



Resting-state fMRI and graph-based methods for analyzing functional connectivity

Alexander Schaefer

Lecture SS 2014

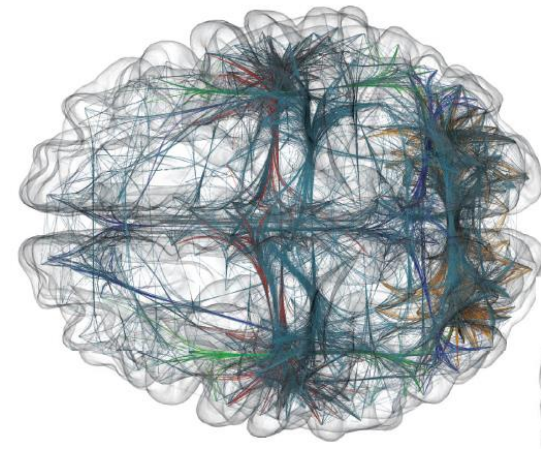
Max Planck Institute
for Human Cognitive and Brain Sciences Leipzig, Germany

Introduction

- Resting State fMRI
- Graphs and their Definition
- Analyze and Compare Graphs



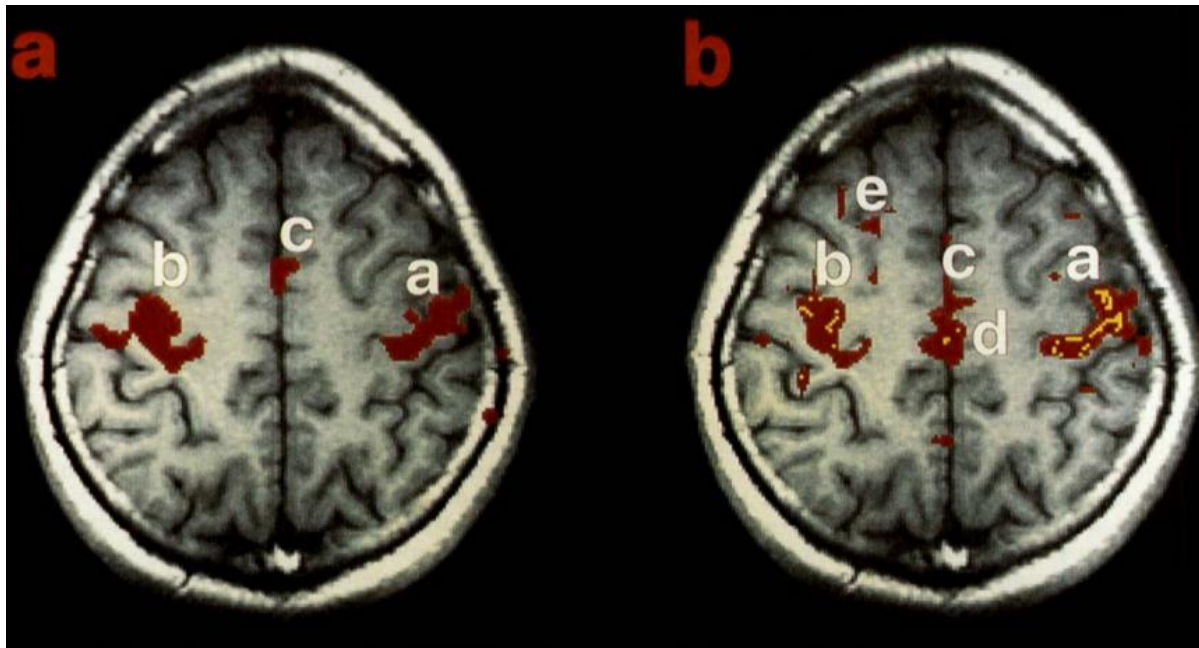
Brain Connectivity, Marie Liebert Publishing



Boettger, IEEE TVCG, 2014

Resting State fMRI

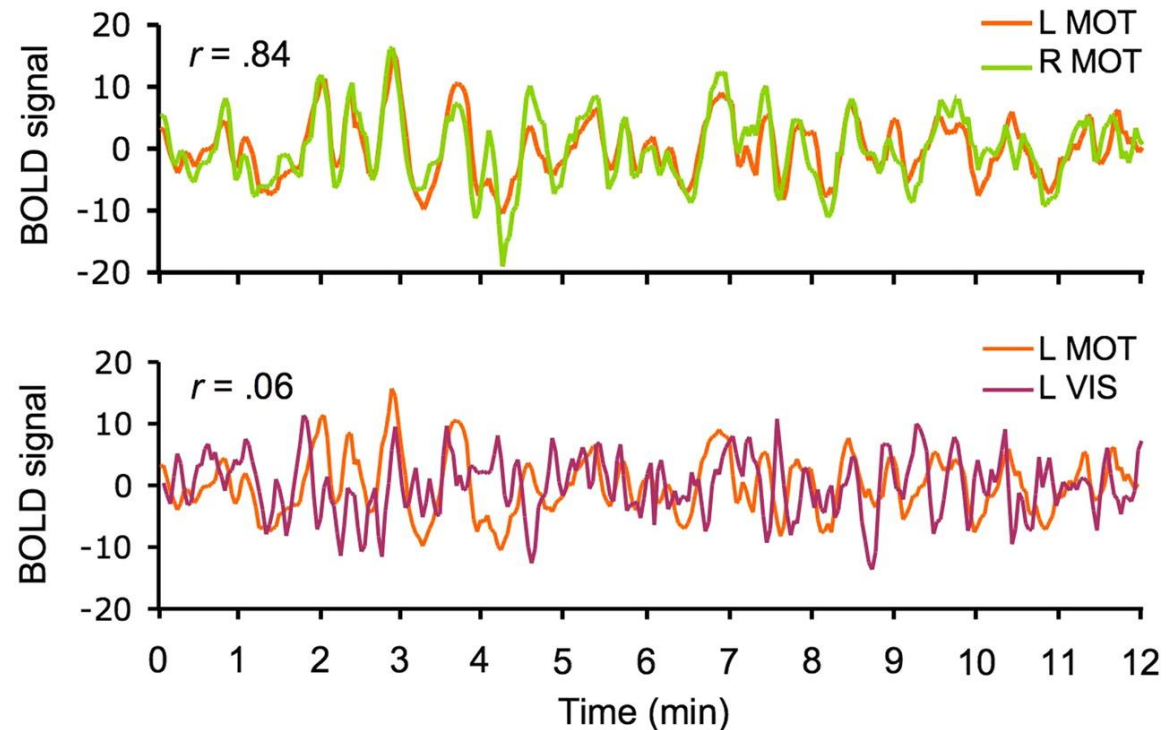
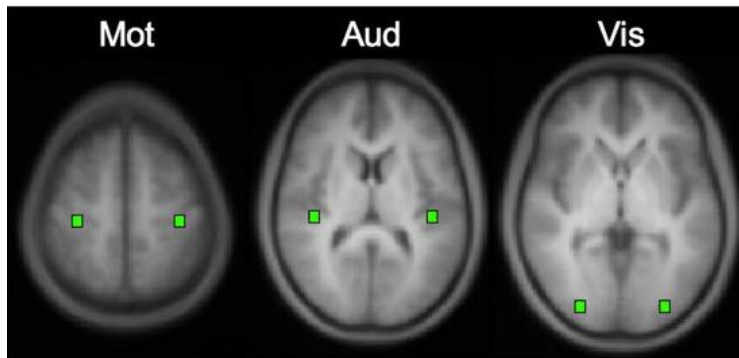
- spontaneous brain activity in the absence of task
- correlated signal in functionally coupled networks



BB Biswal, MRM, 1995

Resting state fMRI

- rs-fMRI observation (Biswal95): correlated signal in functionally coupled networks



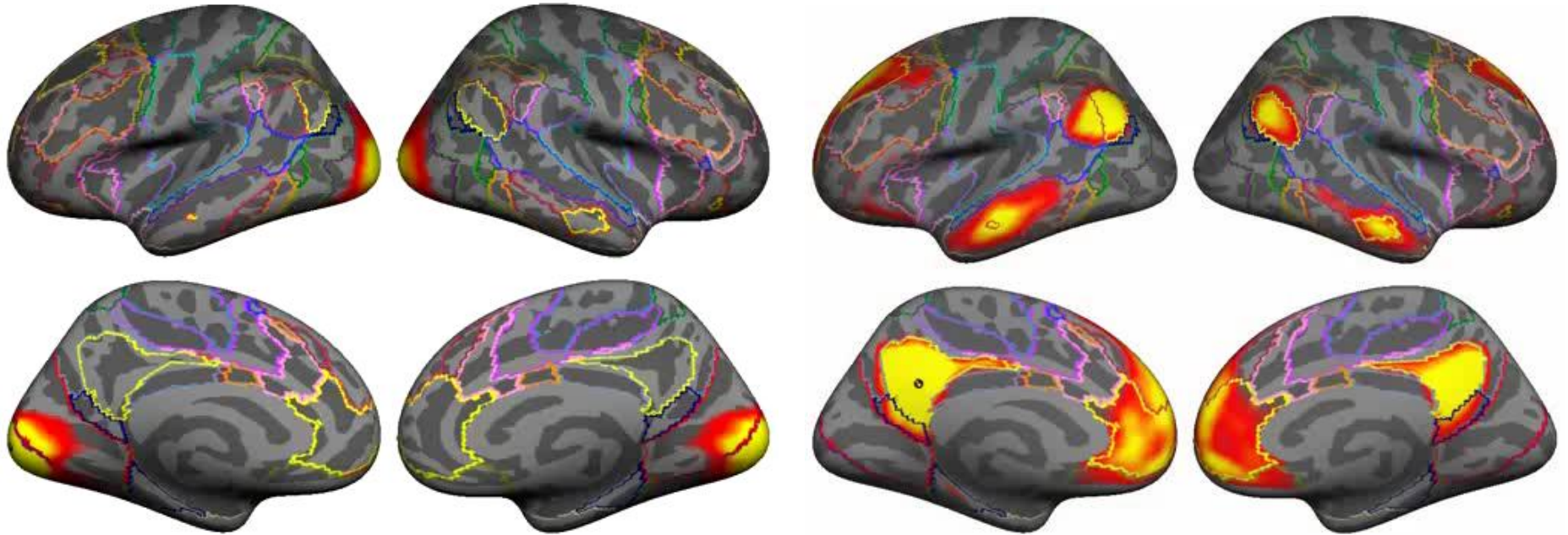
Figures adopted from Van Dijk et al., 2010, Journal of Neurophysiology

Resting State fMRI

- Intrinsic connectivity
 - Present during task, in the absence of task and under anesthesia
 - Majority of the power of the signal is between is in very slow signals (0.01 – 0.05 Hz)
 - correlates with (neuronal) EEG signal (Mantini 2007)

Resting State fMRI

- Correlated signal reflects functionally coupled networks (www.youtube.com/user/YeoKrienen)

