

ICON 2014

# Hubs in Brain Structure and Function

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# Brain Networks

Networks represent complex systems as sets of discrete nodes and edges (e.g. brain regions and interconnections).

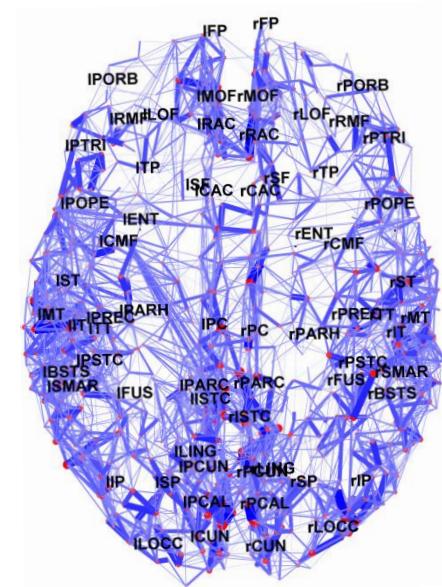
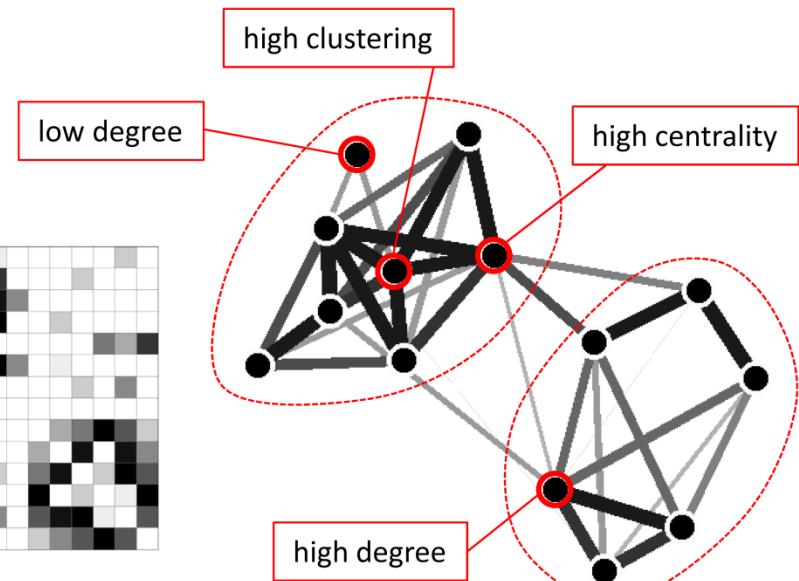
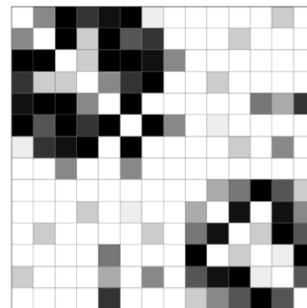
Fundamental distinction:

- Structural networks (anatomical connections, “connectome”)
- Functional networks (statistical dependencies, dynamic interactions)

Important themes in current studies of brain networks:

- Community structure (**modules**)
- Node/edge **influence** and vulnerability
- Network **cores/clubs/cliques**

Virtually all biological networks have  
“network hubs”



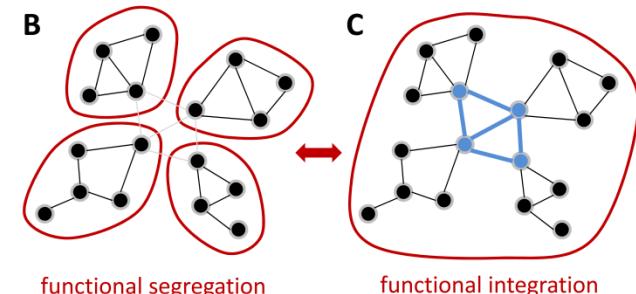
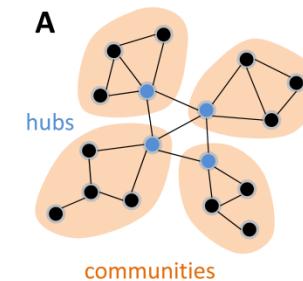
# Hubs – Definition and Detection

Functional roles of network hubs:

- High influence on network dynamics
- Focal points of communication or interaction

Measures for detecting network hubs:

- Degree, strength (local)
- Betweenness or closeness centrality (global)
- Vulnerability
- Participation in community structure



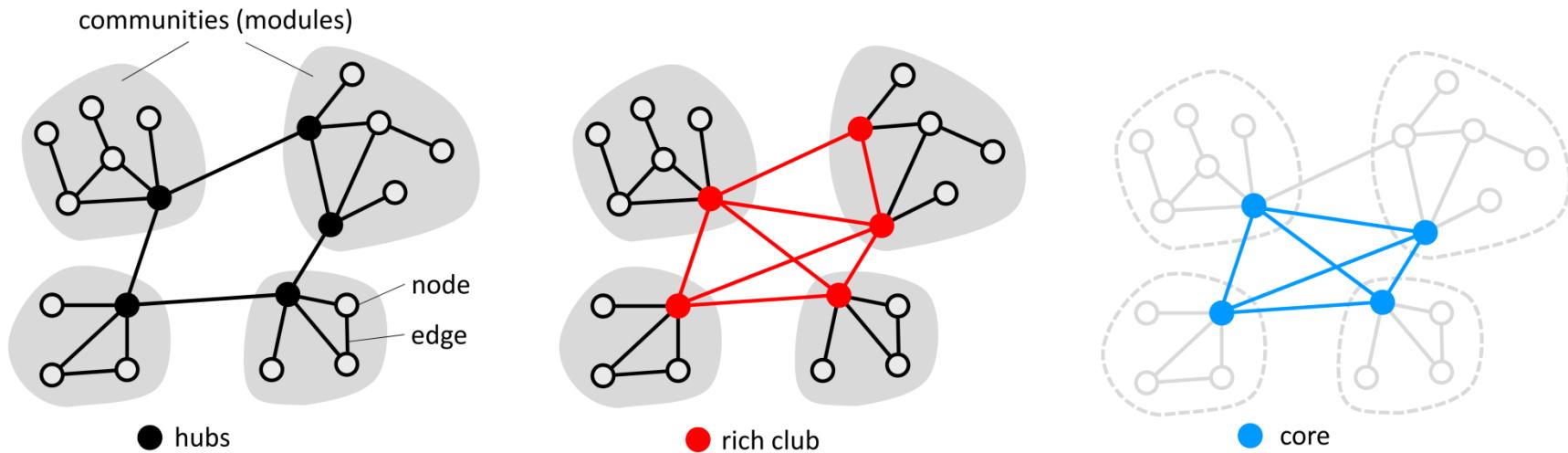
Robust detection of network hubs can be achieved by combining multiple network metrics.

Most network measures are appropriate for use in structural (connectome) networks...

... but use of some measures (degree/strength, path-based centrality) may be biased or potentially inappropriate in functional networks (e.g. resting-state fMRI)

# Modules, Cores, and Rich Clubs

In some networks, highly connected/central hub nodes have a tendency to be **highly connected to each other** (“rich-club” organization).



Hubs, cores and rich clubs may play **important roles in global communication**:

- By creating **short (efficient) paths**
- By supporting **integration of information across diverse brain systems**

# Outline

► Characteristic Properties of Brain Networks

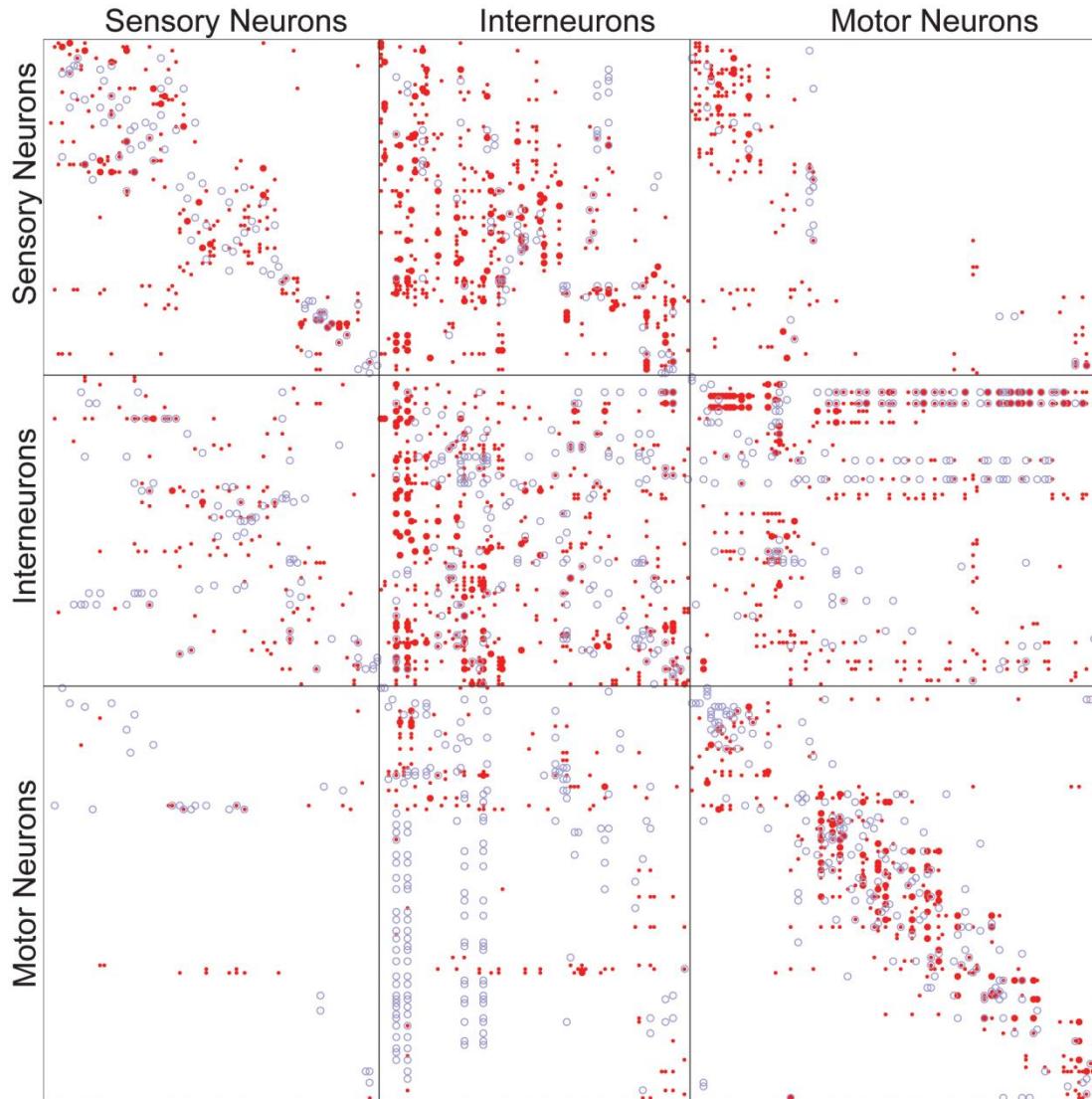
Hubs in the Human Connectome – A Very Brief Summary

Network Hubs, Communication Processes, and Integration

Summary and Conclusion

# Networks – Microscale: *C. elegans*

*C. elegans*



White et al. (1986) Phil Trans R Soc

Varshney et al. (2011) PLOS Comp Biol  
Towlson et al. (2013) J Neurosci

Varshney et al, 2011:

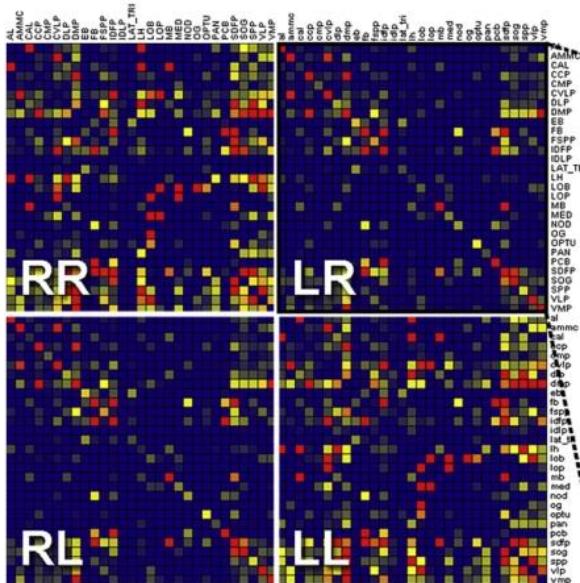
- Full network: 279 neurons, 2990 directed connections (density: 3.9%)
- High clustering, short path length
- Broad (heavy-tailed) degree distribution (neurons with high degree centrality)

Towlson et al, 2013:

- Modules
- Set of neurons with high betweenness, many inter-modular connections (“connector hubs”)
- Hubs are densely interconnected (“rich club”)
- Many hub connections are long-distance

