

Indiana University - 2014

Mapping and Modeling Human Brain Networks

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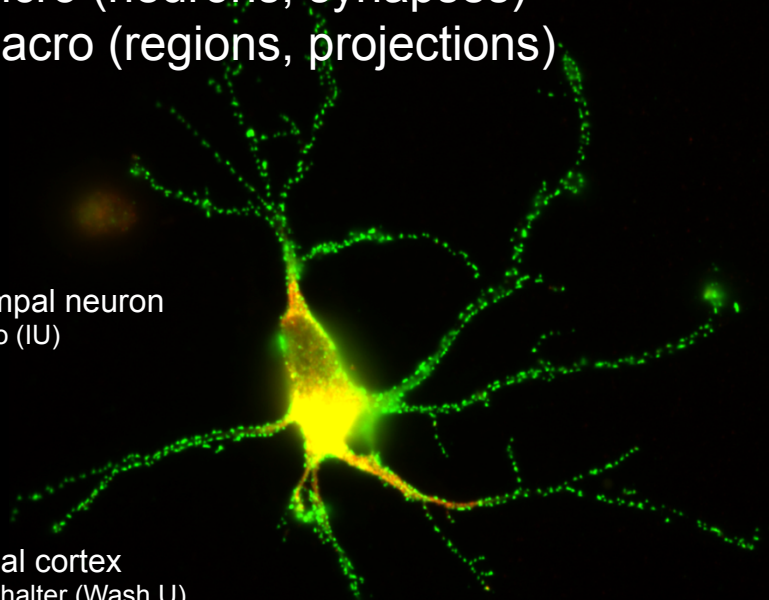
 @spornslab

Neural Systems are Complex Networks

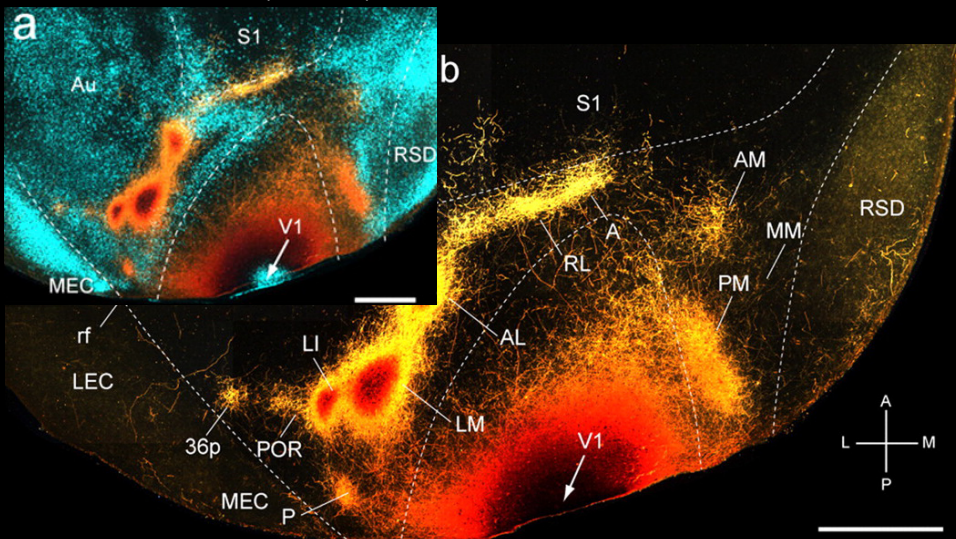
Networks across scales:

- micro (neurons, synapses)
- macro (regions, projections)

Hippocampal neuron
Anne Prieto (IU)



