRETNA/GUI
/home/sandy/sandy_work/matlab_bgl
/home/sandy/sandy_work/matlab_bgl/custom
/home/sandy/sandy_work/matlab_bgl/graphs
/home/sandy/sandy_work/matlab_bgl/libmbgl
/home/sandy/sandy_work/matlab_bgl/libmbgl/include
/home/sandy/sandy_work/matlab_bgl/libmbgl/libmbgl_test
/home/sandy/sandy_work/matlab_bgl/libmbgl/yasmic
/home/sandy/sandy_work/matlab_bgl/libmbgl/yasmic/boost_mod
/home/sandy/sandy_work/matlab_bgl/libmbgl/yasmic/util
/home/sandy/sandy_work/BrainNetViewer
/home/sandy/sandy_work/BrainNetViewer/BrainNet_spm8_files
/home/sandy/sandy_work/BrainNetViewer/Data
/home/sandy/sandy_work/BrainNetViewer/Data/ExampleFiles
```

Click '**Save**' to save your change. If you do not have permission to save your changes on your computer (e.g., on the server), please save pathdef.m to another location where you will often launch MATLAB.

Warning: Please make sure your GRETNA path DOES NOT include blank or special character!

Type 'gretna' to start analyzing on your data! Be sure to type in **lowercase** characters.

```
>>gretna
```



In this version, GRETNA is divided into five sections:

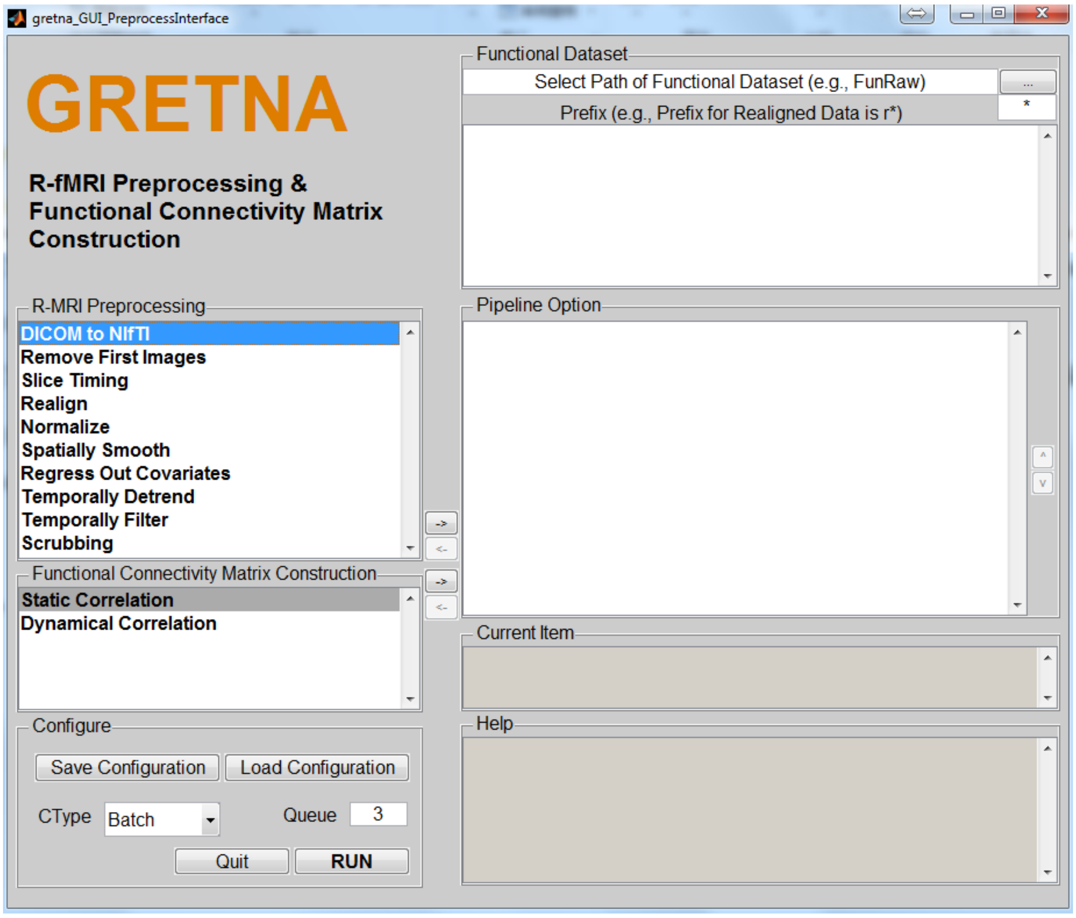
- **FC Matrix Construction:** This section allows researchers to 1) perform R-fMRI data preprocessing, including volume removal, slice timing, realignment, spatial normalization, spatial smoothing, detrend, temporal filtering and removal of confounding variables by regression; and 2) construct static or dynamic region of interest (ROI)-based functional connectivity matrices.
- **Network Analysis:** This section allows researchers to 1) convert individual connectivity matrices into a series of sparse networks according to the pre-assigned parameters of the network type (binary or weighted), network connectivity member (absolute, positive or negative), threshold type (connectivity strength or sparsity), and threshold range; 2) generate benchmark random networks that match real brain networks with respect to the number of nodes and edges and degree distribution; and 3) calculate graph-based global and nodal network metrics.
- **Metric comparison:** This section allows researchers to 1) perform statistical inferencing on global, nodal and connectional network parameters; 2) estimate network-behavior relationships; and 3) generate group-level network.
- **Metric plotting:** This section allows researchers to plot bar charts, dot graphs, violin graphs and shape graphs of the results obtained from metric comparison.

- **GANNM:** This section allows researchers to perform nonparametric statistical inferencing on structural network using permutations.

5. Network Construction

5.1. R-fMRI Preprocessing

In this section, GRETNA allows researchers to perform several commonly used preprocessing steps on R-fMRI data and then construct large-scale brain networks by calculating the pairwise functional connectivity among a set of ROIs according to a brain parcellation scheme. Notably, researchers can arbitrarily designate the order of preprocessing steps (except for **Regress Out Covariates**, which extract time series based on an image mask in MNI space and thus must be executed after Normalization).

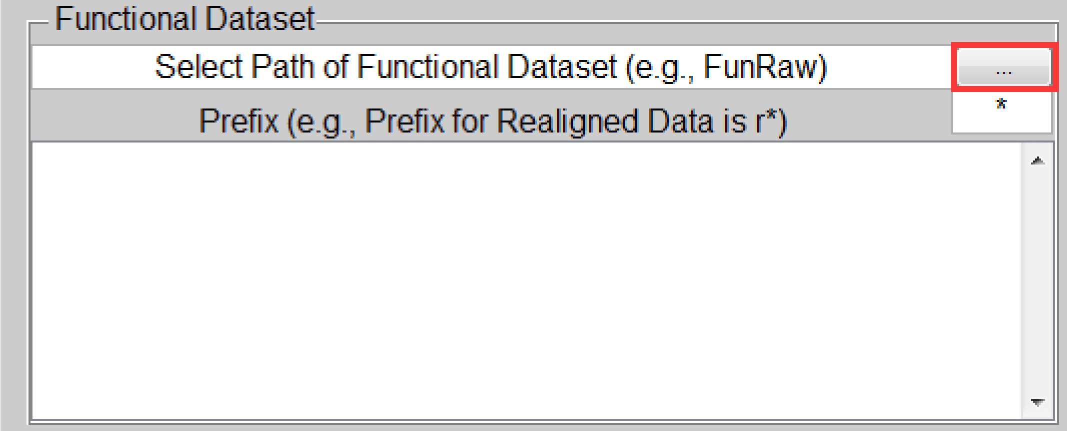


CType Batch

Queue 3

Prefix: *

First, **click the button '…'** next to the 'Select Path of Functional Dataset' in the top-right corner of this panel to select the directory where you store all subjects to input your image data.

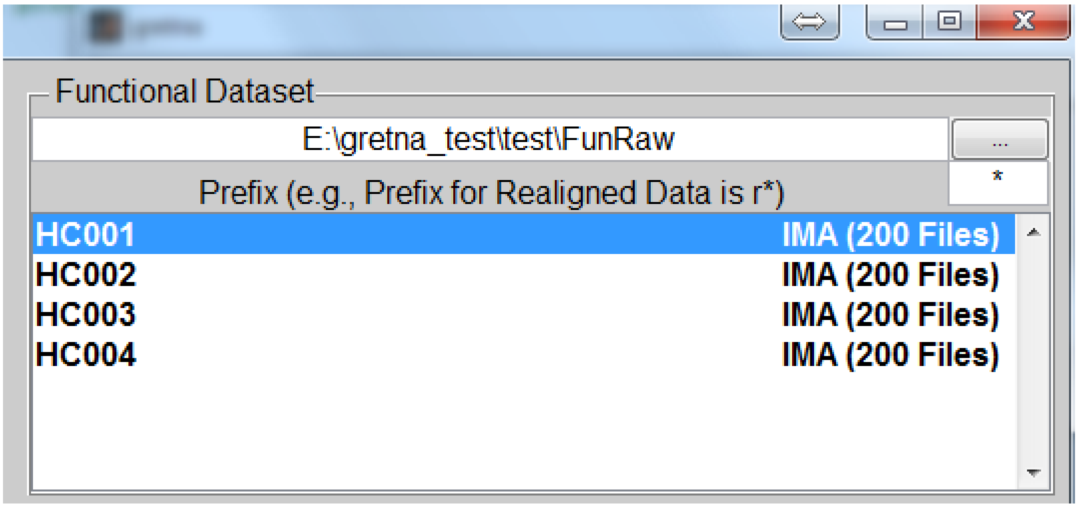


GRETNA supports fMRI sequences with raw DICOM data from scanners or in 3D/4D NIFTI-1 format. The fMRI data should be stored according to the three following rules:

1) The sub-folders of subjects for DICOM data.

2) The sub-folders of subjects for 3D NIFTI-1 files.

3) The sub-folders of subjects for 4D NIFTI-1 files.

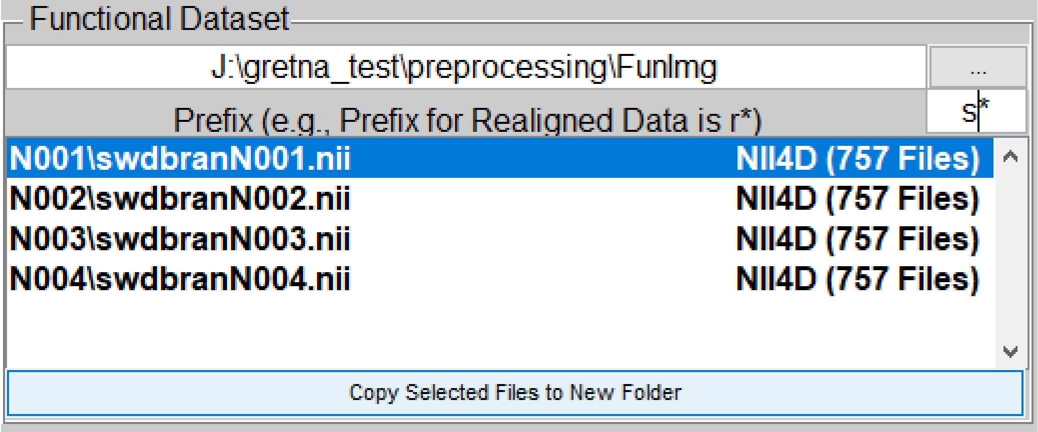


E:\gretna_test\test\FunRaw

*

HC001	IMA (200 Files)
HC002	IMA (200 Files)
HC003	IMA (200 Files)
HC004	IMA (200 Files)

If the folder you store the image data includes other unrelated data, you can use **Prefix** to filter out other data. For example, if you already realigned the data using SPM and the realigned data and raw data are now in the same folder, you can input '**r***' to filter out raw data.



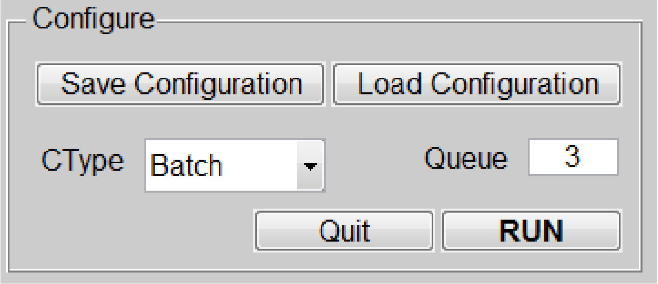
J:\gretna_test\preprocessing\FunImg

Prefix (e.g., Prefix for Realigned Data is r*) s*

N001\swdbranN001.nii	NII4D (757 Files)
N002\swdbranN002.nii	NII4D (757 Files)
N003\swdbranN003.nii	NII4D (757 Files)
N004\swdbranN004.nii	NII4D (757 Files)

Also, you can use **'Copy Selected Files to New Folder'** to save the preprocessed data to a new folder.

After choosing the preprocessing steps, you can save the configuration. Then, you can load the saved configuration when you want to run the same steps next time. **CType** refers to the method for working in parallel and **Queue** is the number of cores in the computer you are operating. Selecting **Session** allows you to execute processes in current MATLAB session, selecting **Batch** creates several MATLAB subprocesses to run the processing task, and selecting **SGE** allows you to submit GRETNA processes to cluster.



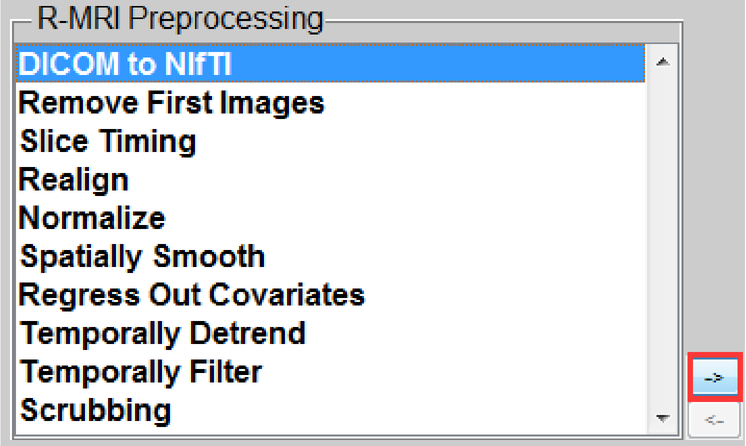
CType Batch

Queue 3

5.1.1. DICOM to NIfTI

Before formal data preprocessing, the DICOM data, a format output by most MRI scanners, is typically transformed into other formats, e.g., NIfTI format. Compared with the previous analyze file format, the NIfTI format contains new and important features, such as affine coordinate definitions that relate a voxel index to a spatial location, indicators of the spatial normalization type and records of the spatio-temporal slice ordering. This conversion is achieved in GRETNA by calling dcm2nii in the MRIcroN software (http://www.mccauslandcenter.sc.edu/mricro/mricron/).

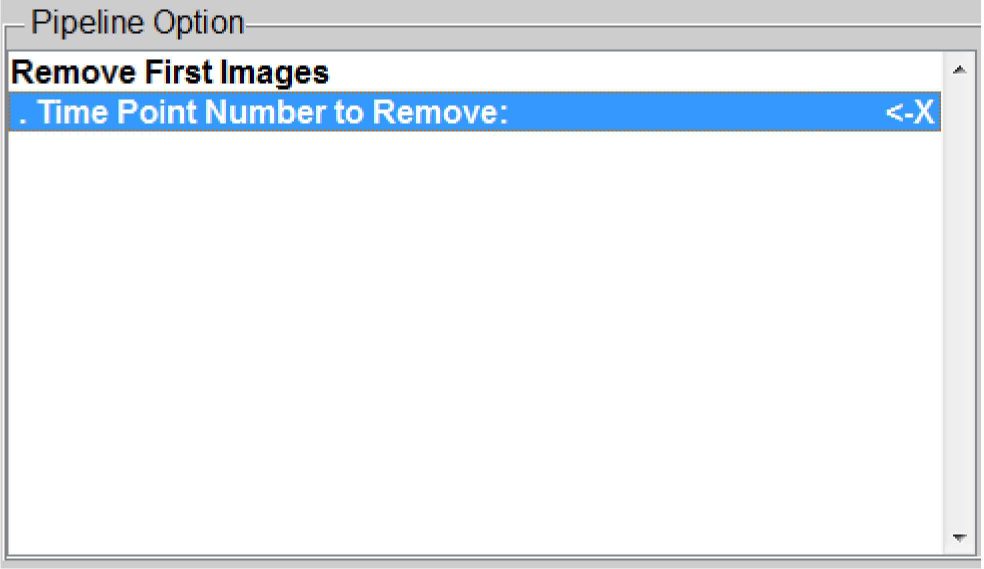
Select the item **'DICOM to NIfTI'** with a mouse click, and click **'->'** in the middle of this panel to select this item (move it into Pipeline Option on the right).



5.1.2. Remove First Images

The first several volumes of individual functional images are often discarded for magnetization equilibrium. GRETNA allows researchers to delete the first several volumes by specifying the number of volumes to be deleted.

Select the item 'Time Point Number to Remove' with a mouse click. Then, press the **Spacebar** or **Enter** on your keyboard, or **double-click** to input the number of time points to remove (e.g., 5 or 10).



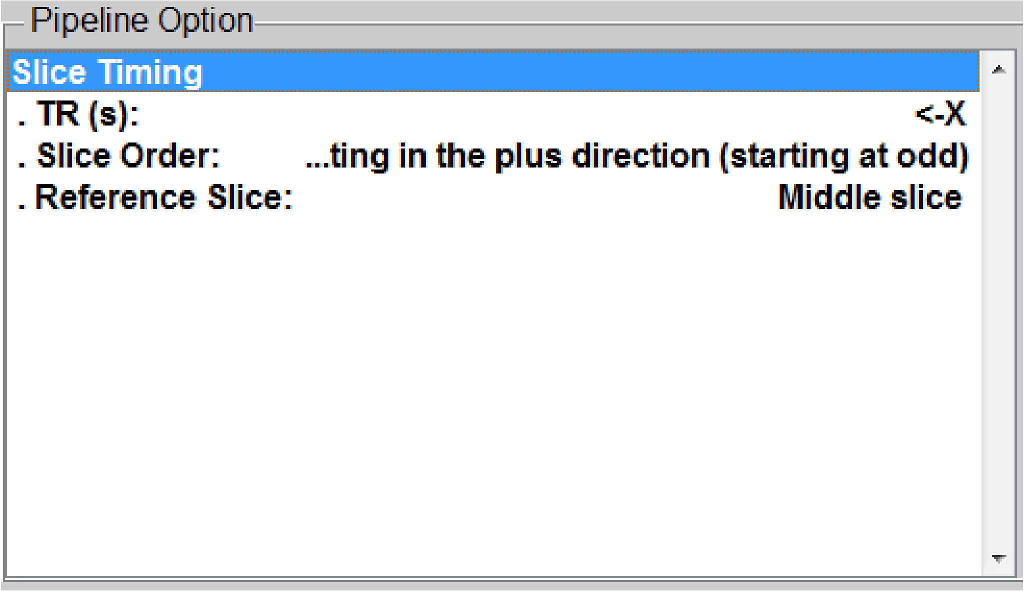
Pipeline Option

Remove First Images

. Time Point Number to Remove: <-X

5.1.3. Slice Timing

R-fMRI datasets are usually acquired using repeated 2D imaging methods, which leads to temporal offsets between slices. Slice timing correction is performed in GRETNA by calling the corresponding SPM8/SPM12 functions. It should be noted that, for a longer repeat time (e.g., > 3 s), within which a whole brain volume is acquired, it is advised to omit the slice time correction step because interpolation in this case becomes less accurate.



Pipeline Option

Slice Timing

. TR (s): <-X

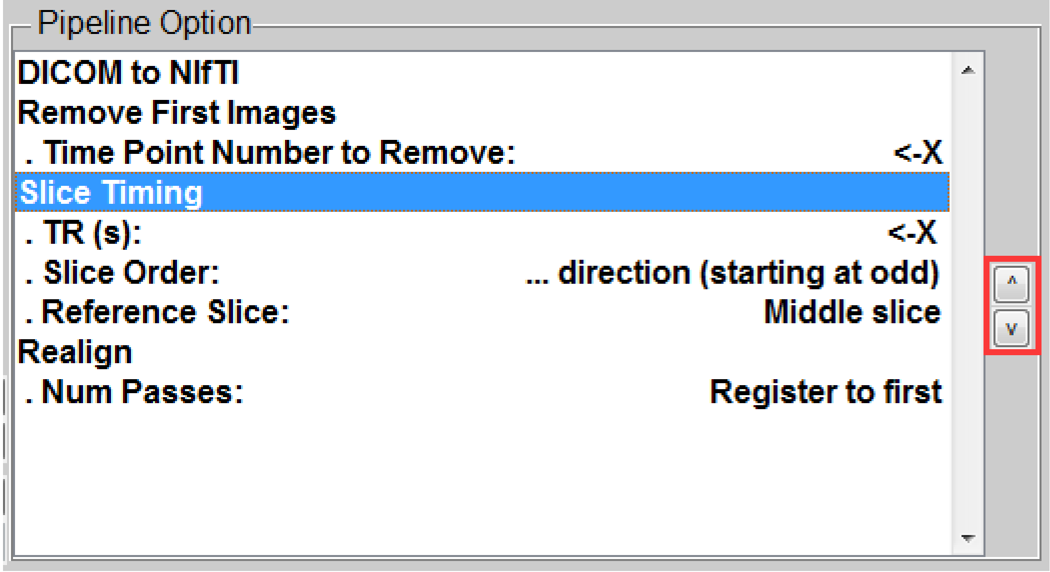
. Slice Order: ...ting in the plus direction (starting at odd)

. Reference Slice: Middle slice

Set the following parameters according to your data.

- **TR (s)**: The time of repeat of an fMRI signal.
- **Slice Order**: The sequence of slices. We have provided six different options: alternating in the plus direction starting with odd-numbered slices (i.e., 1 3 5...2 4 6…), alternating in the plus direction starting with even-numbered slices (i.e., 2 4 6…1 3 5), alternating in the minus direction starting with odd-numbered slices (i.e., 33 31 29...32 30 28…), alternating in the plus direction starting with even-numbered slices (i.e., 32 30 28…33 31 29…), running sequentially in the plus direction (i.e., 1 2 3…31 32 33), and running sequentially in the minus direction (i.e., 33 32 31…3 2 1).
- **Reference Slice**: The slice used as a reference to perform the timing correction. You can choose the first slice, middle slice (middle of time), or last slice as a reference. The default option is middle slice.

When you add several preprocessing steps into the pipeline option, you can use the buttons located on the right to adjust the sequence of the preprocessing steps for fMRI data.



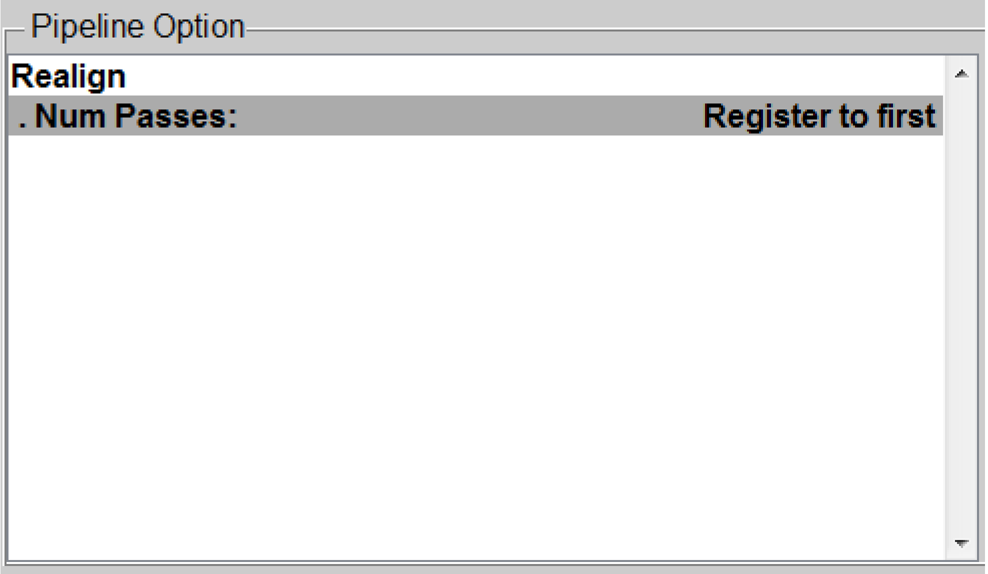
Pipeline Option

DICOM to NIfTI
Remove First Images
. Time Point Number to Remove: <-X
Slice Timing
. TR (s): <-X
. Slice Order: ... direction (starting at odd)
. Reference Slice: Middle slice
Realign
. Num Passes: Register to first

5.1.4. Realign

During an MR scan, participants inevitably undergo various degrees of head movement, even when foam pads are used. The movements break the spatial correspondence of the brain across volumes.