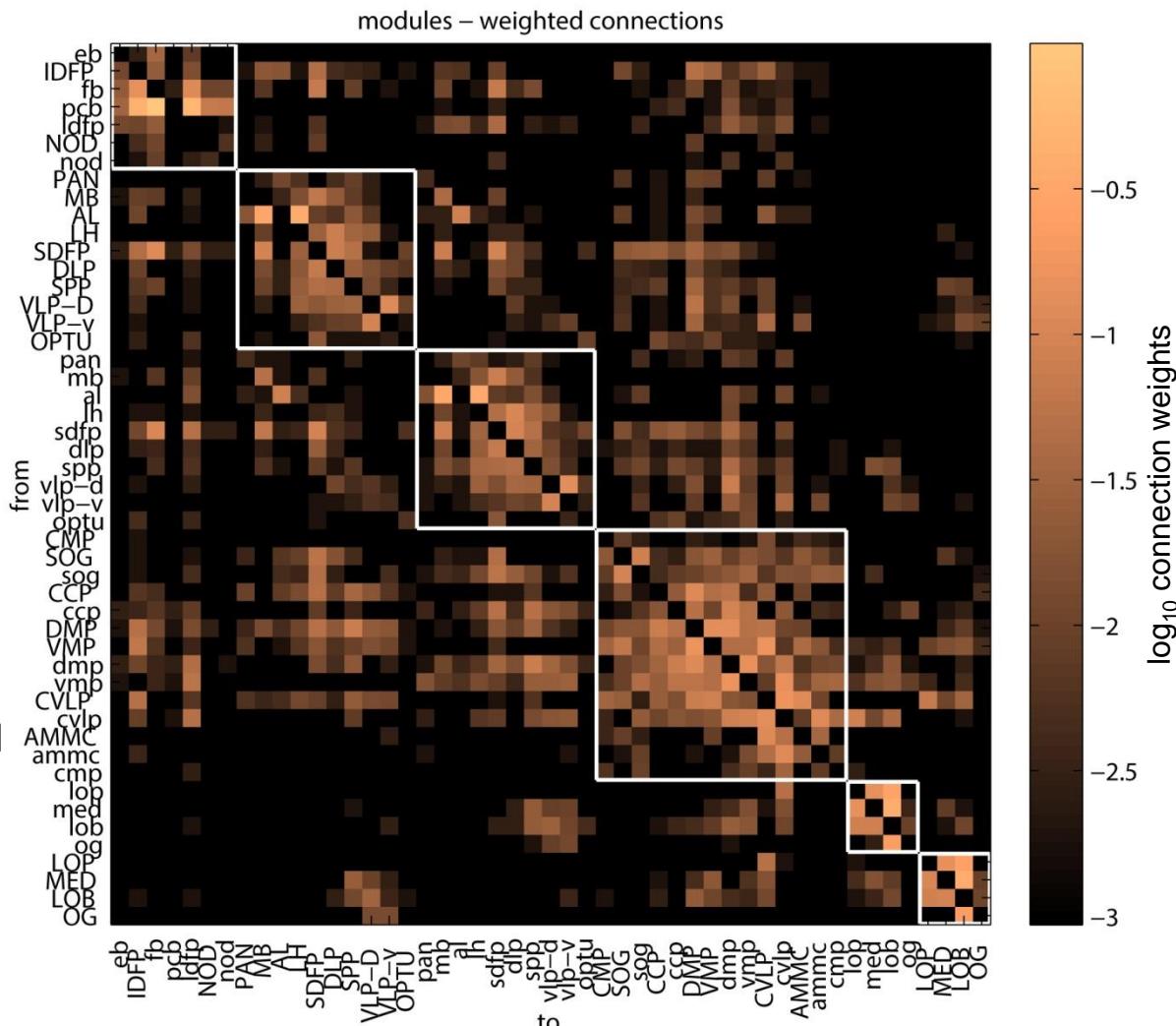
# Networks – *Drosophila* Brain

## *Drosophila* macroscale connectome

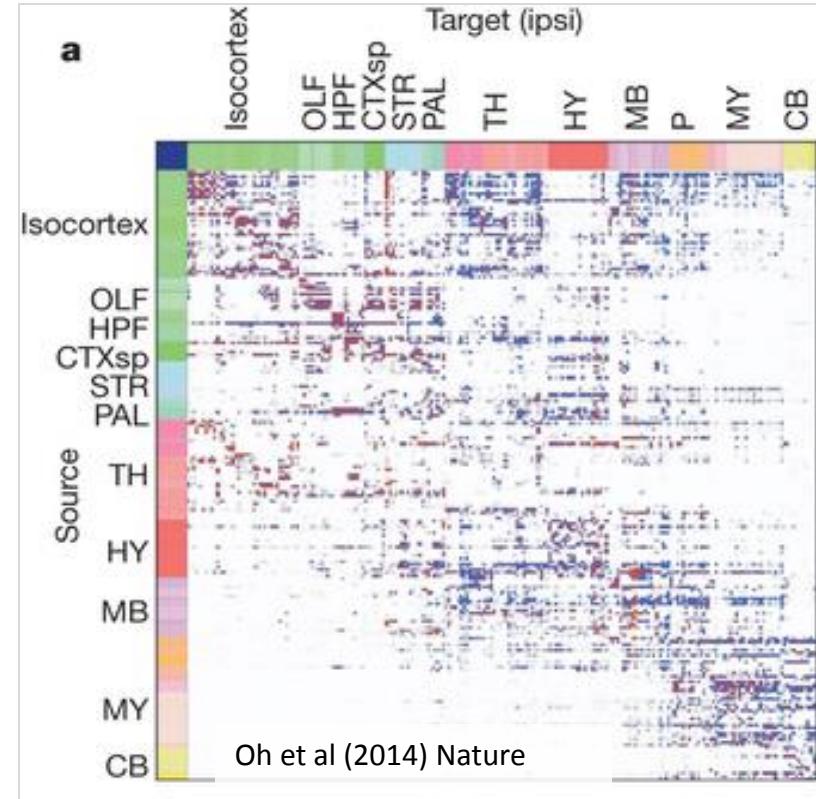
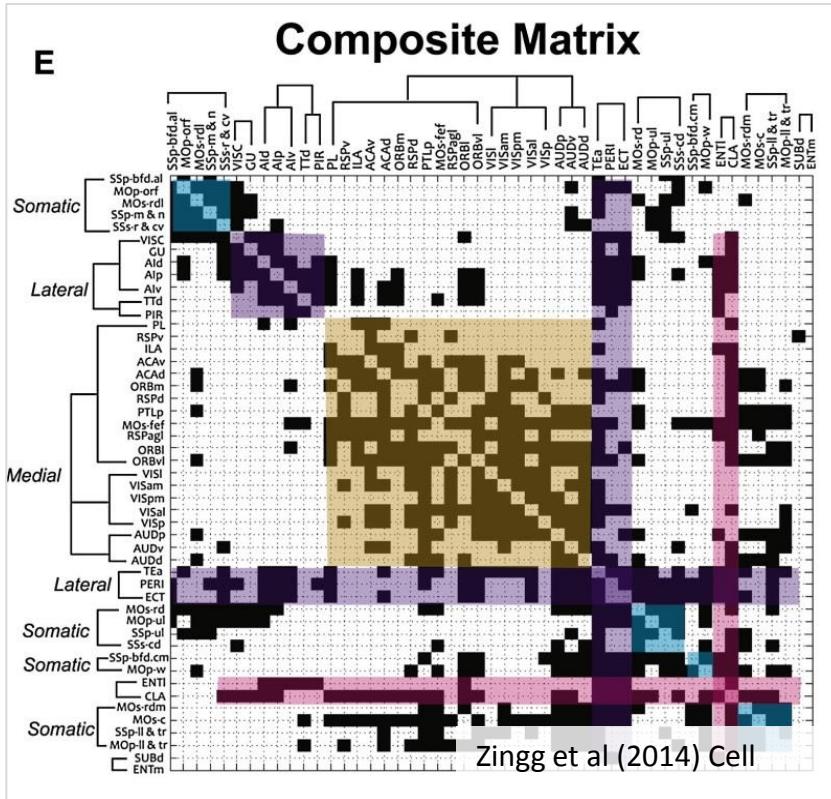
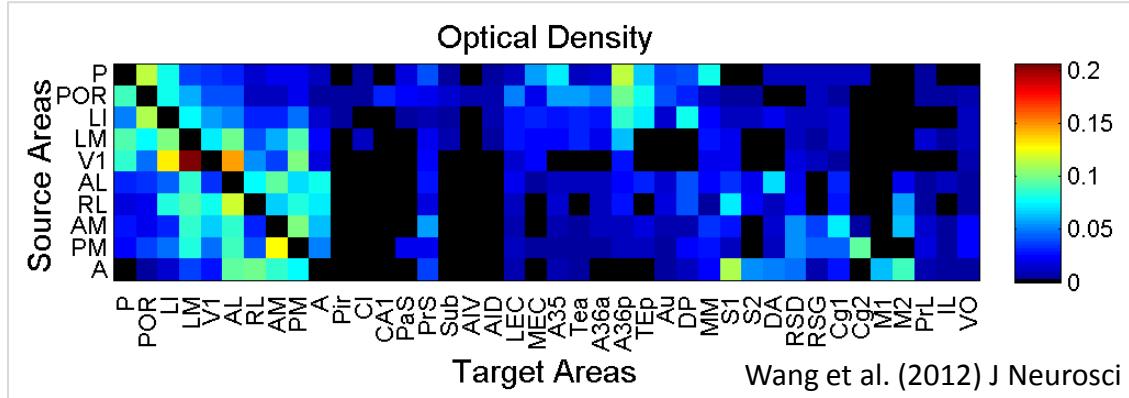


Shi et al:

- 49 LPUs, 1193 directed weighted connections (50% density)
- High clustering, short path length
- Modules (visual L/R, auditory, olfactory L/R, pre-motor)
- Connectors and RC organization

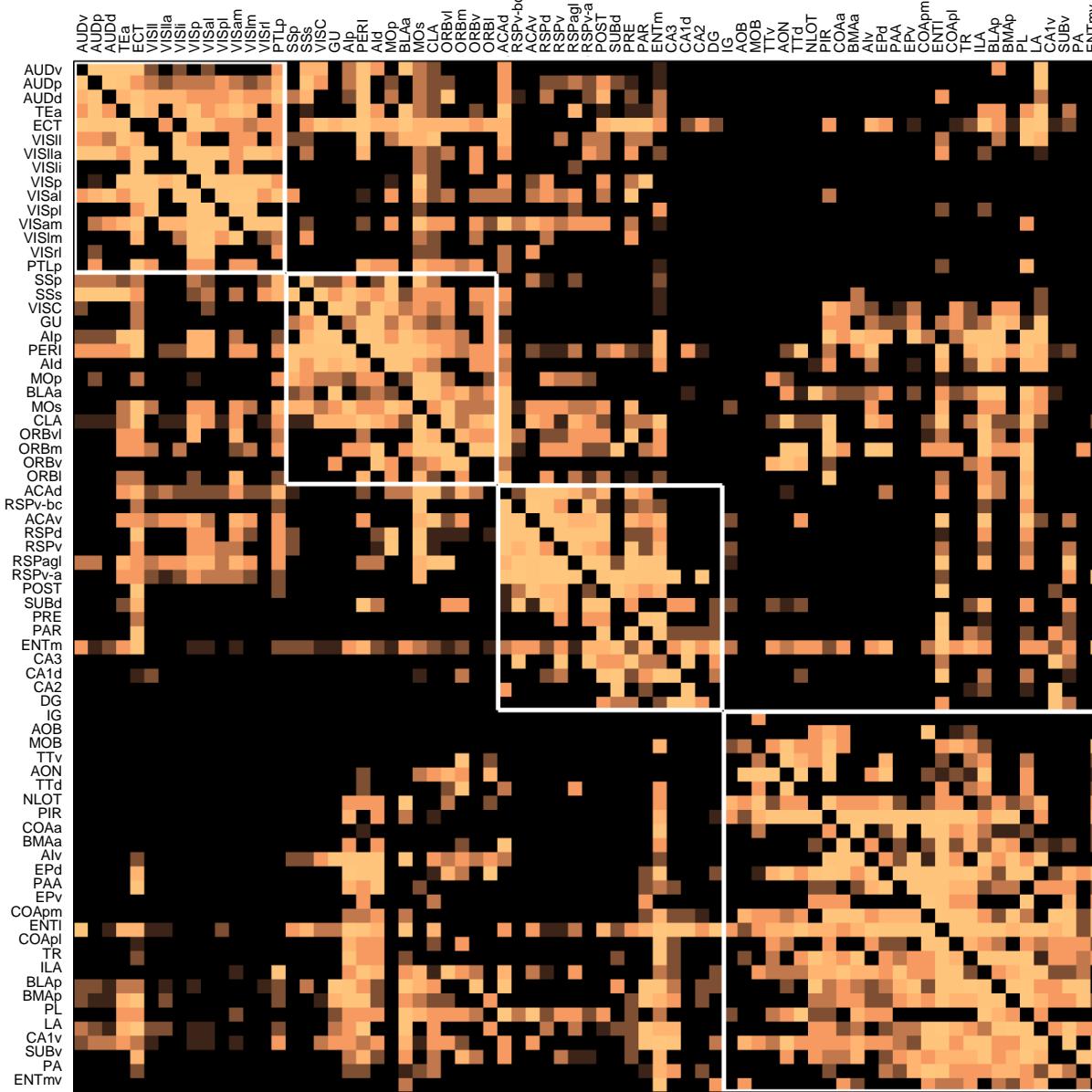


# Networks – Mouse Connectome



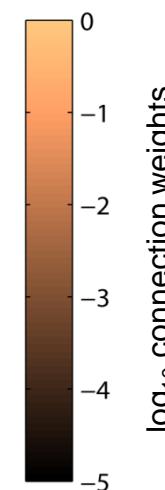
# Networks – Rat Cerebral Cortex Connectome

to



Bota et al:

- 73 areas, 1923 directed weighted connections (37% density)
- High clustering, short path length
- Modules (audiovisual, somatomotor, dorsal limbic, ventral limbic/olfactory)
- Connectors and RC organization

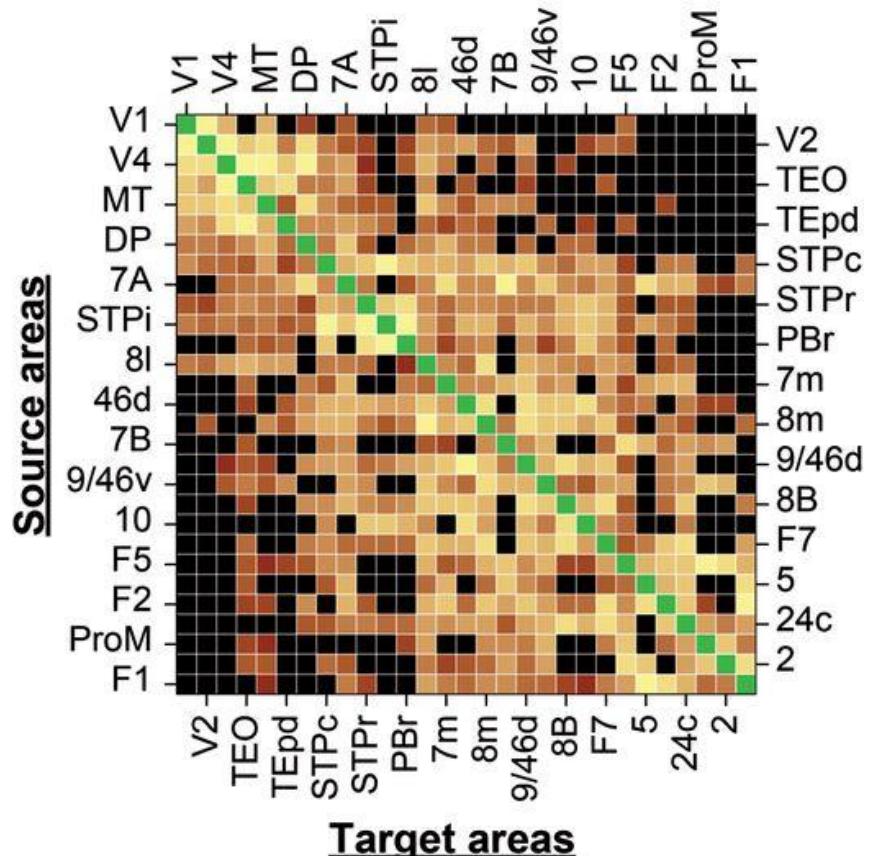


Bota, Sporns, Swanson  
(in preparation)

# Networks – From Cells to Systems

Macaque **macroscale** connectome

From:	OCCIPITAL												TEMPORAL												PARIETAL												FRONTAL								
	V1	V2	V3	VP	V3A	V4	VOT	V1i	MT	FST	PITd	PITv	CITd	CITv	AlTd	AlTv	STPp	STPs	TF	TH	MSTd	MSTi	PO	PIP	LIP	VIP	MIP	MDP	DP	7a	FEF	A6													
V1	+	+	+	.	+	+	.	NR	+	.	.	.	.	.	.	.	.	.	.	.	?	+	+	.	.	.	.	.	.	.	.	.	.	.	.	.	.								
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Bow-tie core-periphery, rather than RC organization

# Networks – Common Properties

Common topological properties:

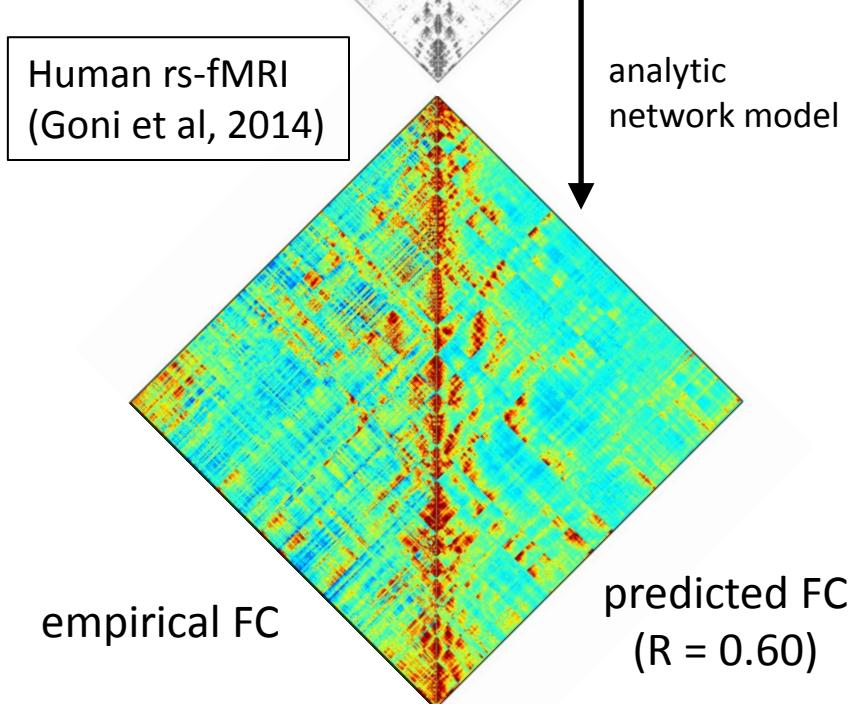
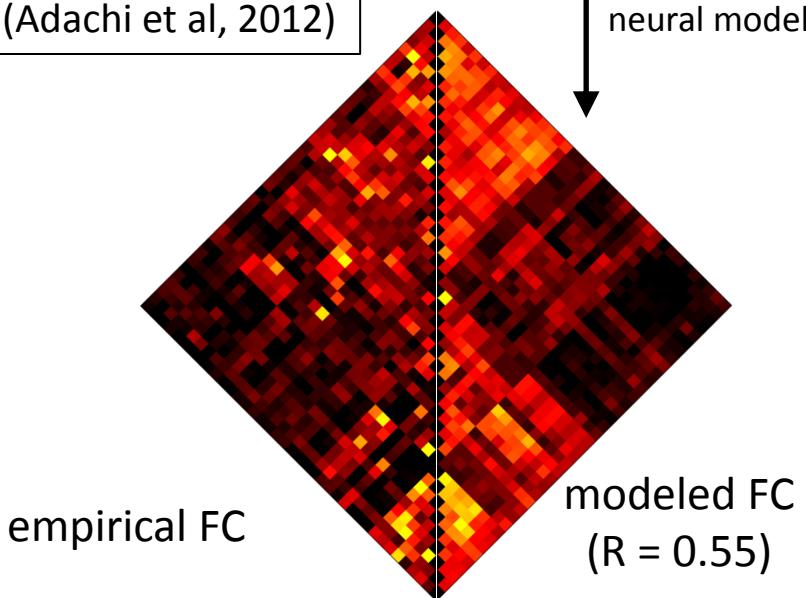
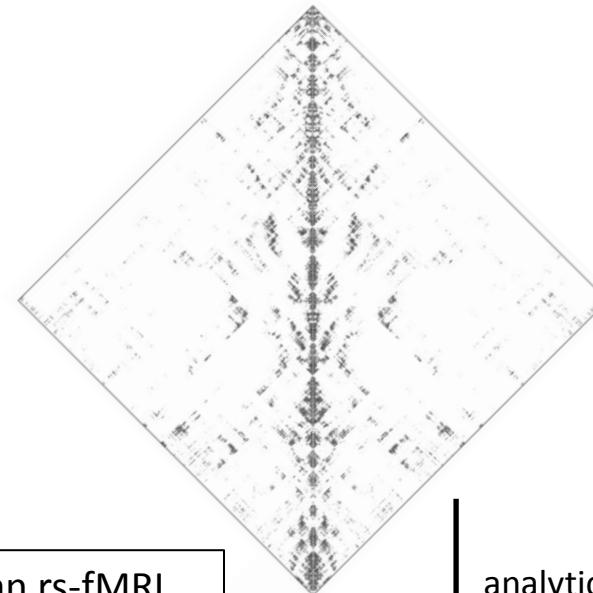
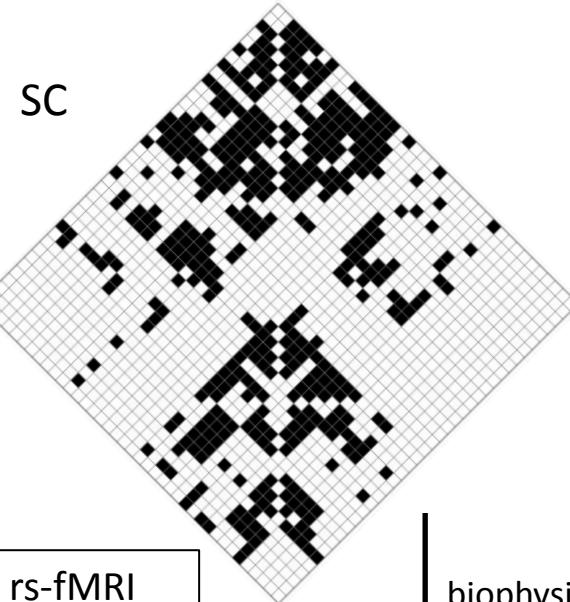
- Broad degree distribution – small subsets of highly connected nodes (hubs)
- Log-normal profiles of connection density (e.g. Markov et al., 2011; Wang et al., 2012; Oh et al 2014)
- Specificity of connection profiles (e.g. Passingham et al., 2002)
- High clustering, short path length
- Interconnected “modules”, or network communities
- A tendency for the formation of a “core” (a central club or clique), as distinct from a set of more peripheral nodes

Features related to spatial embedding:

- Distance-dependent connection density/probability (e.g. Young, 1992)
- Exponential distance rule (Ercsey-Ravasz et al., 2013)
- Near-minimal wiring cost – plus presence of (costly) long-distance projections (Kaiser & Hilgetag, 2006)
- Cost-efficiency trade-off (e.g. Bullmore & Sporns, 2012)

# “Generative” Models for Functional Networks

Can structural connectivity (SC) “generate” functional connectivity (FC)?



biophysical  
neural model

analytic  
network model

# Generative Models for Structural Networks

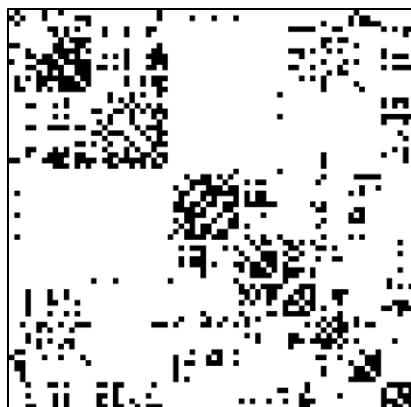
Can spatially-embedded growth (Kaiser & Hilgetag) or distance-based (Ercsey-Ravasz et al., 2013) models account for empirically observed brain networks?

Betzel et al. (in preparation):

- Edges are placed between spatially embedded nodes (human brain) according to some attachment rule.
- For example:

$$\Pi_{ij} \propto D_{ij}^\eta \times K_{ij}^\gamma$$

- $D_{ij}$  is the Euclidean distance between nodes  $i$  and  $j$  and  $K_{ij}$  is the number of neighbors shared between  $i$  and  $j$
- Networks generated by this model are scored based on how well they match empirical networks' degree, clustering, and edge distance distributions.

