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GRETNA

A *Graph-theoretical Network Analysis Toolkit*

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A Brief Introduction of Gretna

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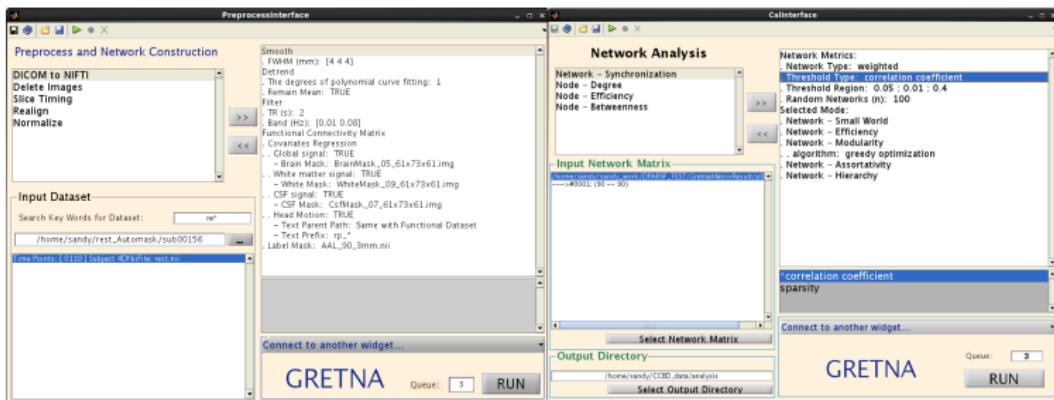
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- This toolkit, termed as Gretna, is designed to perform graph-theoretical network analysis of fMRI data. It can calculate most frequently used network metrics currently, e.g. small world parameters (Watts and Strogatz, 1998), network efficiency (Latora et al., 2001; Marchiori et al., 2003) and etc.



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- Gretna has a simplified interface to calculate brain network metrics.
- Gretna allows you to arrange the order of preprocess.
- Gretna supports 3D/4D NIFTI-1 format.
- Gretna use PSOM (<http://code.google.com/p/psom>) so you can run jobs in parallel as well as check and restart failed jobs.
- you can get this toolkit at
www.nitrc.org/frs/download.php/5534/gretna.zip



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- ① DICOM to NIFTI
- ② Delete Images
- ③ Slice Timing
- ④ Realign
- ⑤ Normalize
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- ⑩ Functional Connectivity Matrix
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DICOM to NIFTI

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NIFTI:
Neuroimaging Informatics
Technology Initiative



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- Scanner Instability
- Subject's State Instability



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- Different Time Points' Signal ↓
Same Time Points' Signal
- NOTE: Slice Order and Reference Slice



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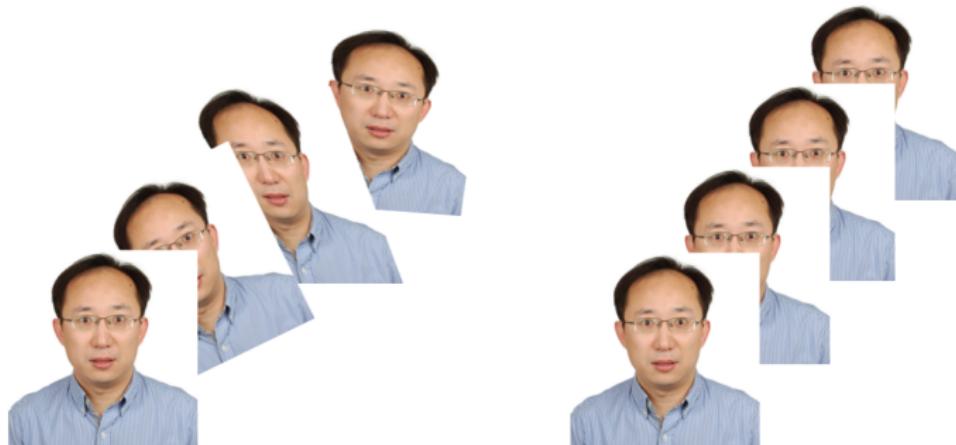
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- Head Motion Correction
- Note: This step DO NOT remove head motion effect!



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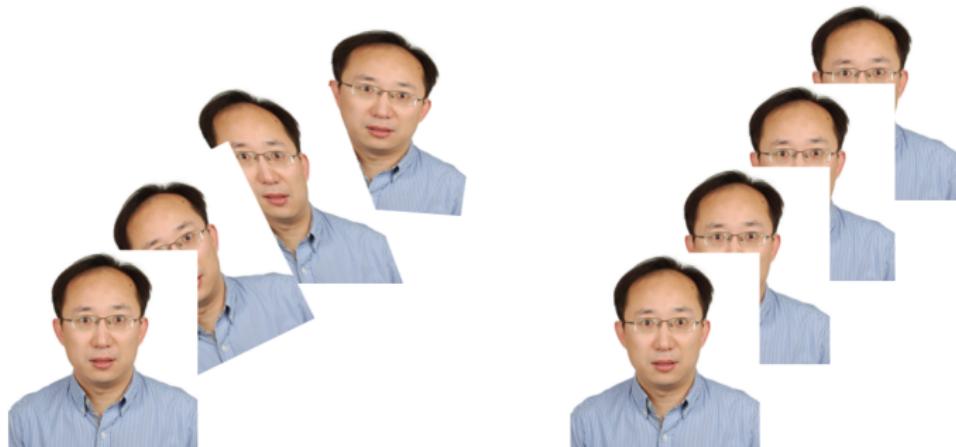
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- Head Motion Correction
- Note: This step DO NOT remove head motion effect!