This step realigns individual images such that each part of the brain in every volume is in the same position. This procedure is performed in GRETNA by calling relevant SPM8/SPM12 functions.



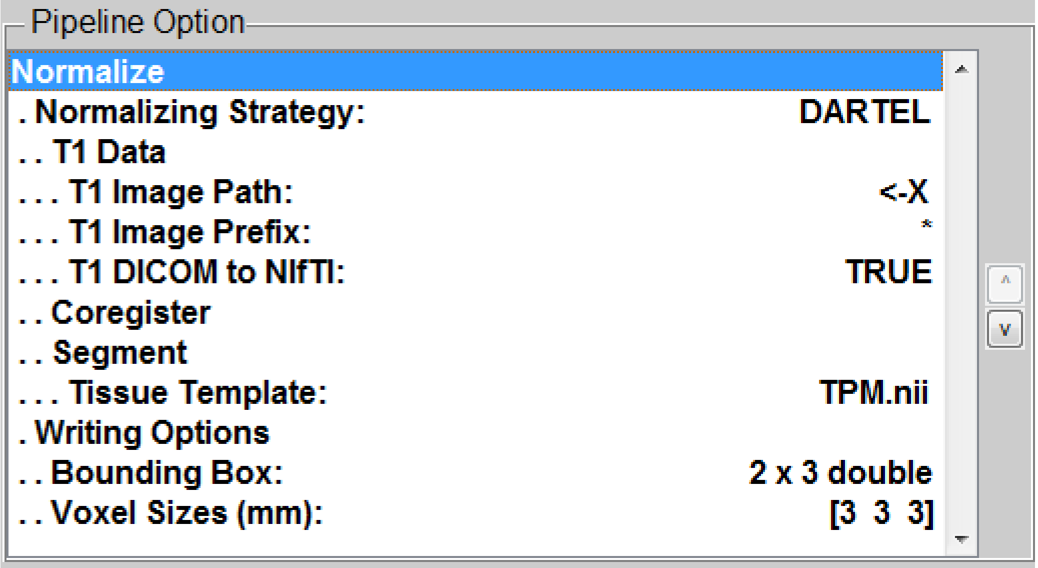
Realign

. Num Passes: Register to first

Set the volume as a reference to register. You can choose to register to the first volume (default) or mean volume (register to the first volume first and then register all volumes to averaged volumes). After completing this process, you can check subjects' head motion parameter in the 'GretnaLogs/HeadMotion' folder.

5.1.5. Normalize

For group average and group comparison, individual data are usually transformed into a standardized space to account for the variability in brain size, shape and anatomy. This transformation can be performed in GRETNA using three methods based on the SPM8/SPM12 functions: 1) directly warping individual functional images to the standard MNI space by estimating their transformation to the echo-planar imaging (EPI) template; 2) warping individual functional images to the standard MNI space by applying the transformation matrix that can be derived by registering the T1 image (co-registered with functional images) into the MNI template by using unified segmentation; and 3) warping individual functional images to the standard MNI space by applying the transformation matrix that can be derived from registering the final Template file generated by DARTEL. Please see the SPM8 reference manual for more details about DARTEL.



Pipeline Option

Normalize

. Normalizing Strategy: DARTEL

. . T1 Data

. . . T1 Image Path: <-X

. . . T1 Image Prefix: *

. . . T1 DICOM to NIfTI: TRUE

. . Coregister

. . Segment

. . . Tissue Template: TPM.nii

. Writing Options

. . Bounding Box: 2 x 3 double

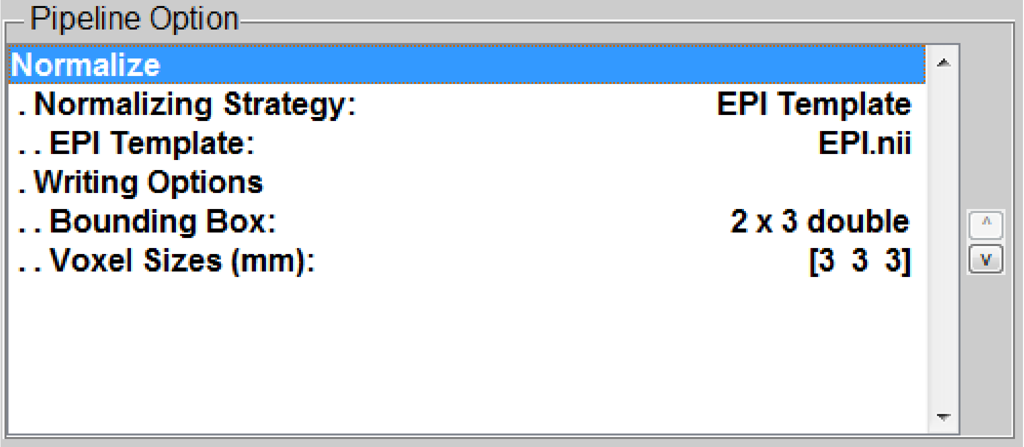
. . Voxel Sizes (mm): [3 3 3]

Set the following parameters according to your data.

- **Normalizing Strategy**: The method of normalization. There are three options, EPI template, T1 unified segmentation and DARTEL.

5.1.5.1. EPI template

- **EPI template:** The target template that is going to warp to match.
- **Bounding Box**: The bounding box (in mm) of the volume that is to be written.
- **Voxel Sizes (mm)**: The voxel size of the written normalized images.



Pipeline Option

Normalize

. Normalizing Strategy: EPI Template

. . EPI Template: EPI.nii

. Writing Options

. . Bounding Box: 2 x 3 double

. . Voxel Sizes (mm): [3 3 3]

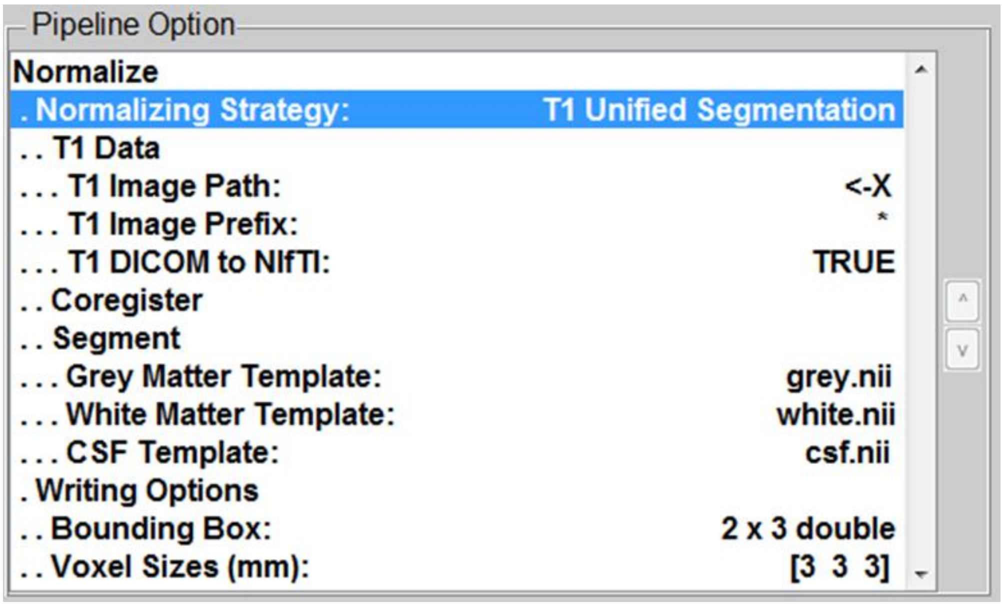
5.1.5.2. T1 unified segmentation

- **T1 Image Path:** The subjects' T1 image directory.
- **T1 Image Prefix:** The prefix of T1 image.
- **DICOM to NIFTI:** Execute DICOM to NIFTI transformation or not.
- **Coregister:** Execute the within-subject coregistration of T1 image to mean functional image.
- **Segment:**

  Grey Matter Template: A prior tissue probability map of grey matter.

  White Matter Template: A prior tissue probability map of white matter.

  CSF Template: A prior tissue probability map of cerebrospinal fluid.
- **Bounding Box**: The bounding box (in mm) of the volume that is to be written.
- **Voxel Sizes (mm)**: The voxel size of the written normalized images.



Normalize	
. Normalizing Strategy:	T1 Unified Segmentation
. . T1 Data	
. . . T1 Image Path:	<-X
. . . T1 Image Prefix:	*
. . . T1 DICOM to NIfTI:	TRUE
. . Coregister	
. . Segment	
. . . Grey Matter Template:	grey.nii
. . . White Matter Template:	white.nii
. . . CSF Template:	csf.nii
. Writing Options	
. . Bounding Box:	2 x 3 double
. . Voxel Sizes (mm):	[3 3 3]

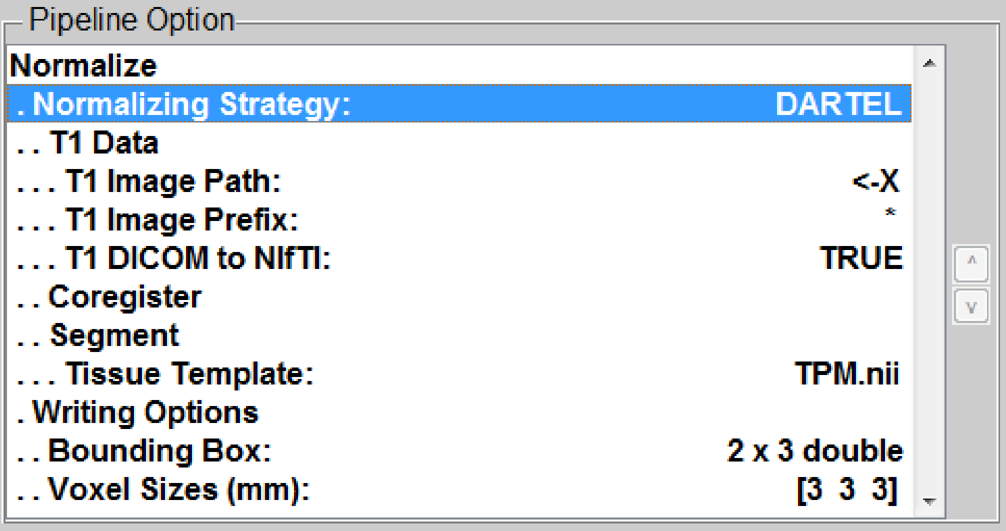
5.1.5.3. DARTEL

- **T1 Image Path:** The subjects' T1 image directory.
- **T1 Image Prefix:** The prefix of T1 image.
- **DICOM to NIFTI:** Execute DICOM to NIFTI transformation or not.
- **Coregister:** Execute the within-subject coregistration of T1 image to mean functional image.

- **Segment:**

  TPM: Tissue probability map for grey matter, white matter, CSF, bone, soft tissue and air/background

- **Bounding Box**: The bounding box (in mm) of the volume that is to be written.
- **Voxel Sizes (mm)**: The voxel size of the written normalized images.

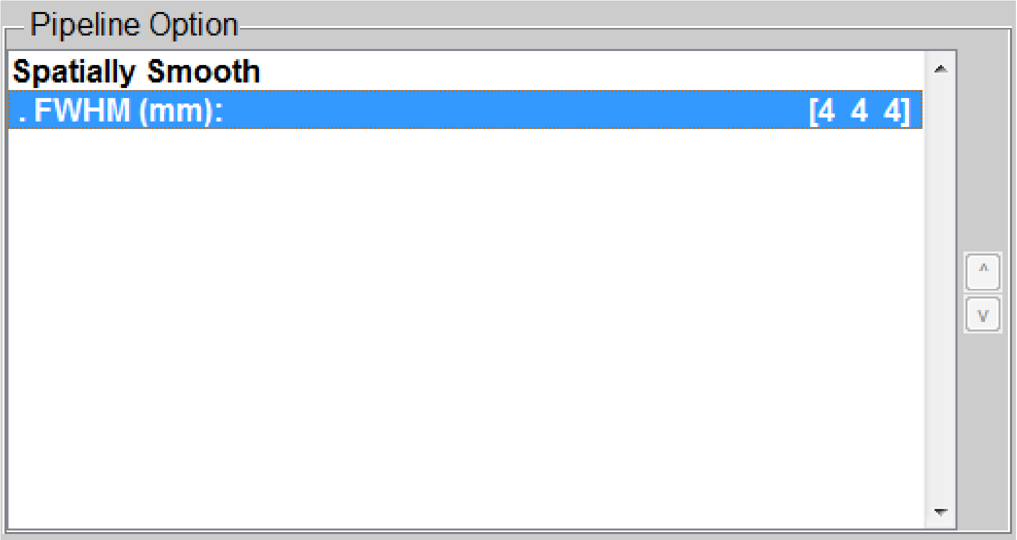


```
Normalize
. Normalizing Strategy:                DARTEL
. . T1 Data
. . . T1 Image Path:                   <-X
. . . T1 Image Prefix:                 *
. . . T1 DICOM to NIfTI:               TRUE
. . Coregister
. . Segment
. . . Tissue Template:                 TPM.nii
. Writing Options
. . Bounding Box:                      2 x 3 double
. . Voxel Sizes (mm):                  [3  3  3]
```

5.1.6. Spatially Smooth

Smoothing, a common preprocessing step performed after spatial normalization, is used to improve the signal-to-noise ratio and attenuate anatomical variances caused by inaccurate inter-subject registration. GRETNA performs spatial smoothing using a Gaussian filter with a shape that can be determined by a 3-value vector of full width at half maximum (FWHM) as implemented in SPM8.

Double-click to set FWHM (mm).



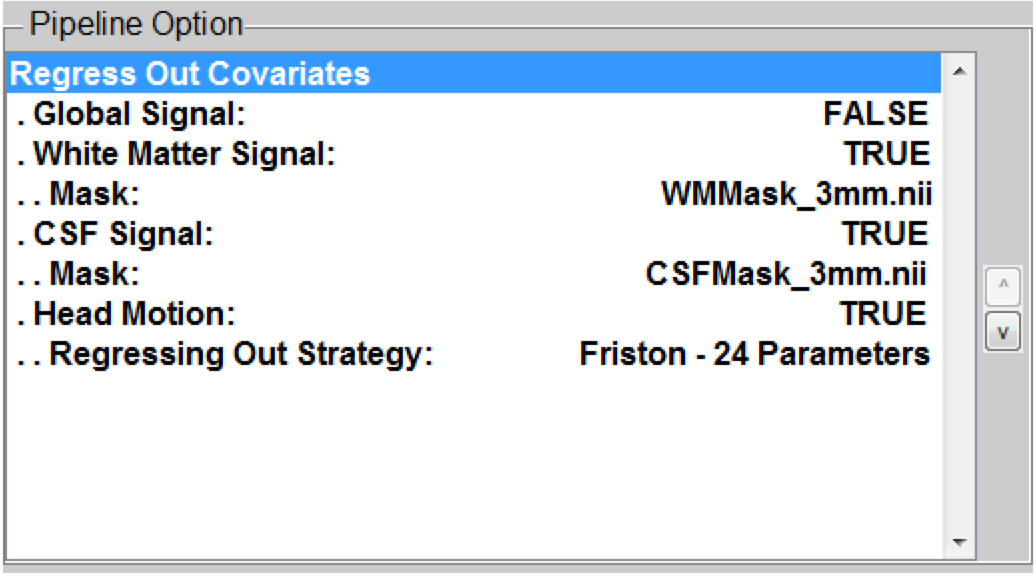
Spatially Smooth

. FWHM (mm): [4 4 4]

5.1.7. Regress Out Covariates

For R-fMRI datasets, several nuisance signals are typically removed from each voxel's time series to reduce the effects of non-neuronal fluctuations, including head motion profiles, the cerebrospinal fluid signal, the white matter signals and/or the global signal. In GRETNA, researchers can assign any combination of these variables to be variables of no interest, which will be regressed out. The global signal, CSF signal and white matter signal are calculated by using the whole brain, cerebral spinal fluid and WM masks in the standard MNI space from the REST toolbox (default). Set the following parameters according to your research purposes.

- **Global Signal:** Regress out global signal or not. You can also change the mask of the whole brain if necessary.
- **White Matter Signal:** Regress out white matter signal or not. You can also change the mask of the white matter if necessary.
- **CSF Signal:** Regress out cerebrospinal fluid signal or not. You can also change the mask of cerebrospinal fluid if necessary.
- **Head Motion:** Regress out head motion parameters or not. Options include the original 6 parameters, the original and relative 12-parameters and the Friston 24 parameters.



Regress Out Covariates

. Global Signal: FALSE

. White Matter Signal: TRUE

. . Mask: WMMask_3mm.nii

. CSF Signal: TRUE

. . Mask: CSFMask_3mm.nii

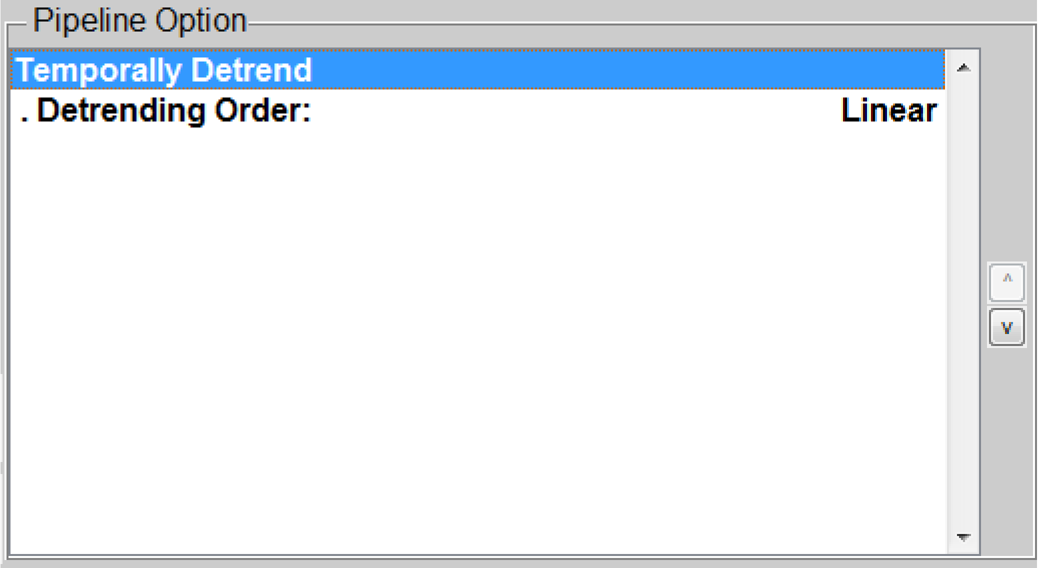
. Head Motion: TRUE

. . Regressing Out Strategy: Friston - 24 Parameters

5.1.8. Temporally Detrend

FMRI datasets may suffer from a systematic increase or decrease in the signal over time, presumably due to long-term physiological shifts or instrumental instability. GRETNA provides an option to reduce the effects of linear and non-linear drift or trends in the signal based on relevant SPM8 functions.

Double-click to choose the removal of only the linear drift or the removal of both linear and non-linear drift.



Temporally Detrend

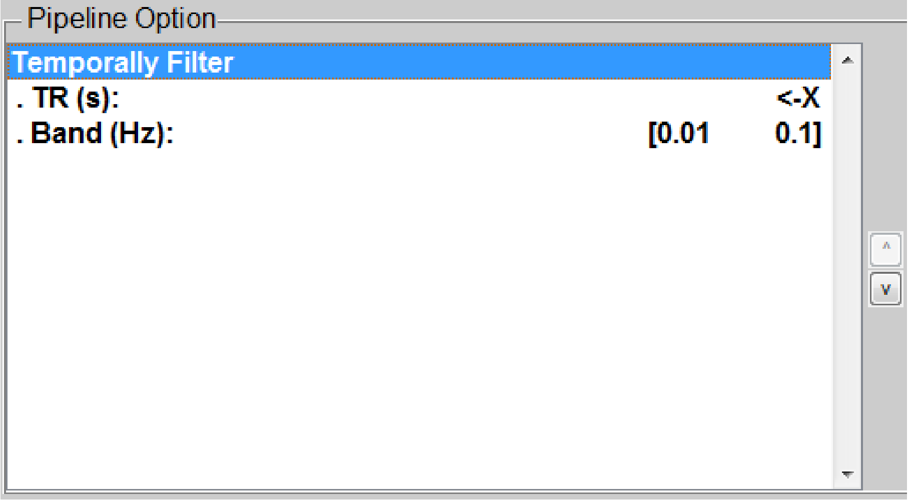
. Detrending Order: Linear

5.1.9. Temporally Filter

R-fMRI data are typically band-pass filtered to reduce the effects of low-frequency drift and high-frequency physiological noises. In GRETNA, we provide an option for researchers to easily choose the frequency ranges over which the data will be filtered with an ideal box filter function. This filtering is performed by converting a time series into a frequency domain using a fast Fourier transform (FFT), retaining the amplitude spectrum for frequency components of interest and setting the amplitude spectrum to 0 for other frequency components, and converting the new amplitude spectrum into a time domain by an inverse FFT.

Set the following parameters according to your data and research purposes.

- **TR (s)**: The time of repeat of an fMRI signal.
- **Band (Hz)**: The frequency band for temporal filtering.



Pipeline Option

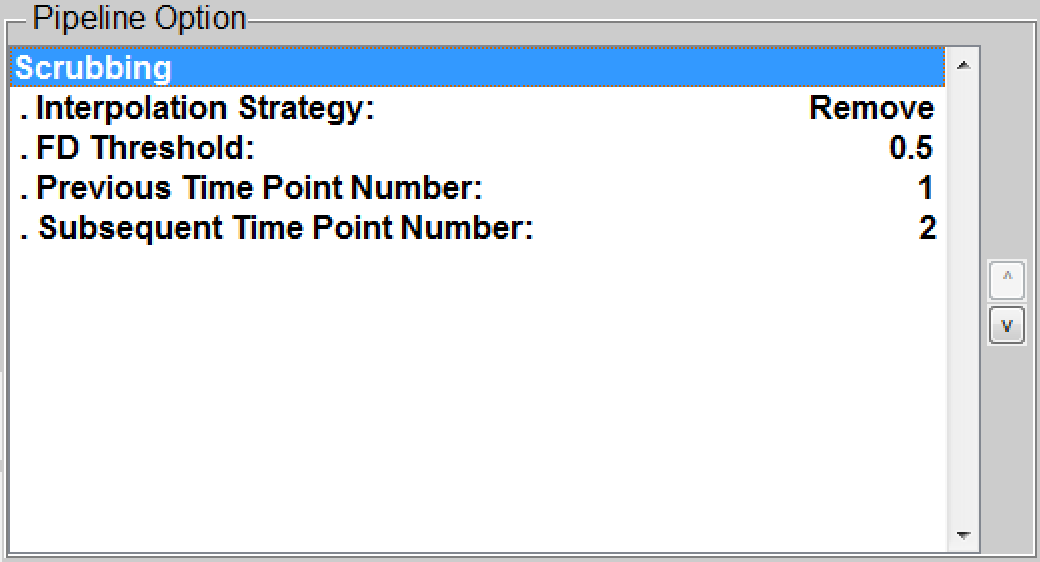
Temporally Filter

. TR (s): <-X

. Band (Hz): [0.01 0.1]

5.1.10. Scrubbing

Scrubbing is a quality control process used to reduce the effects of head motion on R-fMRI data. This process uses realignment parameters to identify frames that may be of poor quality and take apply a certain strategy to these frames (e.g., remove or interpolate).



Pipeline Option

Scrubbing

. Interpolation Strategy: Remove

. FD Threshold: 0.5

. Previous Time Point Number: 1

. Subsequent Time Point Number: 2

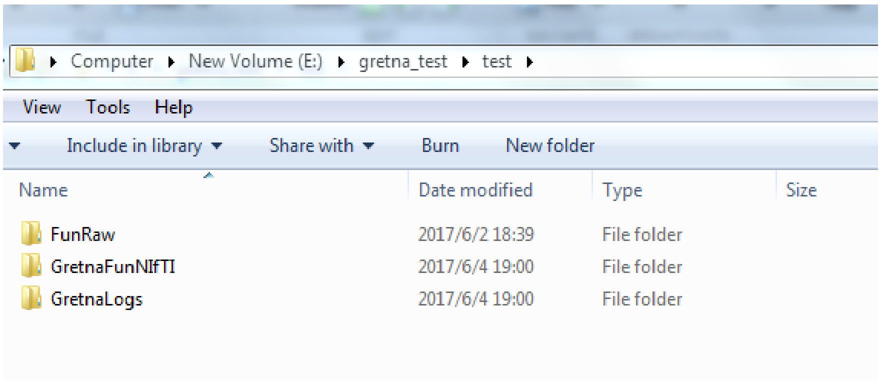
Set the following parameters.

- **Interpolation Strategy:** The strategy adopted to process frames of poor quality. You can choose to remove these flames or replace these flames with the nearest or linear interpolation.