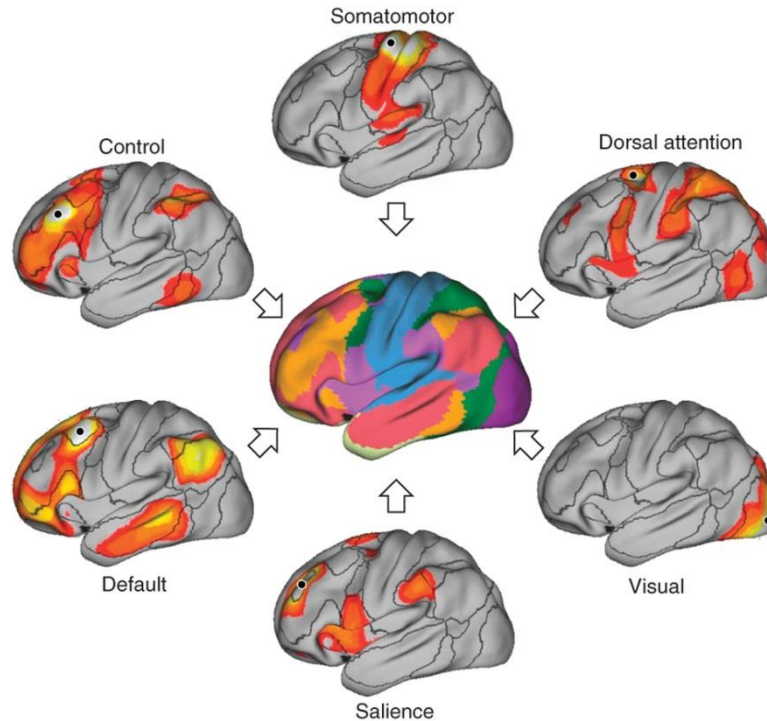


Yeo, *J. Neurophysiol.*, 2011

Yeo, *J. Neurophysiol.*, 2011

Resting State fMRI

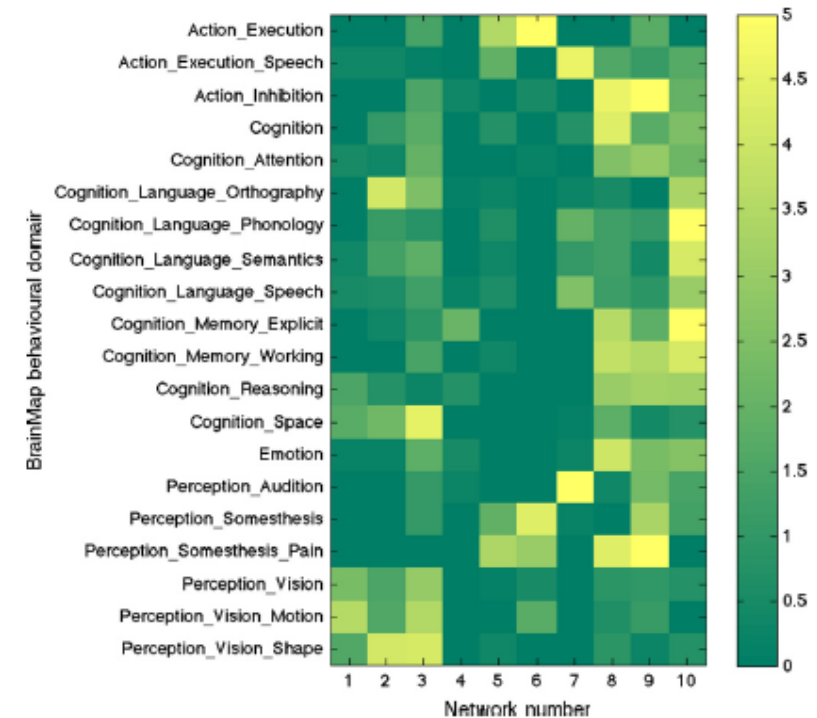
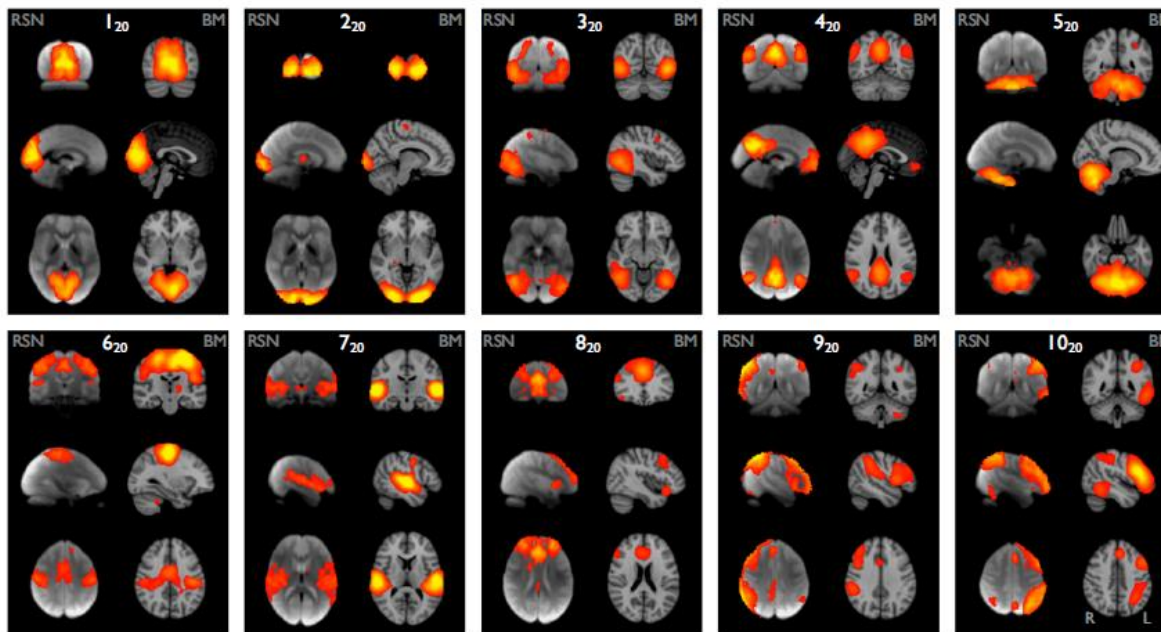
- Correlated signal reflects functionally coupled networks



Yeo, *J. Neurophysiol.*, 2011

Resting State fMRI

- Resembles “task-based” coactivation areas
- Database of 10,000 studies (Smith, PNAS, 2010)

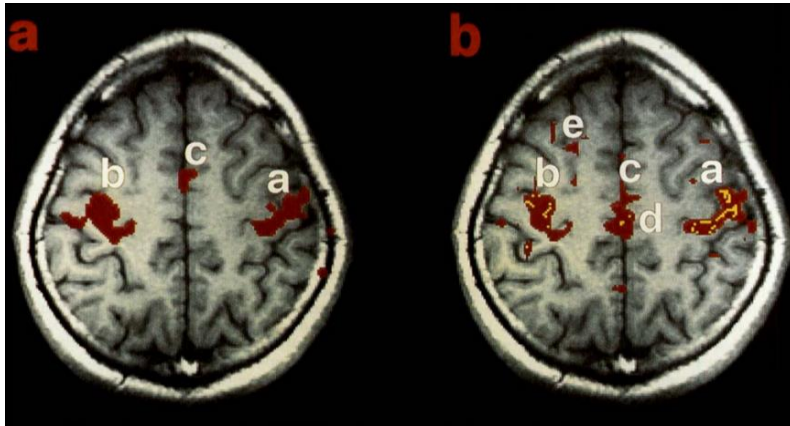


Resting State fMRI

- Good Test-Retest Reliability (Shezad, 2009)
- Can be altered by training a task (Taubert 2010)
- Can predict the age of a subject (Dosenbach 2010)
- Can predict the disease status of a subject e.g. in Depression (Zeng, 2012), ADHD (Fair, 2013) Alzheimer (Sorg, 2007)

Resting State fMRI

- intrinsic brain connectivity → the cross talk of brain areas
- Whole brain cross talk → functional brain network



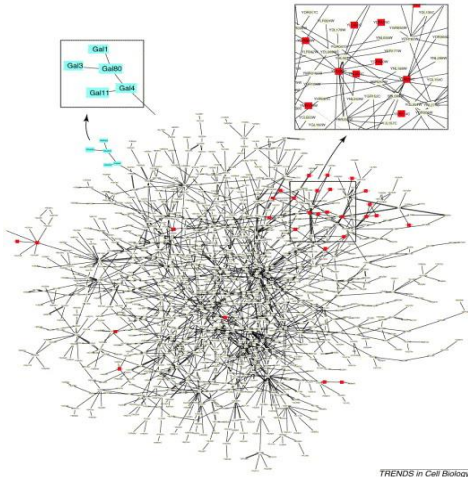
Biswal, MRM, 1995



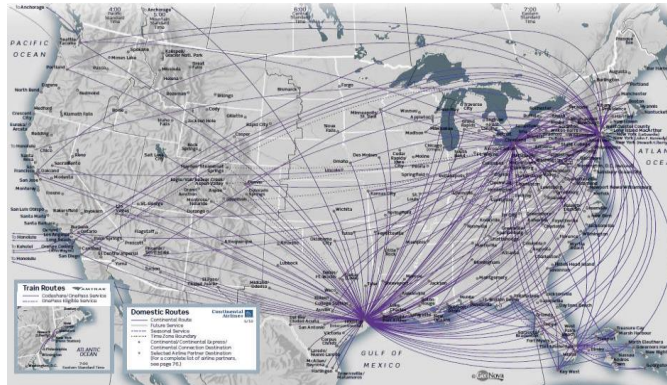
Brain Connectivity, Marie Liebert Publishing

Graph Defintion

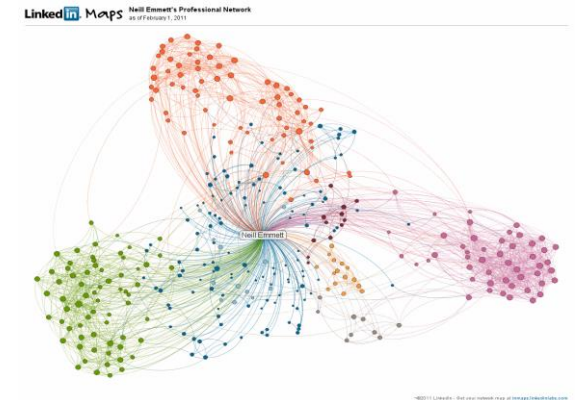
- Some examples of graphs people already work with



Protein Interaction Graph
Tucker 2001



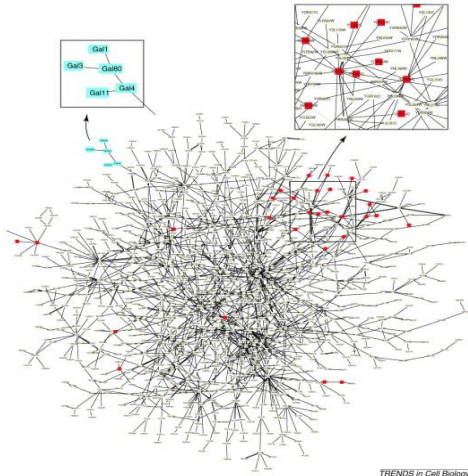
Airplane Graph
Aeorspace.org



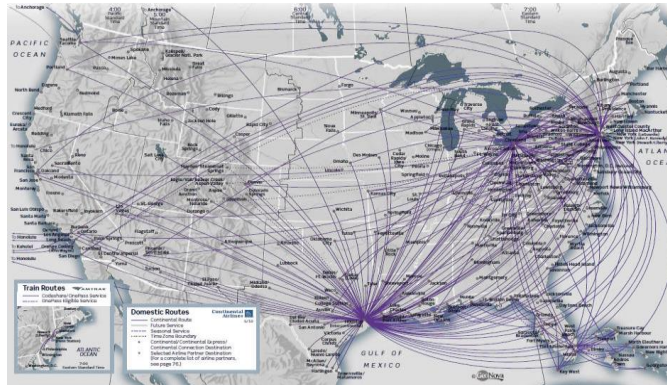
Social Graph
Youarethem.co.uk

Graph Defintion

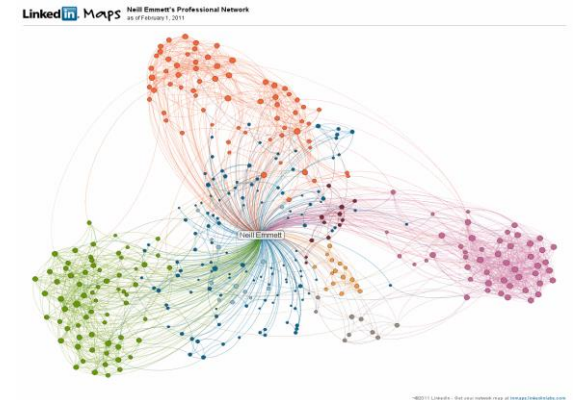
- Some examples of graphs people already work with
- Advantage → we can use the same math for all of them