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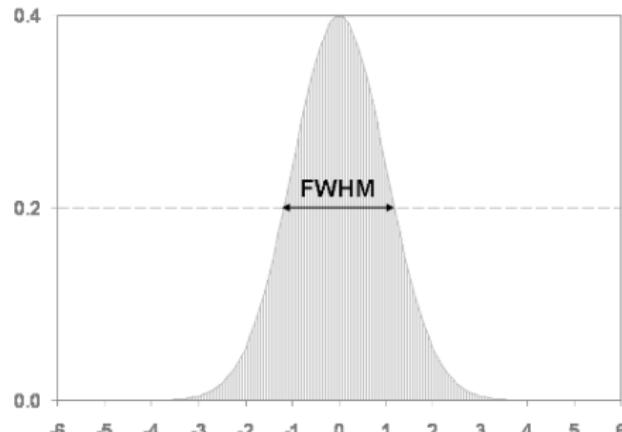
Run

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PyGretna

Acknowledge



- Improve CNR and validity of the statistical tests.
- Accommodation of variations between subjects.
- Note: What is FWHM?



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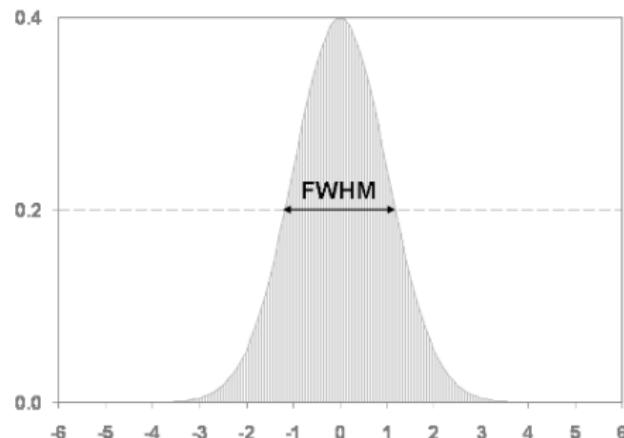
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- Improve CNR and validity of the statistical tests.
- Accommodation of variations between subjects.
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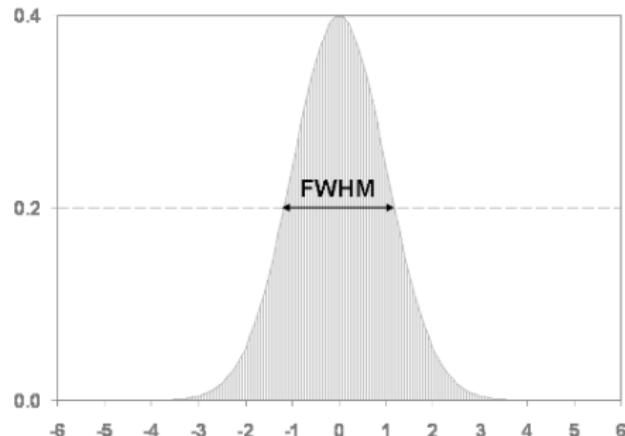
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- Improve CNR and validity of the statistical tests.
- Accommodation of variations between subjects.
- Note: What is FWHM?



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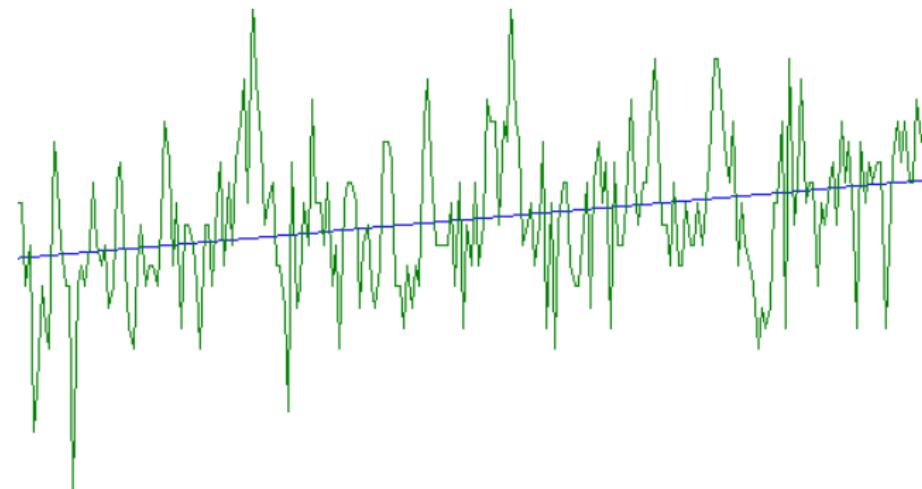
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- What the drift of fMRI signal is?