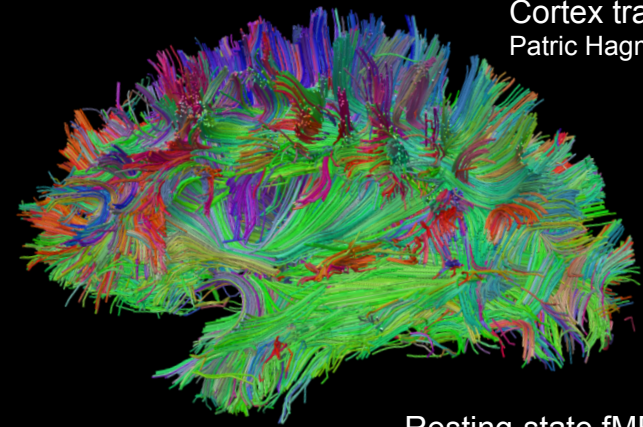
Mouse visual cortex
Andreas Burkhalter (Wash U)



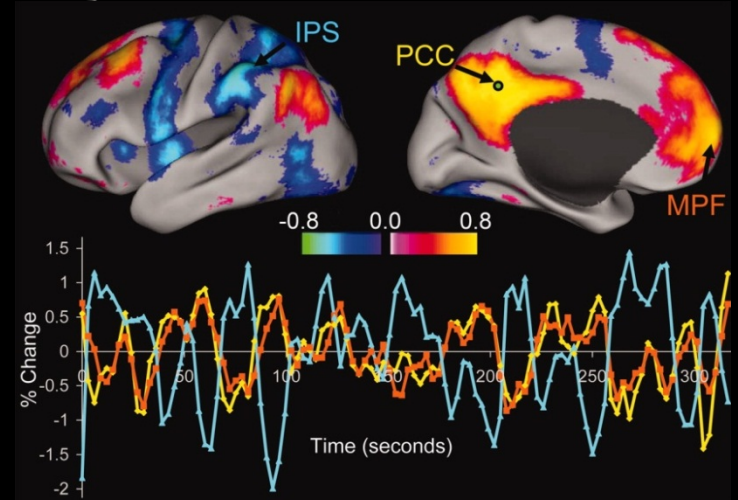
Networks across modes:

- structural (anatomical couplings)
- functional (dynamic interactions)