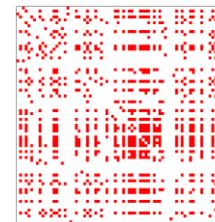
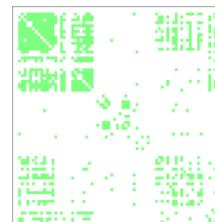
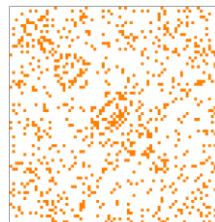
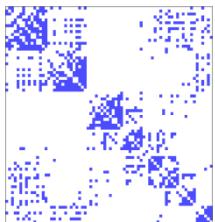
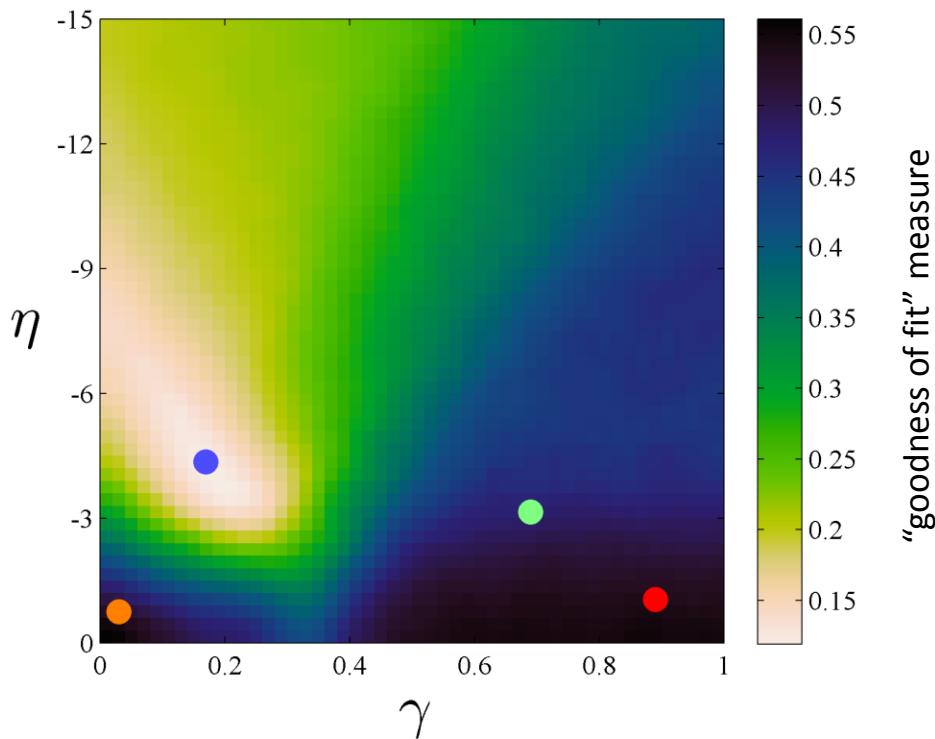


Example empirical network  
(human cortex, NKI lifespan sample, Xi-Nian Zuo, Beijing)

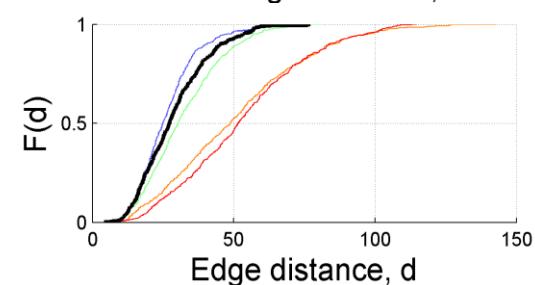
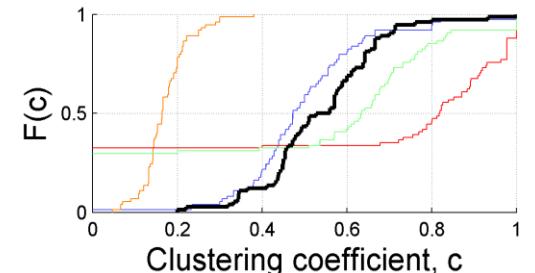
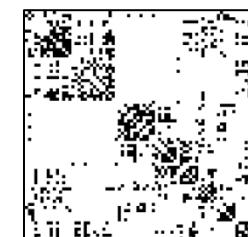
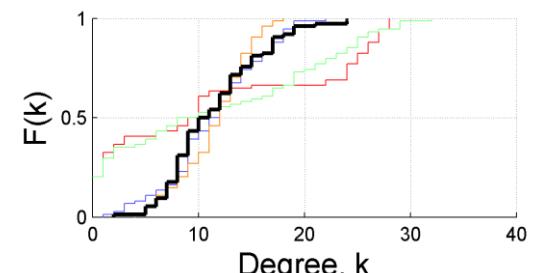
Related work by Vertes et al (2012) in FC modeling,  
and Samu et al. (2014)

# Generative Models for Functional Networks

$$P_{i,j} \propto D_{i,j}^{\eta} \times K_{i,j}^{\gamma}$$



Varying parameters of the generative model allows scoring model networks against empirical networks.



# Outline

## Characteristic Properties of Brain Networks

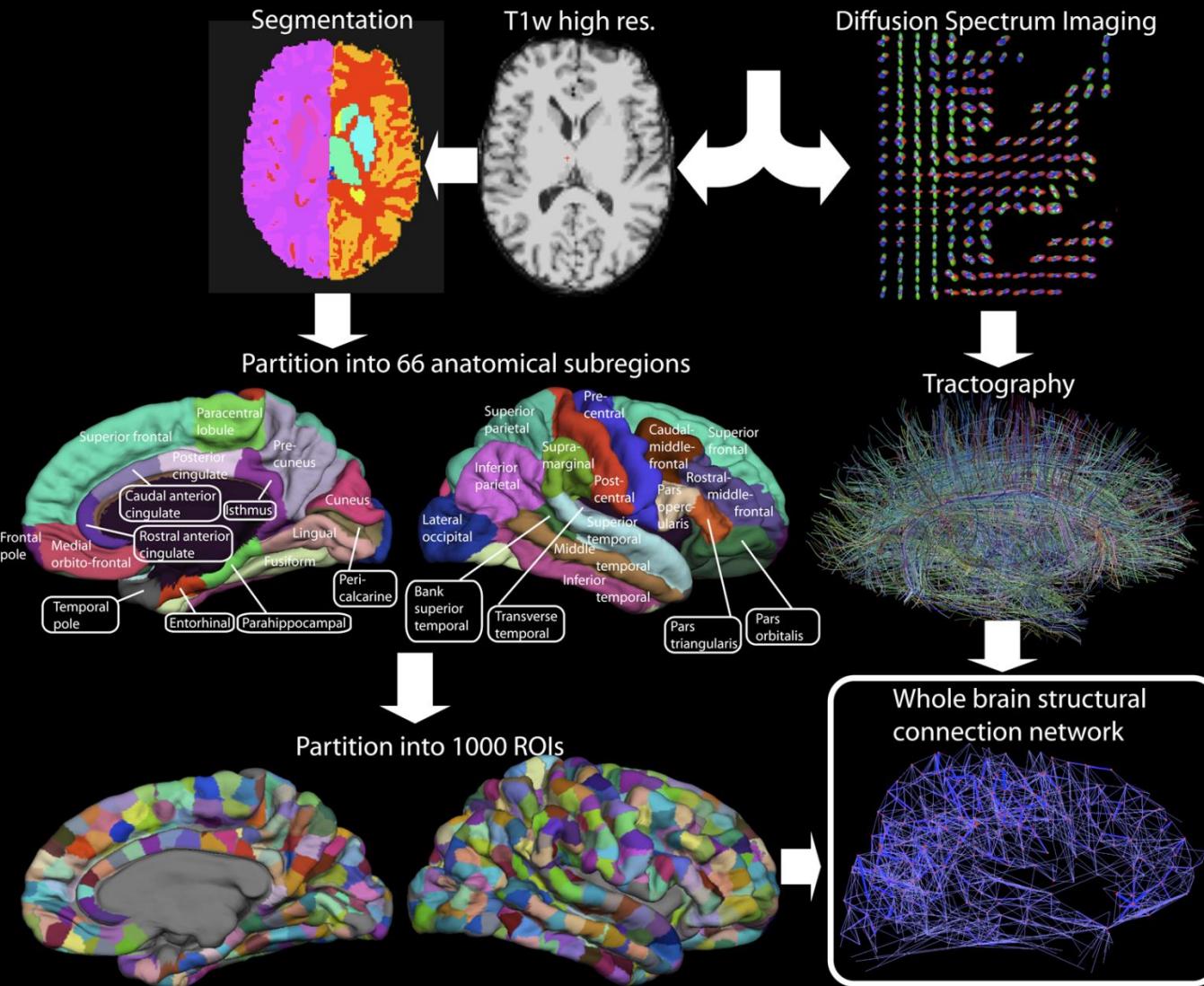
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Network Hubs, Communication Processes, and Integration

Summary and Conclusion

# Mapping Human Brain Structural Connectivity

## MRI Acquisition

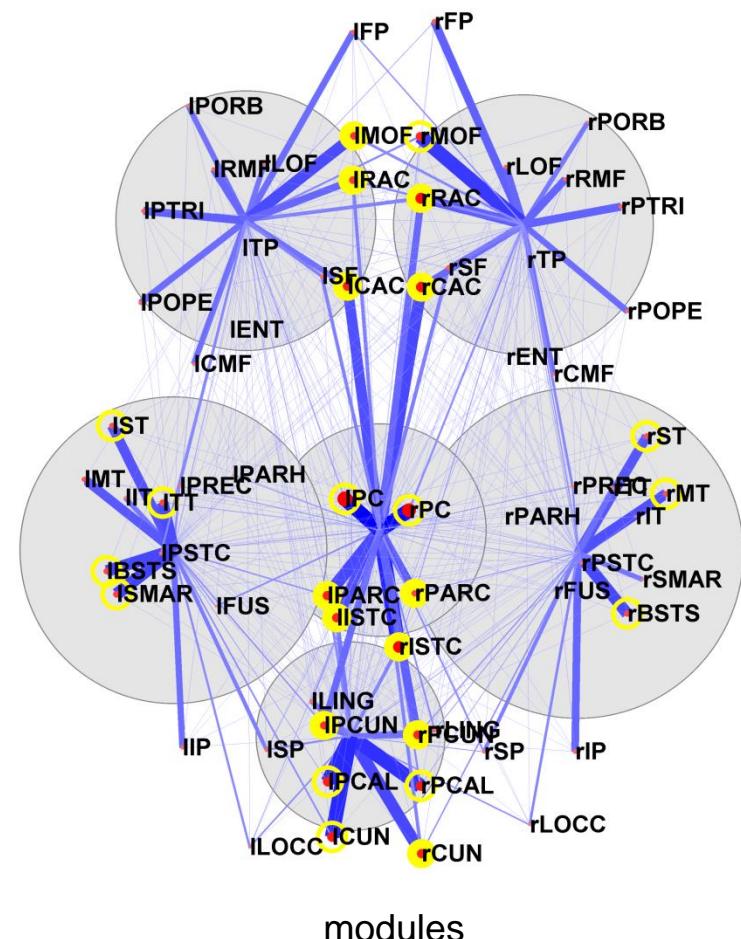
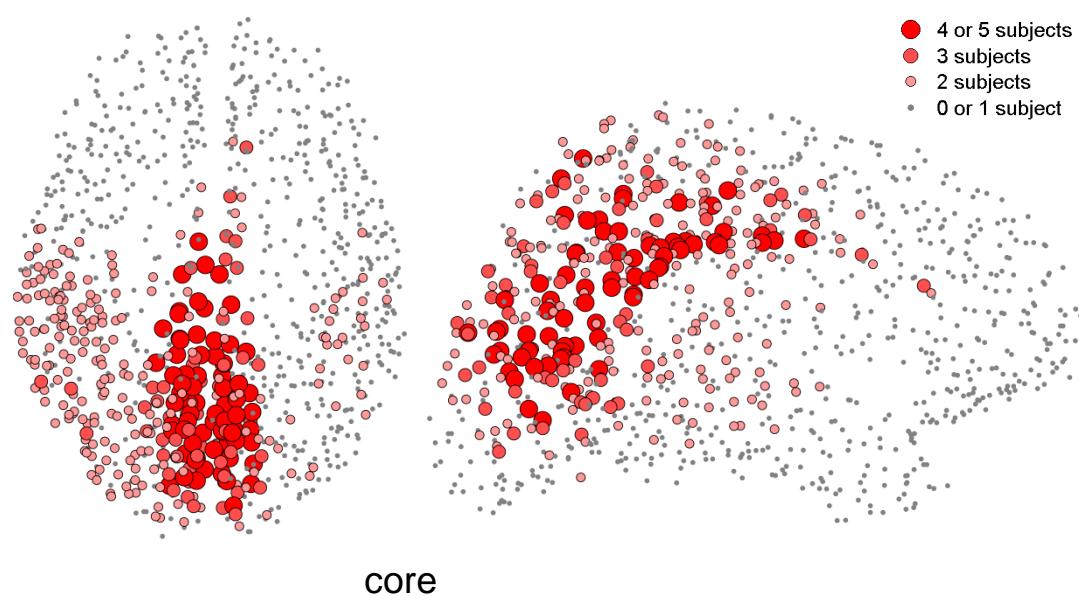


Patric Hagmann

# Network Analysis of the Connectome

## Network analysis revealed

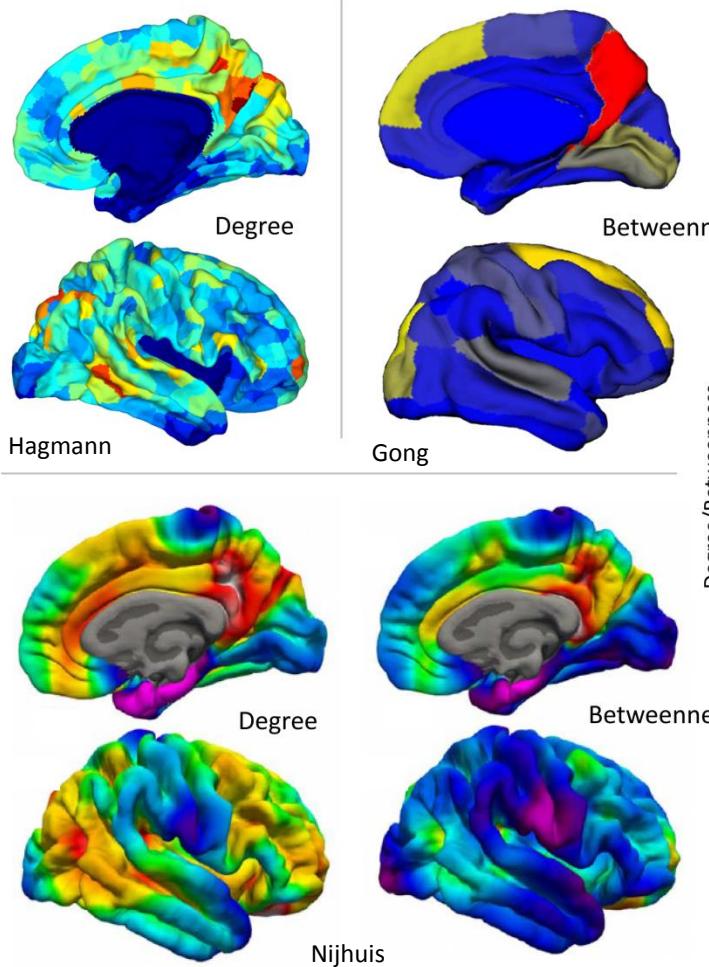
- Unique regional connectivity fingerprints
  - Broad (exponential) degree distribution
  - High clustering, short path length
  - Existence of modules interlinked by hub regions
  - A prominent structural core