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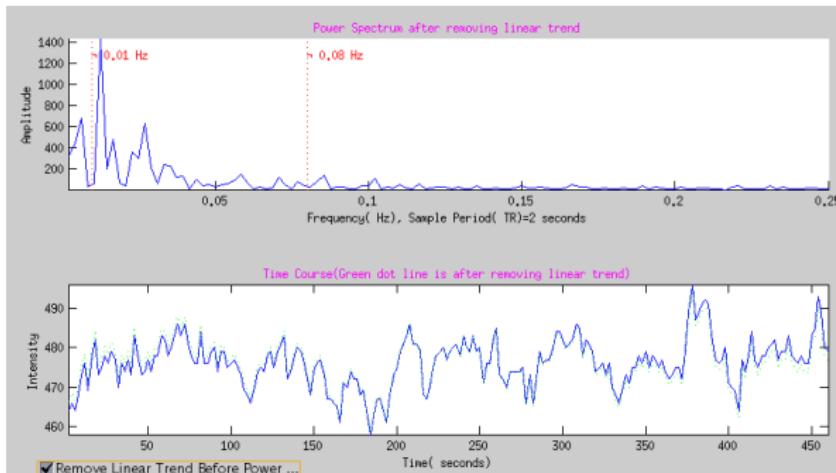
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- Fourier Transform
- Resting-state Band: <0.01Hz



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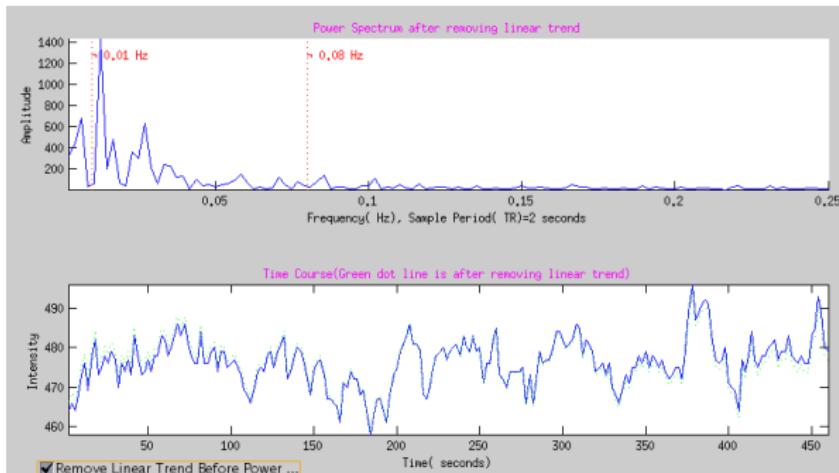
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- Fourier Transform
- Resting-state Band: <0.01Hz



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GLM Model

- Global Signal
- White Matter Signal
- Cerebrospinal Fluid Signal
- Head Motion Parameter: 6, 12, 24, 36
- ...



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Functional Connectivity Matrix

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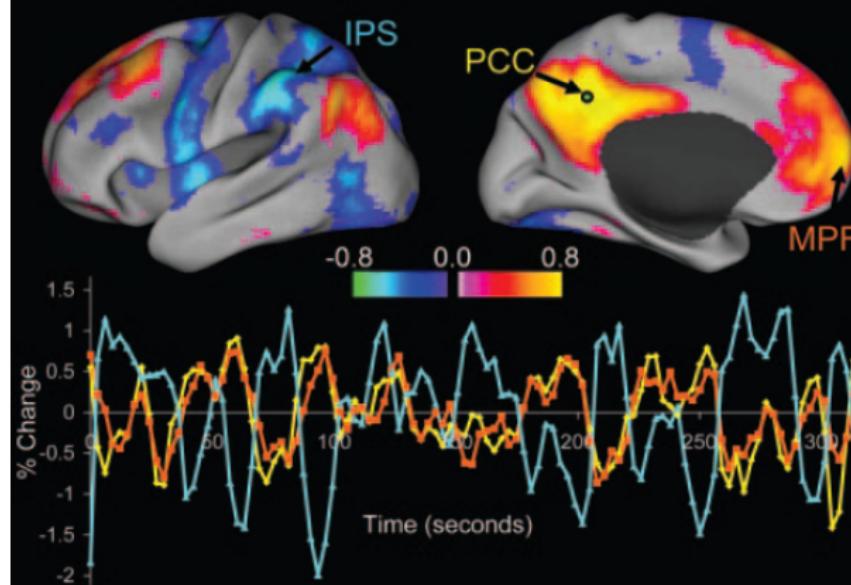
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- M.D. Fox, et al., 2005