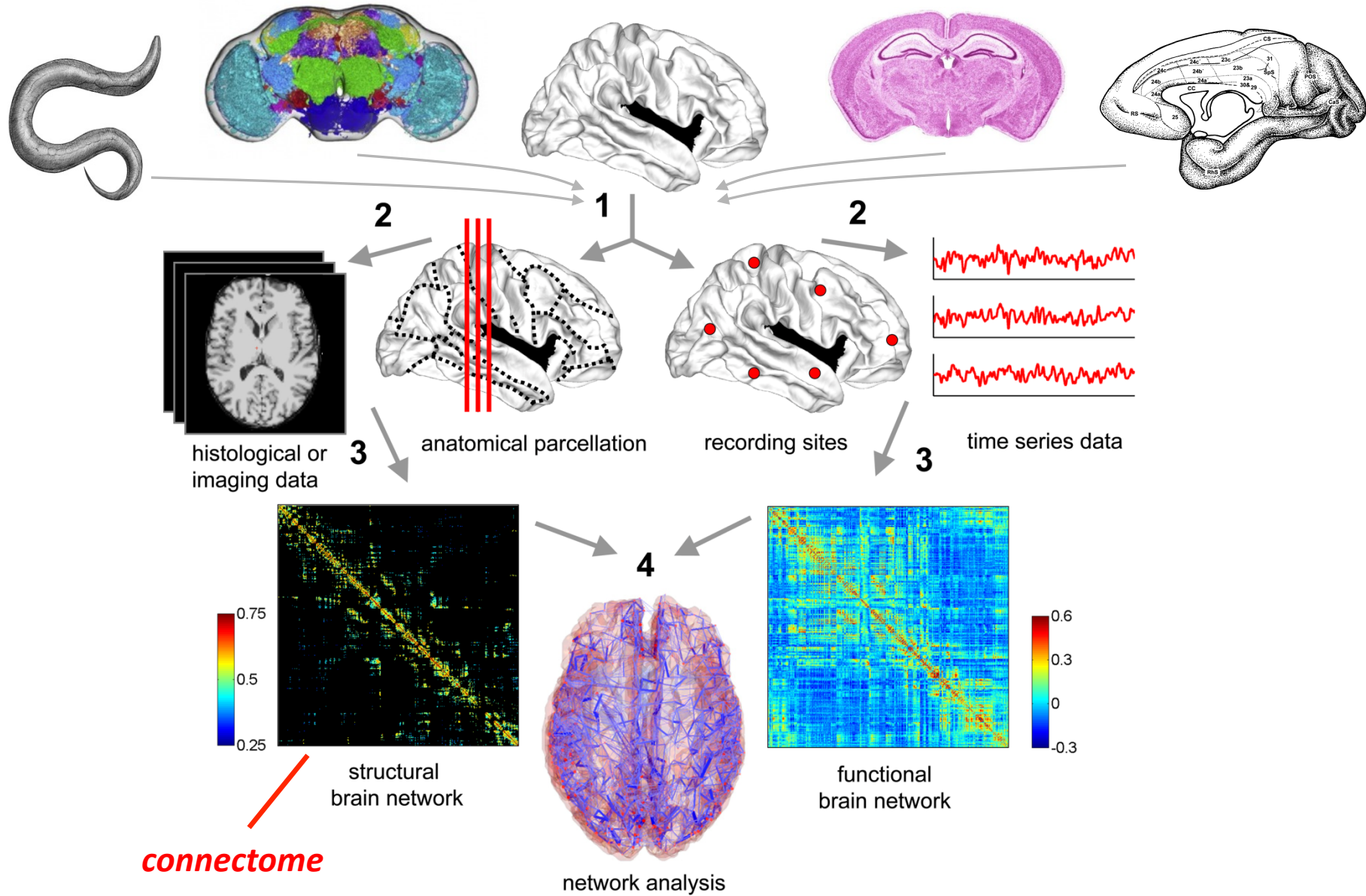
Cortex tractography
Patric Hagmann (EPFL)