- **FD Threshold:** The threshold of frame-wise displacement (FD) above which the frame would be considered to be of with poor quality.

- **Previous Time Point Number:** The number of time point before the frames of poor quality that would be removed or replaced.
- **Subsequent Time Point Number:** The number of time point after the frames of poor quality that would be removed or replaced.

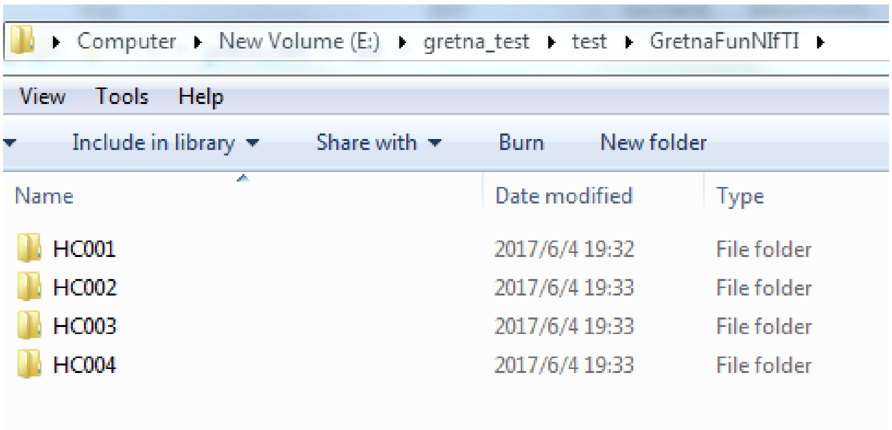
5.1.11. Results of R-fMRI Preprocessing

After completing all preprocessing steps, two folders are generated: **GretnaFunNIfTI** and **GretnaLogs**.



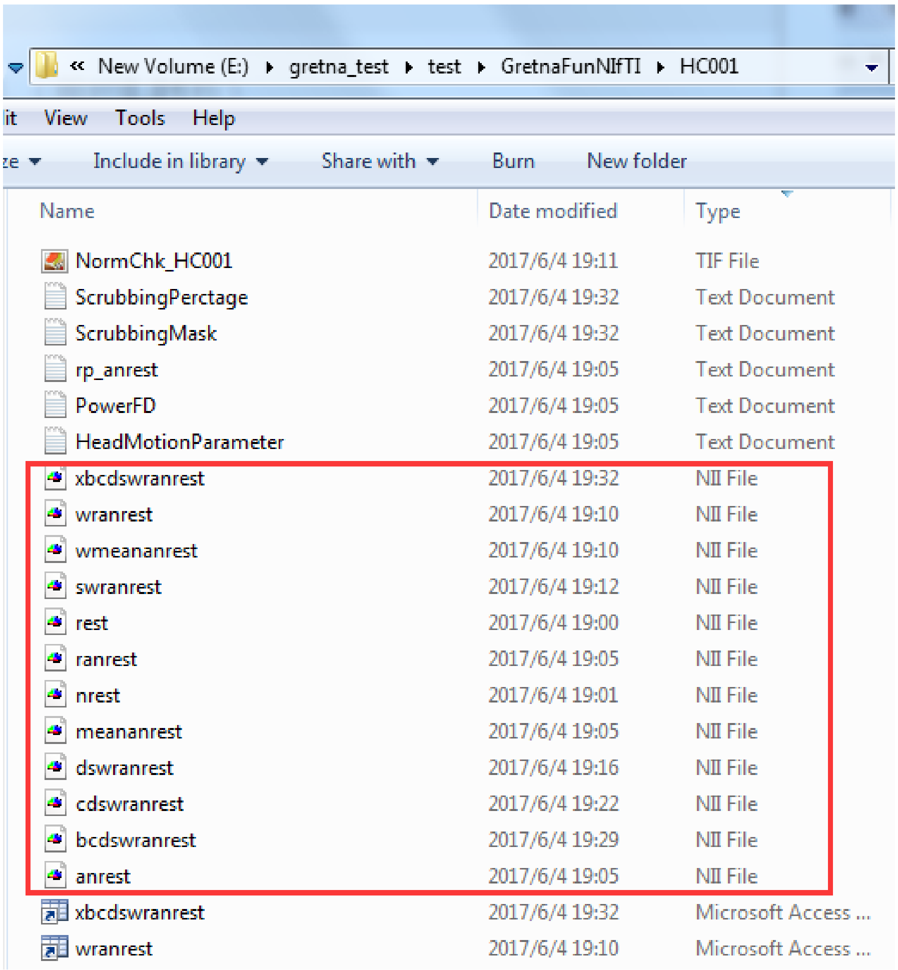
Name	Date modified	Type	Size
FunRaw	2017/6/2 18:39	File folder	
GretnaFunNIfTI	2017/6/4 19:00	File folder	
GretnaLogs	2017/6/4 19:00	File folder	

GretnaFunNIfTI stores the preprocessed files in terms of Subjects ID.



Name	Date modified	Type
HC001	2017/6/4 19:32	File folder
HC002	2017/6/4 19:33	File folder
HC003	2017/6/4 19:33	File folder
HC004	2017/6/4 19:33	File folder

The preprocessed imaging files are stored in the Subject folder:



Name	Date modified	Type
NormChk_HC001	2017/6/4 19:11	TIF File
ScrubbingPerctage	2017/6/4 19:32	Text Document
ScrubbingMask	2017/6/4 19:32	Text Document
rp_anrest	2017/6/4 19:05	Text Document
PowerFD	2017/6/4 19:05	Text Document
HeadMotionParameter	2017/6/4 19:05	Text Document
xbcdswranrest	2017/6/4 19:32	NII File
wranrest	2017/6/4 19:10	NII File
wmeananrest	2017/6/4 19:10	NII File
swranrest	2017/6/4 19:12	NII File
rest	2017/6/4 19:00	NII File
ranrest	2017/6/4 19:05	NII File
nrest	2017/6/4 19:01	NII File
meananrest	2017/6/4 19:05	NII File
dswranrest	2017/6/4 19:16	NII File
cdswranrest	2017/6/4 19:22	NII File
bcdswranrest	2017/6/4 19:29	NII File
anrest	2017/6/4 19:05	NII File
xbcdswranrest	2017/6/4 19:32	Microsoft Access ...
wranrest	2017/6/4 19:10	Microsoft Access ...

The filename prefix indicates specific preprocesses:

n: remove first images

a: slice timing

r: realign

w: normalize

s: smooth

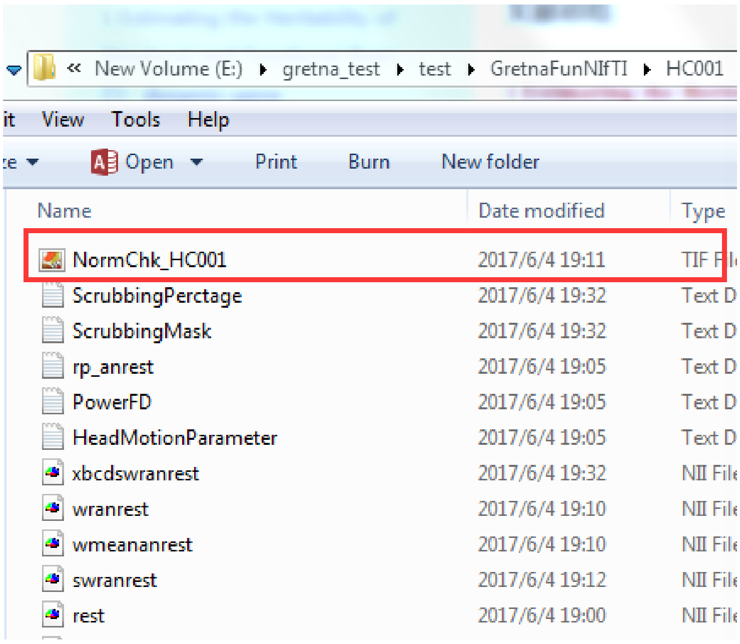
d: detrend

c: regressed out covariates

b: temporally filter

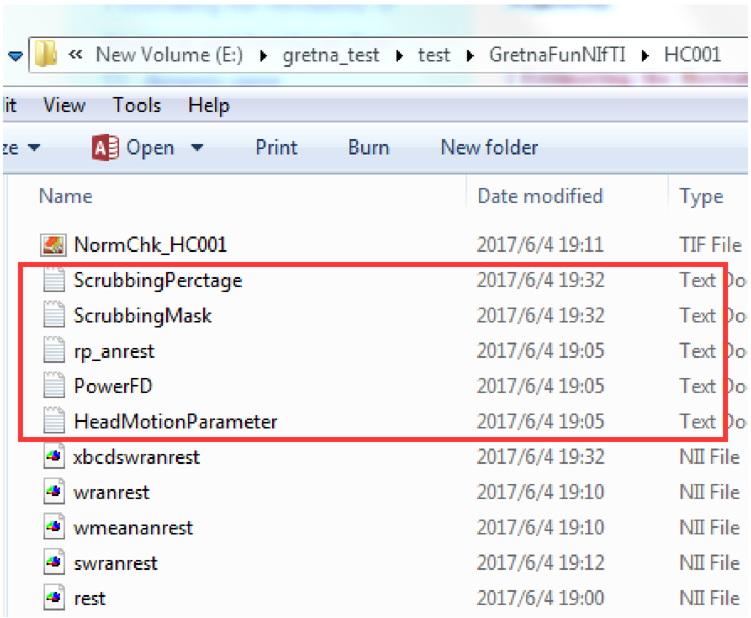
x: scrubbing

rest.nii is the image file obateined after the DICOM to NIfTI transformation. For example, **xbcdswranrest.nii** is the final image file obtained after the DICOM to NIfTI transformation, first images removal, slice timing, realigning, normalization, smoothing, detrending, covariates regression, filtering and scrubbing. **meananrest.nii** and **wmeananrest.nii** are the mean image files across time points before and after normalization to the standard MNI space.



Name	Date modified	Type
NormChk_HC001	2017/6/4 19:11	TIF Fi
ScrubbingPerctage	2017/6/4 19:32	Text D
ScrubbingMask	2017/6/4 19:32	Text D
rp_anrest	2017/6/4 19:05	Text D
PowerFD	2017/6/4 19:05	Text D
HeadMotionParameter	2017/6/4 19:05	Text D
xbcdswranrest	2017/6/4 19:32	NII File
wranrest	2017/6/4 19:10	NII File
wmeananrest	2017/6/4 19:10	NII File
swranrest	2017/6/4 19:12	NII File
rest	2017/6/4 19:00	NII File

NormChk_HC001.tif allows for the quality of Normalization to be visually inspected. To check the quality of Normalization of all subject images, a folder named **NormalizationInfo** in **GretnaLogs** includes Normalization check images for all subjects.

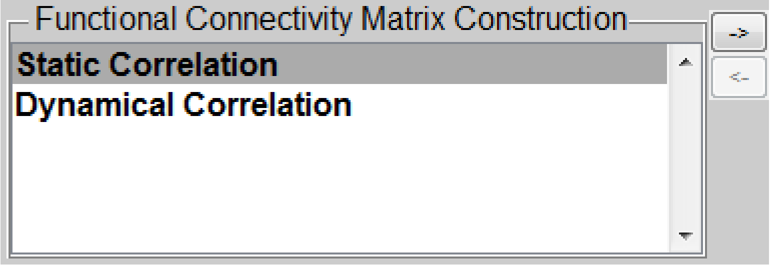


Name	Date modified	Type
NormChk_HC001	2017/6/4 19:11	TIF File
ScrubbingPerctage	2017/6/4 19:32	Text Do
ScrubbingMask	2017/6/4 19:32	Text Do
rp_anrest	2017/6/4 19:05	Text Do
PowerFD	2017/6/4 19:05	Text Do
HeadMotionParameter	2017/6/4 19:05	Text Do
xbcdswranrest	2017/6/4 19:32	NII File
wranrest	2017/6/4 19:10	NII File
wmeananrest	2017/6/4 19:10	NII File
swranrest	2017/6/4 19:12	NII File
rest	2017/6/4 19:00	NII File

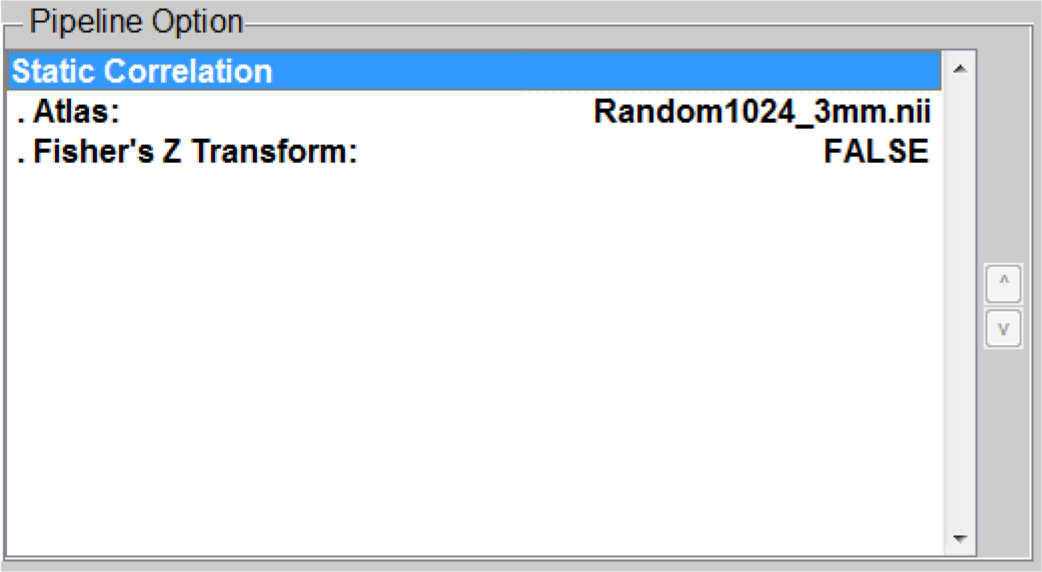
In addition, several head motion parameter files are also generated in this folder. **HeadMotionParameter.txt** stores six head motion parameters, including three translations and three rotations parameters. The Power flame-wise distance (FD) for each time point is also calculated in **PowerFD.txt**. The percentage of flames above a given threshold (e.g. FD>0.05) in scrubbing is calculated in **ScrubbingPerctage.txt**. PowerFD files for all subjects can be found in folder '…\ `GretnaLogs\HeadMotionInfo\PowerFD`'.

5.2. Functional Connectivity Matrix Construction

This option is used to construct individual interregional functional connectivity matrices in two major steps: region parcellation (i.e., network node definition) and functional connectivity estimation (i.e., network edge definition). GRETNA provides options for several different parcellation schemes, including the structurally defined Anatomical Automatic Labeling atlas (AAL-90, AAL116) and Harvard-Oxford atlas (HOA-112) and the functionally defined Dos-160, Crad-200, Power-264 and Fair-34. Additionally, GRETNA contains parcellation schemes defined by randomly parceling the brain into 625 (random-625) or 1024 (random-1024) ROIs. Once a parcellation scheme is chosen, the mean time series will be extracted from each parcellation unit, and pairwise functional connectivity is then estimated among the time series by calculating linear Pearson correlation coefficients. This procedure will generate an N × N correlation matrix for each participant, where N is the number of regions included in the selected brain parcellation. It should be noted that this section also allows researchers to construct a dynamic correlation matrix based on a sliding time-window approach.



5.2.1. Static Correlation

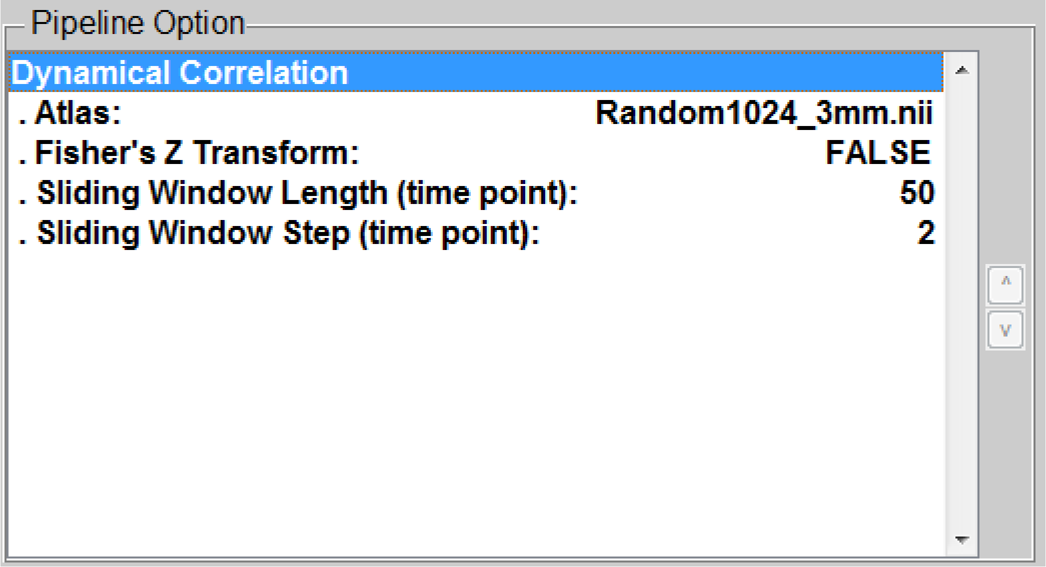


. Atlas: Random1024_3mm.nii
. Fisher's Z Transform: FALSE

Set the following parameters to construct static functional connectivity matrices for each subject in your data.

- **Atlas:** The brain parcellation for network node definition.
- **Fisher's Z Transform**: Perform the Fisher's r-to-z transformation to improve the normality of the correlations or not.

5.2.2. Dynamical Correlation

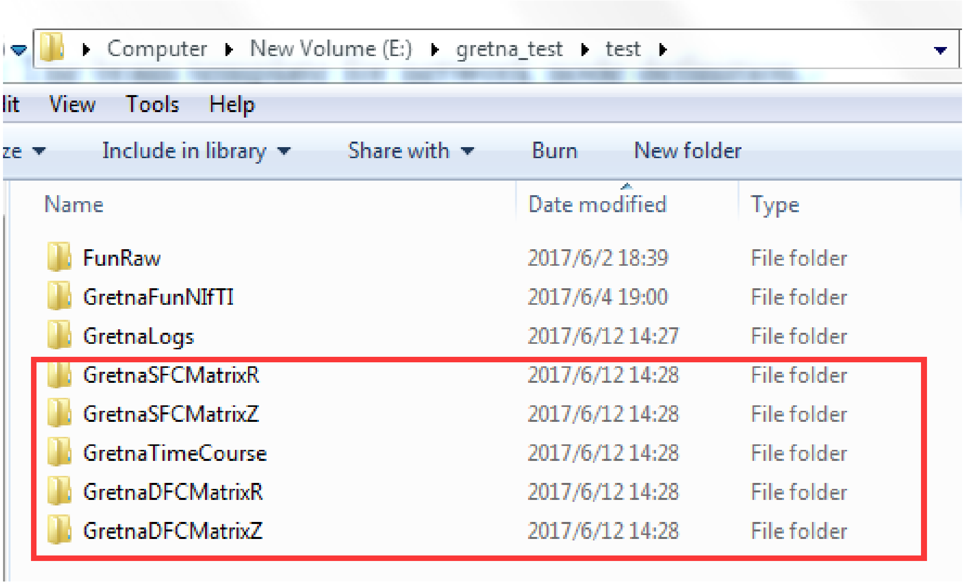


. Atlas: Random1024_3mm.nii
. Fisher's Z Transform: FALSE
. Sliding Window Length (time point): 50
. Sliding Window Step (time point): 2

Set the following parameters to construct time-varying dynamic functional connectivity matrices for each subject in your data.

- **Atlas:** The brain template for network node definition.
- **Fisher's Z Transform**: Perform the Fisher's r-to-z transformation to improve the normality of the correlations or not.
- **Sliding Window Length (time point):** The number of time points included in each window.
- **Sliding Window Step (time point)**: The number of time points for a step in which the time window is shifted forward.

5.2.3. Results of Functional Connectivity Matrix Construction



Name	Date modified	Type
FunRaw	2017/6/2 18:39	File folder
GretnaFunNIfTI	2017/6/4 19:00	File folder
GretnaLogs	2017/6/12 14:27	File folder
GretnaSFCMatrixR	2017/6/12 14:28	File folder
GretnaSFCMatrixZ	2017/6/12 14:28	File folder
GretnaTimeCourse	2017/6/12 14:28	File folder
GretnaDFCMatrixR	2017/6/12 14:28	File folder
GretnaDFCMatrixZ	2017/6/12 14:28	File folder

After constructing functional connectivity matrix, several folders are generated: **GretnaTimeCourse, GretnaSFCMatrixR, GretnaSFCMatrixZ, GretnaDFCMatrixR** and **GretnaDFCMatrixZ**.

GretnaTimeCourse includes the time series of each node based on a given template (the atlas you chose before, e.g. AAL 90) for each subject. Each row indicates one time point and each column indicates one node.

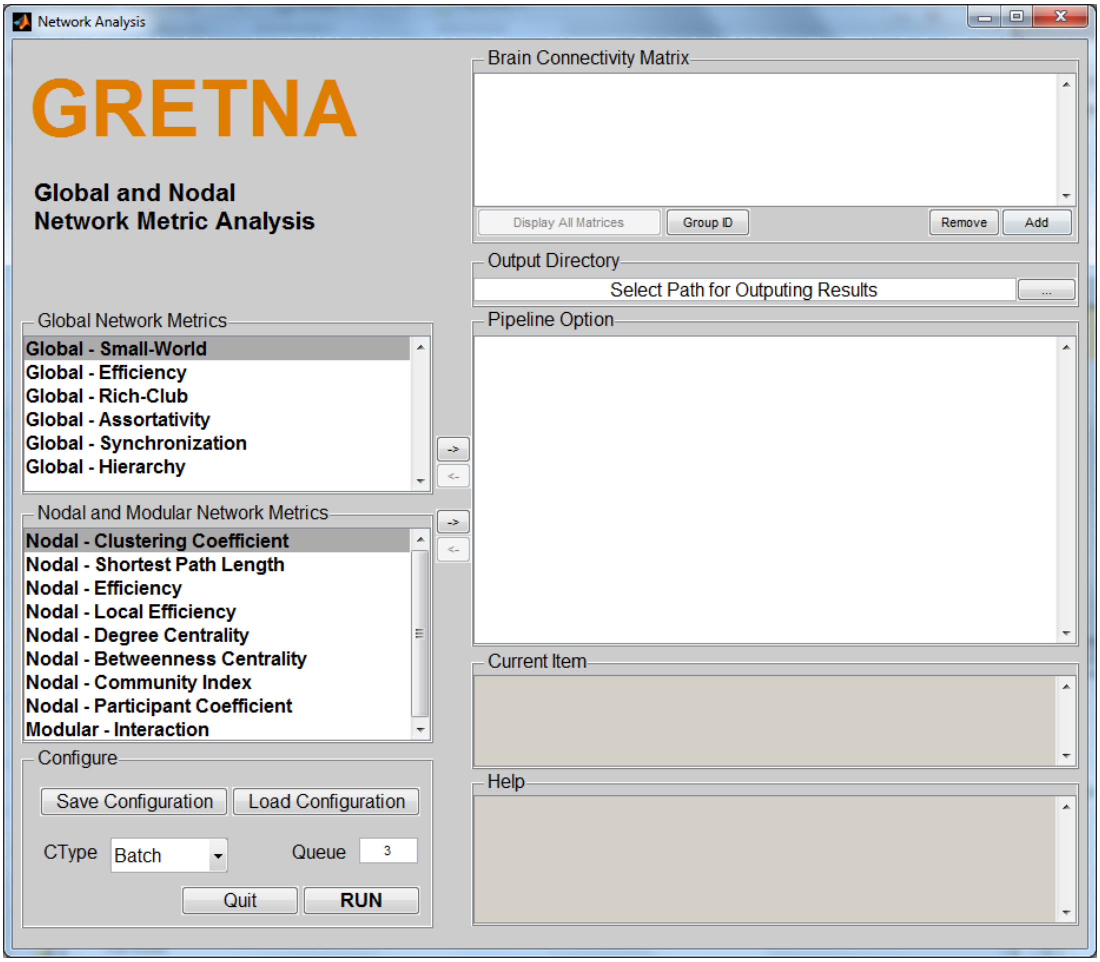
GretnaSFCMatrixR and **GretnaSFCMatrixZ** includes the static functional connectivity matrix (N

× N, N = number of nodes) for all subjects before and after Fisher z transformation.

GretnaDFCMatrixR and **GretnaDFCMatrixZ** includes the dynamic functional connectivity matrix (N × N × T, N = number of nodes and T = number of time windows) for all subjects before and after Fisher z transformation.

6. Network Analysis

In this section, GRETNA can calculate various topological properties of a network/graph from both global and nodal characteristics, which can be compared with random network counterparts to determine the non-randomness.