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Voxel-based Degree

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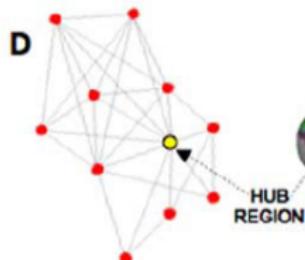
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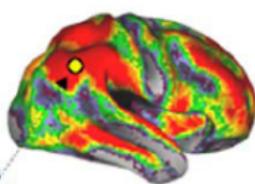
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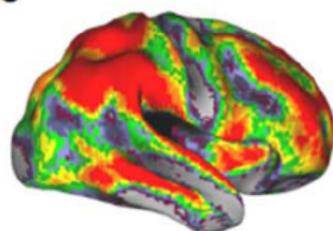
NETWORK ANALYSIS OF HUBS



$$D_i = \sum d_{ij}$$



C





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Calculating Brain network metrics

- Network - Small World
- Network - Efficiency
- Network - Modularity
- Network - Assortativity
- Network - Hierarchy
- Network - Synchronization
- Node - Degree
- Node - Efficiency
- Node - Betweenness



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Network - Small World

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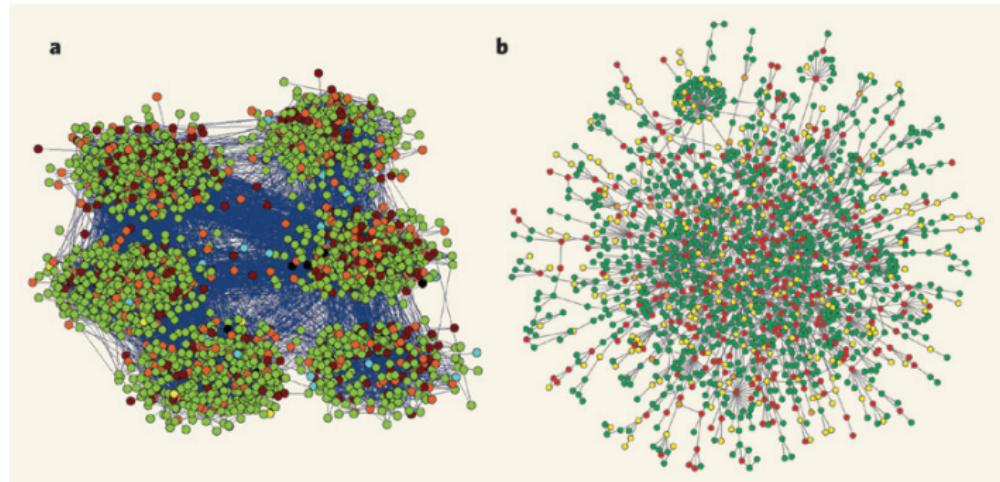
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- S. Redner, 2008



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Network - Hierarchy

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Install Gretna in MATLAB

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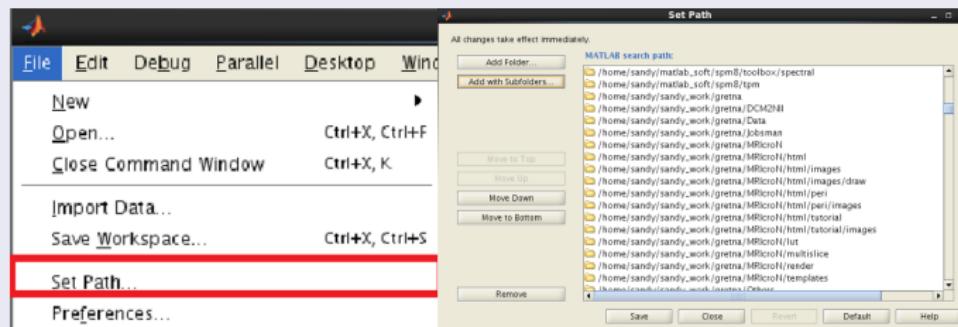
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Acknowledge

Add Gretna to MATLAB search path and save it



- Gretna support MATLAB(2010a) and above at Windows/Linux/Mac OS
- Gretna call SPM8 to preprocess your fMRI data, so please ensure you have installed SPM8



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Initiate Gretna

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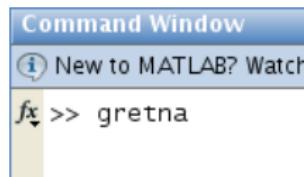
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- Gretna includes two parts:
 - ① Network construction
 - ② Network metrics.