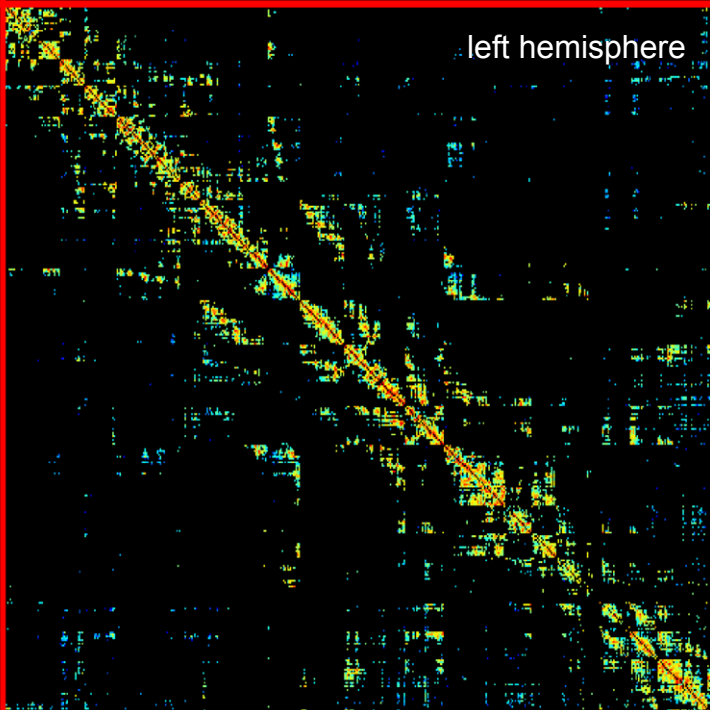
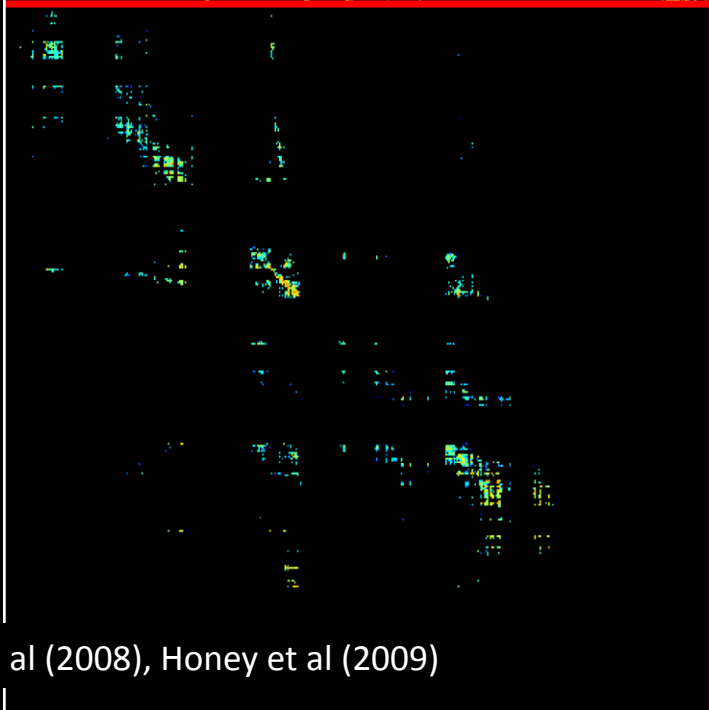
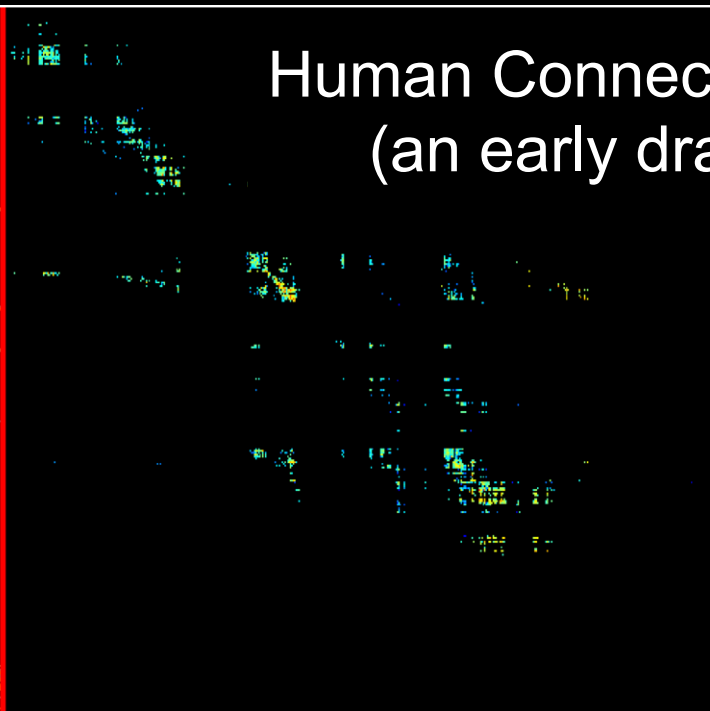
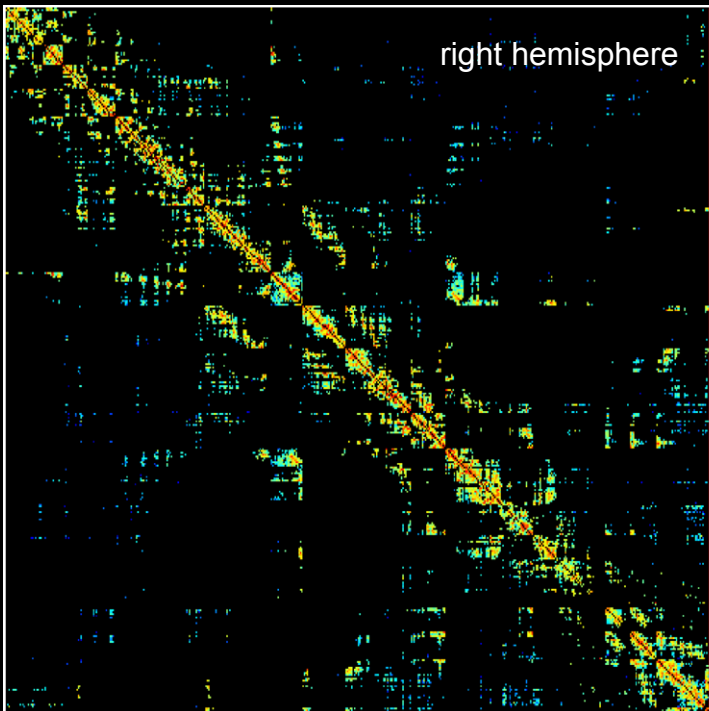
Resting-state fMRI recording
Michael Fox, Marc Raichle (Wash U)