Protein Interaction Graph
Tucker 2001



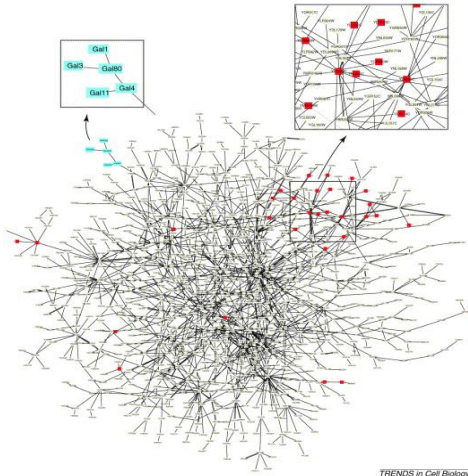
Airplane Graph
Aeospace.org



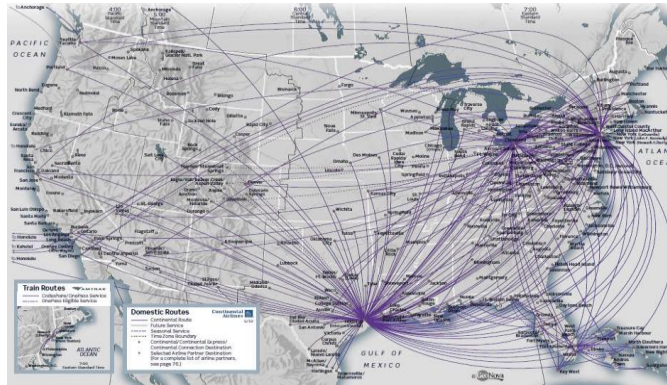
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Graph Definition

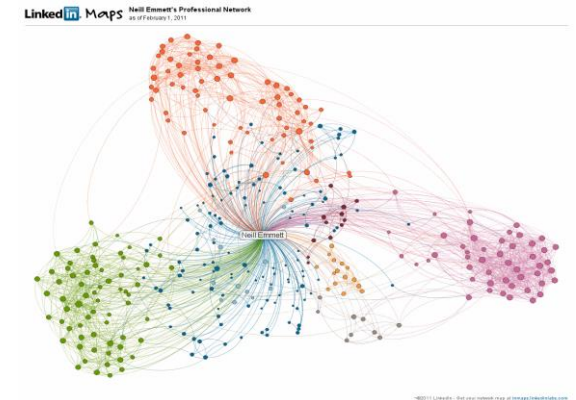
- A Graph is a tuple (V, E)
- V is a set of vertices
- E is a set of edges, where $e \in E: V \times V$



Protein Interaction Graph
Tucker 2001



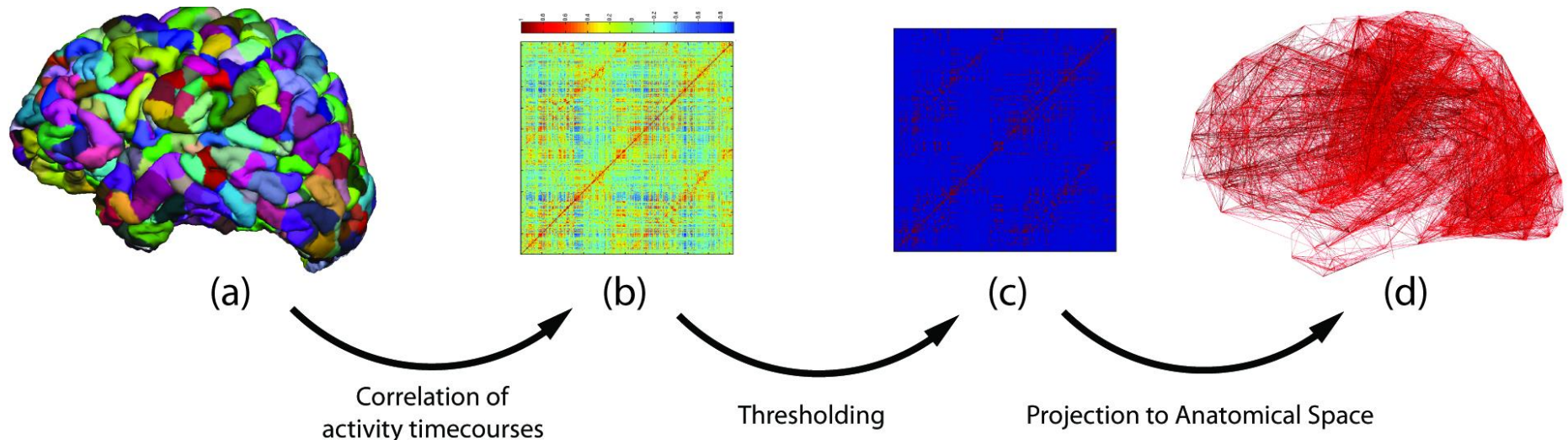
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Aeospace.org



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Graph Definition

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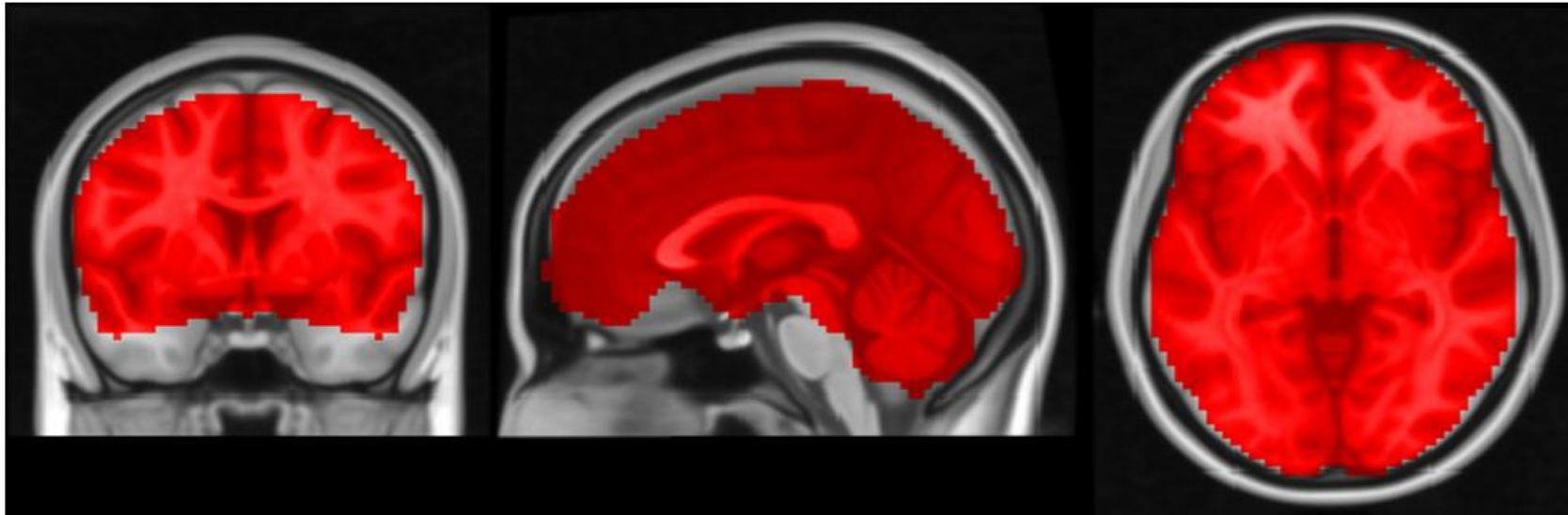
Boettger, IEEE TVCG 2014

Set of Vertices

- “Good” definition of vertices is crucial for the following graph analysis

Set of Vertices

- Voxel-based
 - Each voxel represents a distinct node



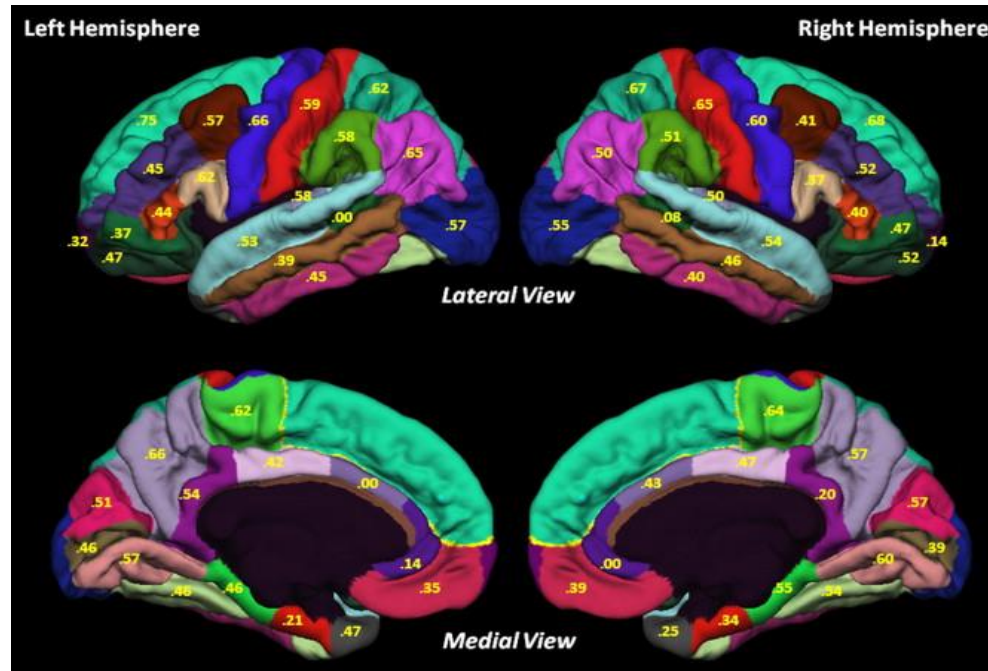
Lohmann, PloS One, 2010

Set of Vertices

- Voxel-based
 - Pro:
 - Data Driven
 - Good reliability
 - High Resolution
 - Con:
 - Unclear Validity
 - Computational intensive
 - Higher risk of false positive short range connections

Set of Vertices

- Anatomical
 - Base on prior anatomical information



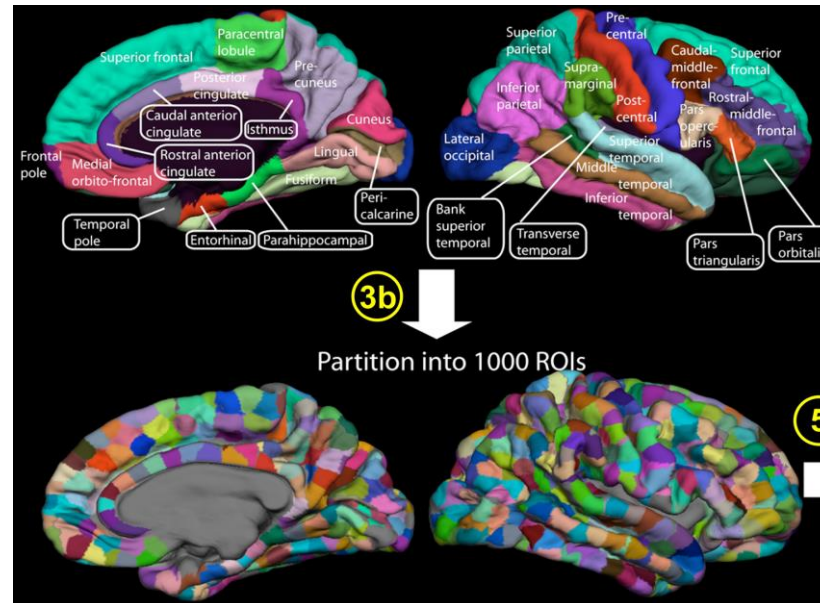
Desikan, NeurolImage 2006

Set of Vertices

- Anatomical
 - Pro:
 - Intuitive parcellation
 - Fast to compute
 - High reliability
 - Con:
 - Low Resolution
 - Variation in node size?
 - Low validity?