# Hubs in the Human Connectome

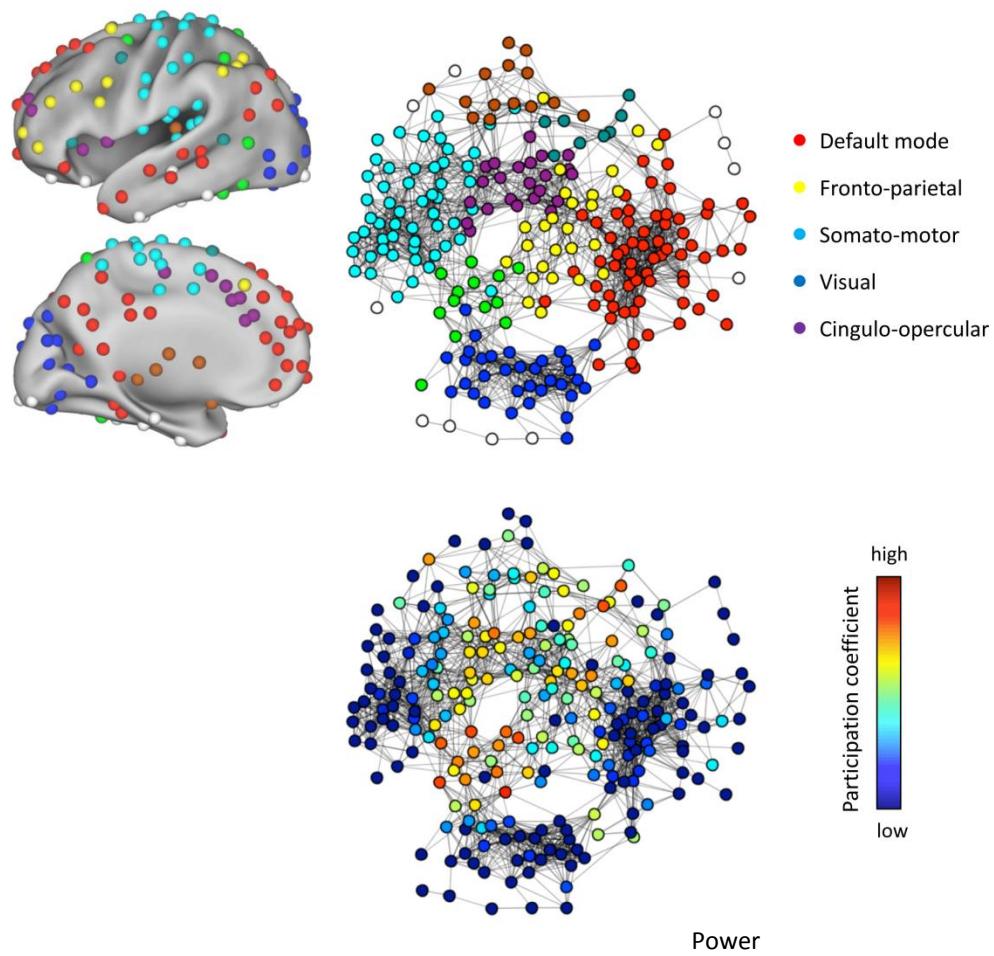
## Structural Connectivity

a



## Functional Connectivity

b



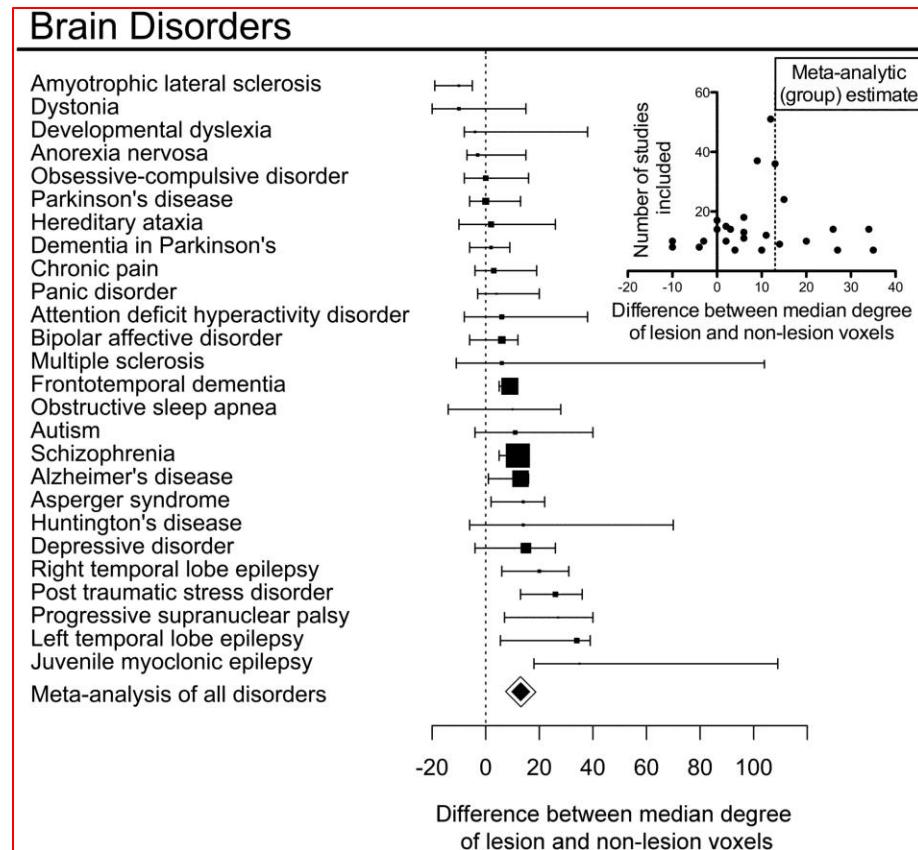
Hagmann et al. (2008) *PLoS Biol.* 6, e159.  
Nijhuis et al. (2013) *PLOS ONE* 8, e65511.

Gong et al. (2009) *Cereb Cortex* 19, 524.  
Power et al. (2011) *Neuron* 72, 665.

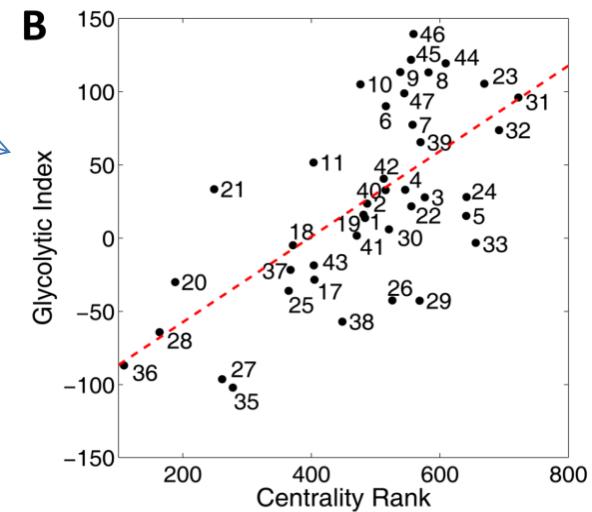
# Hubs in the Human Connectome

## Hub regions:

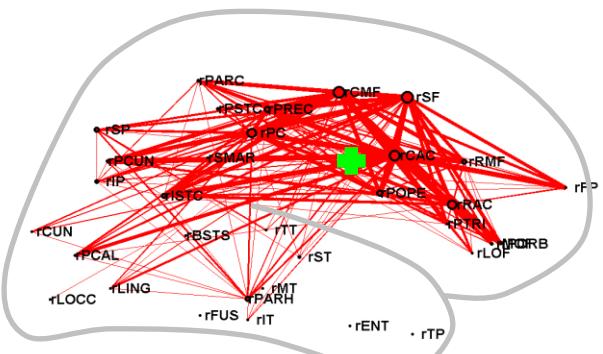
- Relation to brain metabolism and energy demand
- Points of vulnerability in brain damage and disorders (see recent review/meta-analysis by Crossley et al. 2014)



Crossley



Vaihsnavi; Bullmore & Sporns



Alstott

# Outline

## Characteristic Properties of Brain Networks

### Hubs in the Human Connectome – A Very Brief Summary

- ▶ Network Hubs, Communication Processes, and Integration

### Summary and Conclusion

# Rich-Club Organization of the Human Connectome

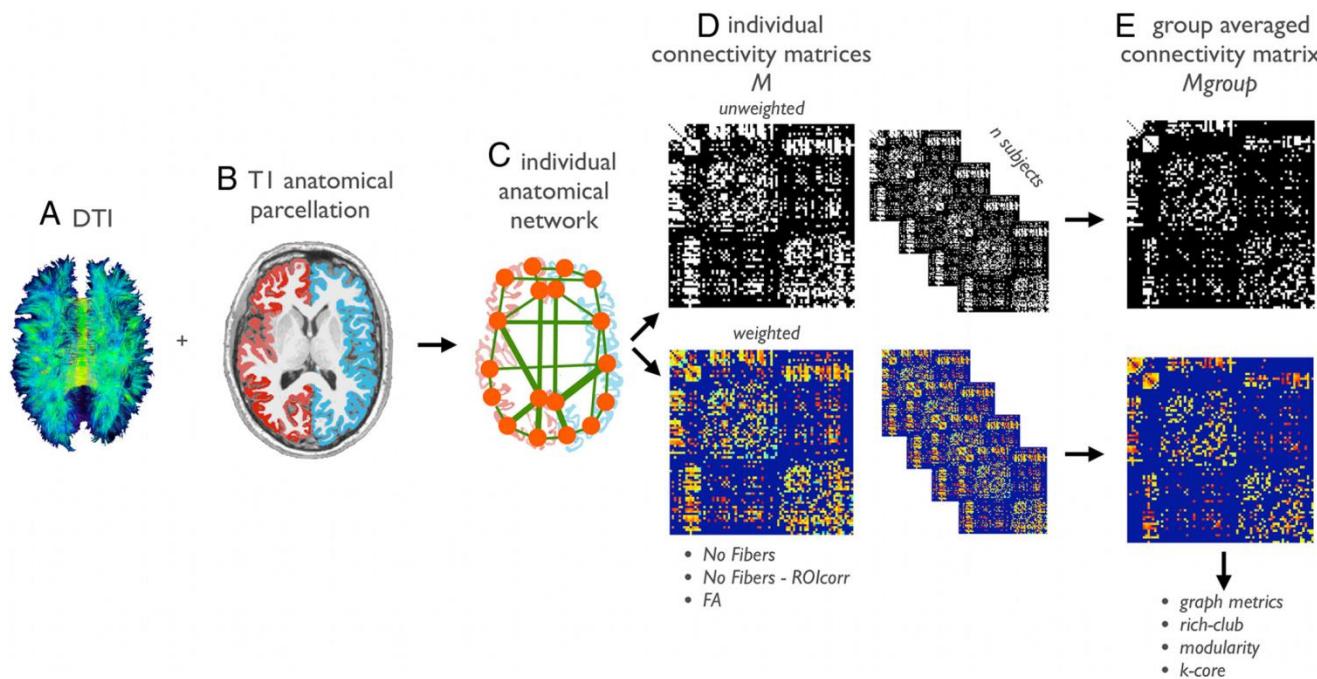
Human connectome data sets exhibit a prominent **rich club**, comprising cortical and subcortical regions.

Presence of rich-club (RC) organization suggests **central role in information integration** and communication.