Extraction of Brain Networks from Empirical Data

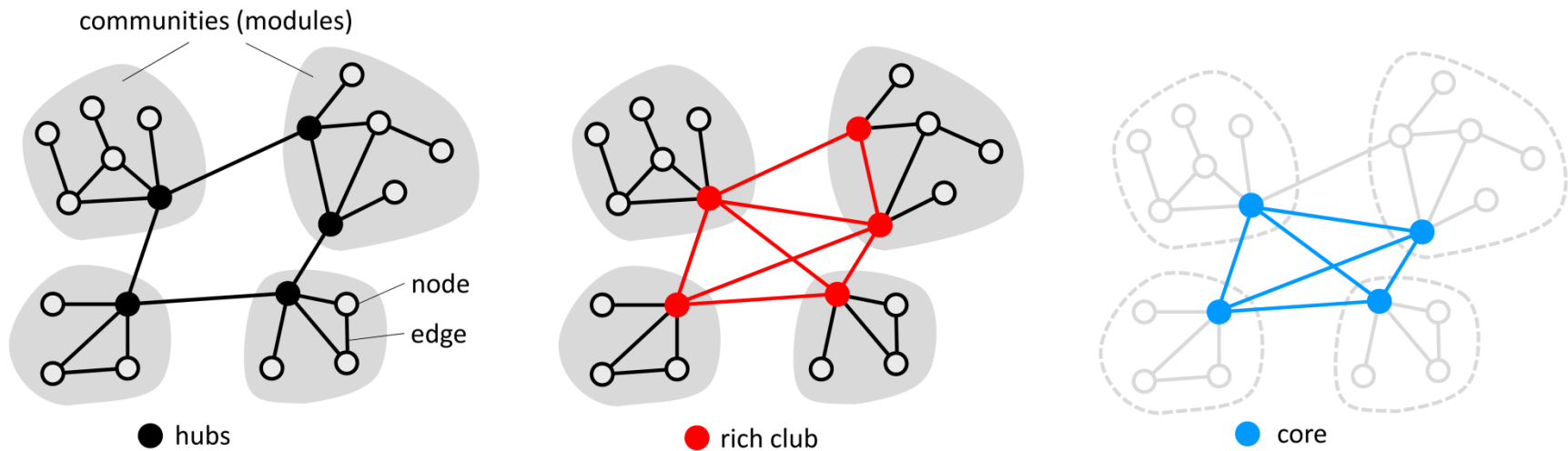


Human Connectome (an early draft)