Set of Vertices

- Random Parcellation
 - Randomly into regions with similar size
 - Allows multi resolutions:



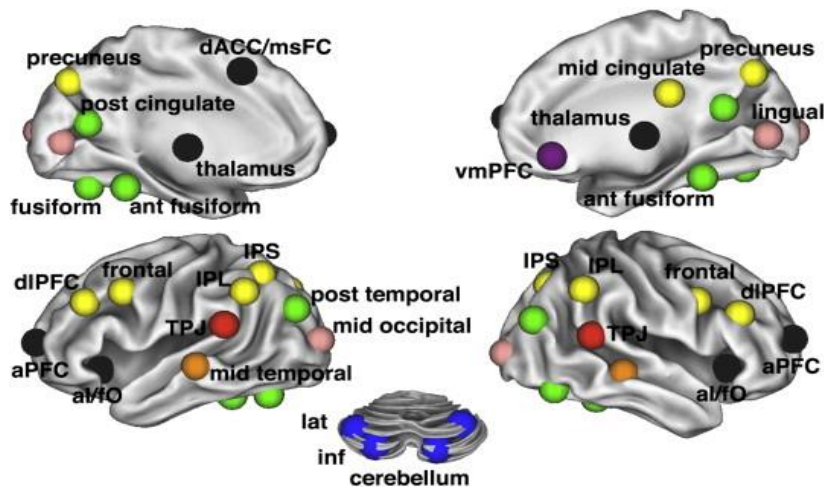
Hagmann, PloS Bio, 2007

Set of Vertices

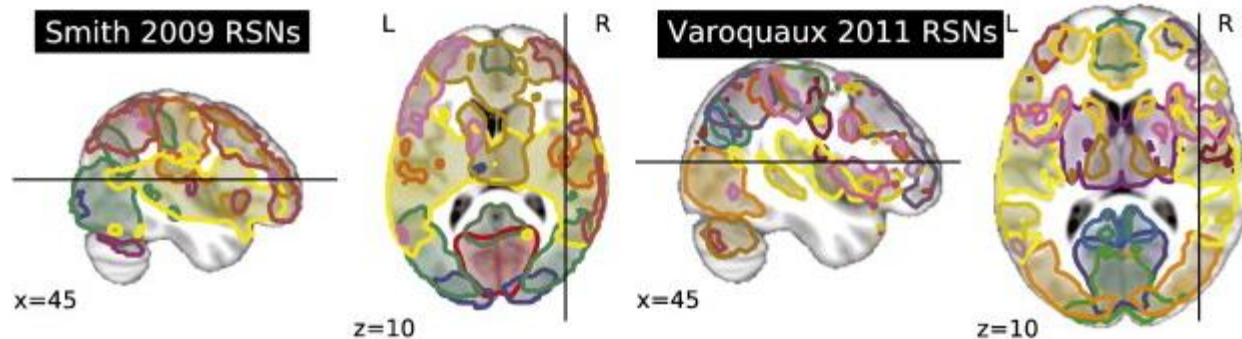
- Random
 - Pro:
 - Minimize node size variations
 - Multi resolution
 - Con:
 - Unclear validity / reliability

Set of Vertices

- Functional Parcellation
 - Based on prior functional information
 - Coordinates from meta analysis or functional homogeneity analysis



Dosenbach, Science, 2010



Smith, PNAS, 2009

Varoquaux, Inf Proc Med, 2011

Set of Vertices

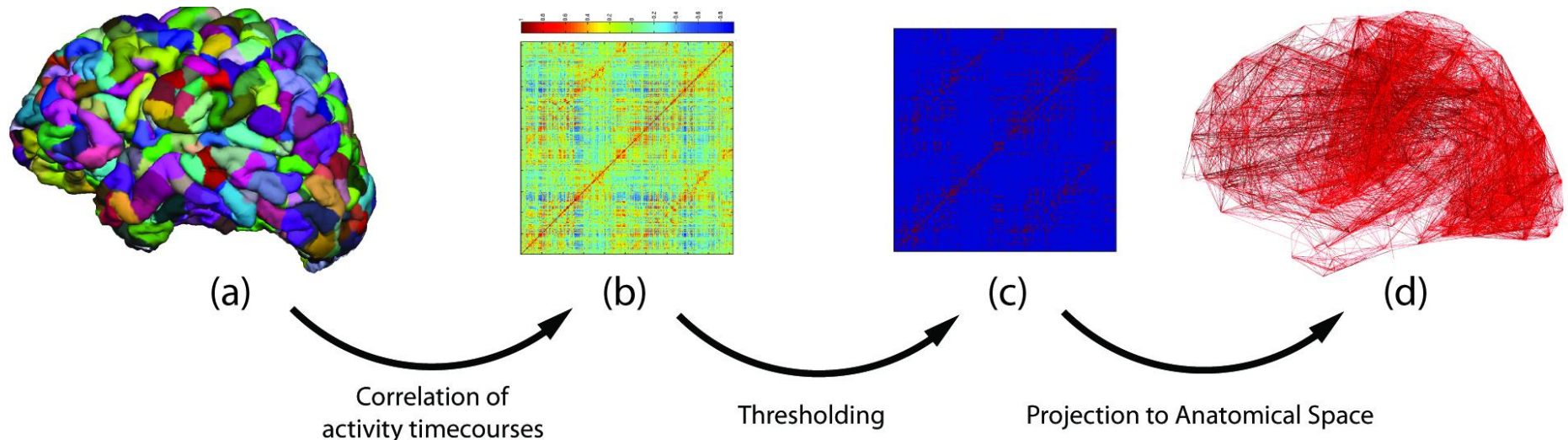
- functional
 - Pro:
 - Good reliability
 - Good validity
 - Con:
 - May miss regions
 - Difficult to apply to DTI

Set of Vertices

- “Good” definition of vertices is crucial for the following graph analysis
- “Good”
 - functional intra-homogeneous
 - Ideally functional inter-heterogeneous
 - reliable
 - account for spatial relationships

Graph Definition

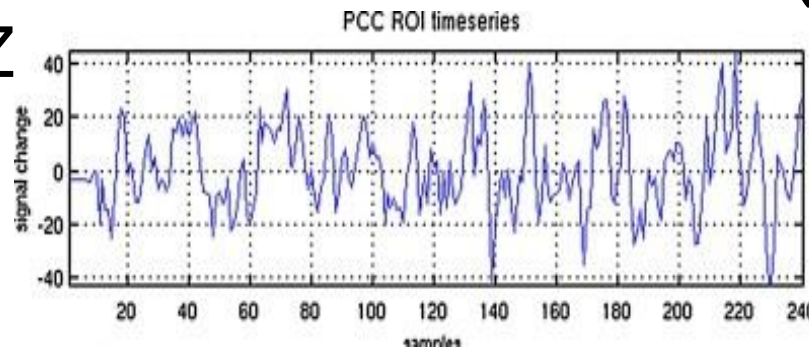
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- V is a set of vertices
- E is a set of edges, where $e \in E: V \times V$



Boettger, IEEE TVCG 2014

Set of Edges

- Estimate a “functional connection” between ROIs
- Data?
 - Average signal over Parcell
 - First eigenvector of PCA over ROI (lower reliability; Z

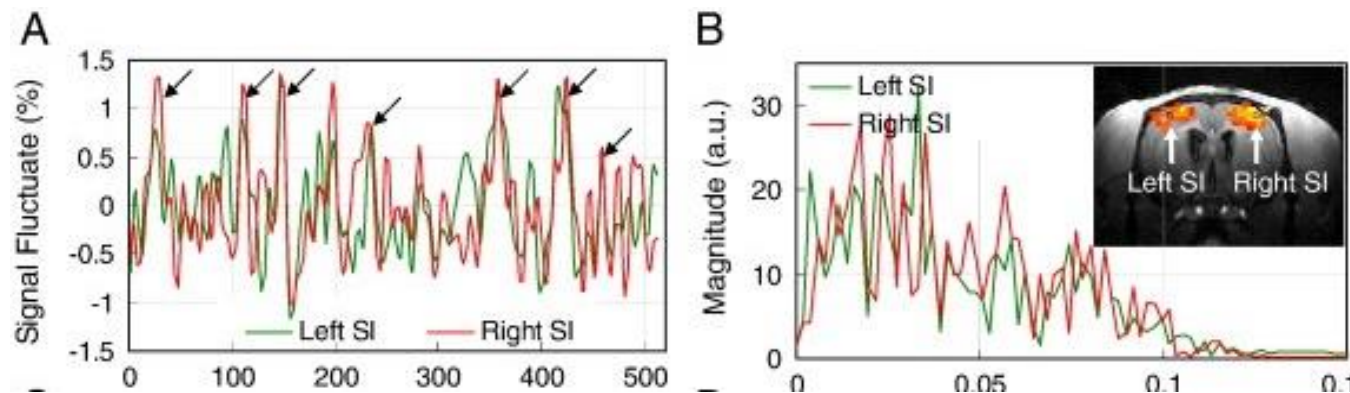


Chang, NeuroImage, 2008

- What do we do with the Data? There are many different ideas.