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Procedure: Begin to Calculate

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Preprocess and Network Construction

DICOM to NIFTI

Delete Images

Slice Timing

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Normalize

Smooth

Detrend

Filter

Covariates Regression

>>

<<



Preprocess and Network Construction

DICOM to NIFTI

Filter

Covariates Regression

Functional Connectivity Matrix

>>

<<

Delete Images

. The delete type: Delete

. . Delete first 10 time points

Slice Timing

. Number of Slices: 33

. TR (s): 2

. Slice order: 1:2:33,2:2:32

. Reference Slice: 33

Realign

Normalize

. Normalize Method: EPI

. Source Image Path: Same with Functional Dataset

. Source Image Prefix: mean*





GUIDE

Network construction Window - Input

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The screenshot displays four separate windows titled "Input Dataset" arranged in a 2x2 grid. Each window contains a search bar labeled "Search Key Words for Dataset" and a list of entries.

- Top Left:** Shows "DICOM File: [10320] DICOM Directory: p001" and "DICOM File: [10320] DICOM Directory: p002".
- Top Right:** Shows "Time Points: [0230] Subject Directory: 0001/" through "Time Points: [0230] Subject Directory: 0006/".
- Bottom Left:** Shows "Time Points: [0240] Subject Directory: sub01077/rest.nii" through "Time Points: [0240] Subject Directory: sub01236/rest.nii".
- Bottom Right:** Shows "Time Points: [0230] Subject 4DNiiFile: 20100514_140449qefu" through "Time Points: [0220] Subject 4DNiiFile: dswran20100514_140449".

- You need to select a parent folder which includes:
 - ① folders of DICOM files,
 - ② folders of 3D Analyze/Nifti files,
 - ③ folders of 4D Nifti files
 - ④ 4D Nifti files.



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Network metrics Window - Input

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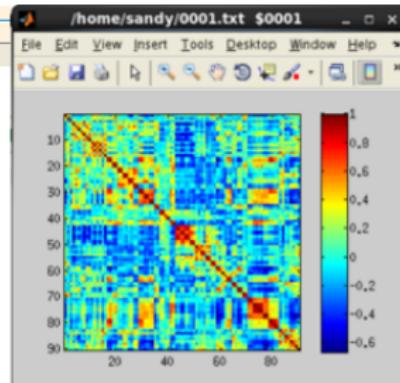
Metrics

PyGretna

Acknowledge

Input Network Matrix

```
/home/sandy/0001.txt  
--->#0001: (90 -- 90)  
/home/sandy/a.mat  
--->#0002: (90 -- 90)  
/home/sandy/b.mat  
--->#0003: (90 -- 90)  
--->#0004: (90 -- 90)  
--->#0005: (90 -- 90)  
--->#0006: (90 -- 90)  
--->#0007: (90 -- 90)  
--->#0008: (90 -- 90)  
--->#0009: (90 -- 90)  
--->#0010: (90 -- 90)  
--->#0011: (90 -- 90)  
--->#0012: (90 -- 90)
```



- You can select three format matrixs includes:
 - ① matrixs saved with *.txt files
 - ② matrixs saved in a *.mat files
 - ③ a cell of matrixs saved in a *.mat files
- You can check inputed matrixs with double click



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Logs: Record your “GUILT”

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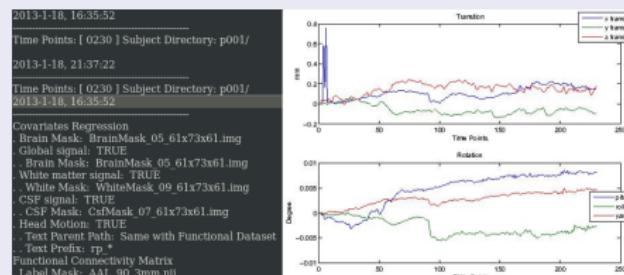
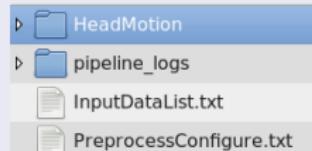
Construction

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Acknowledge

You can find logs in a folder named “GretnaLogs”





GUIDE

Toolbar: Configure and Control Your Pipeline

GRETNA

Sandy Wang



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Easy to use toolbar (from left to right)

- ① Change Default Configure
- ② Gretna Manual
- ③ Load your Configure
- ④ Save current Configure
- ⑤ Run Jobs
- ⑥ Refresh Jobs Status
- ⑦ Stop current Jobs



GUIDE

Run: Computer is hard-working, not you!

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Start Network Construction



Input Dataset

Search Key Words for Dataset:

*

/home/sandy/sandy_work/DPARSF_TEST/Gretna_4 ...