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

Rich-Club Organization of the Human Connectome

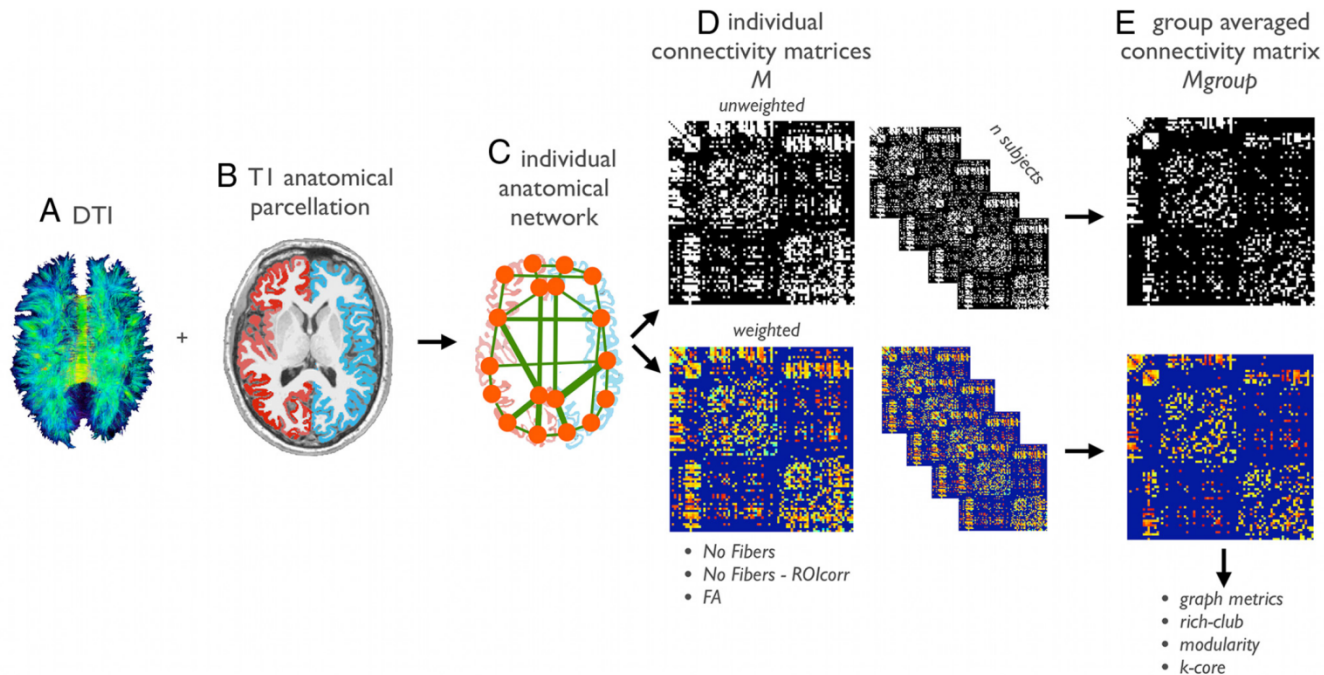
Human connectome data sets exhibit a prominent **rich club**, comprising cortical and subcortical regions.

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

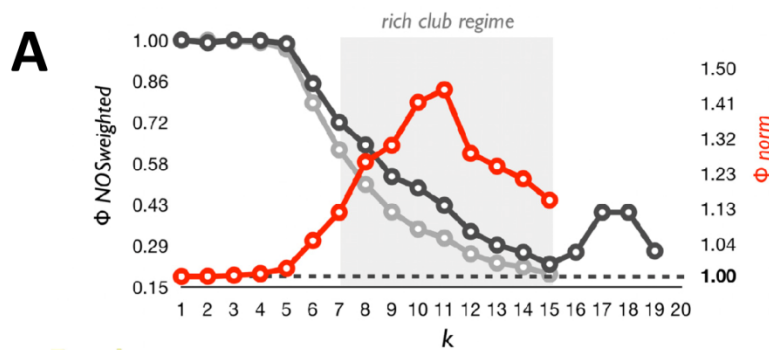
DTI study, 21 participants, low (82 nodes) and high-resolution (1170 nodes) partition, streamline tractography