DTI study, 21 participants, low (82 nodes) and high-resolution (1170 nodes) partition, streamline tractography

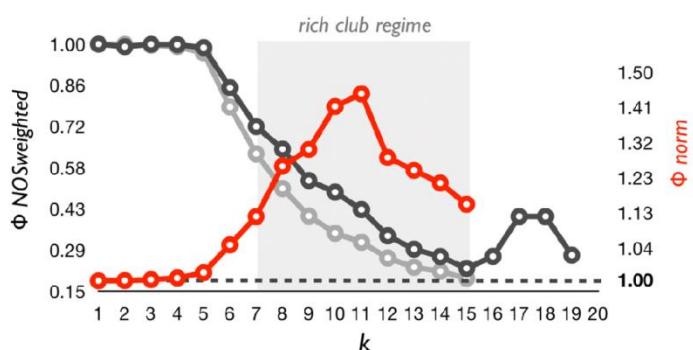


Martijn van den Heuvel



# Rich-Club Organization of the Human Connectome

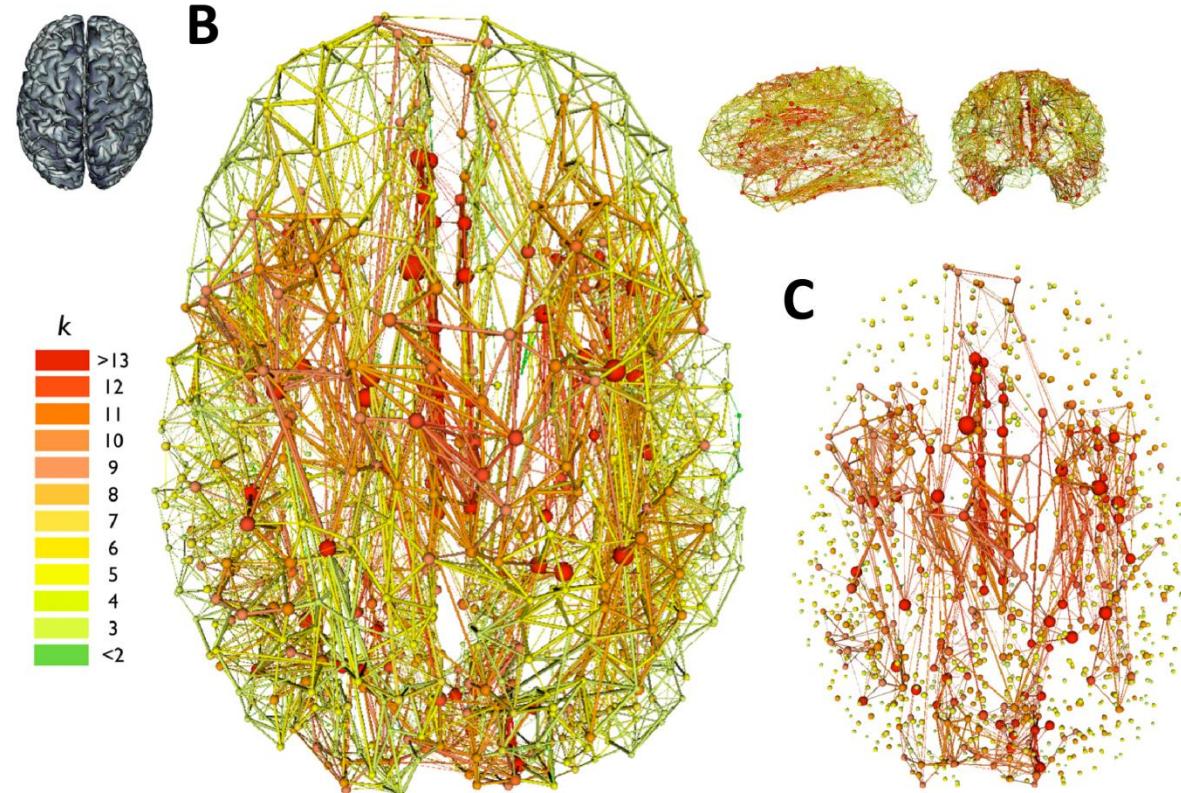
A



RC members include:

precuneus, posterior cingulate cortex, superior frontal cortex, medial orbitofrontal cortex, caudal anterior cingulate cortex, insula, portions of medial temporal cortex.

B



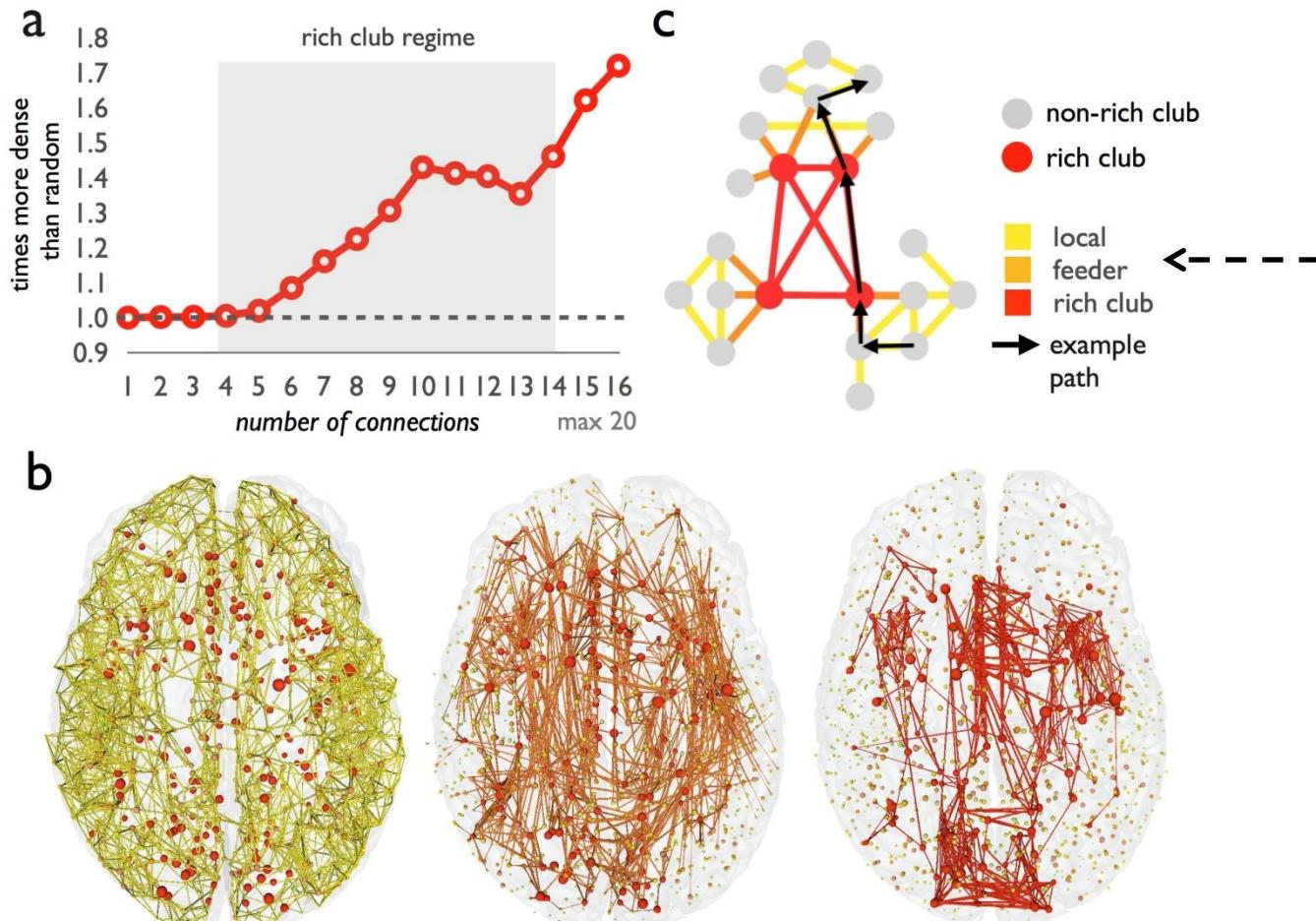
Overlap of RC and structural core.

High proportion (89%) of short communication paths travel through at least one RC node (66% through an RC edge).

RC damage (node/edge deletion) has large effects on network integrity and efficiency.

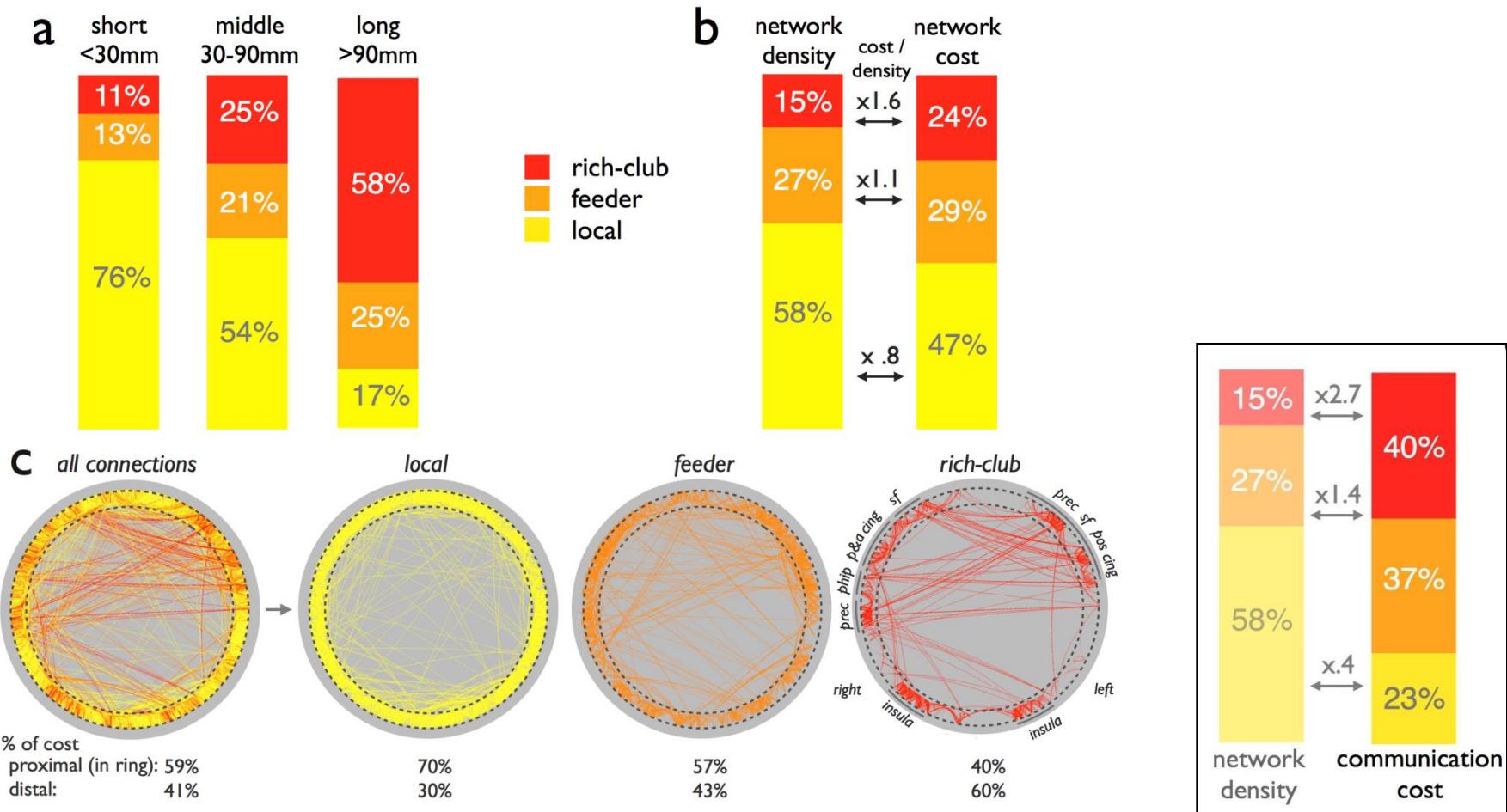
# Rich-Club Organization of the Human Connectome

Replication



Once the RC is identified, connections can be classified as RC, feeder, local.

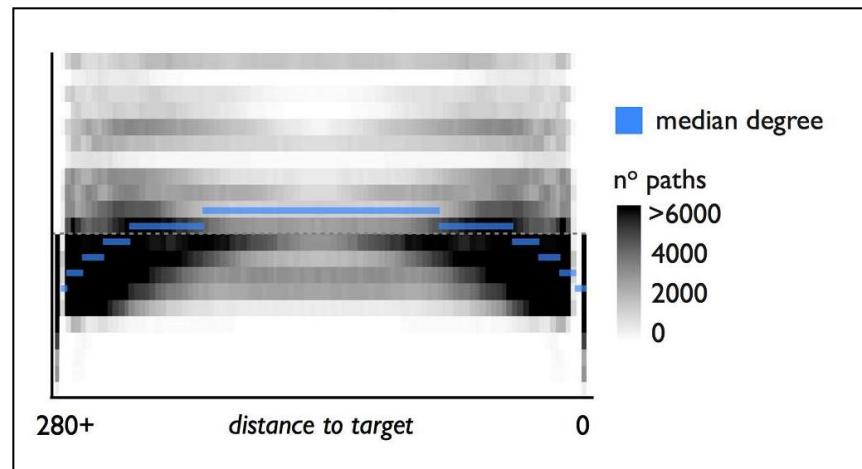
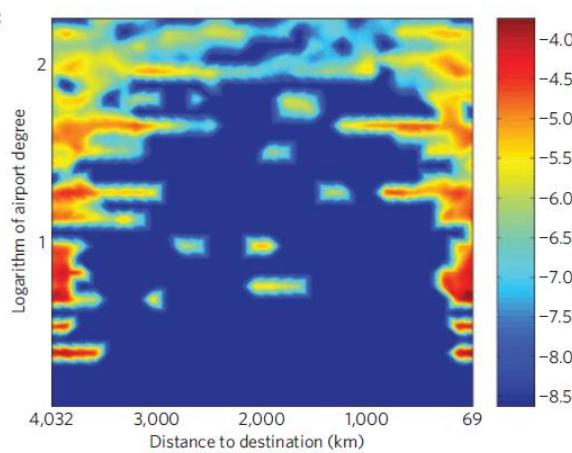
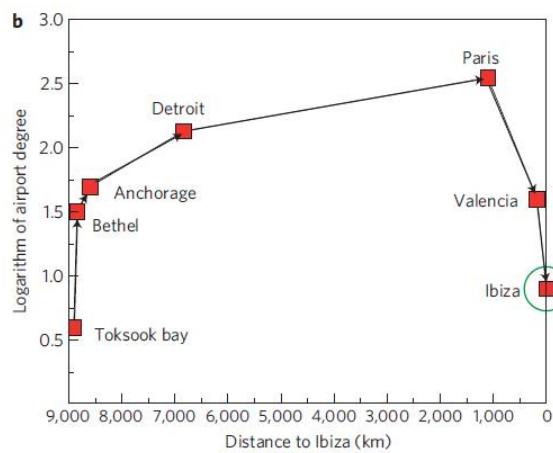
# Rich-Club Organization of the Human Connectome



RC connections are mainly long-distance, and thus represent a high-cost feature of cortical organization – they also account for a large share of short paths.