(p001/Dcm2Nii): running

(p002/Dcm2Nii): none



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PreprocessInterface

Preprocess and Network Construction

DICOM to NIFTI

Filter

Covariates Regression

Functional Connectivity Matrix

Input Dataset

Search Key Words for Dataset:

/home/sandy/RSorSR/SR/ec/FunImg

Time Points: [0230] Subject Directory: 0001/
Time Points: [0230] Subject Directory: 0002/
Time Points: [0230] Subject Directory: 0003/
Time Points: [0230] Subject Directory: 0004/
Time Points: [0230] Subject Directory: 0006/
Time Points: [0230] Subject Directory: 0007/
Time Points: [0230] Subject Directory: 0008/
Time Points: [0230] Subject Directory: 0009/
Time Points: [0230] Subject Directory: 0010/
Time Points: [0230] Subject Directory: 0012/
Time Points: [0230] Subject Directory: 0013/
Time Points: [0230] Subject Directory: 0014/
Time Points: [0230] Subject Directory: 0015/
Time Points: [0230] Subject Directory: 0017/
Time Points: [0230] Subject Directory: 0018/
Time Points: [0230] Subject Directory: 0019/
Time Points: [0230] Subject Directory: 0020/

Delete Images
. The delete type: Delete
. . Delete first 10 time points

Slice Timing
. Number of Slices: 33
. TR (s): 2
. Slice order: 1:2:33,2:2:32
. Reference Slice: 33

Realign

Normalize
. Normalize Method: EPI

. Source Image Path: Same with Functional Dataset
. Source Image Prefix: mean*
. Voxel Sizes (mm): [3 3 3]
. Bounding box: [-90 , -126 , -72 ; 90 , 90 , 108]

Smooth
. FWHM (mm): [4 4 4]

Detrend
. The degrees of polynomial curve fitting: 1

. Remain Mean: TRUE

*EPI
T1

Connect to another widget...

GRETNA

Queue: 3

RUN

Navigation icons: back, forward, search, etc.



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DICOM to NIFTI

- . Time Point: 240
- . Delete Images
- . The delete type: Delete
 - .. Delete first 10 time points
- . Slice Timing
- . Number of Slices: 33
- . TR (s): 2
- . Slice order: 1:2:33,2:2:32
- . Reference Slice: 33

Realign

Normalize

- . Normalize Method: EPI
- . Source Image Path: Same with Functional Dataset
- . Source Image Prefix: mean*
- . Voxel Sizes (mm): [3 3 3]
- . Bounding box: [-90 , -126 , -72 ; 90 , 90 , 108]

Normalize

Normalize Method: T1

- .. T1 Path <-X
 - .. DICOM to Nifti: FALSE
 - .. Coregister: TRUE
 - .. Segment: TRUE
 - Source Image Path: Same with Functional Dataset
 - Source Image Prefix: mean*
 - T1 Images Prefix: co*
 - Affine Regularisation: mni
 - .. Mat Suffix: *_seg_sn.mat
 - . Voxel Sizes (mm): [3 3 3]
 - . Bounding box: [-90 , -126 , -72 ; 90 , 90 , 108]
- Smooth
- . FWHM (mm): [4 4 4]
- Detrend
- . The degrees of polynomial curve fitting: 1
 - . Remain Mean: TRUE

Filter

- . TR (s): 2
- . Band (Hz): [0.01 0.08]
- Covariates Regression
- . Brain Mask: BrainMask_05_61x73x61.img
- . Global signal: TRUE
- . Brain Mask: BrainMask_05_61x73x61.img
- . White matter signal: TRUE
- . White Mask: WhiteMask_09_61x73x61.img
- . CSF signal: TRUE
- . CSF Mask: CsfMask_07_61x73x61.img
- . Head Motion: TRUE
- . Text Parent Path: Same with Functional Dataset
- .. Text Prefix: rp_*
- Functional Connectivity Matrix
- . Label Mask: AAL_90_3mm.nii



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DICOM to NIFTI

|. Time Point: 240

- Provide the number of your dataset's time points



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Network construction Window - Delete Images

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Acknowledge

Delete Images

- . The delete type: Delete
 - .. Delete first 10 time points

- Select Deleting Type
- Provide the number of images deleted



GUIDE

Network construction Window - Slice Timing

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Slice Timing

- . Number of Slices: 43
- . TR (s): 2
- . Slice order: 1:2:43,2:2:42
- . Reference Slice: 33

- The number of slices
- TR of scans
- A slice order sequence
- A reference slice (like SPM)



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Network construction Window - Realign