Set of Edges

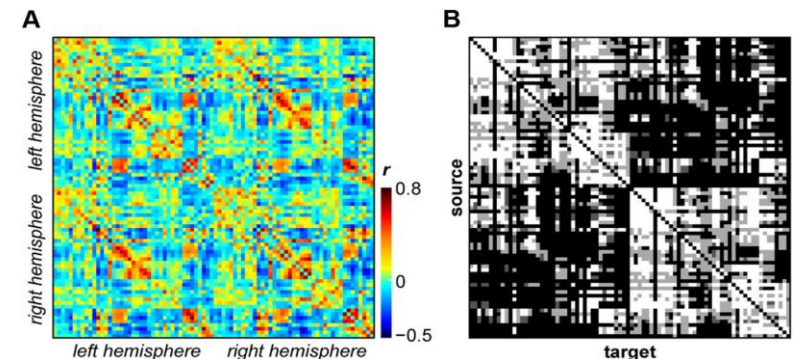
- What do we do with the Data? There are many different ideas.
- Simplest idea (maybe best): measure the pairwise similarity between regions



Zhao, NeuroImage, 2008

Set of Edges

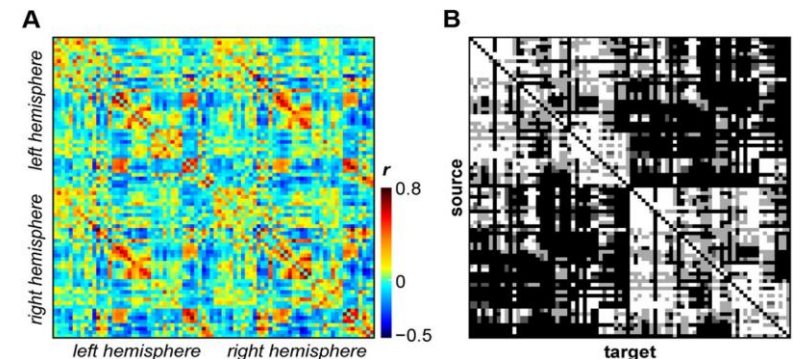
- Pearson Correlation:
$$r = \frac{\sum_{i=1}^n (X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum_{i=1}^n (X_i - \bar{X})^2} \sqrt{\sum_{i=1}^n (Y_i - \bar{Y})^2}}$$
- Notice: → Correlation Matrix: normalized Covariance Matrix
- Positive correlations indicate a functional connection
- Matrix has dimension Vertices x Vertices
- Matrix can describe the complete Graph



Shen, J Neuro, 2012

Set of Edges

- Pearson Correlation:
$$r = \frac{\sum_{i=1}^n (X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum_{i=1}^n (X_i - \bar{X})^2} \sqrt{\sum_{i=1}^n (Y_i - \bar{Y})^2}}$$
- Notice: → Correlation Matrix: normalized Covariance Matrix
- Performs quite well
- But induces indirect connections
- $A \rightarrow B \rightarrow C$
- False positive $A - C$



Shen, J Neuro, 2012

Set of Edges

- Solution → Partial Correlation:
 - Regress out all other timeseries from the data and then perform correlation
 - Gets rid of indirect connections!
 - Problem in (rs-) fMRI: low number of timepoints

Set of Edges

- Solution → Partial Correlation:
 - Regress out all other timeseries from the data and then perform correlation (or compute the inverse Covariance Matrix)
 - Gets rid of indirect connections!
 - Problem in (rs-) fMRI: low number of timepoints
 - Voxel-level: 60 000 voxels * 200 timepoints
 - Rank of Correlation Matrix?

Set of Edges

- Solution → Sparse Inverse Covariance:
 - Idea: regress less by eliminating some connections from the regression process (sparse matrix)
 - some connections are not essential to explain data
 - Problem: Finding this sparse matrix is computationally hard
 - Solution: approximation algorithm (graphical lasso)

Set of Edges

- Conclusion
 - Pearson Correlation has problems with false positives
 - Partial Correlation performs better but has problems with low d.o.f. in fMRI
 - Sparse methods might help



Network modelling methods for FMRI

Stephen M. Smith ^{a,*}, Karla L. Miller ^a, Gholamreza Salimi-Khorshidi ^a, Matthew Webster ^a,
Christian F. Beckmann ^{a,b}, Thomas E. Nichols ^{a,c}, Joseph D. Ramsey ^d, Mark W. Woolrich ^{a,e}

^a FMRI (Oxford University Centre for Functional MRI of the Brain), Dept. Clinical Neurology, University of Oxford, UK

^b Department of Clinical Neuroscience, Imperial College London, UK

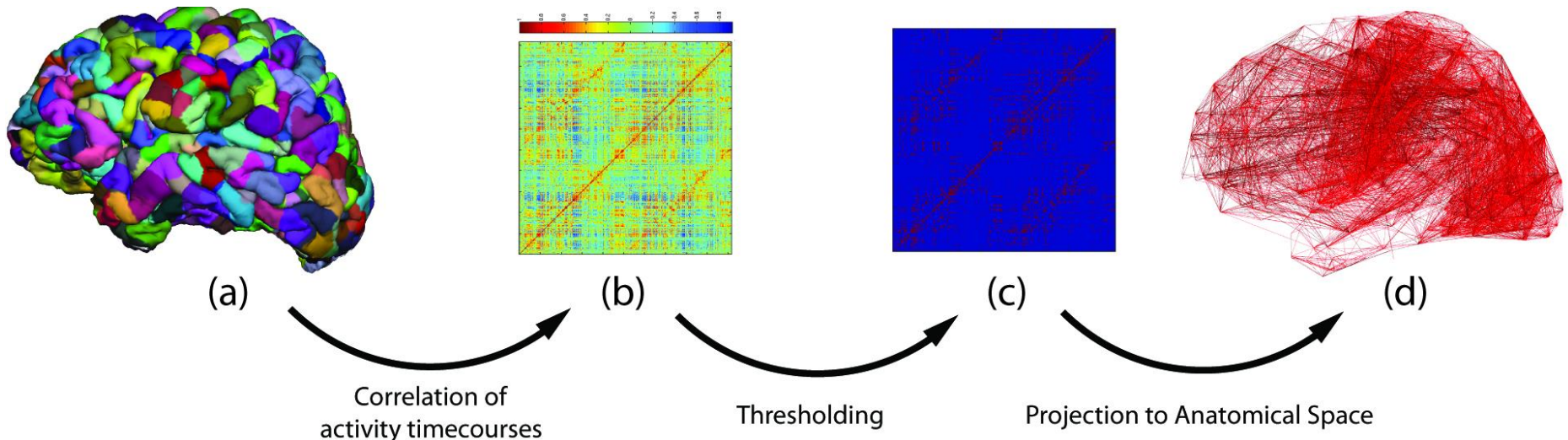
^c Departments of Statistics and Manufacturing, Warwick University, UK

^d Department of Philosophy, Carnegie Mellon University, Pittsburgh, PA, USA

^e OHBA (Oxford University Centre for Human Brain Activity), Dept. Psychiatry, University of Oxford, UK

Graph Definition

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- V is a set of vertices
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Boettger, IEEE TVCG 2014

Thresholding

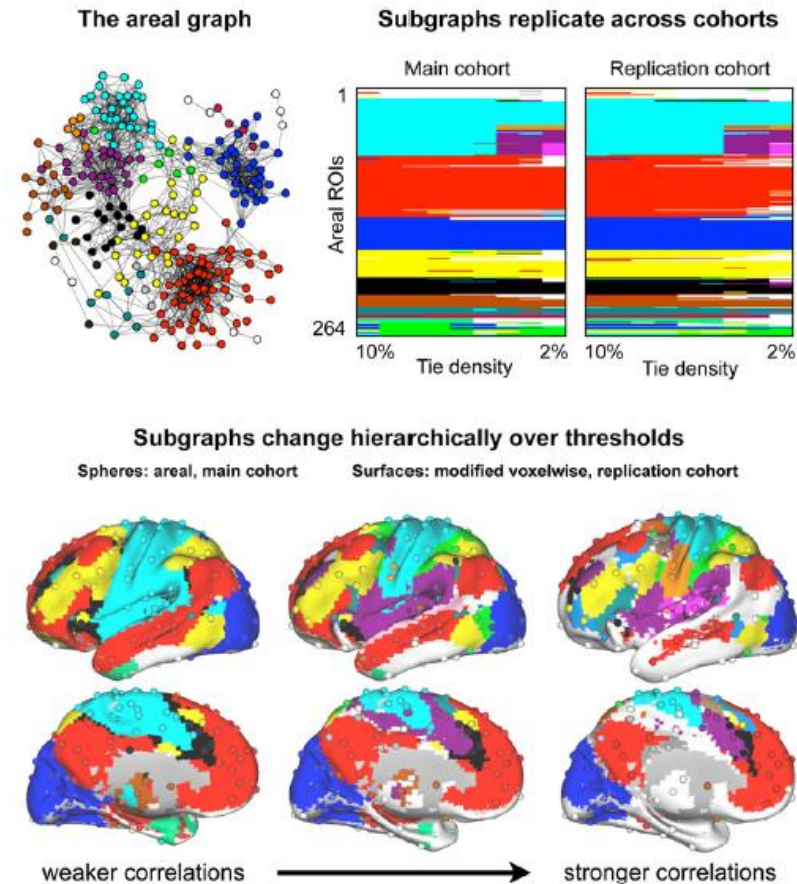
- Validity: mix of correlations and anti-correlations
- Reliability: higher for stronger correlations
- Strategies:
 - Sparsity Thresholding: use only the strongest $x\%$ of edges
 - Soft Thresholding: use only edges above value x
 - Hard Thresholding: use only edges above value x and set them to 1 (binarization)

Graph Analysis / Graph Comparison

- Analysis of Brain Organization
- Comparing Graphs / Brains
 - Centrality Mapping
 - Graph-topological metrics
 - Predictive Modeling

Graph Analysis / Graph Comparison

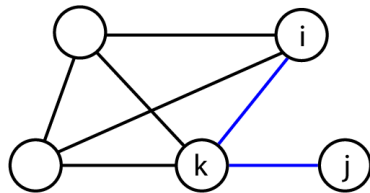
- Investigate Brain Organization
- Unsupervised machine learning
- Power, Neuron, 2011
 - info map algorithm (Rosvall, Bergstrom, 2008)
 - random walk
 - optimal code to describe this random walk
 - code word -> subgraph