# Rich-Club Organization of the Human Connectome

Hidden metric spaces enable “greedy routing” strategies in large communication networks (e.g. air travel)

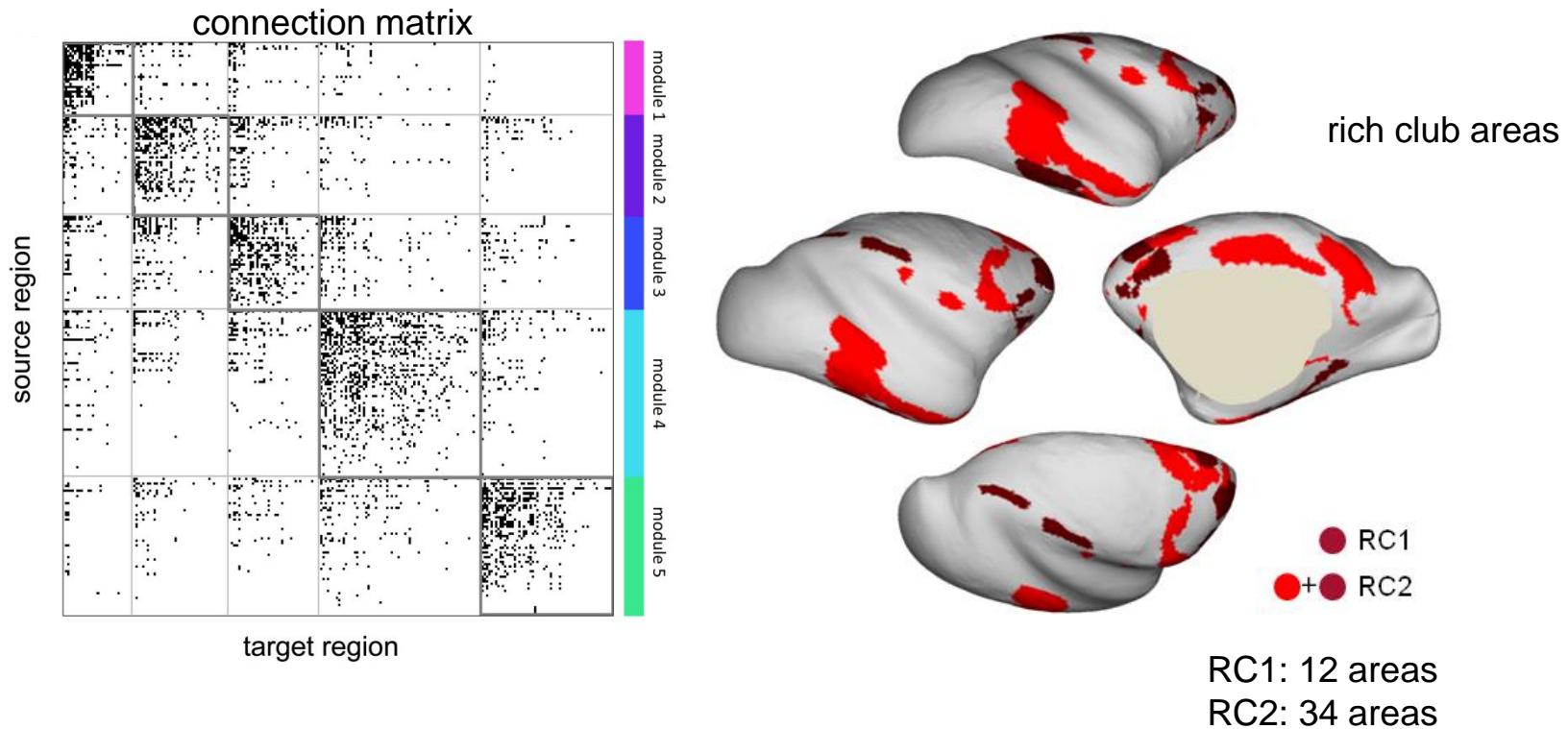


Short paths in human brain structural networks exhibit patterned degree sequences, with a central role of RC nodes and edges.

# Rich-Club Organization of the Macaque Connectome

RC is detected also in **macaque cerebral cortex** (242 areas, 4090 directed projections, collated from Cocomac by Modha & Singh, 2010):

- Mostly composed of **multimodal/association areas** (RC1: areas 9, 46, 4b, LIP, 13a, 32, 12o, 12l, 11, 24, TF, TH)
- RC areas overlap and **interconnect all structural network communities** (modules)

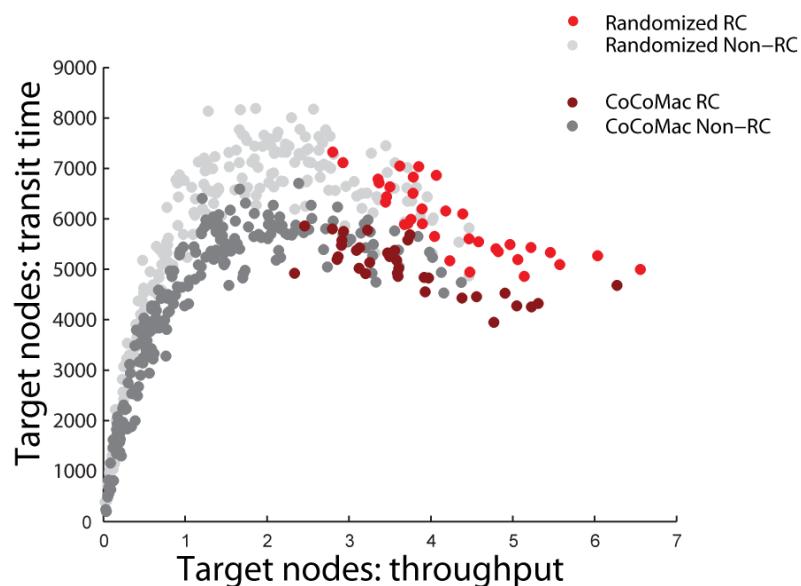
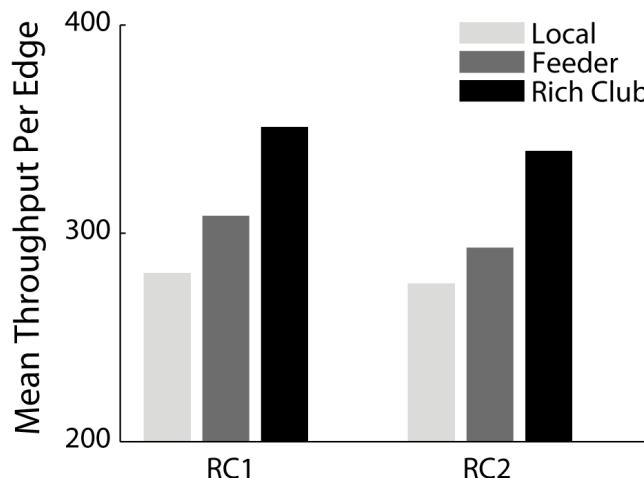


# A Model of Communication in the Macaque Cortex

Use of a communication model to estimate metrics of information flow (Misic et al, 2014)

Units of information are modeled as packets that traverse the macaque cortical network. Allows, for example, to track **mean throughput** (mean number of signals carried by each connection) and **transit time**.

Model suggests that **signal traffic concentrates on RC connections**, and that RC nodes with high mean throughput **receive and transmit signals faster** than lower throughput (non-RC) nodes.



# Rich-Club and Resting-State Networks (RC-RSN)

Resting-state neural activity can be decomposed into independent components or network modules (“resting-state networks” - RSNs).

Functional connectivity and RSNs have an **anatomical/structural basis**:

- Robust (but complex) relationship between SC and FC
- RSNs are internally linked via structural projections (e.g. Greicius et al., 2009; van den Heuvel et al., 2009)

Non-stationary fluctuations in resting brain dynamics (reviewed in Hutchison et al., 2013 – **see Zalesky et al., 2014**):

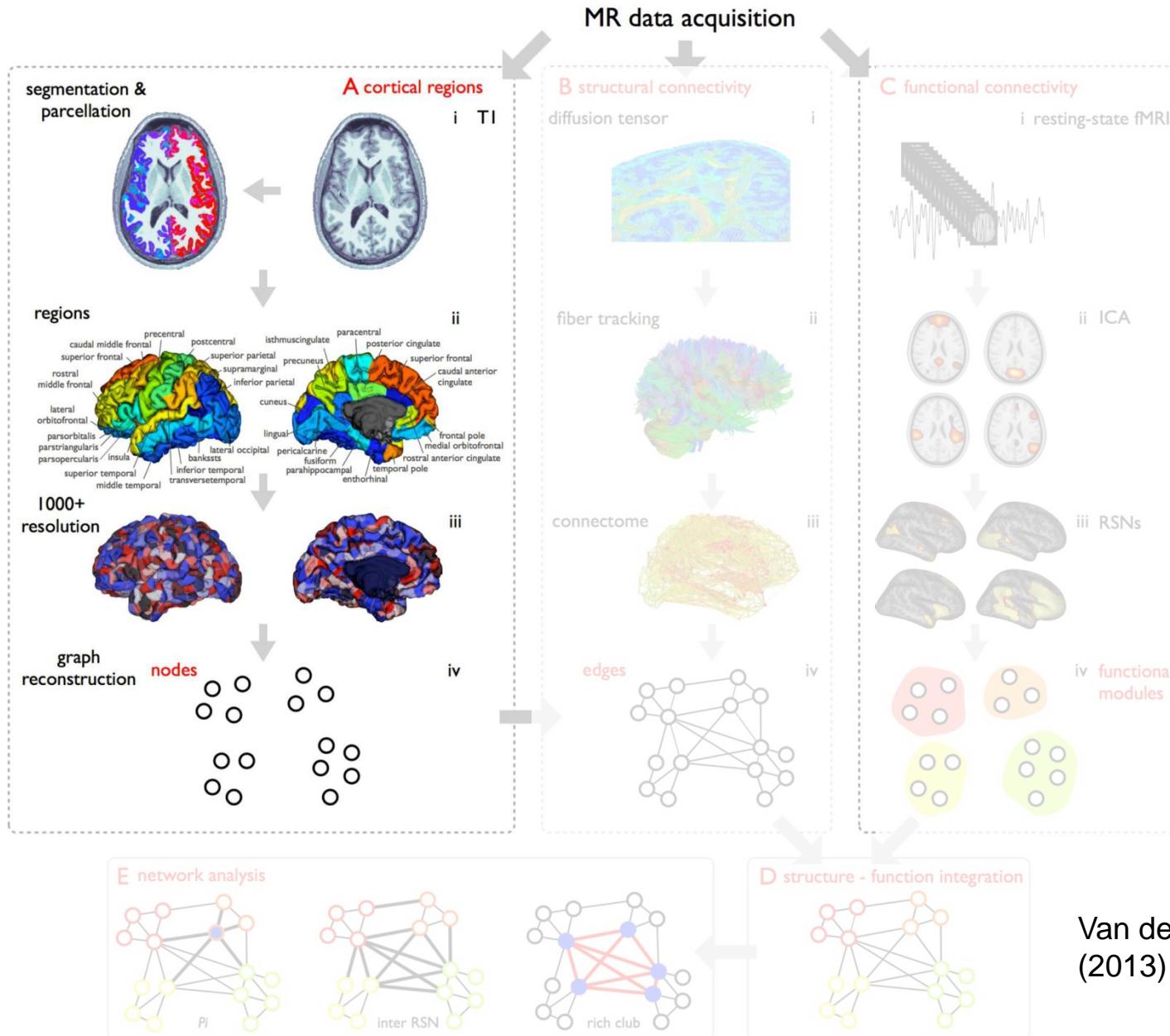
- Possible changes in internal **coherence within** RSNs
- Possible changes in **coupling between** RSNs

**How does RC organization (in structural connectivity) relate to functional RSNs?**

Hypothesis:

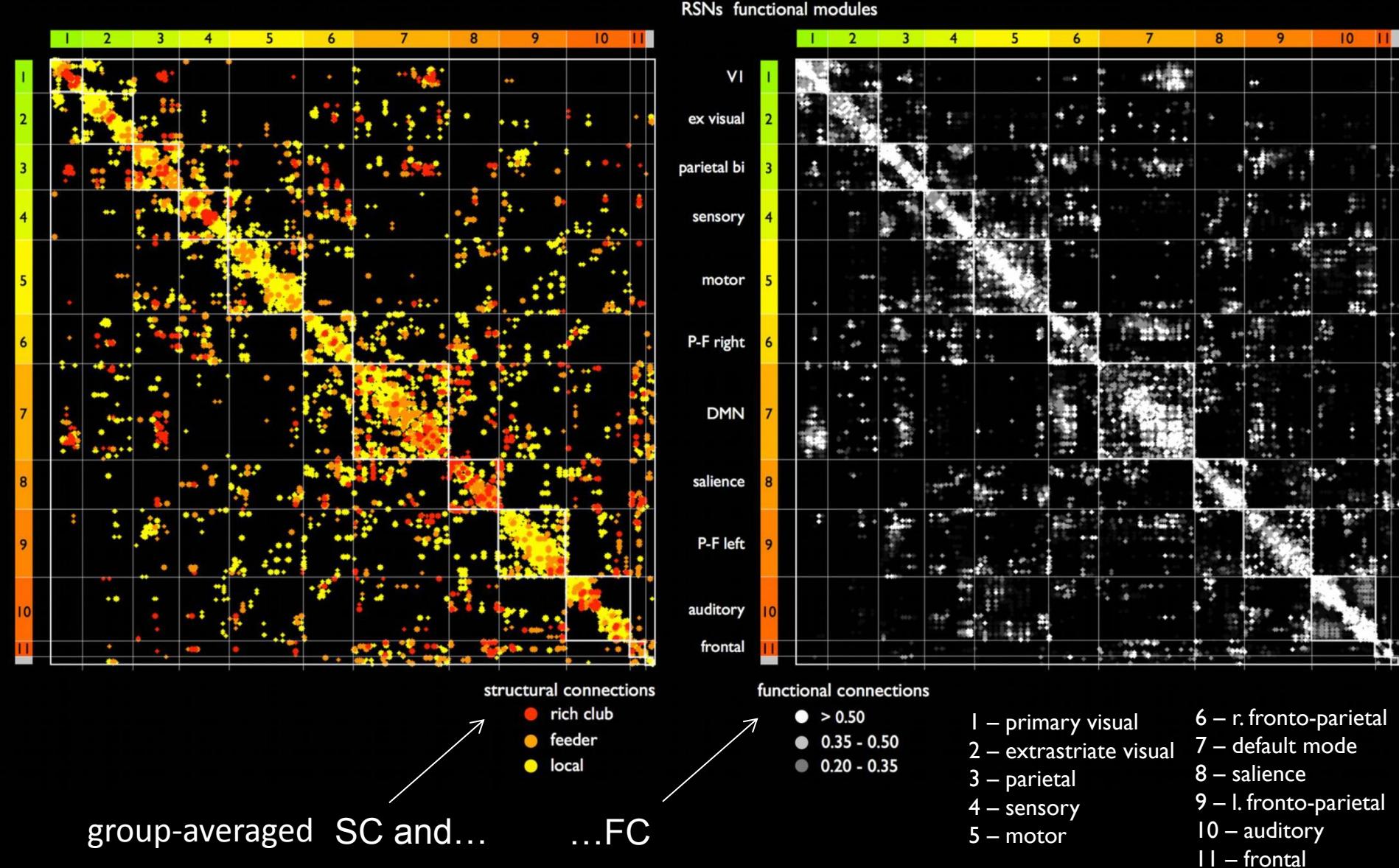
- Structural RC cross-links functional RSNs
- Structural RC is topologically positioned to act as a “central switch” or integrator for time-varying cross-RSN communication.

# RC-RSN: Acquisition and Analysis Workflow



Van den Heuvel & Sporns  
(2013) *J Neurosci*

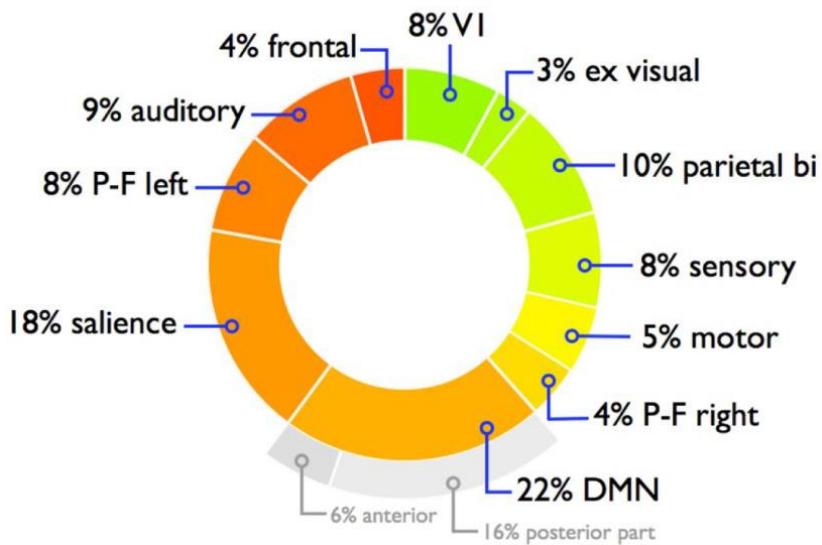
# RC-RSN: Structural and Functional Networks



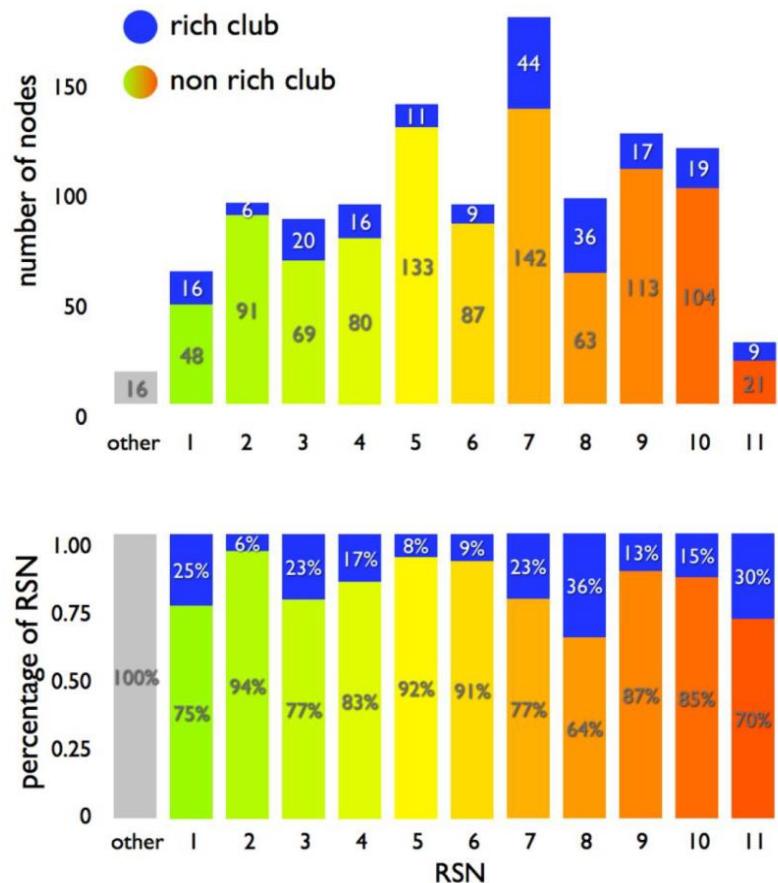
# RC-RSN: RC Node Distribution

RC nodes overlap with all 11 RSNs – with varying levels of participation.

distribution of rich club nodes



- |                         |                        |
|-------------------------|------------------------|
| 1 – primary visual      | 6 – r. fronto-parietal |
| 2 – extrastriate visual | 7 – default mode       |
| 3 – parietal            | 8 – salience           |
| 4 – sensory             | 9 – l. fronto-parietal |
| 5 – motor               | 10 – auditory          |
|                         | 11 – frontal           |



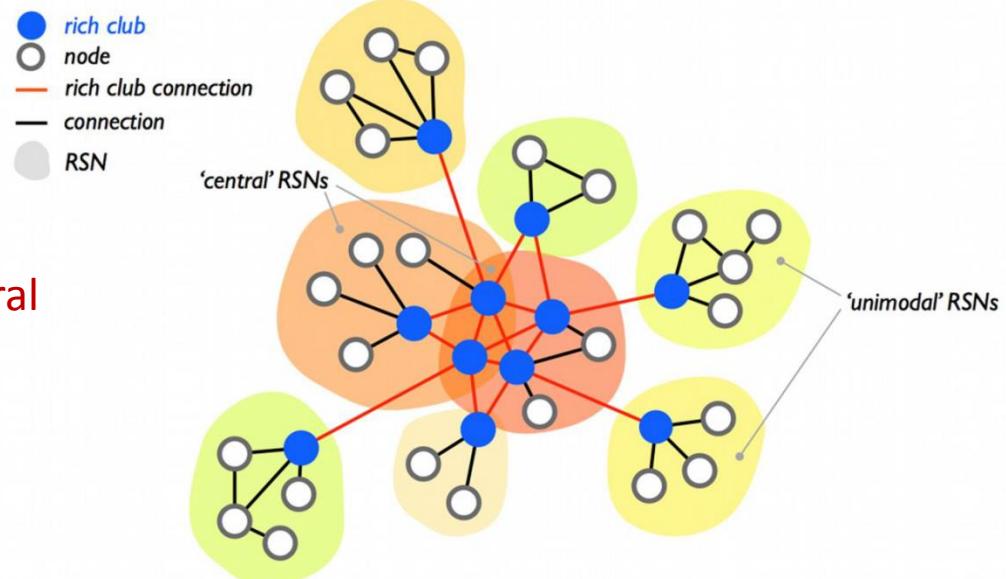
## RC-RSN: Other Results and Summary

Many RC nodes (determined from SC) are **connector hubs** (linking RSN modules determined from FC).

9 out of 11 RSNs contain RC connector hubs – **highest proportion in DMN**.

RC nodes were found at or near regions of the cortical surface where multiple RSNs overlap.

RC and feeder connections are over-represented in short communication paths that cross RSN boundaries.



Proposal:  
**Hierarchical model for structural  
relations among RSNs**

# Outline

Introduction – Brain Networks

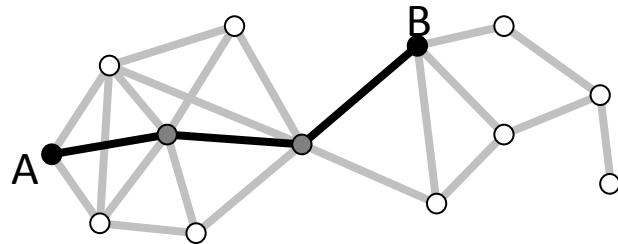
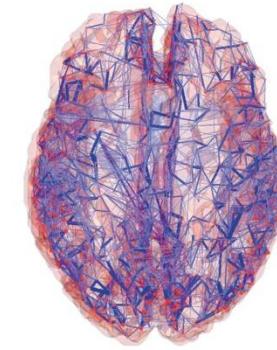
The Human Connectome – A Very Brief Summary

Rich-Club Organization – Network Hubs and Integrative Processes

► Summary and Conclusion

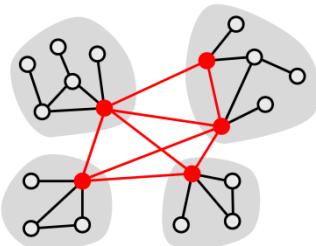
# Summary and Conclusion

Connectomics is beginning to reveal the network architecture of the human brain.



Network science approaches are increasingly important for analysis and modeling of connectome data.

Highly connected and highly central **hub nodes** are a prominent feature in human and non-human connectome networks.



Hubs are densely interconnected to form a “rich club” – a high-cost and high-efficiency attribute of the connectome.

Network hubs and their interconnections may provide an important structural substrate for **functional integration** across segregated brain regions and resting-state networks.

# Further Reading and Acknowledgements

## Further Reading:

- van den Heuvel M, Bullmore E. Human brain network organization. *Opin Neurobiol*. 2013;23(1):1059-1069.
- Bullmore E, Behrens T, Rubinov M. Graph-theory of brain connectome. *Nature Rev Neurosci* 10, 186-198.

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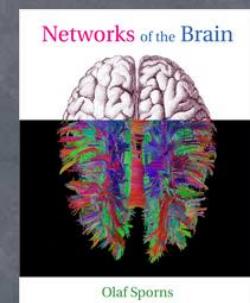
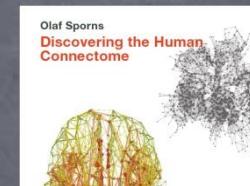
*Nature Rev Neurosci* 10, 186-198.

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NIH Human Connectome Project:  
[www.humanconnectome.org](http://www.humanconnectome.org)

The Virtual Brain Project:  
<http://thevirtualbrain.org>

Network Analysis Toolbox (Matlab):  
[www.brain-connectivity-toolbox.net](http://www.brain-connectivity-toolbox.net)