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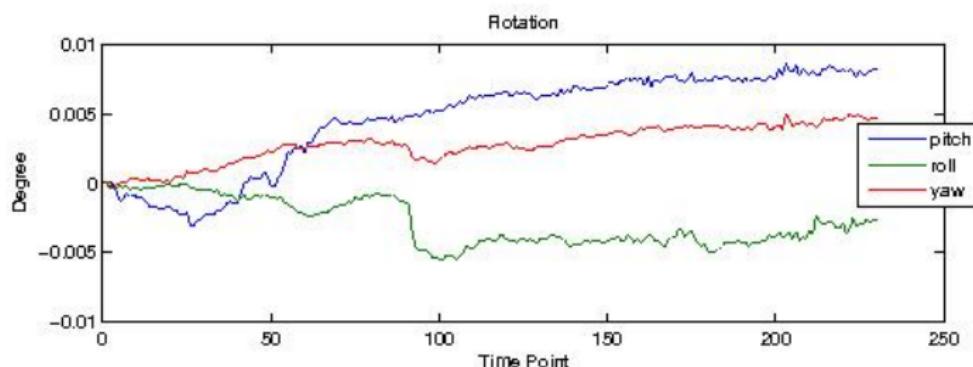
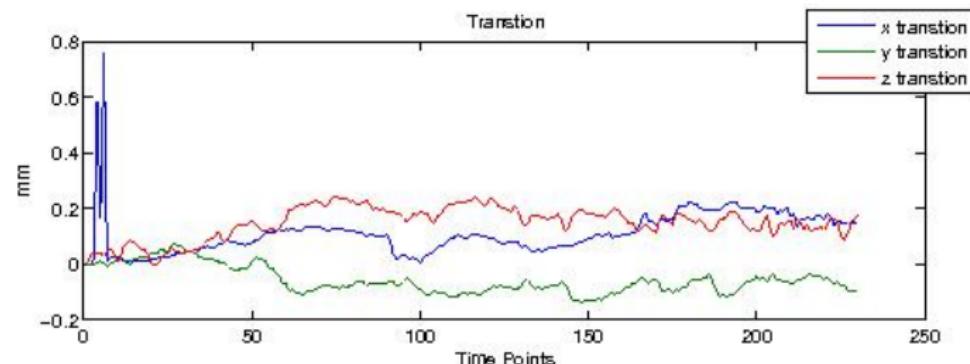
Run

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Normalize

- . Normalize Method: EPI
- . Source Image Path: Same with Functional Dataset
- . Source Image Prefix: mean*
- . Voxel Sizes (mm): [3 3 3]
- . Bounding box: [-90 , -126 , -72 ; 90 , 90 , 108]

Normalize

- . Normalize Method: T1
 - .. T1 Path <-X
 - .. DICOM to Nifti: FALSE
 - .. Coregister: TRUE
 - .. Segment: TRUE
 - Source Image Path: Same with Functional Dataset
 - Source Image Prefix: mean*
 - T1 Images Prefix: co*
 - Affine Regularisation: mni
 - .. Mat Suffix: *_seg_sn.mat
 - . Voxel Sizes (mm): [3 3 3]
 - . Bounding box: [-90 , -126 , -72 ; 90 , 90 , 108]

- EPI
- T1 Segment
- Prefix and Suffix
- Voxel Size
- Bounding Box



GUIDE

Network construction Window - Smooth

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Smooth

. FWHM (mm): [4 4 4]

- 4, 6, 8, 12



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Network construction Window - Detrend

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Detrend

- . The degrees of polynomial curve fitting: 1
- . Remain Mean: TRUE

- Linear or nonlinear



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Network construction Window - Filter

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Acknowledge

Filter

- . TR (s): 2
- . Band (Hz): [0.01 0.08]

- Resting-state Band



GUIDE

Network construction Window - Covariates Regression

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Covariates Regression

- . Brain Mask: BrainMask_05_61x73x61.img
- . Global signal: TRUE
- . . Brain Mask: BrainMask_05_61x73x61.img
- . White matter signal: TRUE
- . . White Mask: WhiteMask_09_61x73x61.img
- . CSF signal: TRUE
- . . CSF Mask: CsfMask_07_61x73x61.img
- . Head Motion: TRUE
- . . Text Parent Path: Same with Functional Dataset
- . . Text Prefix: rp_*
- . . Add Derivative (12): FALSE

- Extract average signal in MASK
- Add derivative head motion



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Network construction Window - Functional Connectivity Matrix

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Functional Connectivity Matrix

. Label Mask: AAL_90_3mm.nii

- What is Lab MASK?
- How to generate a Lab MASK (REST Image Calculator)



GUIDE

Network construction Window - Voxel-based Degree

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Voxel-based Degree

- . Degree Mask: BrainMask_05_61x73x61.img
- . Connectional Threshold: 0.3
- . Connectional Distance: 75

- Consider connectional distance



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Network metrics Window

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CallInterface

Network Analysis

Network – Synchronization
Node – Degree
Node – Efficiency
Node – Betweenness

>>
<<

Input Network Matrix
/home/sandy/sandy_work/DPARSF_TEST/GretnaMatrixResults/p0
--->#0001: (90 -- 90)

*correlation coefficient
sparsity

Connect to another widget...