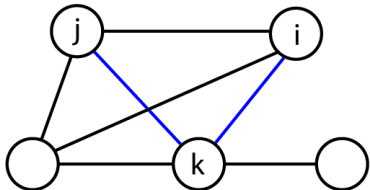
Graph Analysis / Graph Comparison

- Edge clustering
- Similarity between connections
- Hierarchical clustering

A



B



C

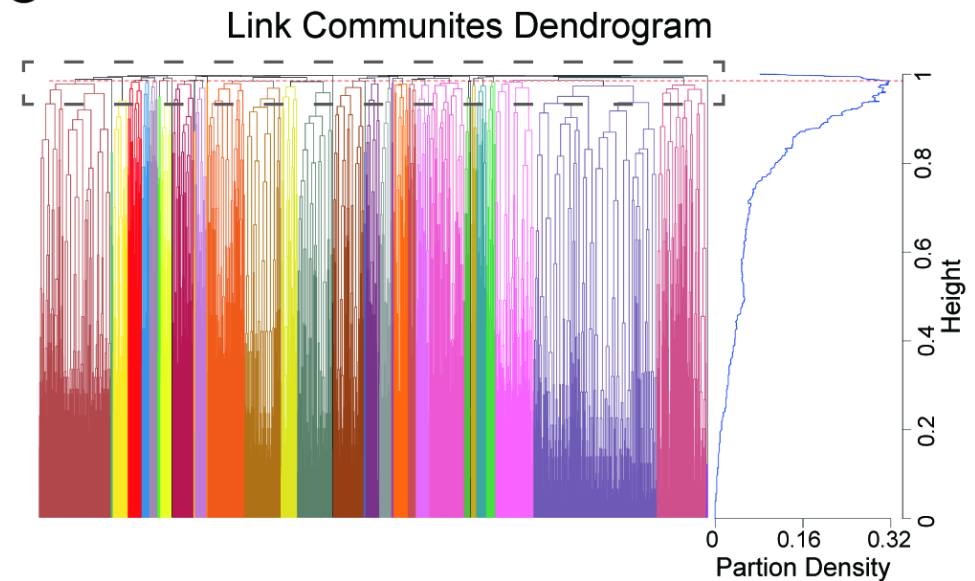


Figure adopted from Schaefer et al., 2014, Frontiers in Human Neuroscience

Graph Analysis / Graph Comparison

- Edge clustering
- <http://openscience.cbs.mpg.de/schaefer/>

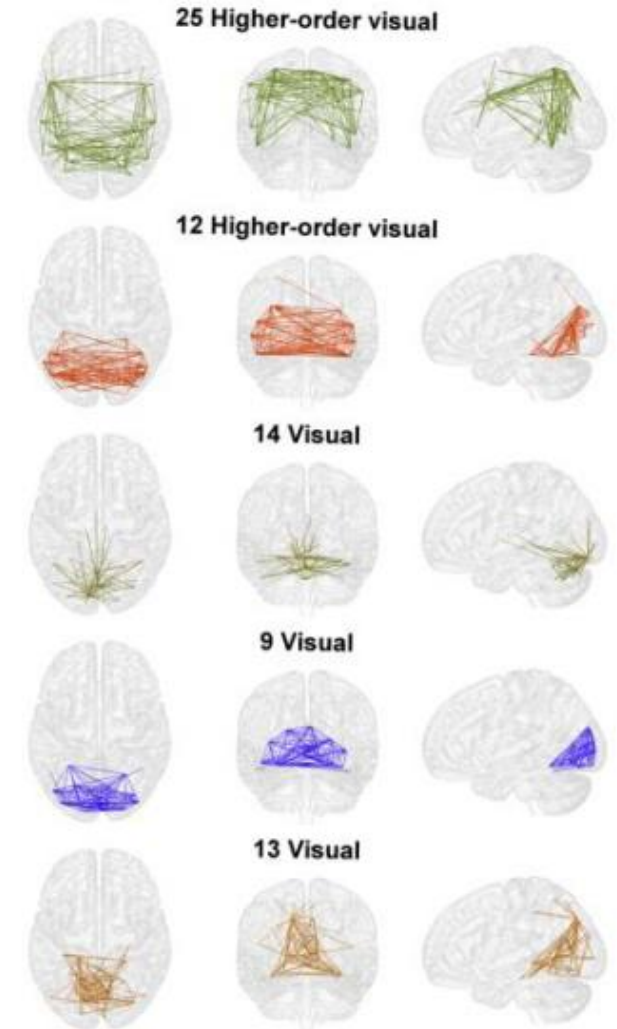
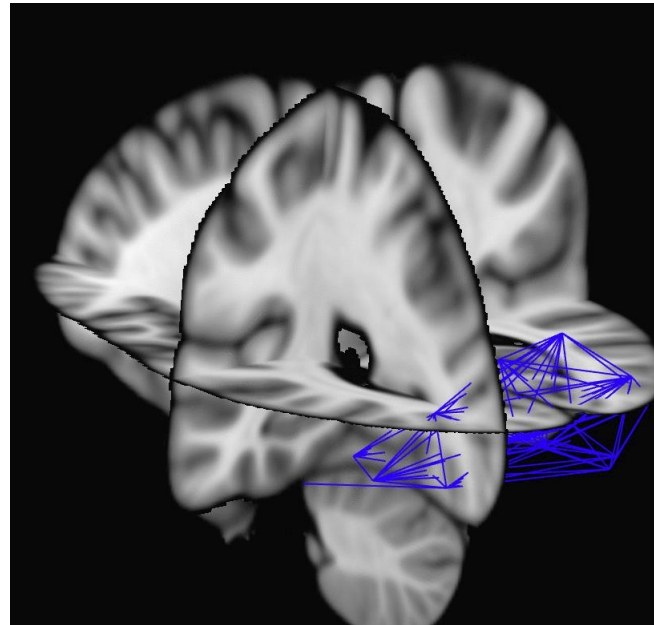
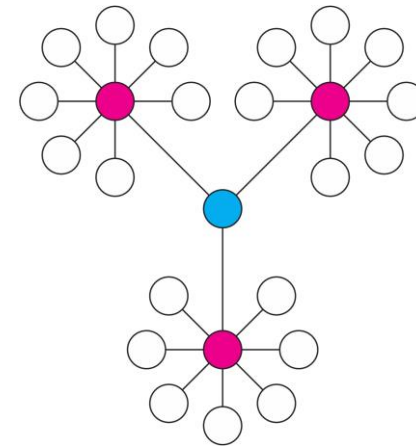


Figure adopted from Schaefer et al., 2014, Frontiers in Human Neuroscience

Graph Analysis / Graph Comparison

- Comparing Graphs
- Centrality Analysis
 - Degree Centrality
 - Assign each Vertex the Sum over its weighted edges:

$$DC(i) = \sum_{j=1}^N a_{ij}.$$

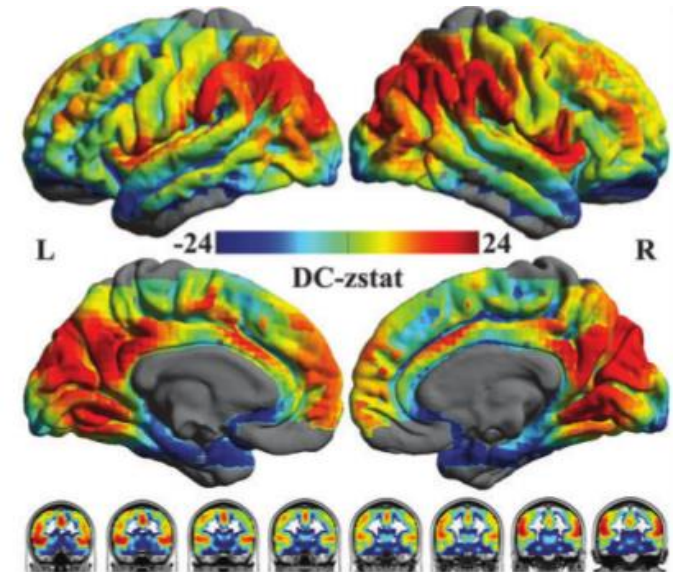


Junker, BioInf, 2006

Graph Analysis / Graph Comparison

- Centrality Mapping
 - Degree Centrality
 - Assign each Vertex the Sum over its weighted connections:

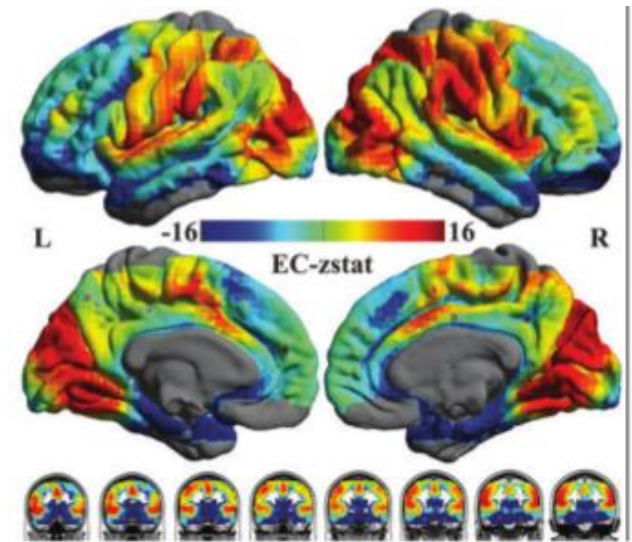
$$\text{DC}(i) = \sum_{j=1}^N a_{ij}.$$



Zuo, Cerb. Cortex, 2010

Graph Analysis / Graph Comparison

- Centrality Mapping
 - Eigenvector Centrality
 - Assign each Vertex the load of its first eigenvector:
- $$EC(i) = \mu_1(i) = \frac{1}{\lambda_1} A \mu_1 = \frac{1}{\lambda_1} \sum_{j=1}^N a_{ij} \mu_1(j).$$
- Cares also about indirect connections



Zuo, Cerb. Cortex, 2010

Graph Analysis / Graph Comparison

- Centrality Mapping
 - Further information in Zuo, Cerebral Cortex, 2012

Cerebral Cortex
doi:10.1093/cercor/bhr269

Network Centrality in the Human Functional Connectome

Xi-Nian Zuo^{1,2}, Ross Ehmke³, Maarten Mennes², Davide Imperati², F. Xavier Castellanos^{2,4}, Olaf Sporns³ and Michael P. Milham⁵

Graph Analysis / Graph Comparison

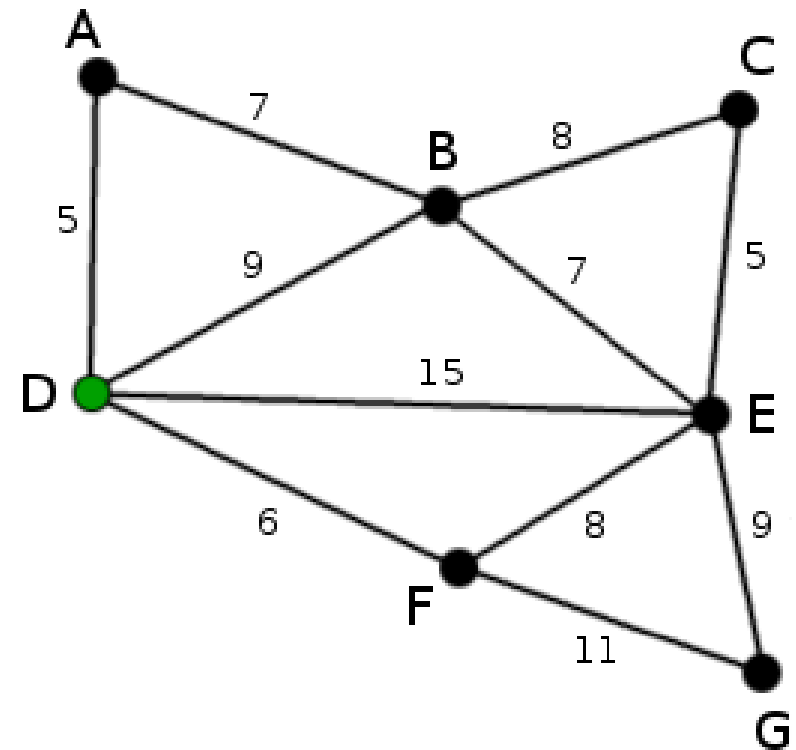
- Graph-topological metrics

- Path Length

$$d_{ij} = \sum_{a_{uv} \in gi \leftrightarrow j} a_{uv},$$

- Average Path Length

$$L = \frac{1}{n} \sum_{i \in N} L_i = \frac{1}{n} \sum_{i \in N} \frac{\sum_{j \in N, j \neq i} d_{ij}}{n - 1},$$



Wikipedia

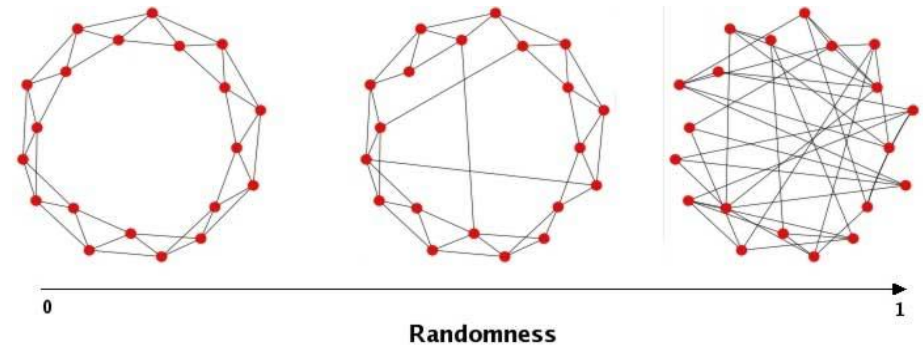
Graph Analysis / Graph Comparison

- Graph-topological metrics
 - Clustering Coefficient

$$C = \frac{1}{n} \sum_{i \in N} C_i = \frac{1}{n} \sum_{i \in N} \frac{2t_i}{k_i(k_i - 1)},$$

- Small Worldness

$$S = \frac{C / C_{\text{rand}}}{L / L_{\text{rand}}},$$



Watts, Nature, 1998

- Problem: What is random, what is artificial?