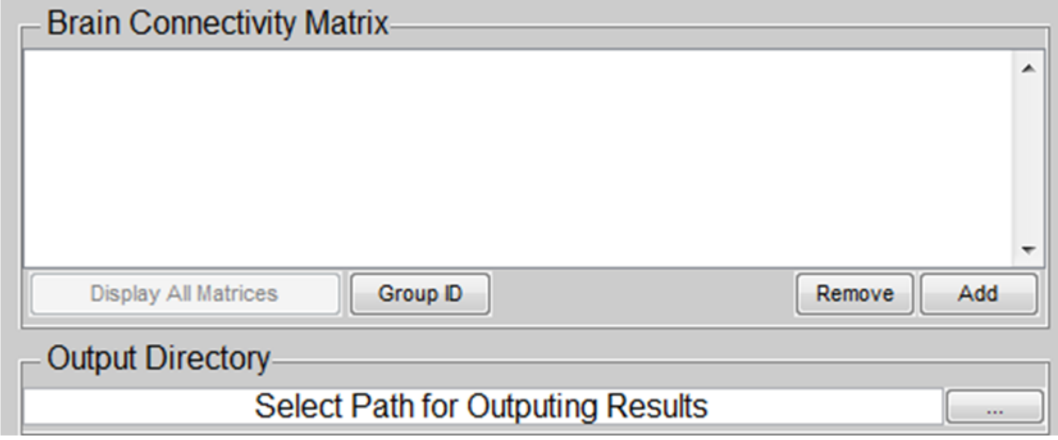


Select Path for Outputing Results

CType Batch

Queue 3

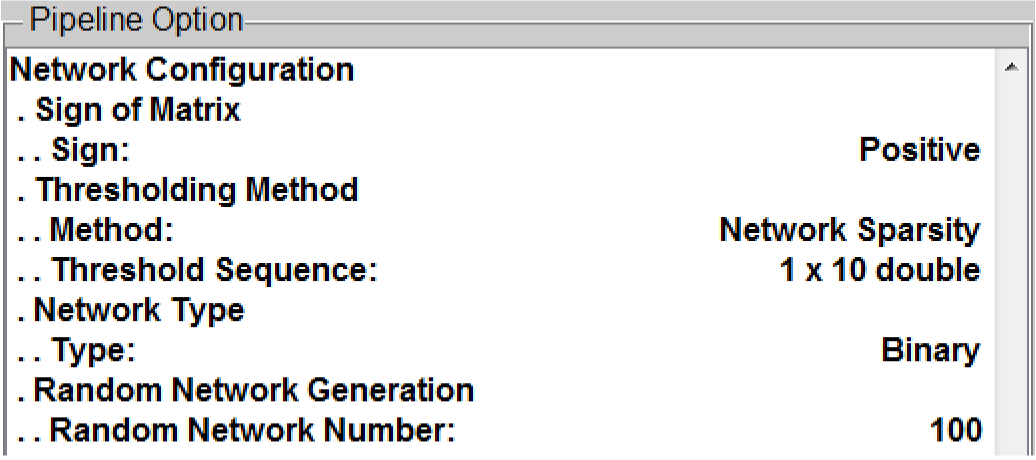
First, **click the button 'Add'** in the top-right corner of this panel to select the text files that store the connectivity matrix you want to use.



After inputting your matrix, you can **click 'Group ID'** to input the group index for each matrix. The results will then be organized into groups (different folders store the results of network analysis for different groups).

Click the button '…' to select the path for outputting results.

Regardless of the network metrics you click into the pipeline option, the following parameters must first be determined before calculating the metrics.



Network Configuration
. Sign of Matrix
. . Sign: Positive
. Thresholding Method
. . Method: Network Sparsity
. . Threshold Sequence: 1 x 10 double
. Network Type
. . Type: Binary
. Random Network Generation
. . Random Network Number: 100

- **Sign of Matrix**

Previous R-fMRI studies have shown that certain functional systems are anti-correlated (i.e., have a negative correlation) in their spontaneous brain activity. However, negative correlations may also be introduced by global signal removal, a preprocessing step that is currently controversial. For network topology, negative correlations may have detrimental effects on TRT reliability and exhibit organizations different from positive correlations. Accordingly, GRETNA provides options for researchers to determine network connectivity members, based on which subsequent graph analyses are implemented: **positive** (composed of only positive correlations), **negative** (composed of only absolute values of negative correlations) or **absolute** (composed of both positive correlations and the absolute values of the negative correlations).

- **Thresholding Method**

Prior to topological characterization, a thresholding procedure is typically applied to exclude the confounding effects of spurious relationships in interregional connectivity matrices. Two thresholding strategies are provided in GRETNA: the **'Network Sparsity'** and **'Value of Matrix Element'**. Specifically, for '**Network Sparsity'**, the threshold value is defined as the ratio of the number of actual edges divided by the maximum possible number of edges in a network. For networks with the same number of nodes, the sparsity threshold ensures the same number of edges for each network by applying a subject-specific connectivity strength threshold and therefore allowing for an examination of relative network organization. For '**Value of Matrix Element'**, researchers can define a threshold value such that network connections with weights greater than the given threshold are retained and others are ignored (i.e., set to 0). This connectivity strength threshold method allows for the examination of absolute network organization. Note that the same connectivity strength threshold usually leads to a different number of edges in the resultant networks, which could confound between-group comparisons in network topology. These two thresholding strategies are complementary and together provide a comprehensive method for testing network organization. Finally, given the absence of a definitive method for selecting a single threshold, researchers can input a range of continuous threshold values to study network properties in GRETNA. Double-click '**Threshold Sequence'** to set a range of continuous threshold values.

- **Network Type**

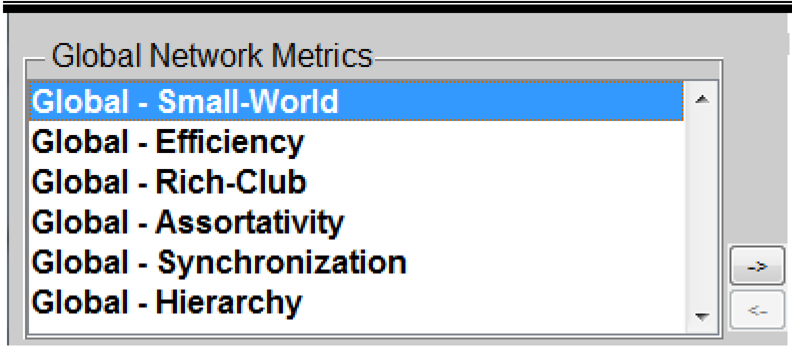
Networks can be binarized or weighted depending on whether connectivity strength is considered. Previous brain network studies have mainly focused on binary networks because of the reduction in computational complexity and clarity of network metric definitions. Notably, binary networks neglect the strength of connections above the threshold and therefore fail to identify subtle network organizations. In GRETNA, all network analyses can be conducted for both **binary** and **weighted** networks.

- **Random Networks**

Brain networks are typically compared with random networks to test whether they are configured with significantly non-random topology. In GRETNA, random networks are generated by a Markov wiring algorithm [Maslov and Sneppen, 2002], which preserves the same number of nodes and edges and the same degree distribution as real brain networks.

6.1. Global Network Metrics

GRETNA can calculate several widely used network metrics in brain network studies for both binary and weighted networks. Generally, these measures can be categorized into global and nodal metrics. Global metrics include small-world parameters of the clustering coefficient and characteristic path length, local efficiency and global efficiency, modularity, assortativity, synchronization and hierarchy. For the formula, usage and interpretation of these measures, see [Rubinov and Sporns, 2010] and [Wang et al., 2011]. Finally, GRETNA can also calculate the area under the curve (AUC) for each network measure to provide a scalar that does not depend on a specific threshold selection. It should be noted that this module can perform topological analysis of brain networks, independent of imaging modality and species. For example, the structural brain connectivity matrices in humans or macaques that are obtained from the PANDA toolbox [Cui et al., 2013] or the CoCoMac database can be entered into this module for graph analysis.



Global Network Metrics

Global - Small-World

Global - Efficiency

Global - Rich-Club

Global - Assortativity

Global - Synchronization

Global - Hierarchy

6.1.1. Small-World

Small-world networks have a shorter characteristic path length than regular networks (high clustering and long path lengths) but greater local interconnectivity than random networks (low clustering coefficient and short path lengths). The small-world metric supports both specialized/modularized and integrated/distributed information processing and maximizes the efficiency of information transfer at a relatively low wiring cost.

6.1.2. Efficiency

Global efficiency measures the global efficiency of parallel information transfer in a network. The local efficiency of the network measures how efficient communication is among the first neighbors of a given node when it is removed.

6.1.3. Rich-Club

Rich-club architecture is a nontrivial topological property of a brain network, indicating that the hub nodes are more densely connected among themselves than non-hub nodes and thus form a highly interconnected club.

6.1.4. Assortativity

Assortativity reflects the tendency of nodes to link those nodes with similar numbers of edges.

6.1.5. Synchronization

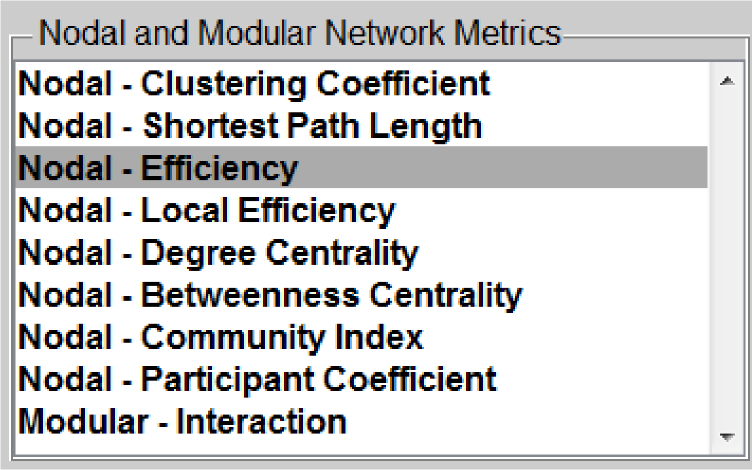
Synchronization measures how likely it is that all nodes fluctuate in the same wave pattern.

6.1.6. Hierarchy

The hierarchy coefficient is used to identify the presence of a hierarchical organization in a network [Ravasz and Barabási, 2003].

6.2. Nodal and Modular Network Metrics

Nodal metrics include nodal degree, nodal efficiency and nodal betweenness centrality. For the formula, usage and interpretation of these measures, see [Rubinov and Sporns, 2010] and [Wang et al., 2011].



Nodal and Modular Network Metrics

- Nodal - Clustering Coefficient
- Nodal - Shortest Path Length
- Nodal - Efficiency
- Nodal - Local Efficiency
- Nodal - Degree Centrality
- Nodal - Betweenness Centrality
- Nodal - Community Index
- Nodal - Participant Coefficient
- Modular - Interaction

6.2.1. Clustering Coefficient

The clustering coefficient of a given node measures the likelihood its neighborhoods are connected to each other.

6.2.2. Shortest Path Length

The shortest path length of a given node quantifies the mean distance or routing efficiency between this node and all the other nodes in the network.

6.2.3. Efficiency

The nodal efficiency for a given node characterizes the efficiency of parallel information transfer of that node in the network.

6.2.4. Local Efficiency

The local efficiency for a given node measures how efficient the communication is among the first neighbors of this node when it is removed.

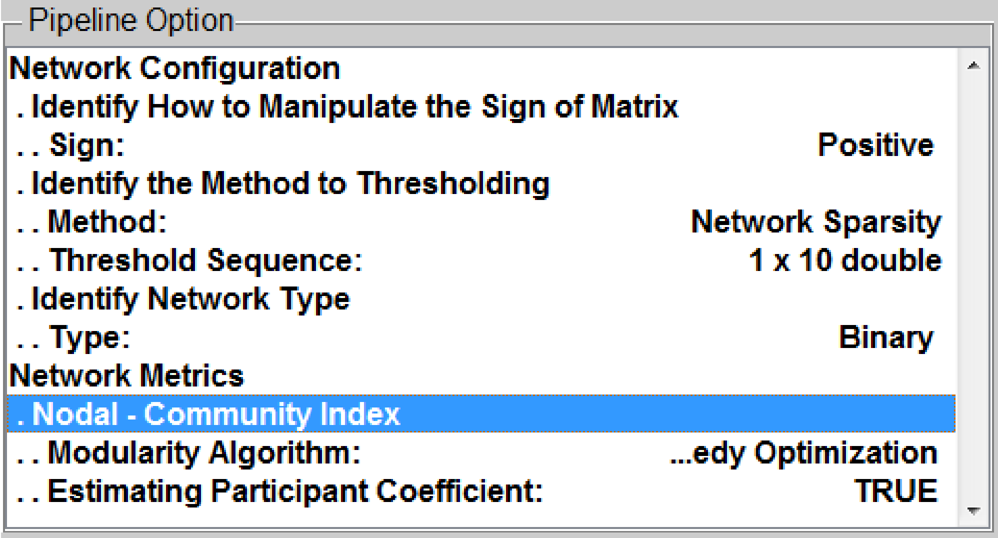
6.2.5. Degree Centrality

The nodal degree for a given node reflects its information communication ability in the functional network.

6.2.6. Betweenness Centrality

The nodal betweenness for a given node characterizes its effect on information flow between other nodes.

6.2.7. Community Index



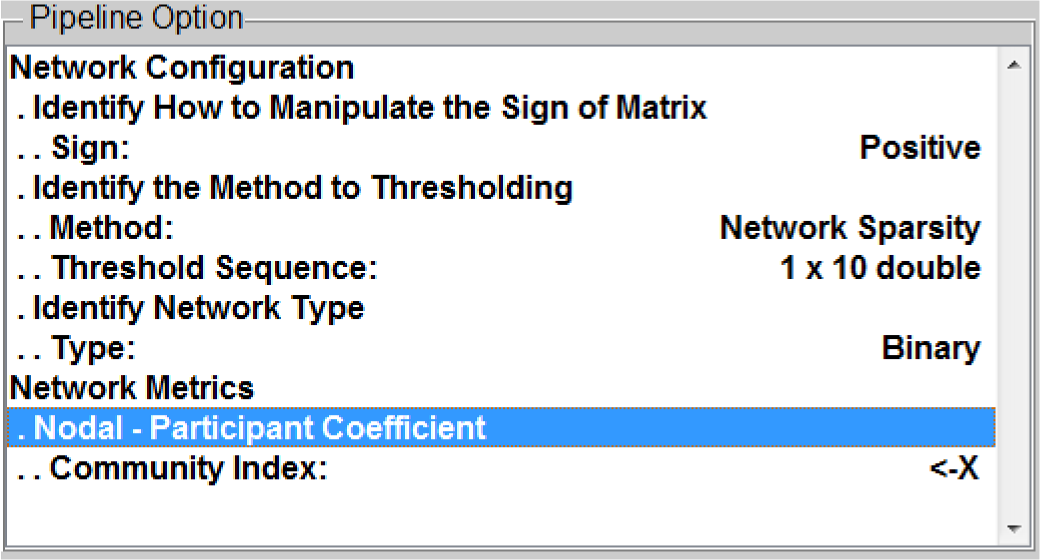
Network Configuration
. Identify How to Manipulate the Sign of Matrix
. . Sign: Positive
. Identify the Method to Thresholding
. . Method: Network Sparsity
. . Threshold Sequence: 1 x 10 double
. Identify Network Type
. . Type: Binary
Network Metrics
. Nodal - Community Index
. . Modularity Algorithm: ...edy Optimization
. . Estimating Participant Coefficient: TRUE

Modularity refers to the existence of multiple densely connected communities of regions in a brain network.

- **Modularity Algorithm:** We have provided two common modularity algorithms to perform modularity analysis: **Modified Greedy Optimization** and **Spectral Optimization**.

- **Estimating Participant Coefficient:** This setting determines whether to calculate the nodal participant coefficient based on the modularity division results obtained in the previous step. If a predefined module division is desired for PC calculation, please use the Nodal- Participant Coefficient in the Nodal Metrics section.

6.2.8. Participant Coefficient

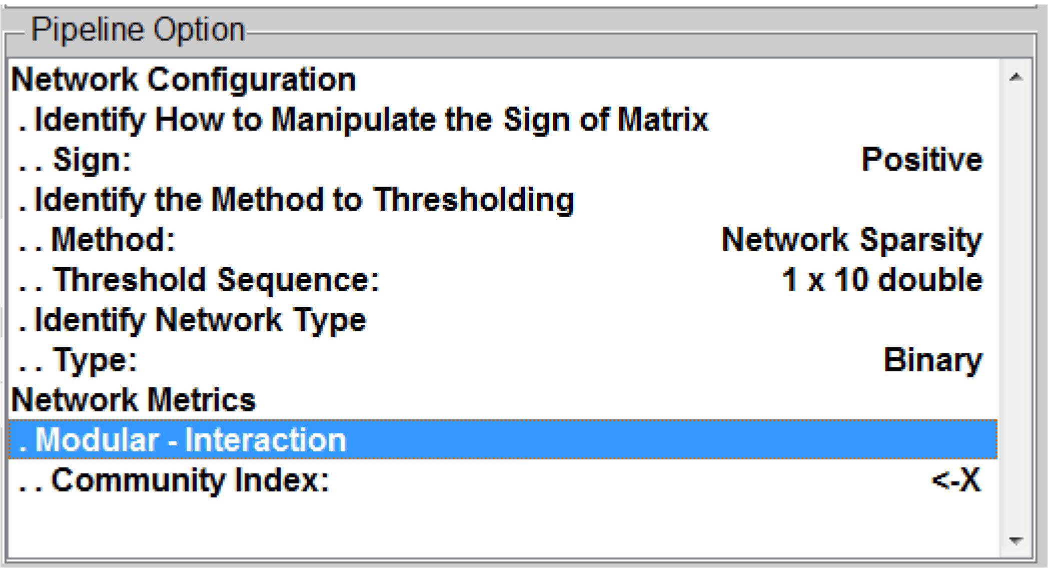


Network Configuration
. Identify How to Manipulate the Sign of Matrix
. . Sign: Positive
. Identify the Method to Thresholding
. . Method: Network Sparsity
. . Threshold Sequence: 1 x 10 double
. Identify Network Type
. . Type: Binary
Network Metrics
. Nodal - Participant Coefficient
. . Community Index: <-X

The participant coefficient reflects the ability of an index node in keeping communication between its own module and the other modules.

- **Community Index:** A list of numbers that represent the predefined module division for each node in your matrices. The value of the community index must be consistent with the number of nodes in the matrix. The community index will be used for all subjects, and in this case, the participant coefficients of nodes for all subjects are calculated based on the same module structure.

6.2.9. Modular Interaction



Pipeline Option

Network Configuration
. Identify How to Manipulate the Sign of Matrix
. . Sign: Positive
. Identify the Method to Thresholding
. . Method: Network Sparsity
. . Threshold Sequence: 1 x 10 double
. Identify Network Type
. . Type: Binary
Network Metrics
. Modular - Interaction
. . Community Index: <-X

In this section, the averaged functional connectivity strength within and between modules can be obtained, which is defined by the community index input here.

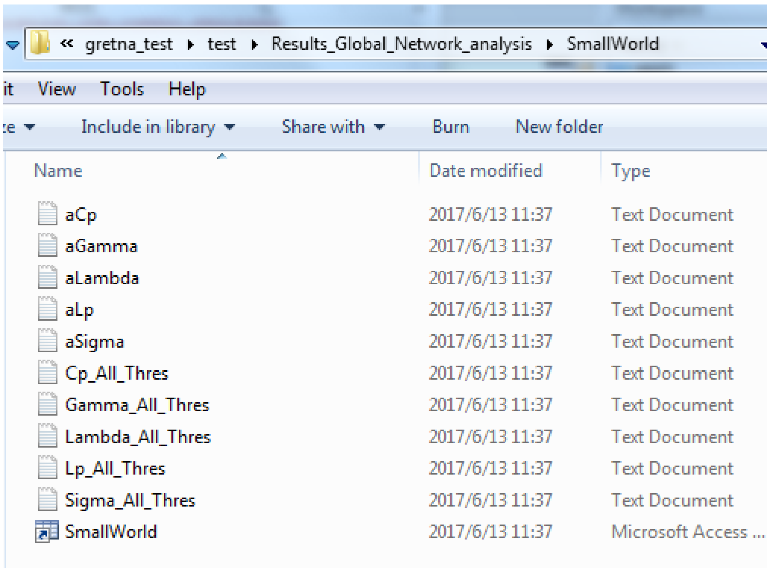
- **Community Index:** A list of numbers that represent the predefined module division for each node in your matrices. The value of the community index must be consistent with the number of nodes in the matrix. The community index will be used for all subjects, and in this case, the participant coefficients of nodes for all subjects are calculated based on the same module structure.

6.3. Results of Network Analysis

All results of the network metrics are stored in different folders (one folder for each metric) using two file types: MAT-file and TEXT-file.

6.3.1. Global Network Metrics

- **Small-World**



Name	Date modified	Type
aCp	2017/6/13 11:37	Text Document
aGamma	2017/6/13 11:37	Text Document
aLambda	2017/6/13 11:37	Text Document
aLp	2017/6/13 11:37	Text Document
aSigma	2017/6/13 11:37	Text Document
Cp_All_Thres	2017/6/13 11:37	Text Document
Gamma_All_Thres	2017/6/13 11:37	Text Document
Lambda_All_Thres	2017/6/13 11:37	Text Document
Lp_All_Thres	2017/6/13 11:37	Text Document
Sigma_All_Thres	2017/6/13 11:37	Text Document
SmallWorld	2017/6/13 11:37	Microsoft Access ...

aCp: The AUC (area under curve) of the clustering coefficient of a network for each subject.

aGamma: The AUC of the Gamma of a network for each subject.

aLambda: The AUC of the Lambda of a network for each subject.

aLp: The AUC of the shortest path length of a network for each subject.

aSigma: The AUC of the Sigma of a network for each subject.

Cp_All_Thres: Clustering coefficient of a network at each threshold for each subject. Each row represents one subject, and each column represents one threshold.

Gamma_All_Thres: The Gamma of a network at each threshold for each subject.

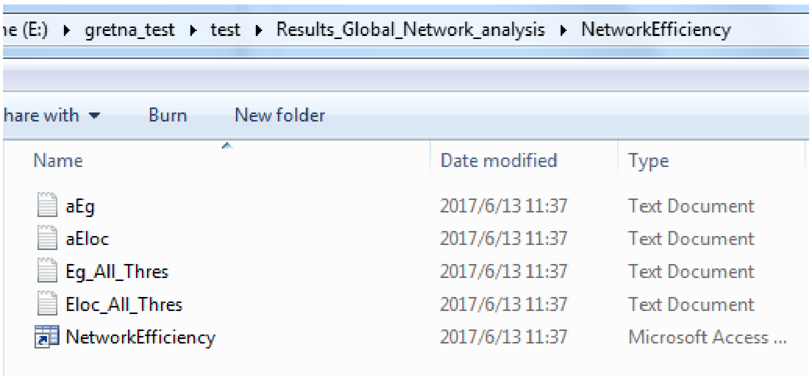
Lambda_All_Thres: The Lambda of a network at each threshold for each subject.

Lp_All_Thres: The shortest path length of a network at each threshold for each subject.

Sigma_All_Thres: The Sigma of network at each threshold for each subject.

SmallWorld.mat includes all of these metrics and can loaded in MATLAB.

- **Network Efficiency**



Name	Date modified	Type
aEg	2017/6/13 11:37	Text Document
aEloc	2017/6/13 11:37	Text Document
Eg_All_Thres	2017/6/13 11:37	Text Document
Eloc_All_Thres	2017/6/13 11:37	Text Document
NetworkEfficiency	2017/6/13 11:37	Microsoft Access ...

aEg: The AUC of the global efficiency of a network for each subject.

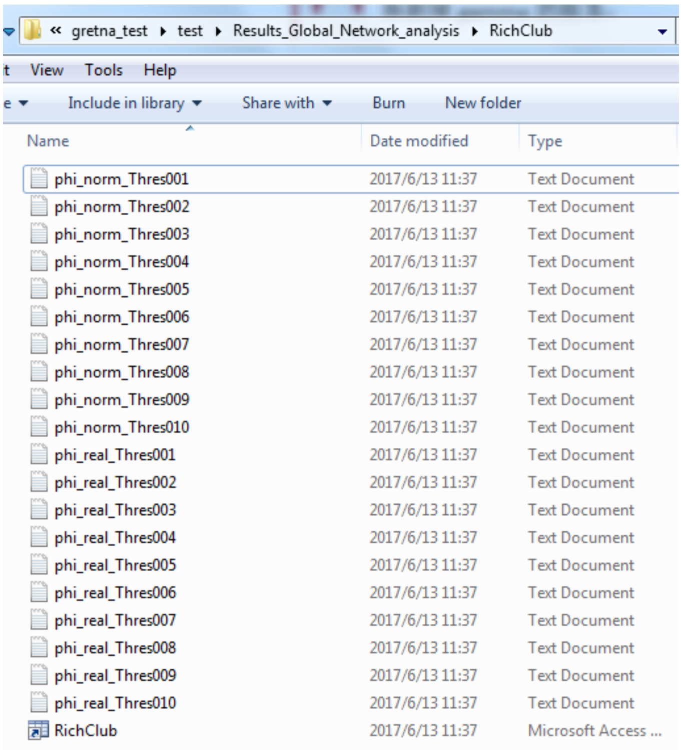
aEloc: The AUC of the local efficiency of a network for each subject.