Queue: 3

GRETNNA

RUN

The screenshot shows the GRETNNA software interface. On the left, there's a vertical sidebar with links for Overview, Introduction, Why Gretna, Construction, Metrics, Guide, Install, Initialize, Procedure, Input, Logs, Toolbar, Run, Construction, Metrics, PyGretna, and Acknowledge. The main window has a title bar 'CallInterface'. It features a 'Network Analysis' panel on the left with a list of metrics: Network – Synchronization, Node – Degree, Node – Efficiency, and Node – Betweenness. There are '">>>' and '<<' buttons between this panel and the central workspace. The central workspace contains an 'Input Network Matrix' field showing the path '/home/sandy/sandy_work/DPARSF_TEST/GretnaMatrixResults/p0' and a preview '--->#0001: (90 -- 90)'. Below it is an 'Output Directory' field set to '/home/sandy/CCBD_data/analysis' with a 'Select Output Directory' button. To the right of the workspace is a 'Network Metrics' section with a list of options: Network Type: weighted, Threshold Type: correlation coefficient (which is highlighted in blue), Threshold Region: 0.05 : 0.01 : 0.4, Random Networks (n): 100, Selected Mode: Network – Small World, Network – Efficiency, Network – Modularity, algorithm: greedy optimization, Network – Assortativity, and Network – Hierarchy. Below this is a 'correlation coefficient' entry and a 'sparsity' entry. At the bottom right is a 'Connect to another widget...' button, a 'Queue: 3' button, and a large 'GRETNNA' logo with a 'RUN' button.



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Network metrics Window - Configure

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Network Metrics:

- . Network Type: weighted
 - . Threshold Type: correlation coefficient
 - . Threshold Region: 0.05 : 0.01 : 0.4
 - . Random Networks (n): 100
-
- Network Type: Wei or Bin
 - Threshold Type: R value or Sparsity
 - Threshold Region: Read paper and consider your function of machine
 - Random Networks: 100 or more



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Network metrics Window - Network - Small World

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- Cp: Clustering Coefficient of Network
- Cprand: Clustering Coefficient of Random Network
- Cp_zscore: $(Cp - \text{mean}(Cprand)) / \text{std}(Cprand)$
- nodalCp: Clustering Coefficient of Nodes
- Lp: Shortest Path of Network
- Lprand: Shortest Path of Random Network
- Lp_zscore: $(Lp - \text{mean}(Lprand)) / \text{std}(Lprand)$
- nodalLp: Shortest Path of Nodes
- Gamma: Cp/Cprand
- Lambda: Lp/Lprand
- Sigma: Gamma/Lambda
- a*: Multi-thresholds



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Network metrics Window - Network - Efficiency

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- locE: Local Efficiency of Network
- locErand: Local Efficiency of Random Network
- locE_zscore: $(\text{locE}-\text{mean}(\text{locErand}))/\text{std}(\text{locErand})$
- nodallocE: Local Efficiency of Nodes
- gE: Global Efficiency of Network
- gErand: Global Efficiency of Random Network
- gE_zscore: $(\text{gE}-\text{mean}(\text{gErand}))/\text{std}(\text{gErand})$
- nodalgE: Global Efficiency of Nodes
- Gamma: locE/locErand
- Lambda: gE/gErand
- Sigma: Gamma/Lambda
- a*: Multi-thresholds



GUIDE

Network metrics Window - Network - Modularity

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- C_i : The communities (listed for each node)
- modularity_real: The modularity of real network
- numberofmodule_real: The number of module
- modularity_zscore: The z score of the modularity
- numberofmodule_zscore: The z score of the numbers



GUIDE

Network metrics Window - Network - Assortativity

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Acknowledge

- real: The assortativity of network
- rand: The assortativity of random network
- zscore: $(\text{real}-\text{mean}(\text{rand}))/\text{std}(\text{rand})$



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Network metrics Window - Network - Hierarchy

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Acknowledge

- real: The hierarchy of network
- rand: The hierarchy of random network
- zscore: $(\text{real}-\text{mean}(\text{rand}))/\text{std}(\text{rand})$



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Network metrics Window - Network - Synchronization

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- real: The synchronization of network
- rand: The synchronization of random network
- zscore: $(\text{real}-\text{mean}(\text{rand}))/\text{std}(\text{rand})$



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Network metrics Window - Node - Degree

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- degree: Degree of Nodes
- adegree: Multi-thresholds



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Network metrics Window - Node - Efficiency

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- gE: Global Efficiency of Nodes
- agE: Multi-thresholds



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Network metrics Window - Node - Betweenness

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Acknowledge

- bi: Betweenness of Nodes
- abi: Multi-thresholds



OUTLINE

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PYGRETNA

Gretna Based on Python

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Network - Small World
Network - Efficiency
Network - Assortativity
Network - Hierarchy
Network - Synchronization
Node - Degree
Node - Efficiency
Node - Betweenness

Network Type: Binary Weighted
 Normalized Network Matrix

Clustering Algorithm: Barrat Onnela

Threshold Start: 0.1
Threshold Step: 0.05
Threshold Stop: 0.4

Threshold Type: Correlation Value Sparsity Number of Edges

Random Network: 1000
Generate Way: Randomize Edges Randomize Edges and Nodes

Results Folder: /home/sandy/sandy_work/ Clear "Result" Folder
Queue Size: 4

Run



OUTLINE

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Acknowledge

- Gretna call SPM8 and reference some functions in DPARSF
- Dr. He reserves the right of final interpretation for this toolkit
- Thanks Jin-hui Wang, Ming-rui Xia, Zheng-jia Dai, Xun-hong Liao, Rui Hou, Xin-di Wang and others in He's group who develop this toolkit
- Thanks for your attention!