Martijn van den Heuvel

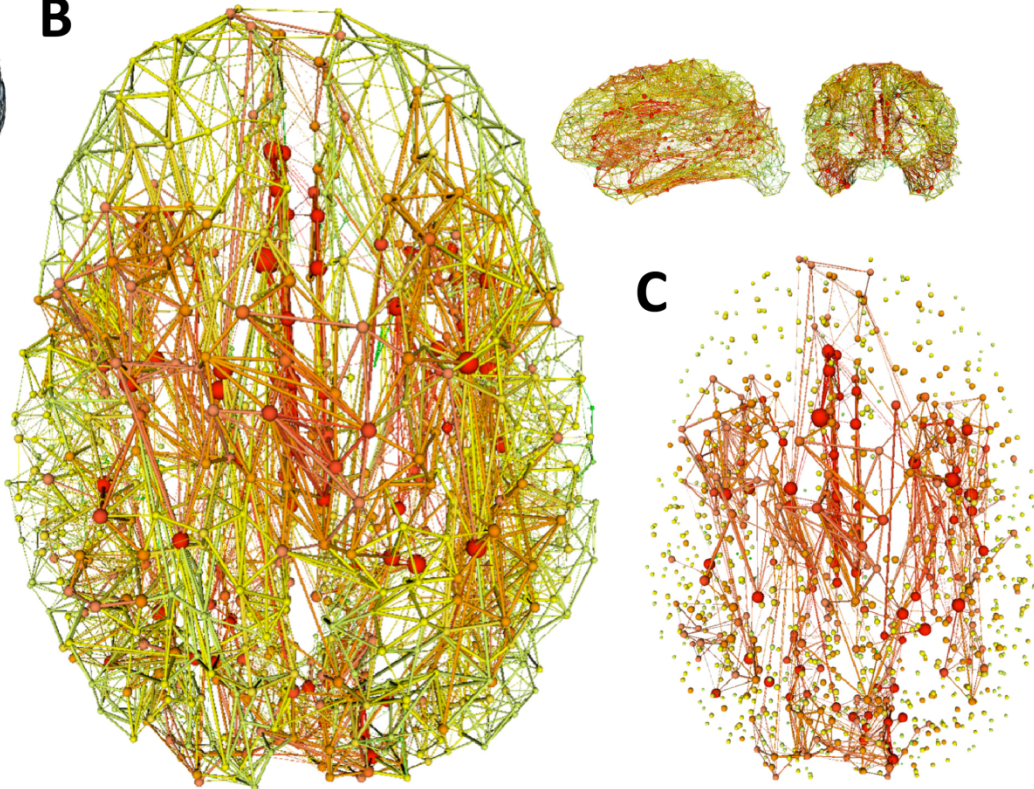


Rich-Club Organization of the Human Connectome



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

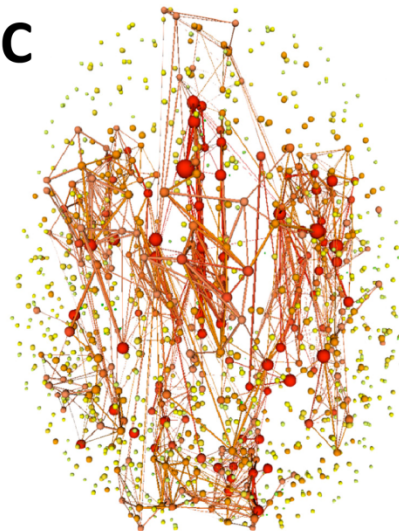
B



Overlap of RC and structural core.