Eg_All_Thres: The global efficiency of a network at each threshold for each subject.

Eloc_All_Thres: The local efficiency of a network at each threshold for each subject.

NetworkEfficiency.mat includes all of these metrics and can loaded in MATLAB.

- **Rich-Club**



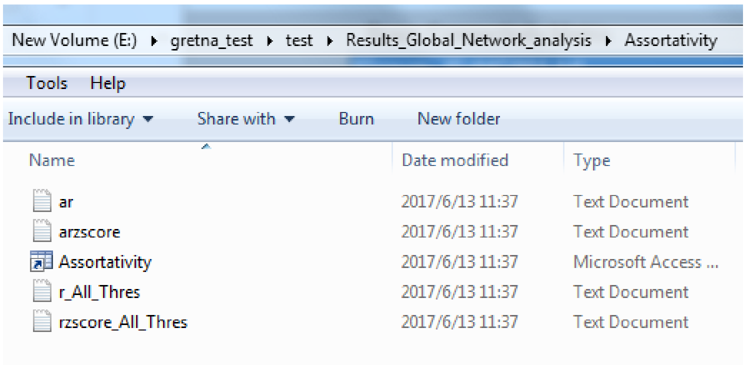
Name	Date modified	Type
phi_norm_Thres001	2017/6/13 11:37	Text Document
phi_norm_Thres002	2017/6/13 11:37	Text Document
phi_norm_Thres003	2017/6/13 11:37	Text Document
phi_norm_Thres004	2017/6/13 11:37	Text Document
phi_norm_Thres005	2017/6/13 11:37	Text Document
phi_norm_Thres006	2017/6/13 11:37	Text Document
phi_norm_Thres007	2017/6/13 11:37	Text Document
phi_norm_Thres008	2017/6/13 11:37	Text Document
phi_norm_Thres009	2017/6/13 11:37	Text Document
phi_norm_Thres010	2017/6/13 11:37	Text Document
phi_real_Thres001	2017/6/13 11:37	Text Document
phi_real_Thres002	2017/6/13 11:37	Text Document
phi_real_Thres003	2017/6/13 11:37	Text Document
phi_real_Thres004	2017/6/13 11:37	Text Document
phi_real_Thres005	2017/6/13 11:37	Text Document
phi_real_Thres006	2017/6/13 11:37	Text Document
phi_real_Thres007	2017/6/13 11:37	Text Document
phi_real_Thres008	2017/6/13 11:37	Text Document
phi_real_Thres009	2017/6/13 11:37	Text Document
phi_real_Thres010	2017/6/13 11:37	Text Document
RichClub	2017/6/13 11:37	Microsoft Access ...

phi_real_Thres001: The rich club coefficient of a network at a given threshold 1. Each row represents one subject, and each column represents one binary node degree K (from 1 to Node-1).

phi_norm_Thres001: The normalized rich-club coefficient of a real network at a given threshold 1.

RichClub.mat includes all of these metrics and can loaded in MATLAB.

- **Assortativity**



Name	Date modified	Type
ar	2017/6/13 11:37	Text Document
arzscore	2017/6/13 11:37	Text Document
Assortativity	2017/6/13 11:37	Microsoft Access ...
r_All_Thres	2017/6/13 11:37	Text Document
rzscore_All_Thres	2017/6/13 11:37	Text Document

ar: The AUC of the assortativity of a network for each subject.

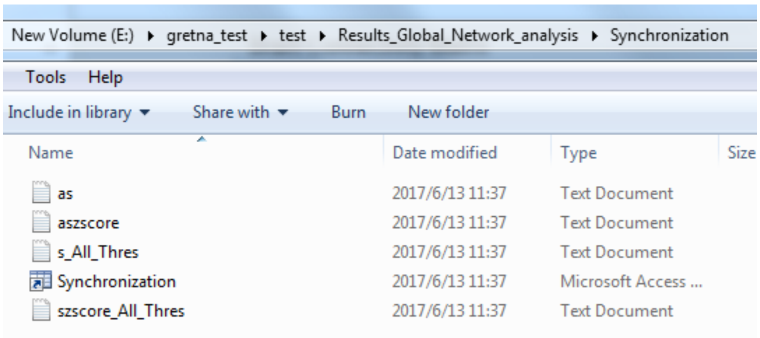
arzscore: The AUC of the z-score of the assortativity of a network determined for each subject by subtracting the average assortativity across random networks and then dividing it by the standard deviation of the assortativity of random networks.

r_All_Thres: The assortativity of a network at each threshold for each subject.

rzscore_All_Thres: The z-score of the assortativity of a network at each threshold for each subject.

Assortativity.mat includes all of these metrics and can loaded in MATLAB.

- **Synchronization**



Name	Date modified	Type	Size
as	2017/6/13 11:37	Text Document	
aszscore	2017/6/13 11:37	Text Document	
s_All_Thres	2017/6/13 11:37	Text Document	
Synchronization	2017/6/13 11:37	Microsoft Access ...	
szscore_All_Thres	2017/6/13 11:37	Text Document	

as: The AUC of the synchronization of a network for each subject.

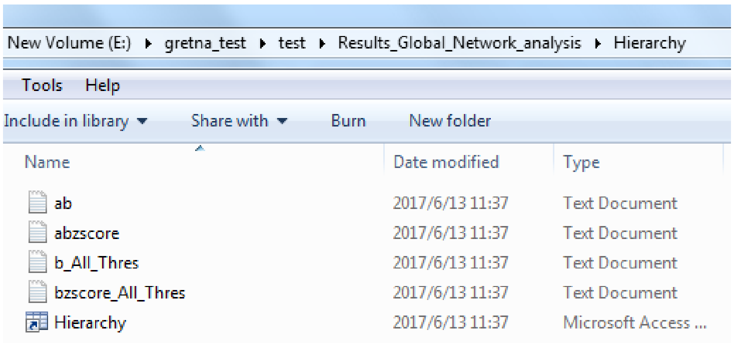
aszscore: The AUC of the z-score of the synchronization of a network determined for each subject by subtracting the average synchronization across random networks and then dividing it by the standard deviation of the synchronization of random networks.

s_All_Thres: The synchronization of a network at each threshold for each subject.

szscore_All_Thres: The z-score of the synchronization of a network at each threshold for each subject.

Synchronization.mat includes all of these metrics and can loaded in MATLAB.

- **Hierarchy**



Name	Date modified	Type
ab	2017/6/13 11:37	Text Document
abzscore	2017/6/13 11:37	Text Document
b_All_Thres	2017/6/13 11:37	Text Document
bzscore_All_Thres	2017/6/13 11:37	Text Document
Hierarchy	2017/6/13 11:37	Microsoft Access ...

ab: The AUC of the hierarchy of a network for each subject.

abzscore: The AUC of the z-score of the hierarchy of a network for each subject by subtracting the average hierarchy across random networks and then dividing it by the standard deviation of the hierarchy of random networks.

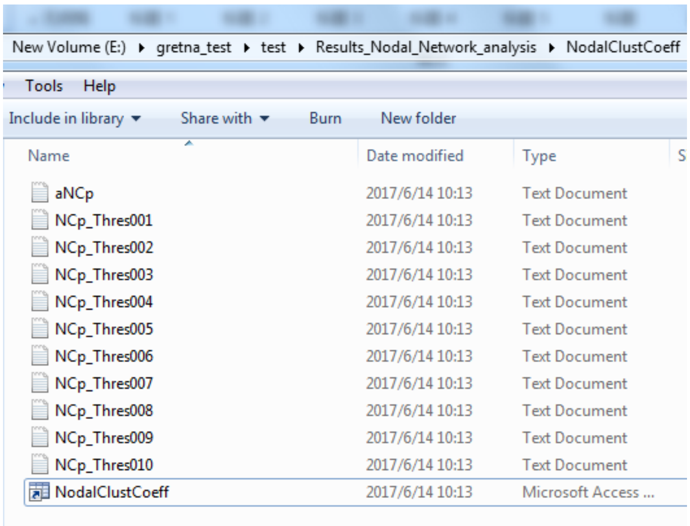
b_All_Thres: The hierarchy of a network at each threshold for each subject.

bzscore_All_Thres: The z-score of the hierarchy of a network at each threshold for each subject.

Hierarchy.mat includes all of these metrics and can loaded in MATLAB.

6.3.2. Nodal and Modular Network Metrics

- **Clustering Coefficient**



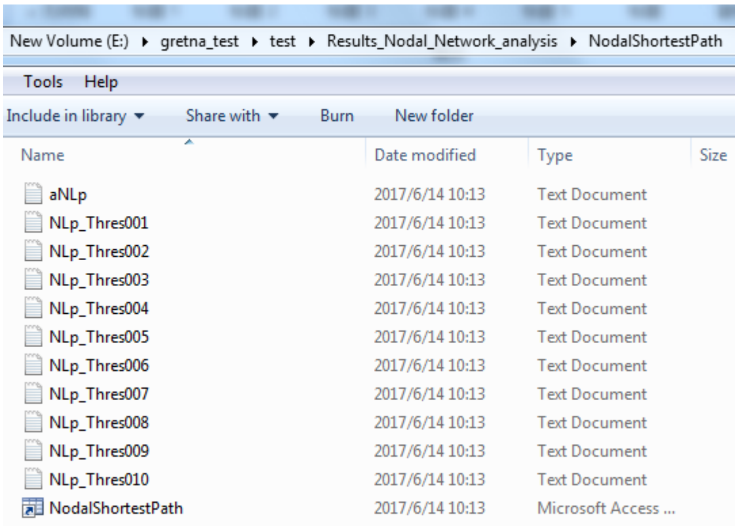
Name	Date modified	Type
aNCp	2017/6/14 10:13	Text Document
NCp_Thres001	2017/6/14 10:13	Text Document
NCp_Thres002	2017/6/14 10:13	Text Document
NCp_Thres003	2017/6/14 10:13	Text Document
NCp_Thres004	2017/6/14 10:13	Text Document
NCp_Thres005	2017/6/14 10:13	Text Document
NCp_Thres006	2017/6/14 10:13	Text Document
NCp_Thres007	2017/6/14 10:13	Text Document
NCp_Thres008	2017/6/14 10:13	Text Document
NCp_Thres009	2017/6/14 10:13	Text Document
NCp_Thres010	2017/6/14 10:13	Text Document
NodalClustCoeff	2017/6/14 10:13	Microsoft Access ...

aNCp: The AUC of the nodal clustering coefficient for each subject.

NCp_Thres001: The nodal clustering coefficient for each subject at a given threshold 1.

NodalClustCoeff.mat includes all of these metrics and can loaded in MATLAB.

- **Shortest Path Length**



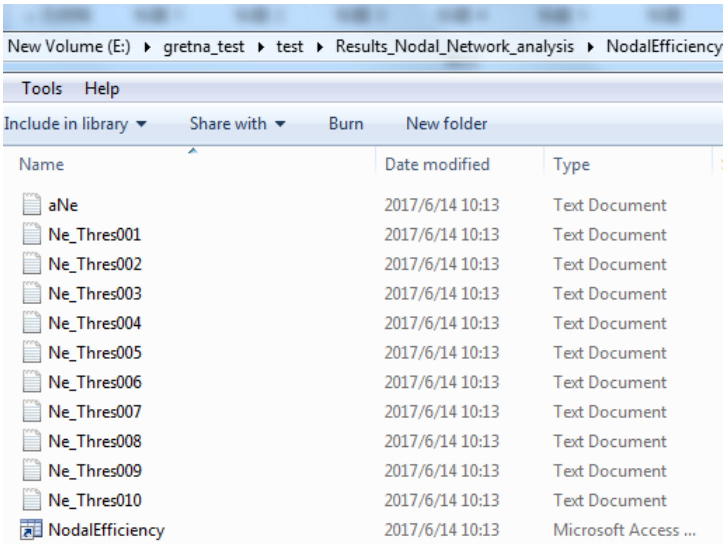
Name	Date modified	Type	Size
aNLp	2017/6/14 10:13	Text Document	
NLp_Thres001	2017/6/14 10:13	Text Document	
NLp_Thres002	2017/6/14 10:13	Text Document	
NLp_Thres003	2017/6/14 10:13	Text Document	
NLp_Thres004	2017/6/14 10:13	Text Document	
NLp_Thres005	2017/6/14 10:13	Text Document	
NLp_Thres006	2017/6/14 10:13	Text Document	
NLp_Thres007	2017/6/14 10:13	Text Document	
NLp_Thres008	2017/6/14 10:13	Text Document	
NLp_Thres009	2017/6/14 10:13	Text Document	
NLp_Thres010	2017/6/14 10:13	Text Document	
NodalShortestPath	2017/6/14 10:13	Microsoft Access ...	

aNLp: The AUC of the nodal shortest path length for each subject.

NLp_Thres001: The nodal shortest path length for each subject at a given threshold 1.

NodalShortestPath.mat includes all of these metrics and can loaded in MATLAB.

- **Efficiency**



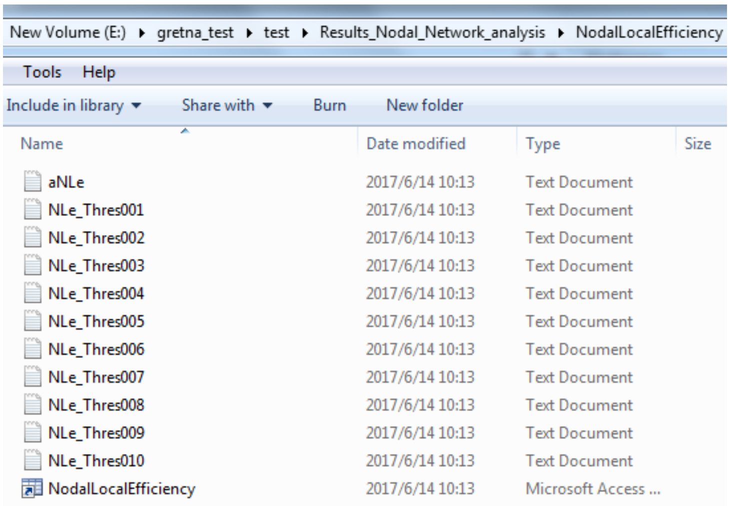
Name	Date modified	Type
aNe	2017/6/14 10:13	Text Document
Ne_Thres001	2017/6/14 10:13	Text Document
Ne_Thres002	2017/6/14 10:13	Text Document
Ne_Thres003	2017/6/14 10:13	Text Document
Ne_Thres004	2017/6/14 10:13	Text Document
Ne_Thres005	2017/6/14 10:13	Text Document
Ne_Thres006	2017/6/14 10:13	Text Document
Ne_Thres007	2017/6/14 10:13	Text Document
Ne_Thres008	2017/6/14 10:13	Text Document
Ne_Thres009	2017/6/14 10:13	Text Document
Ne_Thres010	2017/6/14 10:13	Text Document
NodalEfficiency	2017/6/14 10:13	Microsoft Access ...

aNe: The AUC of the nodal efficiency for each subject.

Ne_Thres001: The nodal efficiency for each subject at a given threshold 1.

NodalEfficiency.mat includes all of these metrics and can loaded in MATLAB.

- **Local Efficiency**



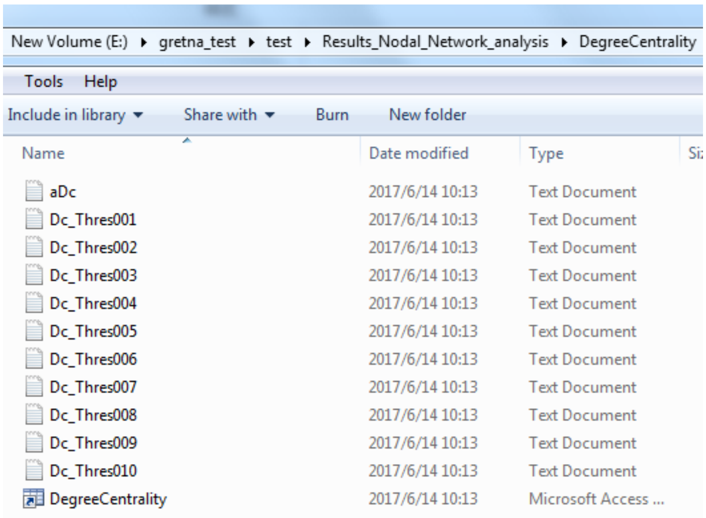
Name	Date modified	Type	Size
aNLe	2017/6/14 10:13	Text Document	
NLe_Thres001	2017/6/14 10:13	Text Document	
NLe_Thres002	2017/6/14 10:13	Text Document	
NLe_Thres003	2017/6/14 10:13	Text Document	
NLe_Thres004	2017/6/14 10:13	Text Document	
NLe_Thres005	2017/6/14 10:13	Text Document	
NLe_Thres006	2017/6/14 10:13	Text Document	
NLe_Thres007	2017/6/14 10:13	Text Document	
NLe_Thres008	2017/6/14 10:13	Text Document	
NLe_Thres009	2017/6/14 10:13	Text Document	
NLe_Thres010	2017/6/14 10:13	Text Document	
NodalLocalEfficiency	2017/6/14 10:13	Microsoft Access ...	

aNLe: The AUC of the nodal local efficiency for each subject.

NLe_Thres001: The nodal local efficiency for each subject at a given threshold 1.

NodalLocalEfficiency.mat includes all of these metrics and can loaded in MATLAB.

- **Degree Centrality**



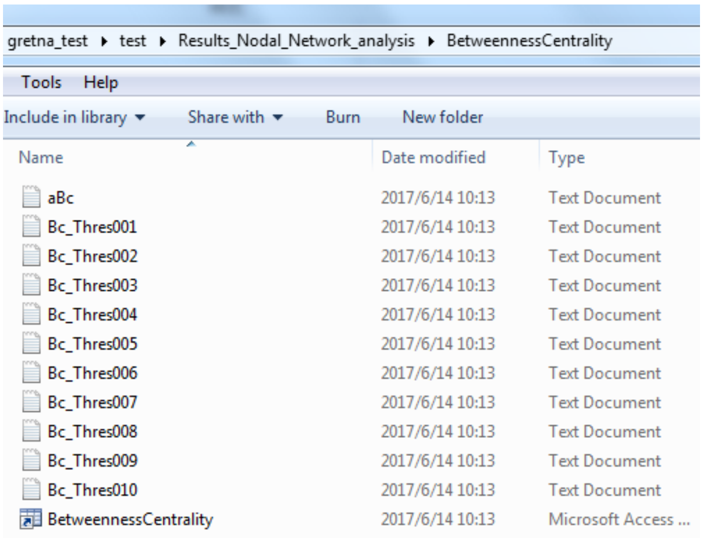
Name	Date modified	Type
aDc	2017/6/14 10:13	Text Document
Dc_Thres001	2017/6/14 10:13	Text Document
Dc_Thres002	2017/6/14 10:13	Text Document
Dc_Thres003	2017/6/14 10:13	Text Document
Dc_Thres004	2017/6/14 10:13	Text Document
Dc_Thres005	2017/6/14 10:13	Text Document
Dc_Thres006	2017/6/14 10:13	Text Document
Dc_Thres007	2017/6/14 10:13	Text Document
Dc_Thres008	2017/6/14 10:13	Text Document
Dc_Thres009	2017/6/14 10:13	Text Document
Dc_Thres010	2017/6/14 10:13	Text Document
DegreeCentrality	2017/6/14 10:13	Microsoft Access ...

aDc: The AUC of the nodal degree centrality for each subject.

Dc_Thres001: The nodal degree centrality for each subject at a given threshold 1.

DegreeCentrality.mat includes all of these metrics and can loaded in MATLAB.

- **Betweenness Centrality**



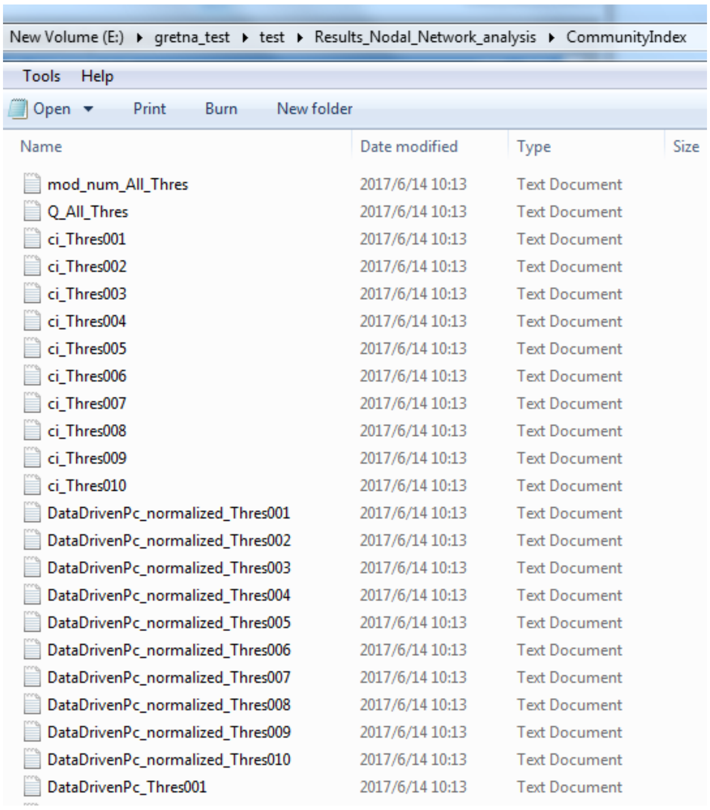
Name	Date modified	Type
aBc	2017/6/14 10:13	Text Document
Bc_Thres001	2017/6/14 10:13	Text Document
Bc_Thres002	2017/6/14 10:13	Text Document
Bc_Thres003	2017/6/14 10:13	Text Document
Bc_Thres004	2017/6/14 10:13	Text Document
Bc_Thres005	2017/6/14 10:13	Text Document
Bc_Thres006	2017/6/14 10:13	Text Document
Bc_Thres007	2017/6/14 10:13	Text Document
Bc_Thres008	2017/6/14 10:13	Text Document
Bc_Thres009	2017/6/14 10:13	Text Document
Bc_Thres010	2017/6/14 10:13	Text Document
BetweennessCentrality	2017/6/14 10:13	Microsoft Access ...

aBc: The AUC of the nodal betweenness for each subject.

Bc_Thres001: The nodal betweenness for each subject at a given threshold 1.

BetweennessCentrality.mat includes all of these metrics and can loaded in MATLAB.

- **Community Index**



Name	Date modified	Type	Size
mod_num_All_Thres	2017/6/14 10:13	Text Document	
Q_All_Thres	2017/6/14 10:13	Text Document	
ci_Thres001	2017/6/14 10:13	Text Document	
ci_Thres002	2017/6/14 10:13	Text Document	
ci_Thres003	2017/6/14 10:13	Text Document	
ci_Thres004	2017/6/14 10:13	Text Document	
ci_Thres005	2017/6/14 10:13	Text Document	
ci_Thres006	2017/6/14 10:13	Text Document	
ci_Thres007	2017/6/14 10:13	Text Document	
ci_Thres008	2017/6/14 10:13	Text Document	
ci_Thres009	2017/6/14 10:13	Text Document	
ci_Thres010	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres001	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres002	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres003	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres004	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres005	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres006	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres007	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres008	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres009	2017/6/14 10:13	Text Document	
DataDrivenPc_normalized_Thres010	2017/6/14 10:13	Text Document	
DataDrivenPc_Thres001	2017/6/14 10:13	Text Document	

mod_num_All_Thres: The number of modules in a network for each subject under each threshold.

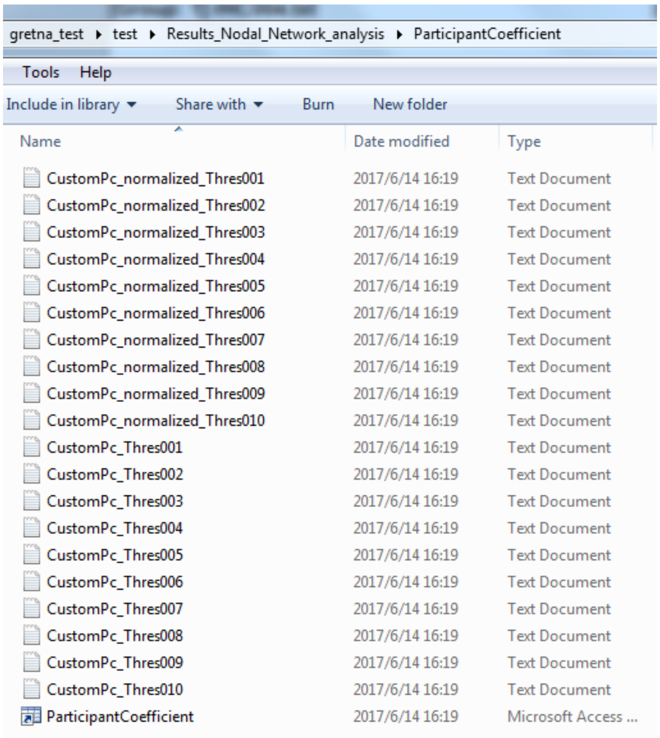
Q_All_Thres: The modularity of a network for each subject under each threshold.