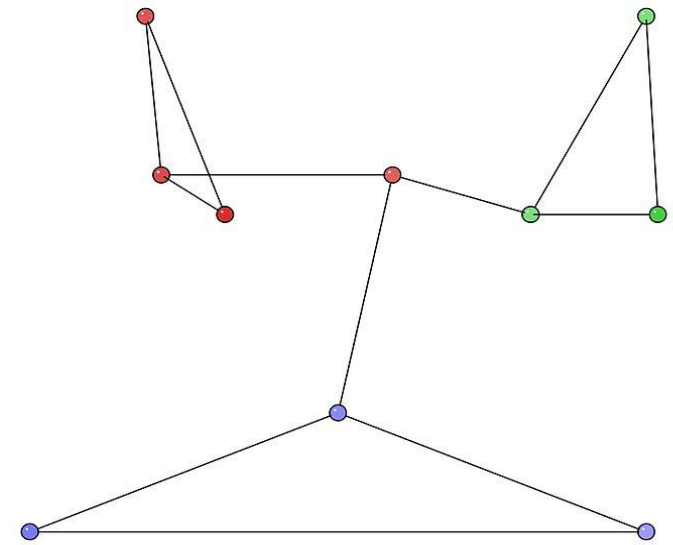
Graph Analysis / Graph Comparison

- Graph-topological metrics

- Modularity:

$$Q = \sum_{u \in M} \left[e_{uu} - \left(\sum_{v \in M} e_{uv} \right)^2 \right],$$

- within module connections
 - (inter module connections)²



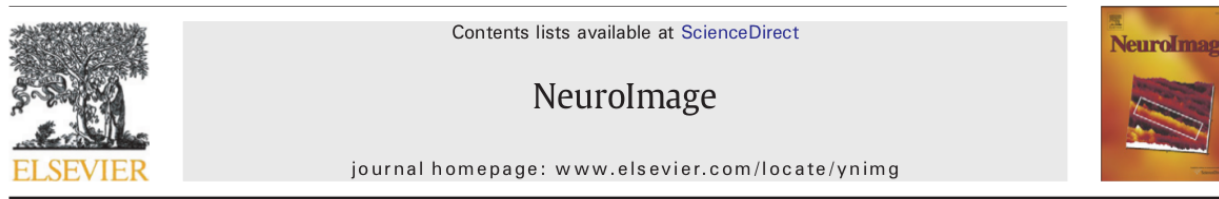
Wikipedia

Graph Analysis / Graph Comparison

- Graph-topological metrics
 - Pro:
 - Many of these Measures are quite intuitive
 - Con:
 - The topology itself is reduced to a single number. Too simplistic?
 - Results are not very reliable

Graph Analysis / Graph Comparison

- Graph-topological metrics
 - Further Reading



Complex network measures of brain connectivity: Uses and interpretations

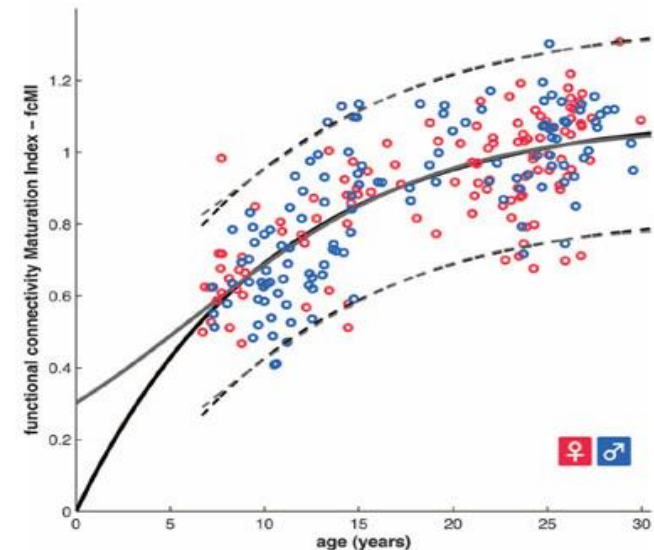
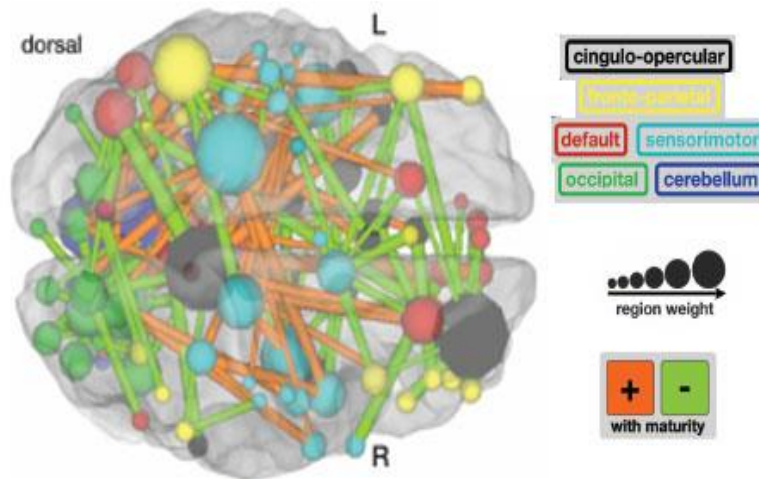
Mikhail Rubinov^{a,b,c}, Olaf Sporns^{d,*}

Graph Analysis / Graph Comparison

- Predictive Modeling
 - Supervised machine learning problem
 - Targets of prediction: age, disease or cognitive state
 - Features are connectivity, centrality or topology metrics
 - To prevent over - fitting of the model one uses cross validation

Graph Analysis / Graph Comparison

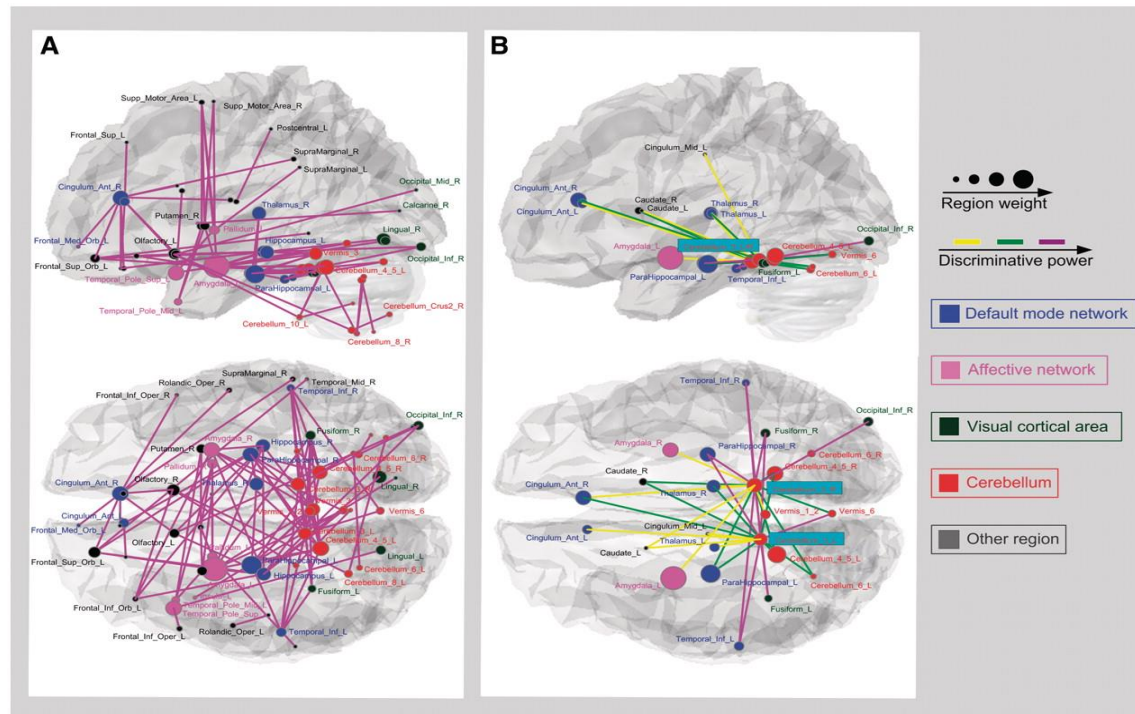
- Predictive Modeling: Predicting Age



Dosenbach, Science, 2010

Graph Analysis / Graph Comparison

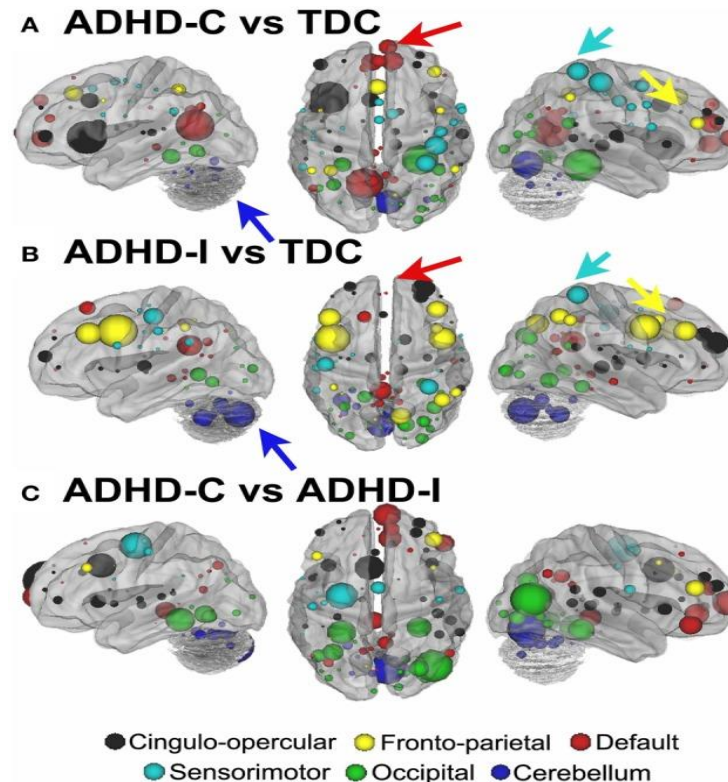
- Predictive Modeling: Predicting Depression



Zeng, Brain, 2012

Graph Analysis / Graph Comparison

- Predictive Modeling: Predicting ADHD



Fair, Fron Hum, 2013

Graph Analysis / Graph Comparison

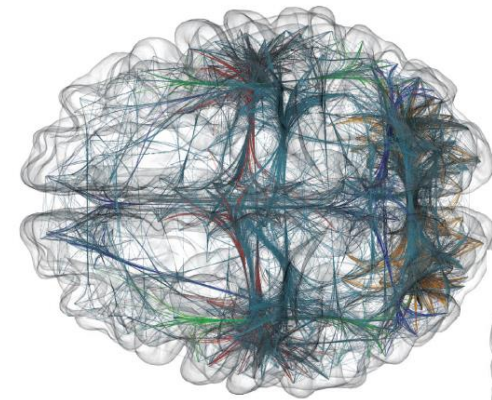
- Predictive Modelling
 - Pro:
 - Allows more complex interactions
 - “multivariate like the brain”
 - Closer to the single subject level
 - Con:
 - Complex models on high dimensional data with very few samples (over fitting!)

