## Brain Network Analysis with Pluto

Micah Chambers Laboratory of Neuro Imaging

# Graph Theory and the Brain

- Made up of Nodes and Edges
  - Node: Brain Region (e.g. V5) or Single Voxel
  - Edge: Direct Connection between Nodes (e.g. Corpus Callosal Fiber)
- Mathematical Formalization of Connectivity
- Allows researchers to characterize communication
  - "small world networks"
  - Random networks
- Look for subtle patterns
  - Not visible at a glance
  - vs. easily visible effects such as lesions
- Pluto Tools makes these fast and easy





## Node Statistics

- Clustering Coefficient
  - Ratio of Realized vs.
     Potential Triangles
- Degree
  - Number of Edges
- Strength
  - Sum of Weights



Degree

3

Strength

#### **Distance Metrics**

- All Shortest Paths
- Edge Betweenness
  - Number of Shortests Paths
     Traversing the edge





**Edge Betweenness** 

#### **Distance** Metrics

- Betweenness Centrality
  - Number of Shortest Paths Containing the Vertex
- Eccentricity
  - Length of the longest shortest path for a vertex
- Characteristic Path Length
  - Average Shortest Path
- Radius
  - Minimum of Eccentricity
- Diameter
  - Maximum of Eccentricity



0

Diameter: 3.5 Characteristc Path Length: 1.8

#### **Distance Metrics**

- Local Efficiency
  - Sum of Reciprocal Shortest
     Paths in subgraph
- Edge Range





## **Other Metrics**

- Louvain Modularity
- Assortivity
  - Correlation of Degree
     Between Connected Vertices
- Matching Index



Louvain Modularity





High Assortivity

Matching Index

Low Assortivity

## **Pluto Tools Overview**

- micor : timeseries similiarity
  - Calculates voxel-voxel mutual information or correlation
- gCalcAdj : Fiber Counts
  - Count between regions or mesh-points
- gRed : Resampling
  - calculate regional averages of connectivity
- gRed : Graph Theory
  - Calculate Metrics using Graph Theory



# **Functional Connectivity Calculation**

- Required Input:
  - fMRI Image
  - Labelmap Image
  - Nearest N. Resampling Handled Internally
- Required Output:
  - Adjacency Matrix Stored in vtkImageData
- Lags: number of TR's to lag in search of maximal connectivity (2L+1)
- Metrics:
  - Correlation, "-c" (Recommended in Pipeline, < 1 hour runtime)</li>
  - Mutual Information (Not Recommended in Pipeline, 10+ Hour runtime)
  - Mutual Information with Interpolation (Not Recommended in Pipeline, Day+ Runtime)
- Outside Pipeline: "-G" to use GPU

micor pluto		×
Name	Prefix	Value
🗹 fMRI Image	(none)	(1) NIFTI GZ (nii.gz)
🖌 Labelmap	(none)	(1) NIFTI GZ (nii.gz)
🗹 Output	-0	(1) vtk file (vtk)
Advanced Mutua	C	(0) File
🔽 Correlation	-с	(0) File
Threshold	-t	(1)Number
Number of Lags	-1	(1)Number
🗌 Don't Ignore No	-1	(0) File
Pre-Average Ea	-A	(0) File
VTK Text Output	-т	(0) File

# Structural Connectivity Calculation

- Required Input:
  - Vertices Either:
    - Point List "-p"
    - Label Map Image "-L"
  - Input Data Either:
    - Existing Adj. Matrix "-a"
    - Fiber Tracts "-t"
- Filter out short tracts with "-m <length>"
  - Very short tracts are often considered noise

gCalcAd	ij	×
Name	Prefix	Value
🔽 Point List	-р	(1) File, csv file (csv
Labelmap	-L	(1) NIFTI GZ (nii.gz)
🔽 Tracts	-t	(1) vtk file (vtk)
Adjacency Matrix	-a	(1) vtk file (vtk)
🔽 Output Adjacen	(none)	(1) vtk file (vtk)
VTK Text	-Т	(0) File
🗌 Log File	-1	(1) File
Minimum Track	-m	(1)Number

# **Graph Modification**

- Keep Only List of Nodes

   e.g. List of cortical Regions
- Remove List of Nodes
  - e.g. Ventricles
  - Extremely important when calculating shortest paths
- Graph Simplification:
  - Average Connectivity over Label-Pairs
  - Percentile over Label-Pairs
  - Optional Inclusion of Zeros in statistics

gRed		×
Name	Prefix	Value
Region-Paired	-a	(0) File
Region-Paired S	-s	(0) File
Keep Labels	-k	(1)String
🔽 Remove Labels	-r	0,1,2,4,5,6,7,8,14,
🗌 Include Zeros in	-z	(0) File
Region-Paired P	-р	(1)Number
🗹 Input Adjacenc	(none)	(1) vtk file (vtk)
🔽 Output Adjacen	(none)	(1) vtk file (vtk)
Normalize to Sel	-N	(0)
Save in ascii fo	-т	(0) File
Compute Statistic	-S	invert_elements

#### Graph Statistics "-S"

- Compute Statistic "-S":
  - Betweenness Centrality
  - Clustering Coefficient
  - Degree
  - Strength
  - Eccentricity
  - Local Efficiency
  - Shortest Path
  - Edge Range
  - Edge Betweeness
  - Matching Index
  - Joint Degree
  - Assortivity
  - Characteristic Path Length
  - Diameter
  - Radius
  - Global Efficiency
  - Louvain Modularity
  - Invert Elements (for converting weight to distance)

gRed pluto		×
Name	Prefix	Value
Region-Paired	-a	(0) File
Region-Paired S	-5	(0) File
Keep Labels	-k	(1)String
🔽 Remove Labels	-r	0,1,2,4,5,6,7,8,14,
Include Zeros in	-z	(0) File
Region-Paired P	-р	(1)Number
🗹 Input Adjacenc	(none)	(1) vtk file (vtk)
V Output Adjacen	(none)	(1) vtk file (vtk)
Normalize to Sel	-N	(0)
Save in ascii fo	-т	(0) File
Compute Statistic	-S	invert_elements

# Odds and Ends

- gTxtToVtk
  - Input: CSV Adjacency Matrix
  - Output: vtkImageData
- gVtkToTxt
  - Input: vtkImageData
  - Output: CSV Adjacency Matrix
- trkToVtk
  - Input: trackvis .trk file
  - Output: vtkPolyLines

gTxtToVtk			
Name	Prefix	Value	
<ul> <li>✓ Input Adj.</li> <li>✓ Ouptut Adj.</li> </ul>	(none) (none)	(1) Text file (txt), c (1) vtk file (vtk)	
gVtkTo pluto Name	o <b>Txt</b> Pref <u>ix</u>	Xalue	
✓ Input Adj. ✓ Output Adj.	(none) (none)	(1) vtk file (vtk) (1) Text file (txt), c	
trkToVtk 🛛 🛛			
Name	Prefix	Value	
Output	(none) (none)	(1) tract (.trk) (1) vtk file (vtk)	

## Conclusions

- Native C++ Code
  - Source Available for Request
  - Compiled Versions at /ifs/students/mchambers/pluto-0.5
- Pipelines Available Now
  - Make interfacing with other tools far easier
- GPU Support for functional connectivity (outside pipeline)
  - More may be added for slower graph-metrics
- Designed For Neuro Imaging Applications
  - Wide Variety of Input Image Types (nifti preferred)
  - Easily Convertible VTK format, tools included
- Please Contact Me at:
  - micahcc@ucla.edu
  - Come talk to me at the Ice Cream Social