ci_Thres001: The community index for each nodes each subject at a given threshold 1. This measure indicates to which community the node belongs. Each row represents one subject, and each column represents one node.

DataDrivenPc Thres001: The nodal participant coefficient for each node each subject based on the subject-specific community index at a given threshold 1.

DataDrivenPc_normalized_Thres001: The nodal normalized participant coefficient (scaled by the max participant coefficient within subject) for each node each subject based on the subject-specific community index at a given threshold 1.

- **Participant Coefficient**



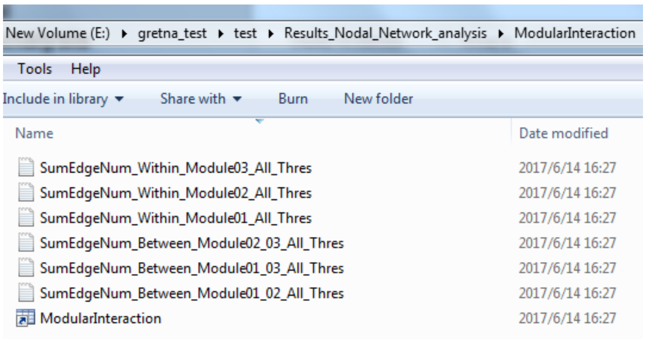
Name	Date modified	Type
CustomPc_normalized_Thres001	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres002	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres003	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres004	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres005	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres006	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres007	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres008	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres009	2017/6/14 16:19	Text Document
CustomPc_normalized_Thres010	2017/6/14 16:19	Text Document
CustomPc_Thres001	2017/6/14 16:19	Text Document
CustomPc_Thres002	2017/6/14 16:19	Text Document
CustomPc_Thres003	2017/6/14 16:19	Text Document
CustomPc_Thres004	2017/6/14 16:19	Text Document
CustomPc_Thres005	2017/6/14 16:19	Text Document
CustomPc_Thres006	2017/6/14 16:19	Text Document
CustomPc_Thres007	2017/6/14 16:19	Text Document
CustomPc_Thres008	2017/6/14 16:19	Text Document
CustomPc_Thres009	2017/6/14 16:19	Text Document
CustomPc_Thres010	2017/6/14 16:19	Text Document
ParticipantCoefficient	2017/6/14 16:19	Microsoft Access ...

CustomPc_Thres001: The nodal participant coefficient for each node each subject based on the same given community index at a given threshold 1.

CustomPc_normalized_Thres001: The nodal normalized participant coefficient (scaled by the max participant coefficient within subject) for each node each subject based on the same given community index at a given threshold 1.

ParticipantCoefficient.mat includes all of these metrics and can loaded in MATLAB.

- **Modular Interaction**



Name	Date modified
SumEdgeNum_Within_Module03_All_Thres	2017/6/14 16:27
SumEdgeNum_Within_Module02_All_Thres	2017/6/14 16:27
SumEdgeNum_Within_Module01_All_Thres	2017/6/14 16:27
SumEdgeNum_Between_Module02_03_All_Thres	2017/6/14 16:27
SumEdgeNum_Between_Module01_03_All_Thres	2017/6/14 16:27
SumEdgeNum_Between_Module01_02_All_Thres	2017/6/14 16:27
ModularInteraction	2017/6/14 16:27

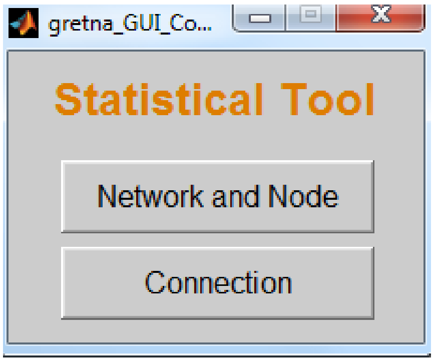
SumEdgeNum_Within_Module01_All_Thres: The total number of edges within module 1 for each subject based on the same given community index at all thresholds.

SumEdgeNum_Between_Module01_02_All_Thres: The total number of edges between module 1 and module 2 for each subject based on the same given community index at all thresholds.

ModularInteraction.mat includes all of these metrics and can loaded in MATLAB.

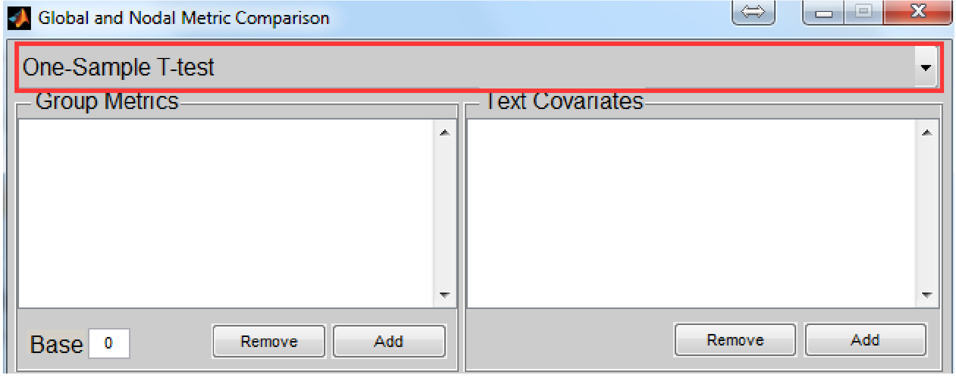
7. Metric Comparison

In this section, GRETNA allows researchers to perform statistical analysis on global, nodal and connectional network measures.

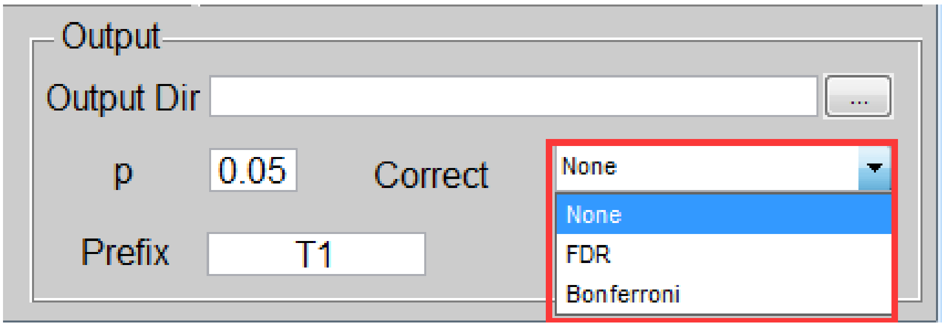


7.1. Network and Node

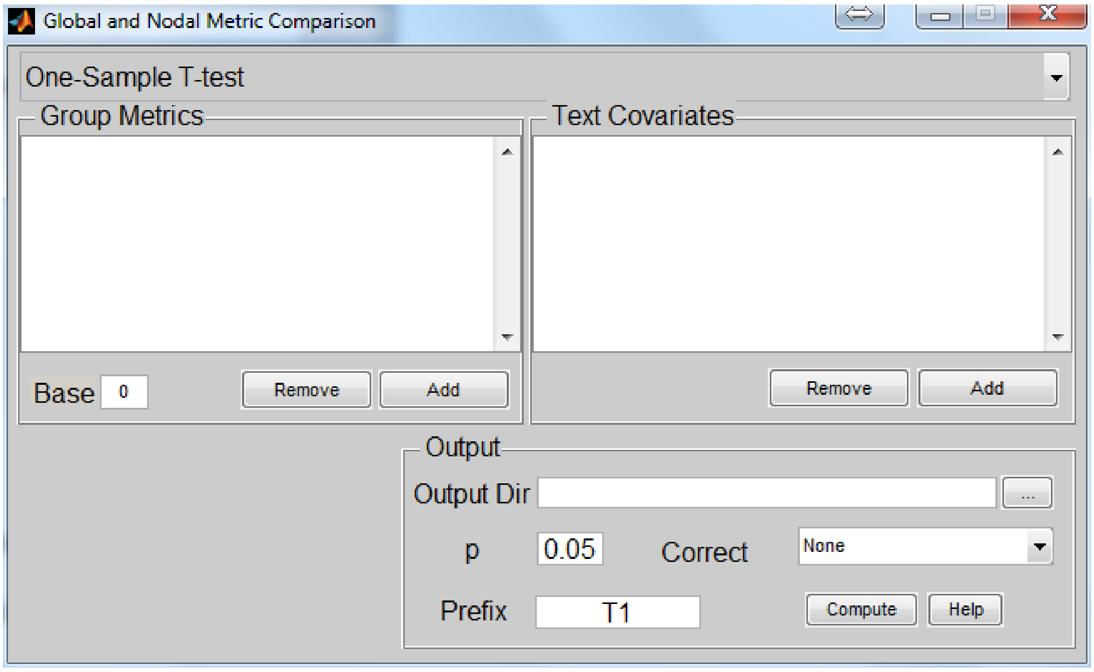
For global and nodal network measures, GRETNA provides several popular parametric models, including the one-sample *t*-test, two-sample *t*-test, paired *t*-test, one-way analysis of variance (ANOVA) and repeated measurement ANOVA.



Finally, the statistical analysis of network-behavior correlation can be implemented in this section. In addition, covariates of no interest (e.g., age, gender and clinical variables) can be added into all of these statistical models. GRETNA also provides multiple comparison correction approaches, including the false discovery rate (FDR) and Bonferroni correction.



7.1.1. One-Sample *t*-Test



p 0.05

Correct None

Base 0

Prefix T1

The one-sample *t*-test can be used to test whether the global and nodal metrics are significantly different from a given value (e.g., 0).

Click 'Add' in the 'Group Metrics' column to input the global or nodal metric for each subject.

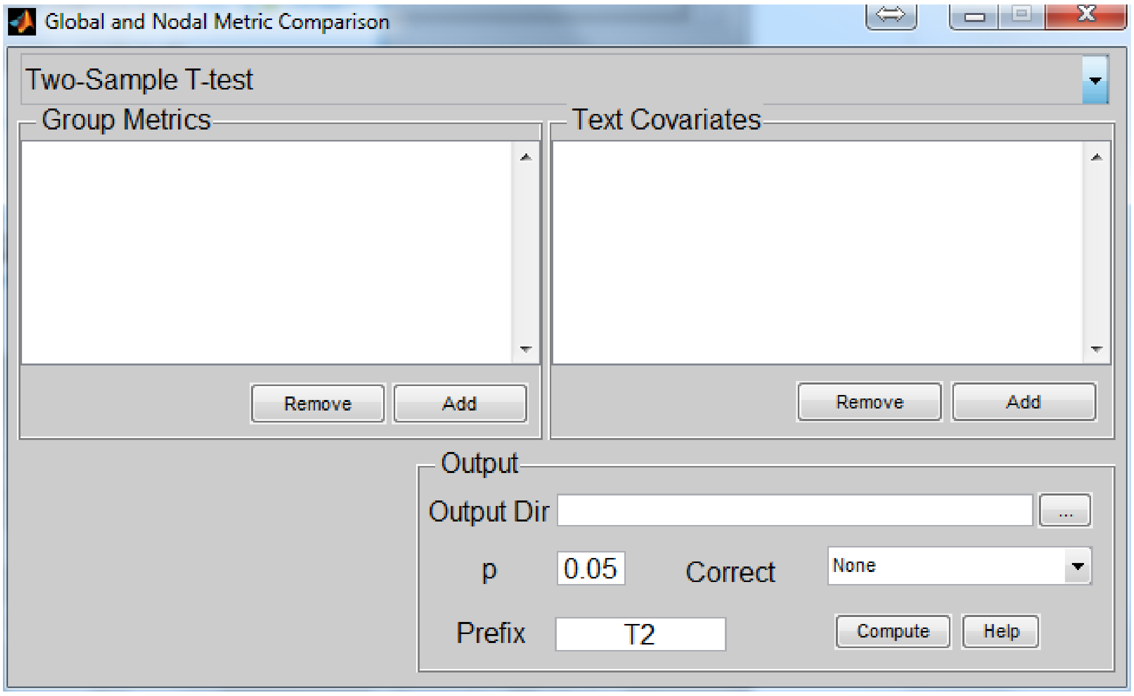
Click 'Add' in the 'Text covariates' column to input the covariates of no interests (e.g., age, gender and clinical variables) to control the effects of these factors.

Click the button '…' to select the path for outputting results. **Prefix** can be changed if necessary.

Choose one of the multiple correction methods by **clicking the small triangle** to the right of **'Correct'**.

After setting all of the parameters, **click 'Compute'** to run this process.

7.1.2. Two-Sample *t*-Test



Two-Sample T-test

p 0.05

Correct None

Prefix T2

The two-sample t-test can be used to test whether the global and nodal metrics in two independent groups are significantly different from each other.

Click ‘Add’ in the ‘Group Metrics’ column to input the global or nodal metrics of two groups.

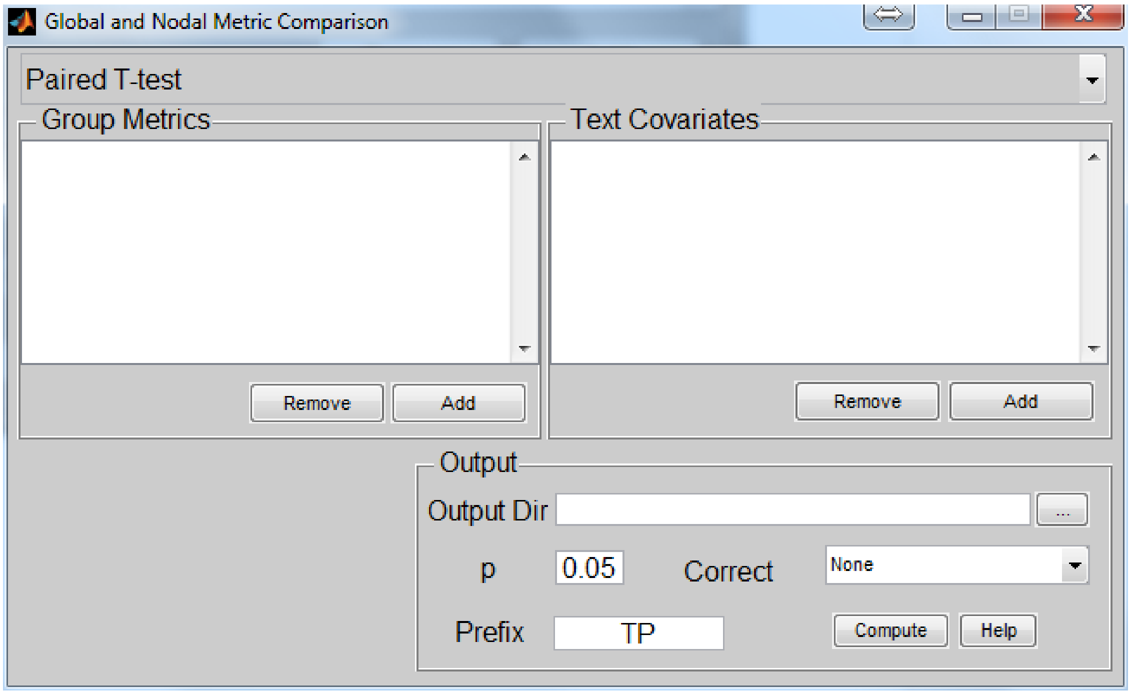
Click ‘Add’ in the ‘Text covariates’ column to input the covariates of no interest (e.g., age, gender and clinical variables) to control the effects of these factors.

Click the button ‘…’ to select the path for outputting results. **Prefix** can be changed if necessary.

Choose one of the multiple correction methods by **clicking the small triangle** to the right of **‘Correct’**.

After setting all of the parameters, **click ‘Compute’** to run this process.

7.1.3. Paired *t*-Test



Paired T-test

p 0.05

Correct None

Prefix TP

The paired t-test can be used to test whether the global and nodal metrics in two related groups are significantly different from each other.

Click 'Add' in the 'Group Metrics' column to input the global or nodal metrics of two groups.

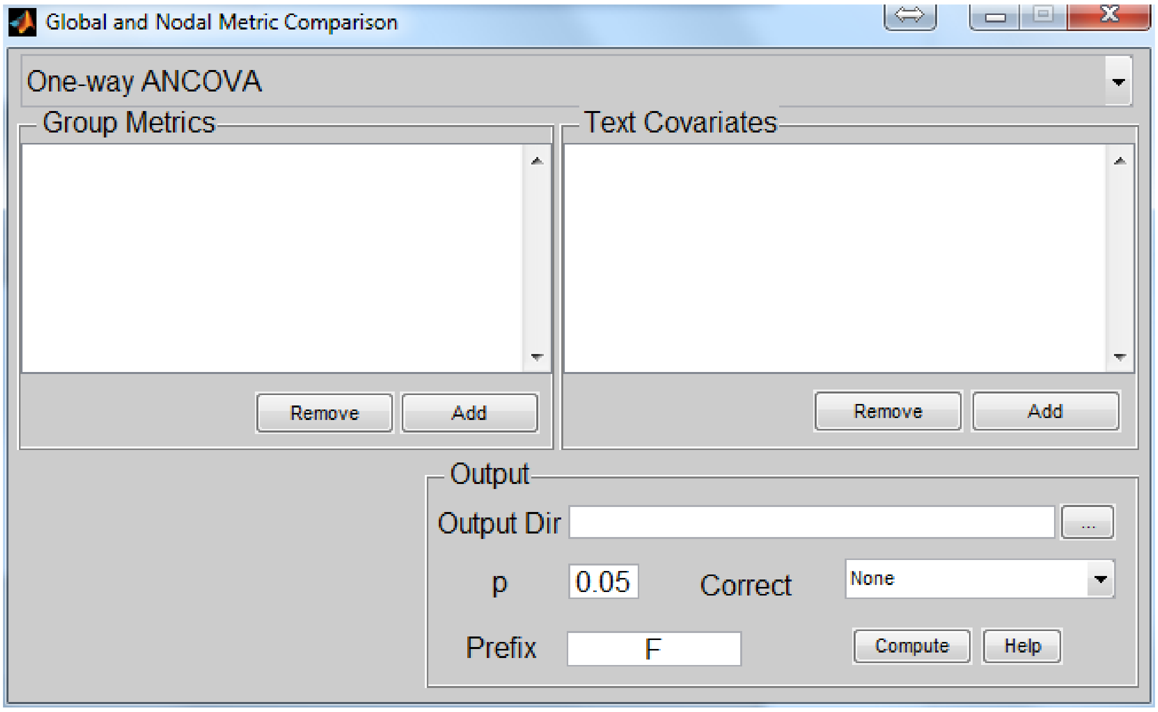
Click 'Add' in the 'Text covariates' column to input the covariates of no interest (e.g., age, gender and clinical variables) to control the effects of these factors.

Click the button '…' to select the path for outputting results. **Prefix** can be changed if necessary.

Choose one of the multiple correction methods by **clicking the small triangle** to the right of **'Correct'**.

After setting all of the parameters, **click 'Compute'** to run this process.

7.1.4. One-Way ANCOVA



One-way ANCOVA can be used to test whether the global and nodal metrics are significantly different across categories/levels of an independent variable while controlling the differences of the covariates.

Click ‘Add’ in the ‘Group Metrics’ column to input the global or nodal metrics.

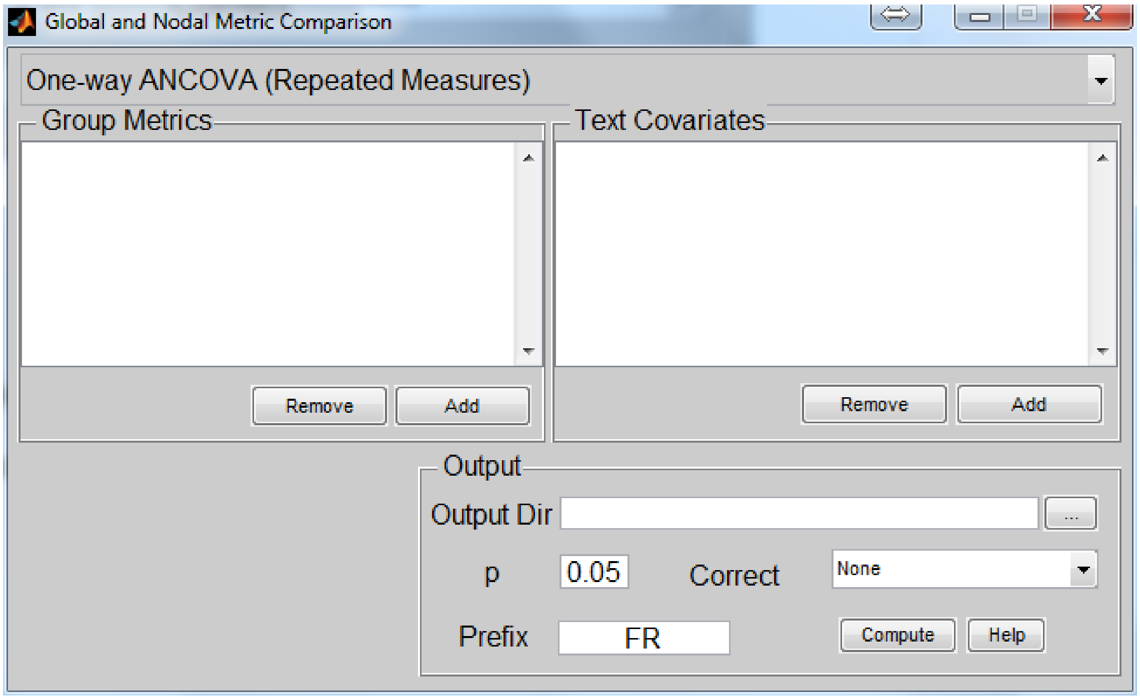
Click ‘Add’ in the ‘Text covariates’ column to input the covariates of no interest (e.g., age, gender and clinical variables) to control the effects of these factors.

Click the button ‘…’ to select the path for outputting results. **Prefix** can be changed if necessary.

Choose one of the multiple correction methods by **clicking the small triangle** to the right of **‘Correct’**.

After setting all of the parameters, **click ‘Compute’** to run this process.

7.1.5. One-Way ANCOVA (Repeated Measures)



One-way ANCOVA (repeated measures) can be used to test whether the global and nodal metrics are significantly different across categories/levels of a repeated variable while controlling the differences of the covariates.

Click 'Add' in the 'Group Metrics' column to input the global or nodal metric.

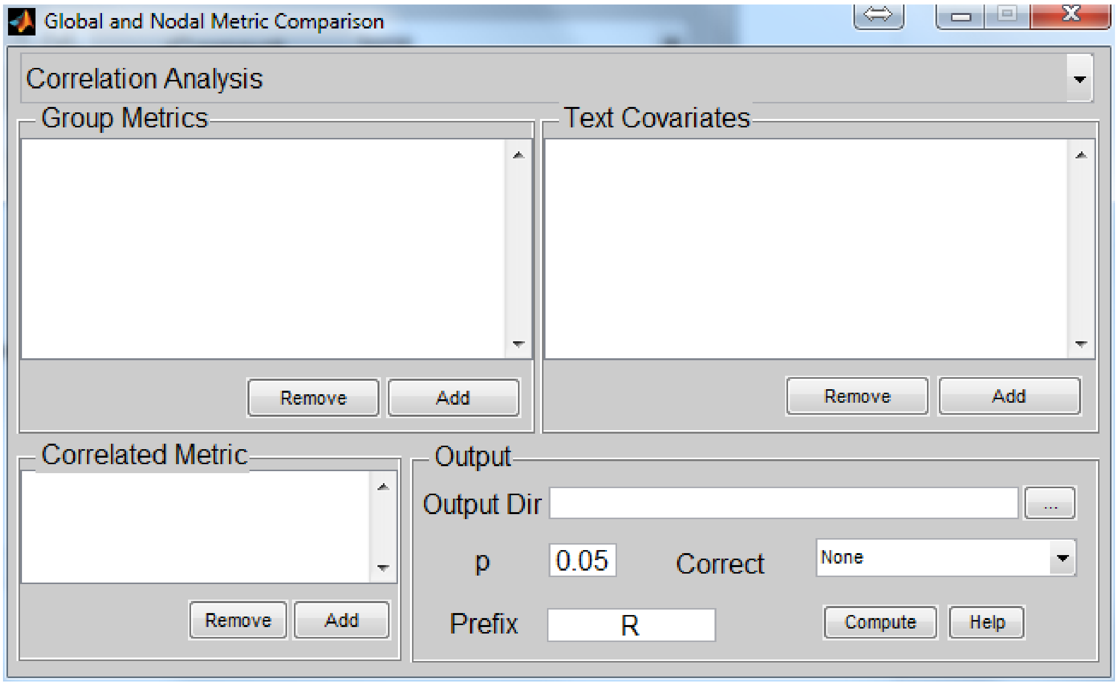
Click 'Add' in the 'Text covariates' column to input the covariates of no interest (e.g., age, gender and clinical variables) control the effects of these factors.