Graph Analysis / Graph Comparison

- Few samples
 - Problem: Scanning is expensive
 - Solution: Data Sharing Initiatives:
 - » ADNI ([*adni.loni.usc.edu/*](http://adni.loni.usc.edu/))
 - » ADHD200
(fcon_1000.projects.nitrc.org/indi/adhd200)
 - » ABIDE ([*fcon_1000.projects.nitrc.org/indi/abide*](http://fcon_1000.projects.nitrc.org/indi/abide))
 - » Human Connectome Project
([*www.humanconnectome.org/*](http://www.humanconnectome.org/))

Software

- Preprocessing rs-fMRI:
 - Nipype (nipy.sourceforge.net/nipype/)
 - FCON1000 (nitrc.org/projects/fcon_1000/)
- Building graphs (learned here)
 - Nipy and Numpy
 - Matlab
- Visualizing Graphs
 - brainGL (<http://code.google.com/p/braingl/>)
 - Gephi (<https://gephi.org/>)



Boettger, IEEE TVCG, 2014

Further Reading

- Varoquaux, Gaël, and R. Cameron Craddock. "Learning and comparing functional connectomes across subjects." *NeuroImage* 80 (2013): 405-415.
- Fornito, Alex, Andrew Zalesky, and Michael Breakspear. "Graph analysis of the human connectome: promise, progress, and pitfalls." *Neuroimage* 80 (2013): 426-444.

Thank you

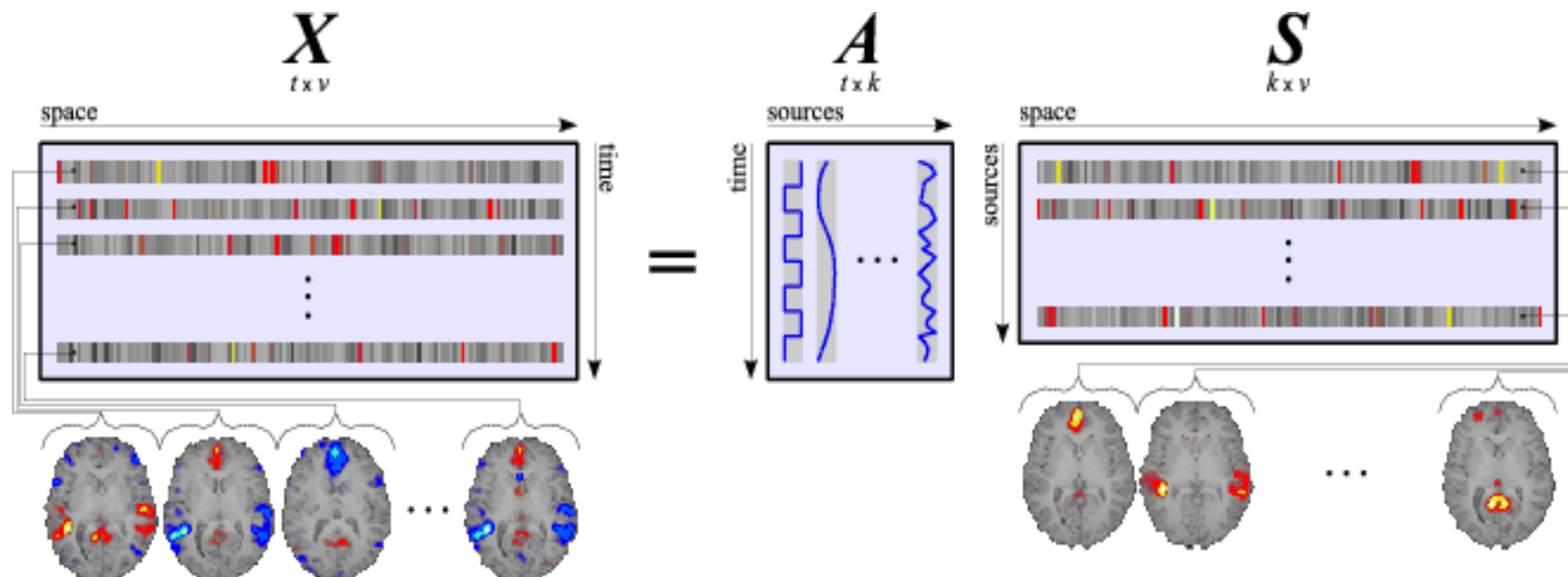
- Dept. of Neurology
- Resting State Group



Zuo, Cereb Cortex, 2012

Appendix

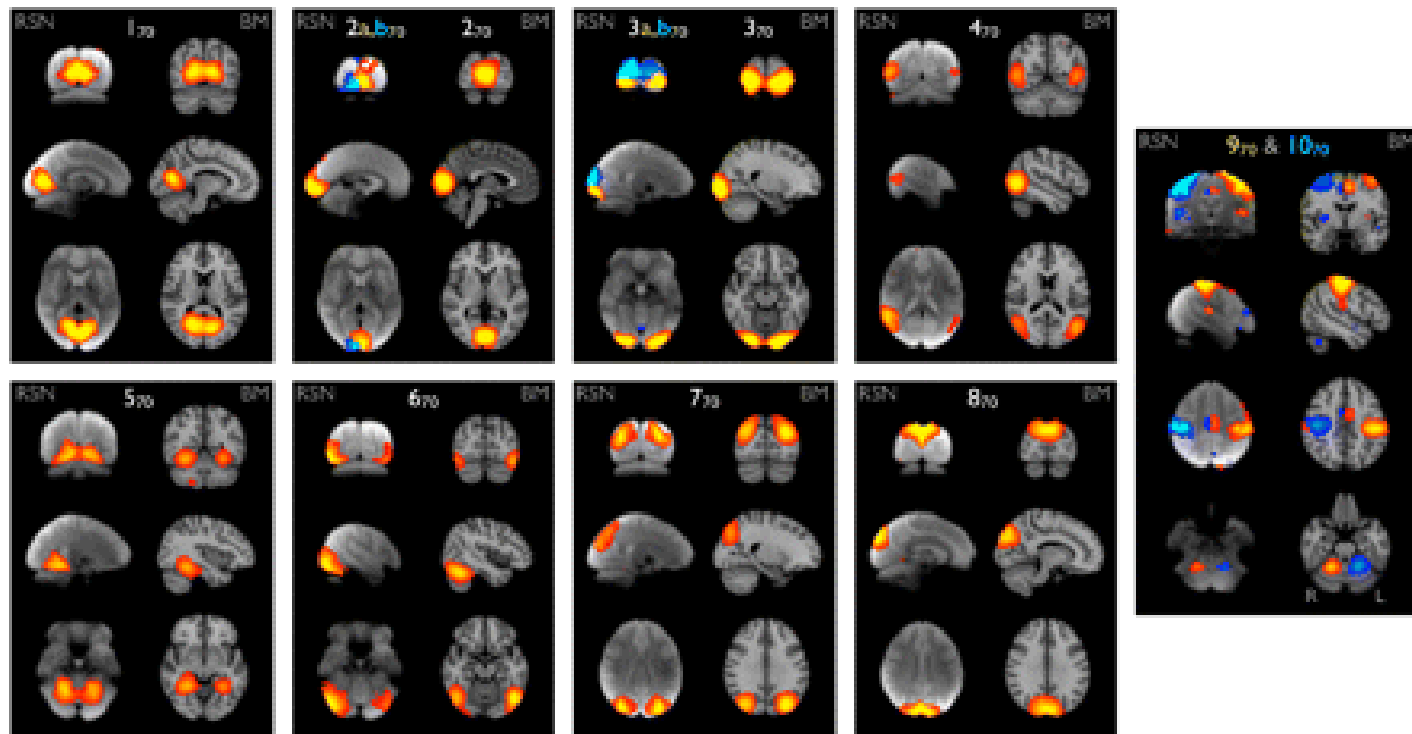
- Ylipaavalniemi, 2005



Ylipaavalniemi, 2005

Appendix

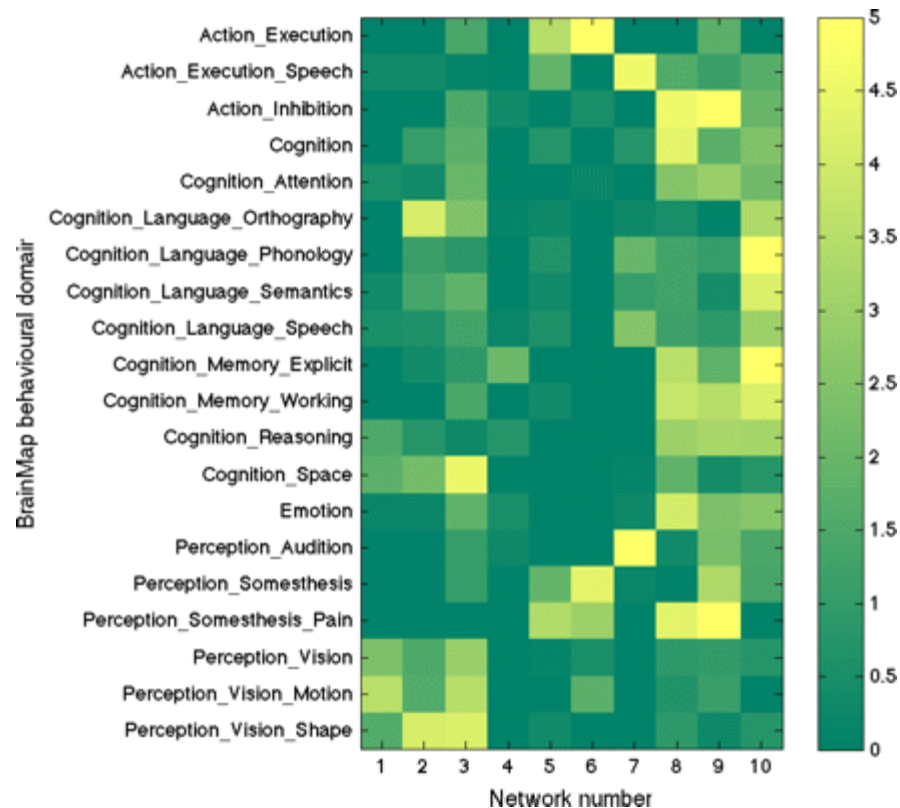
- Smith PNAS 2009



Smith, PNAS, 2009

Appendix

- Smith PNAS 2009



Smith, PNAS, 2009

Appendix

- Preprocessing
 - 1) discarding the first four EPI volumes to allow for signal equilibration,
 - 2) 3D motion correction
 - 3) time series despiking,
 - 4) 4D mean-based intensity normalization,
 - 5) band-pass temporal filtering (0.01-0.1 Hz),
 - 6) removing linear and quadratic trends and
 - 7) regressing out eight nuisance signals (white matter, cerebrospinal fluid and six motion parameters).