Click the button '…' to select the path for outputting results. **Prefix** can be changed if necessary.

Choose one of the multiple correction methods by **clicking the small triangle** to the right of **'Correct'**.

After setting all of the parameters, **click 'Compute'** to run this process.

7.1.6. Correlation Analysis



Correlation analysis can be used to test whether the global and nodal metrics are significantly correlated with the variable of interest (e.g., demographic, or cognitive, or clinical variables) across subjects while controlling the differences of the covariates of no interest.

Click ‘Add’ in the ‘Group Metrics’ column to input the global or nodal metric.

Click ‘Add’ in the ‘Text covariates’ column to input the covariates of no interest (e.g., age, gender and clinical variables) control the effects of these factors.

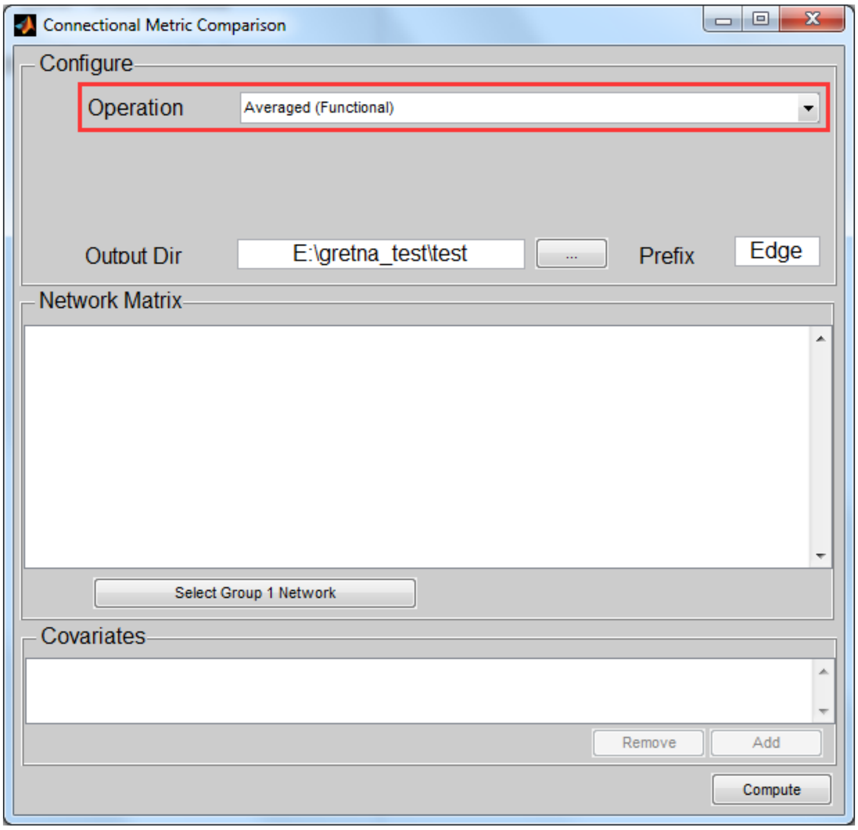
Click ‘Add’ in the ‘Correlated Metric’ column to input the variables of interest.

Click the button ‘…’ to select the path for outputting results. **Prefix** can be changed if necessary.

Choose one of the multiple correction methods by **clicking the small triangle** to the right of **‘Correct’**. After setting all of the parameters, **click ‘Compute’** to run this process.

7.2. Connection

With respect to inter-nodal connection comparisons, the one-sample *t*-test and the two-sample *t*-test are provided, followed by multiple comparison correction procedures, including FDR, Bonferroni and network-based statistic (NBS) methods. Additionally, mean value calculation (for functional connectivity matrix) and backbone extraction (for structural connectivity matrix) are provided in this section.

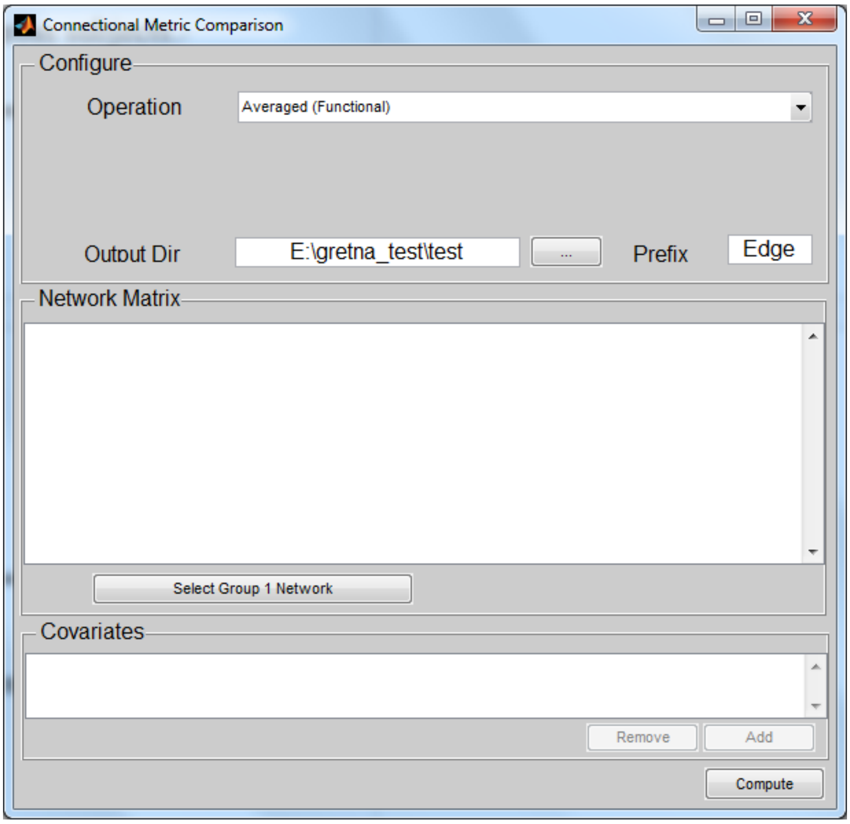


Operation: Averaged (Functional)

Output Dir: E:\gretna_test\test

Prefix: Edge

7.2.1. Averaged (Functional)



Connectional Metric Comparison

Configure

Operation: Averaged (Functional)

Output Dir: E:\gretna_test\test

Prefix: Edge

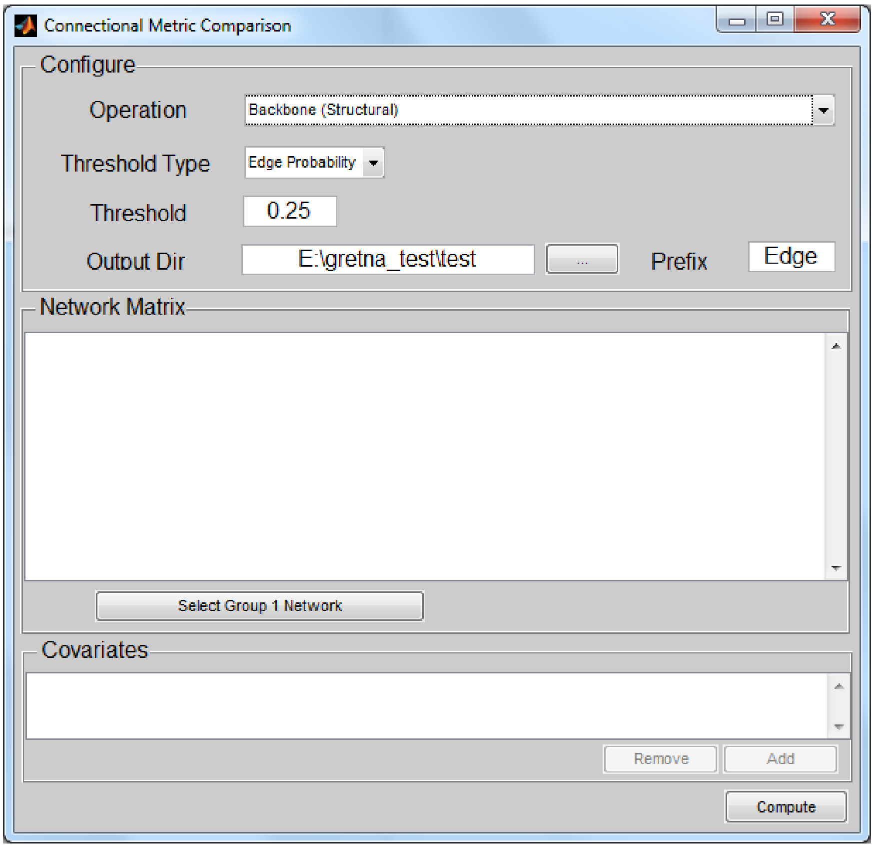
Averaged (Functional) can be used to calculate the mean functional connectivity across subjects.

Click 'Select Group 1 Network' in the 'Network Matrix' column to input the matrix for each subject in a group.

Click the button '…' to select the path for outputting results. **Prefix** can be changed if necessary.

Click 'Compute' to run.

7.2.2. Backbone (Structural)



Operation: Backbone (Structural)
Threshold Type: Edge Probability
Threshold: 0.25
Output Dir: E:\gretna_test\test
Prefix: Edge

Backbone (Structural) can be used to extract the backbone of structural connectivity across subjects.

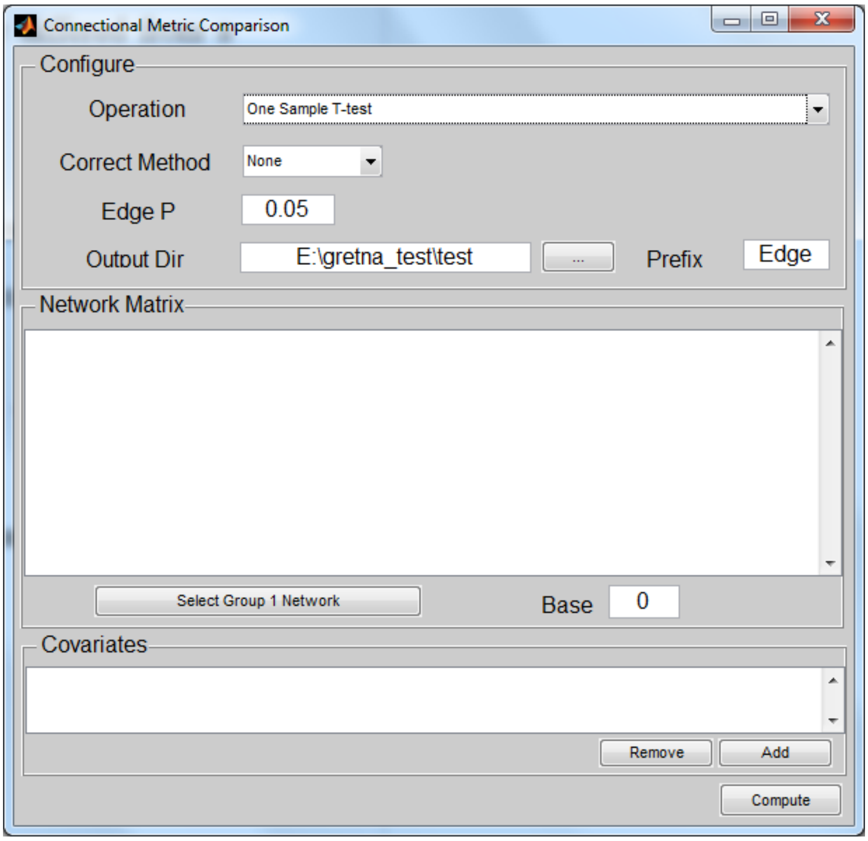
Click 'Select Group 1 Network' in the 'Network Matrix' column to input the matrix for each subject in a group.

Threshold Type refers to edge probability more options will be added in a future release). **Threshold Value** can be changed according to your research purposes.

Click the button '…' to select the path for outputting results. **Prefix** can be changed if necessary.

Click 'Compute' to run.

7.2.3. One-Sample *t*-Test

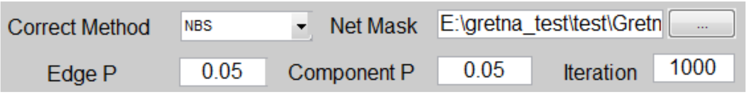


Operation: One Sample T-test
Correct Method: None
Edge P: 0.05
Output Dir: E:\gretna_test\test
Prefix: Edge
Base: 0

One-Sample T-test can be used to examine whether each connection significantly differs from a given value (e.g., 0).

Click ‘Select Group 1 Network’ in the ‘Network Matrix’ column to input the matrix for each subject in a group. You can then **click ‘Add’** in the ‘covariates’ column to input the covariates of no interest.

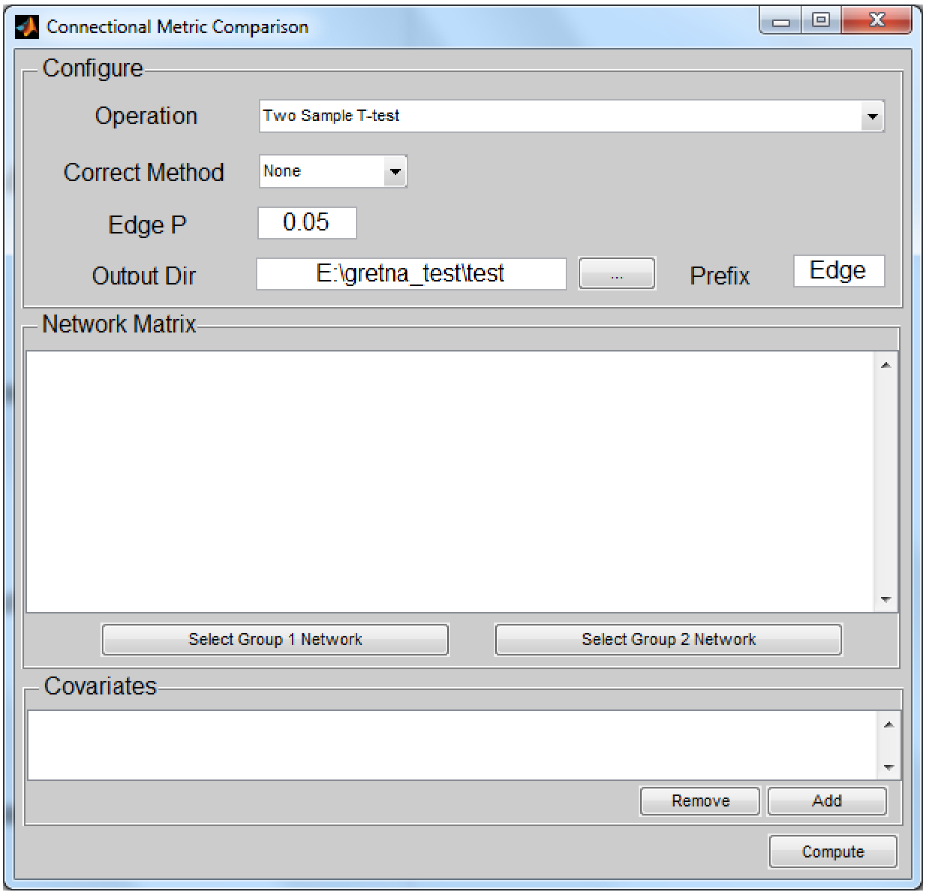
You can choose one of the following **Correct Methods**: FDR, Bonferroni, NBS, or None. You can input a network mask to restrict the statistical scope and set the *p* value of the NBS component and the number of iterations if you choose NBS.



Correct Method: NBS
Net Mask: E:\gretna_test\test\Gretn
Edge P: 0.05
Component P: 0.05
Iteration: 1000

Click the button ‘…’ to select the path for outputting results. **Prefix** can be changed if necessary. **Click ‘Compute’** to run.

7.2.4. Two-Sample *t*-Test



Operation: Two Sample T-test
Correct Method: None
Edge P: 0.05
Output Dir: E:\gretna_test\test ...
Prefix: Edge

Two-Sample T-test can be used to examine whether each connection significantly differs between two groups.

Click 'Select Group 1 Network' in the 'Network Matrix' column to input the matrix for each subject in a group. **Click 'Select Group 2 Network'** to input another group.

Then, you can **click 'Add'** in the 'covariates' column to input the covariates of no interest. You can choose one of the following **Correct Methods**: FDR, Bonferroni, NBS, or None.

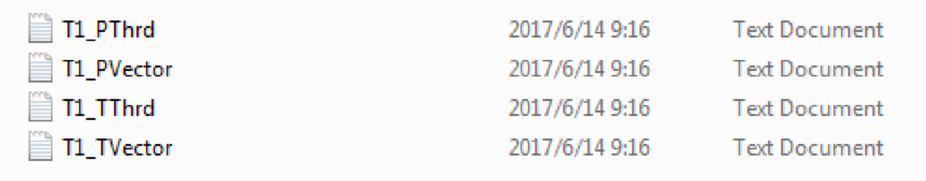
Click the button '…' to select the path for outputting results. **Prefix** can be changed if necessary.

Click 'Compute' to run.

7.3. Results of Metric Comparison

7.3.1. Network and Node

- **One-Sample T-test**



T1_PThrd	2017/6/14 9:16	Text Document
T1_PVector	2017/6/14 9:16	Text Document
T1_TThrd	2017/6/14 9:16	Text Document
T1_TVector	2017/6/14 9:16	Text Document

T1_PVector: The *p* value derived from a one-sample t-test on network metrics for each threshold.

T1_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

T1_TVector: The *t* value derived from a one-sample t-test on network metrics for each threshold.

T1_TThrd: The significance threshold of *t* values after correction of multiple comparisons.

- **Two-Sample T-test**

T2_PThrd	2017/6/14 19:02	Text Document
T2_PVector	2017/6/14 19:02	Text Document
T2_TThrd	2017/6/14 19:02	Text Document
T2_TVector	2017/6/14 19:02	Text Document

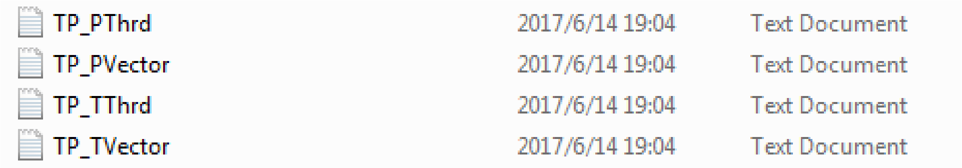
T2_PVector: The *p* value derived from a two-sample t-test on network metrics for each threshold.

T2_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

T2_TVector: The *t* value derived from a two-sample t-test on network metrics for each threshold.

T2_TThrd: The significance threshold of *t* values after correction of multiple comparisons.

- **Paired T-test**



TP_PThrd	2017/6/14 19:04	Text Document
TP_PVector	2017/6/14 19:04	Text Document
TP_TThrd	2017/6/14 19:04	Text Document
TP_TVector	2017/6/14 19:04	Text Document

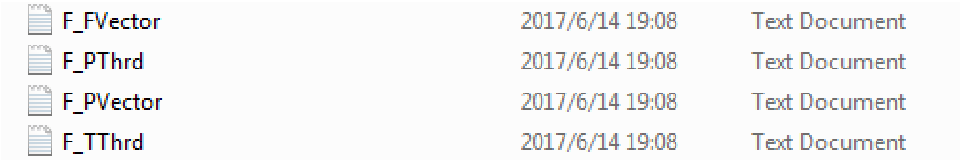
TP_PVector: The *p* value derived from a paired t-test on network metrics for each threshold.

TP_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

TP_TVector: The *t* value derived from a paired t-test on network metrics for each threshold.

TP_TThrd: The significance threshold of *t* values after correction of multiple comparisons.

- **One-way ANCOVA**



F_FVector	2017/6/14 19:08	Text Document
F_PThrd	2017/6/14 19:08	Text Document
F_PVector	2017/6/14 19:08	Text Document
F_TThrd	2017/6/14 19:08	Text Document

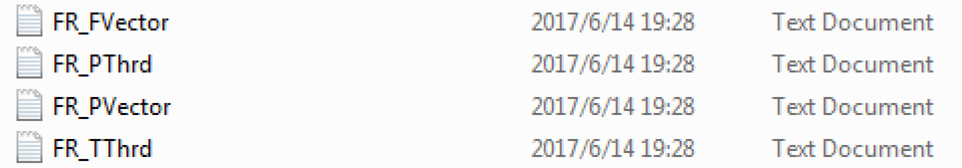
F_FVector: The *F* value derived from one-way ANCOVA on network metrics for each threshold.

F_FThrd: The significance threshold of *F* values after correction of multiple comparisons.

F_PVector: The *p* value derived from one-way ANCOVA on network metrics for each threshold.

F_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

- **One-way ANCOVA (Repeated Measures)**



FR_FVector	2017/6/14 19:28	Text Document
FR_PThrd	2017/6/14 19:28	Text Document
FR_PVector	2017/6/14 19:28	Text Document
FR_TThrd	2017/6/14 19:28	Text Document

FR_FVector: The *F* value derived from repeated one-way ANCOVA on network metrics for each threshold.

FR_FThrd: The significance threshold of *F* values after correction of multiple comparisons.

FR_PVector: The *p* value derived from repeated one-way ANCOVA on network metrics for each threshold.

FR_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

- **Correlation Analysis**

R_PThrd	2017/6/14 19:32	Text Document
R_PVector	2017/6/14 19:32	Text Document
R_RVector	2017/6/14 19:32	Text Document
R_TThrd	2017/6/14 19:32	Text Document

R_PVector: The *p* value derived from correlation analysis between two metrics.

R_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

R_RVector: The *r* value derived from correlation analysis between two metrics.

R_RThrd: The significance threshold of *r* values after correction of multiple comparisons.

7.3.2. Connection

- **Averaged (Functional)**

Edge_Avg	2017/6/15 9:49	Text Document

Edge_Avg: The averaged matrix derived from input functional connectivity matrixes.

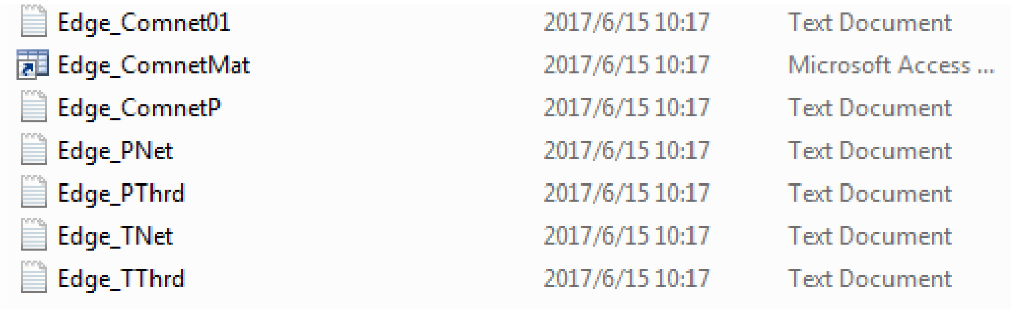
- **Backbone (Structural)**

Edge_Backbone	2017/6/15 9:58	Text Document
Edge_Probability	2017/6/15 9:58	Text Document

Edge_Backbone: The backbone (mask) matrix of input structural matrixes above a given probability threshold.

Edge_Probability: The group probability matrix derived from input individual functional connectivity matrixes.

- **One Sample T-test**



Edge_Comnet01	2017/6/15 10:17	Text Document
Edge_ComnetMat	2017/6/15 10:17	Microsoft Access ...
Edge_ComnetP	2017/6/15 10:17	Text Document
Edge_PNet	2017/6/15 10:17	Text Document
Edge_PThrd	2017/6/15 10:17	Text Document
Edge_TNet	2017/6/15 10:17	Text Document
Edge_TThrd	2017/6/15 10:17	Text Document

R_PNet: The *p* value derived from a one-sample T-test for each connection.

R_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

R_TNet: The *t* value derived from a one-sample t-test for each connection.

R_TThrd: The significance threshold of *t* values after correction of multiple comparisons.

If NBS correction is selected, you will obtain the following:

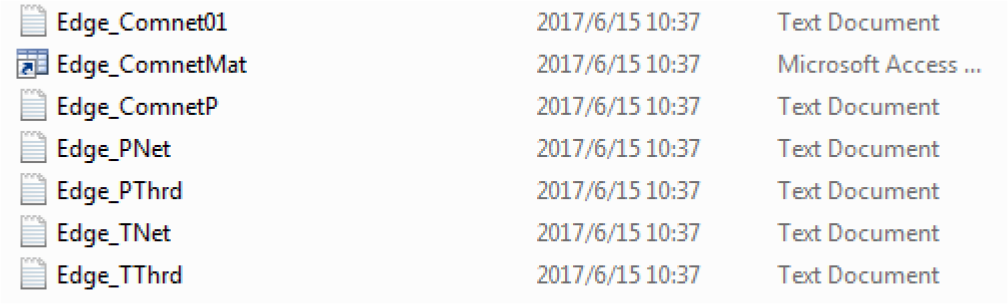
Edge_Comnet01: A matrix (included 1 and 0) indicating the connections in significant component 1.

Edge_ComnetP: The *p* value derived from NBS for each component.

Edge_ComnetMat: A MAT-file including *p* value of the component and matrix mask for significant components.

These files cannot be obtained if no significant results after NBS correction.

- **Two Sample T-test**



Edge_Comnet01	2017/6/15 10:37	Text Document
Edge_ComnetMat	2017/6/15 10:37	Microsoft Access ...
Edge_ComnetP	2017/6/15 10:37	Text Document
Edge_PNet	2017/6/15 10:37	Text Document
Edge_PThrd	2017/6/15 10:37	Text Document
Edge_TNet	2017/6/15 10:37	Text Document
Edge_TThrd	2017/6/15 10:37	Text Document

R_PNet: The *p* value derived from a two-sample t-test for each connection.

R_PThrd: The significance threshold of *p* values after correction of multiple comparisons.

R_TNet: The *t* value derived from a two-sample t-test for each connection.

R_TThrd: The significance threshold of *t* values after correction of multiple comparisons.

If NBS correction is selected, you will obtain the following:

Edge_Comnet01: A matrix (included 1 and 0) indicating the connections in significant component 1.

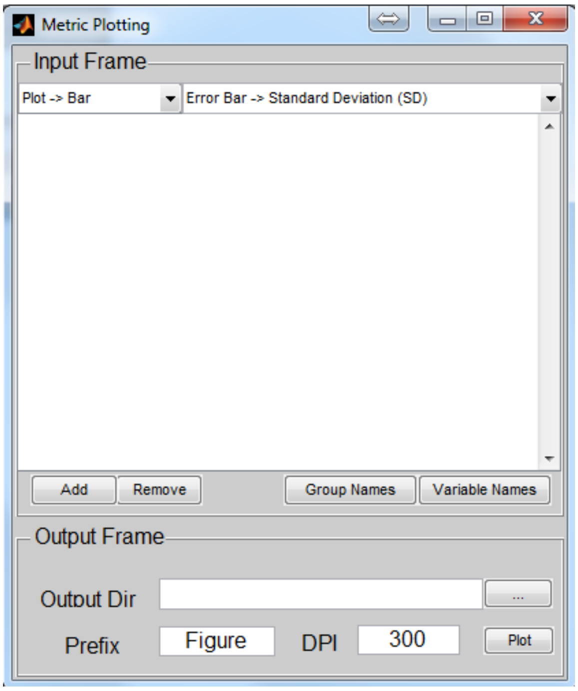
Edge_ComnetP: The *p* value derived from NBS for each component.

Edge_ComnetMat: A MAT-file including the *p* value of the component and matrix mask for significant components.

These files cannot be obtained if no significant results after NBS correction.

8. Metric Plotting

In the new version of GRETNA, we have added a new section to plot four types of charts typically used in research, including bar, dot, violin and shape graphs. This section works well with MATLAB 2014b or later version



Plot -> Bar

Error Bar -> Standard Deviation (SD)

Output Dir

Prefix Figure

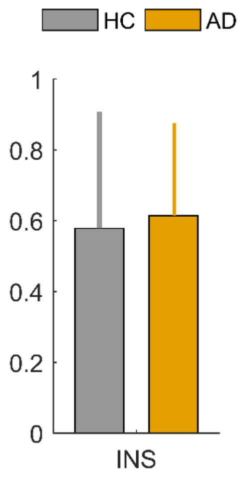
DPI 300

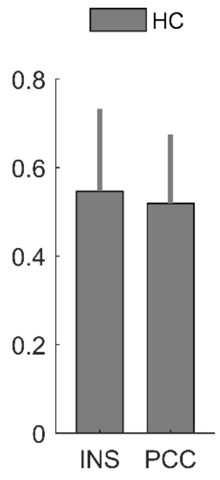
Click 'Add' to input the text for each group. Each row of text represents one participant, and each column of text represents one variable. And **click 'Group Names'** to define the name of each group that will be shown in the caption. **Click 'Variable Names'** to define the name of each variable that will be shown in the label.

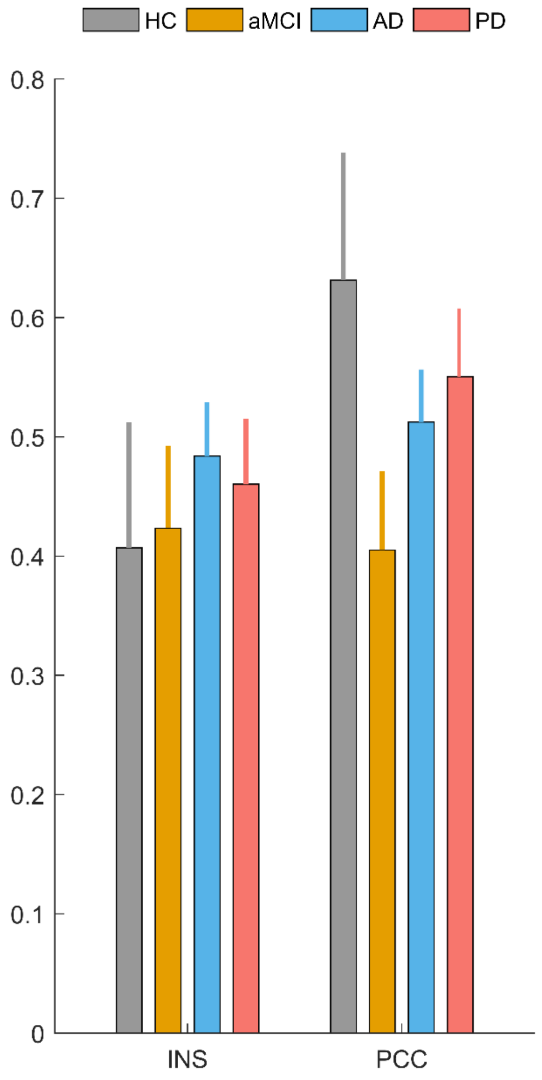
Three types of **Error Bars** can be chosen: standard deviation (SD), standard error of the mean (SEM) and 95% confidence interval (CI). **Click the button '…'** to select the path for outputting results. **Prefix** can be changed if necessary. **DPI** is the image resolution. **Click 'Plot'** to run.

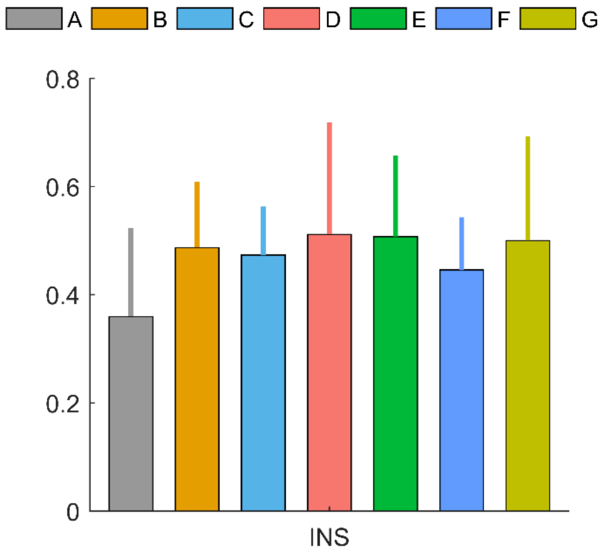
See **test_figure.m** or **Gretna_Plot_Gallery.pdf** **`(…/Gretna/MakeFigures/ and …/Gretna/MakeFigures/Samples/)`** for more complex plotting.

8.1. Bar

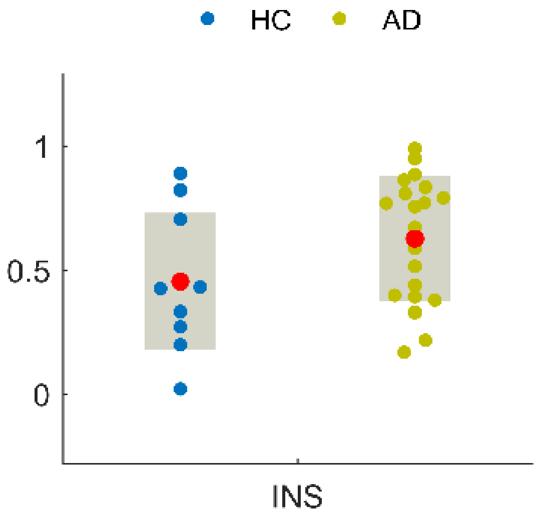

HC
AD
1
0.8
0.6
0.4
0.2
0
INS

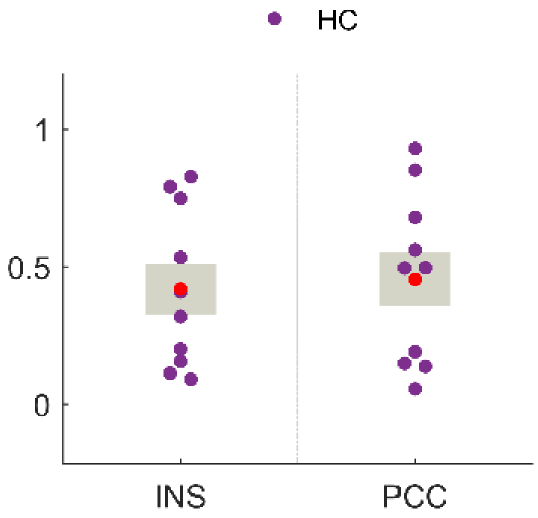

HC
0.8
0.6
0.4
0.2
0
INS
PCC

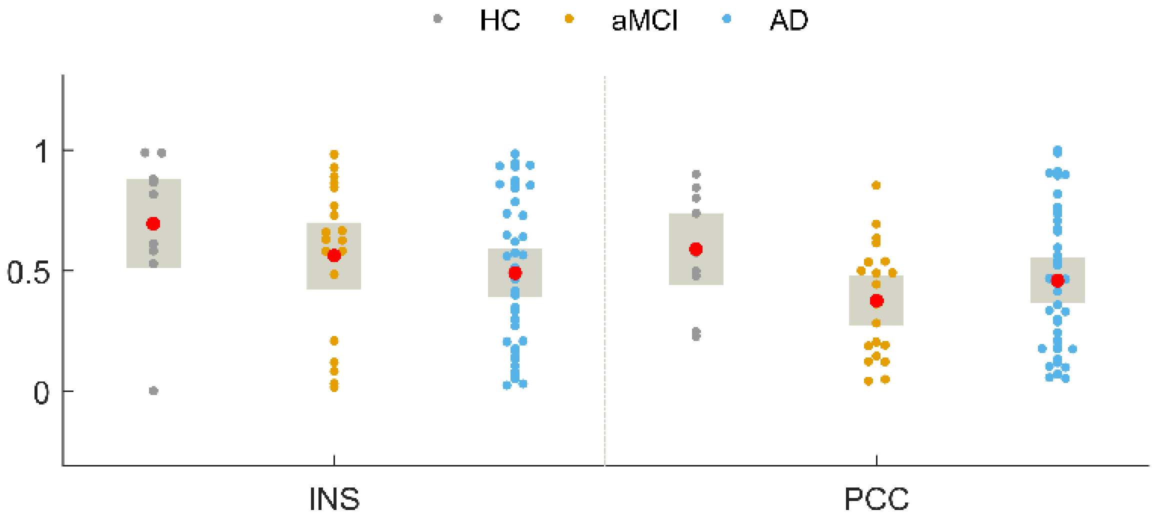

HC
aMCI
AD
PD
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
INS
PCC


A
B
C
D
E
F
G
0.8
0.6
0.4
0.2
0
INS

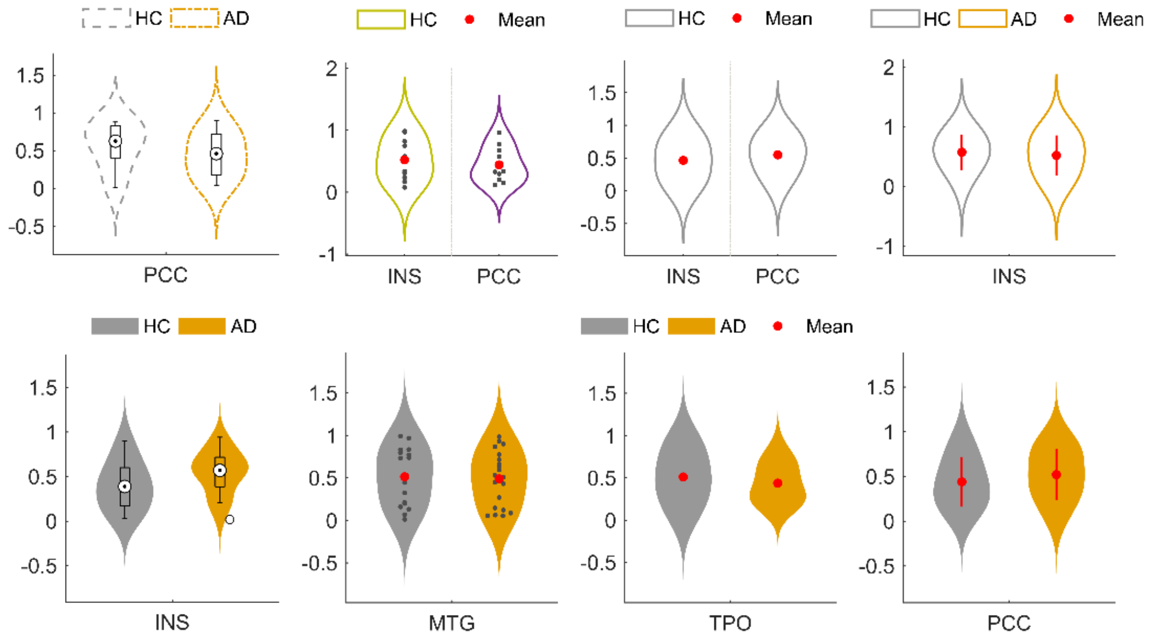
8.2. Dot

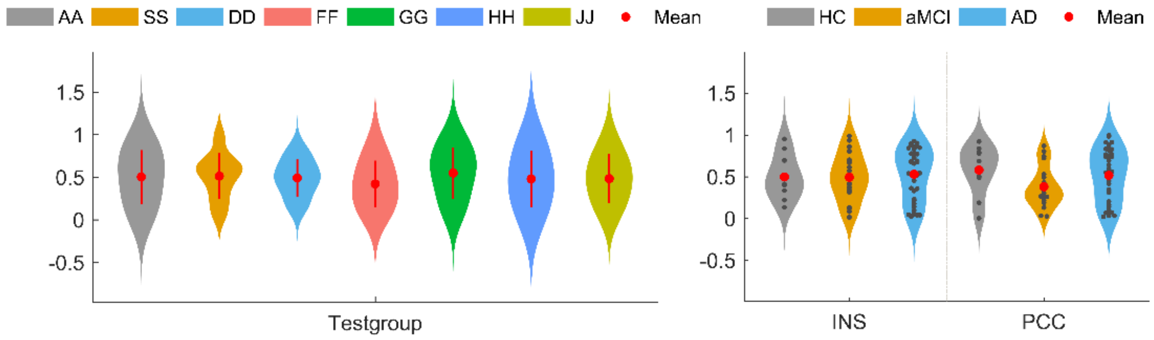




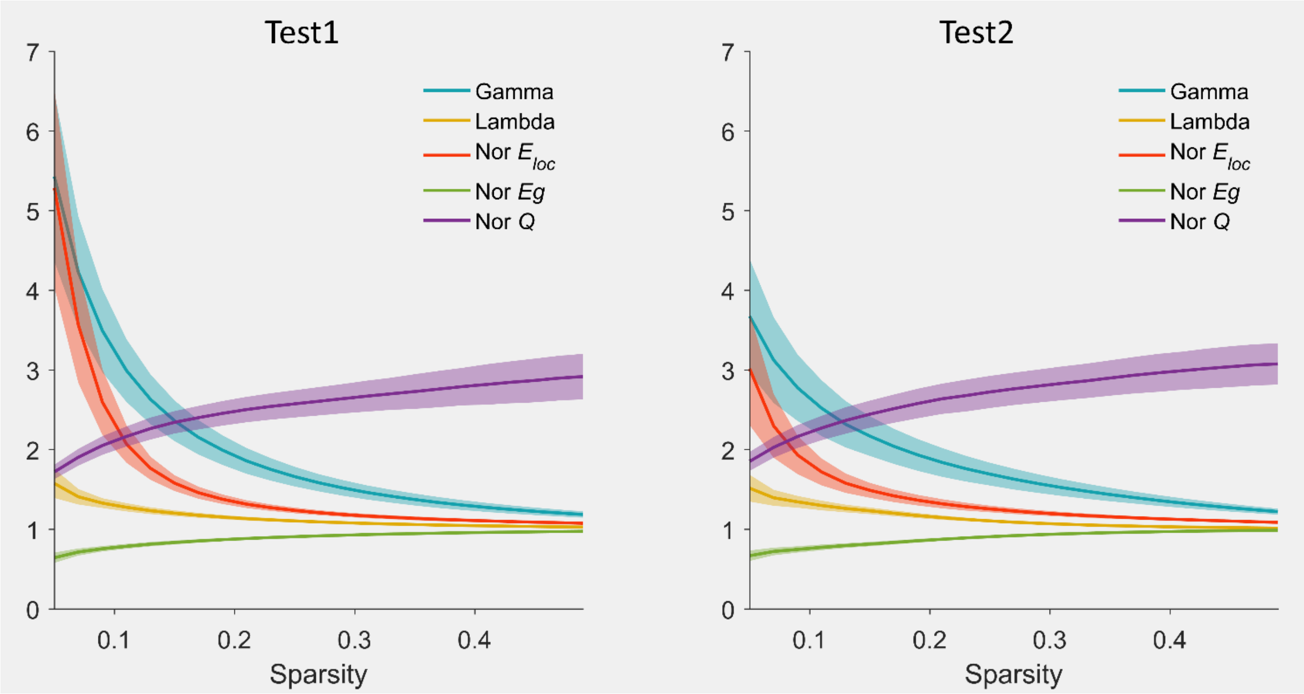


8.3. Violin

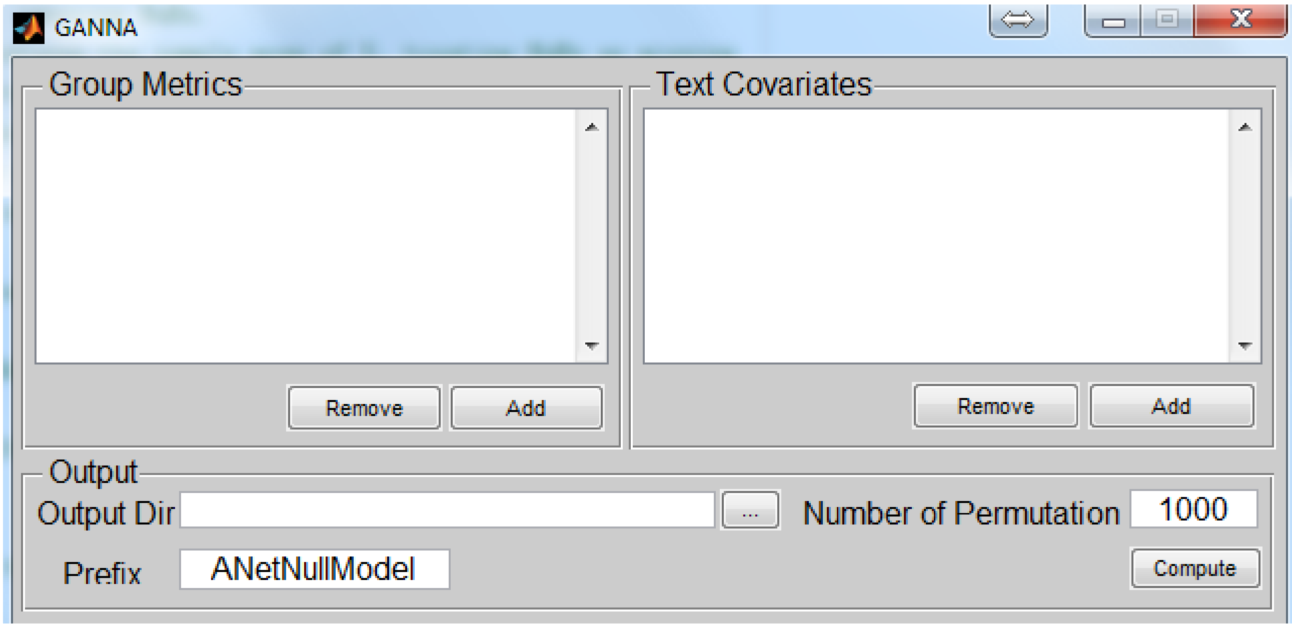

HC AD
1.5
1
0.5
0
-0.5
PCC
HC ● Mean
2
1
0
-1
INS
PCC
HC ● Mean
1.5
1
0.5
0
-0.5
INS
PCC
HC AD ● Mean
2
1
0
-1
INS
HC AD
1.5
1
0.5
0
-0.5
INS
1.5
1
0.5
0
-0.5
MTG
HC AD ● Mean
1.5
1
0.5
0
-0.5
TPO
1.5
1
0.5
0
-0.5
PCC


AA SS DD FF GG HH JJ ● Mean
1.5
1
0.5
0
-0.5
Testgroup
HC aMCI AD ● Mean
1.5
1
0.5
0
-0.5
INS
PCC

8.4. Shade


Test1
Test2
Gamma
Lambda
Nor E_{loc}
Nor Eg
Nor Q
7
6
5
4
3
2
1
0
0.1
0.2
0.3
0.4
Sparsity

9. GANNM



Number of Permutation: 1000

Prefix: ANetNullModel

This section allows researchers to generate a null model of an anatomical (cortical thickness or VBM) associated network using permutations. Users can then adopt this network null model to estimate the null model of network metrics, e.g., small-world coefficient.

Click 'Add' in the 'Group Metrics' column to input the text including anatomical metrics (one set of text represents a group of anatomical metrics, each row indicates one subject and each column indicates one region). Then, you can **click 'Add'** in the 'Text Covariates' column to input the covariates of no interest.

Number of Permutations can be changed according to your research purposes (e.g., 5,000 or 10,000).

Click the button '…' to select the path for outputting results. **Prefix** can be changed if necessary.

Click 'Compute' to run.

Acknowledgements

We thank the following colleagues for their kind helps during GRETNA developing and testing: Mingrui Xia, Xuhong Liao, Miao Cao, Zhengjia Dai, Hao Wang, Zhijiang Wang, Jin Liu, Xiaodan Chen, Yuehua Xu, Zhilei Xu, Qing Ma, Yapei Xie, Xiaoyi Sun, Siqi Wang, Rui Hou, Junjiao Feng, Feng Liu (Tianjin Medical University General Hospital), Qiang Xu (Tianjin Medical University General Hospital), Tao Liu (Beihang University), Chao Dong (Beihang University), Lei Gao (Zhongnan Hospital)， Wei Cheng (Fudan University) and Professor Alan Evans (McGill University, Canada)

We thank the following colleagues for their efforts in manual revising:
Jin Liu, Miao Cao, Xindi Wang

We also thank the developers of the following softwares and toolboxes whose source codes or file formats were referenced during our package developing:

Matlab: www.mathworks.com/products/matlab/
MatlabBGL: www.cs.purdue.edu/homes/dgleich/packages/matlab_bgl/
MRIcroN: www.mccauslandcenter.sc.edu/mricro/mricron/
Brain Connectivity Toolbox: sites.google.com/site/bctnet/
SPM: www.fil.ion.ucl.ac.uk/spm/
REST: www.restfmri.net/

Reference

Cui Z, Zhong S, Xu P, He Y, Gong G (2013): PANDA: a pipeline toolbox for analyzing brain diffusion images. Front Hum Neurosci 7:42.

Maslov S, Sneppen K (2002): Specificity and stability in topology of protein networks. Science 296:910-913.

Ravasz E, Barabási A-L (2003): Hierarchical organization in complex networks. Phys. Rev. E. 67:026112.

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

Wang JH, Zuo XN, Gohel S, Milham MP, Biswal BB, He Y (2011): Graph theoretical analysis of functional brain networks: test-retest evaluation on short- and long-term resting-state functional MRI data. PLoS One 6:e21976.