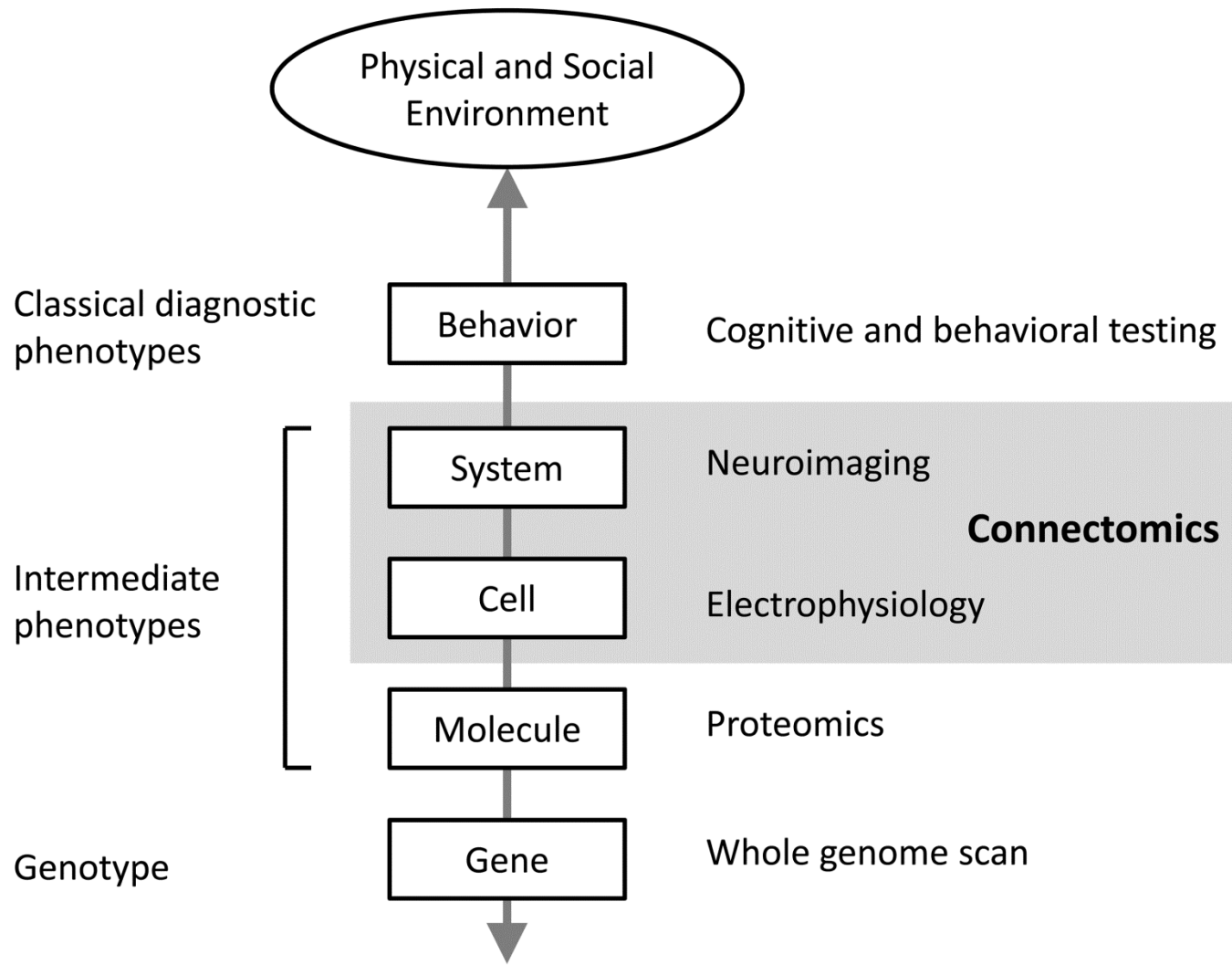
High proportion (89%) of **short communication paths** travel through at least one RC node (66% through an RC edge).

C

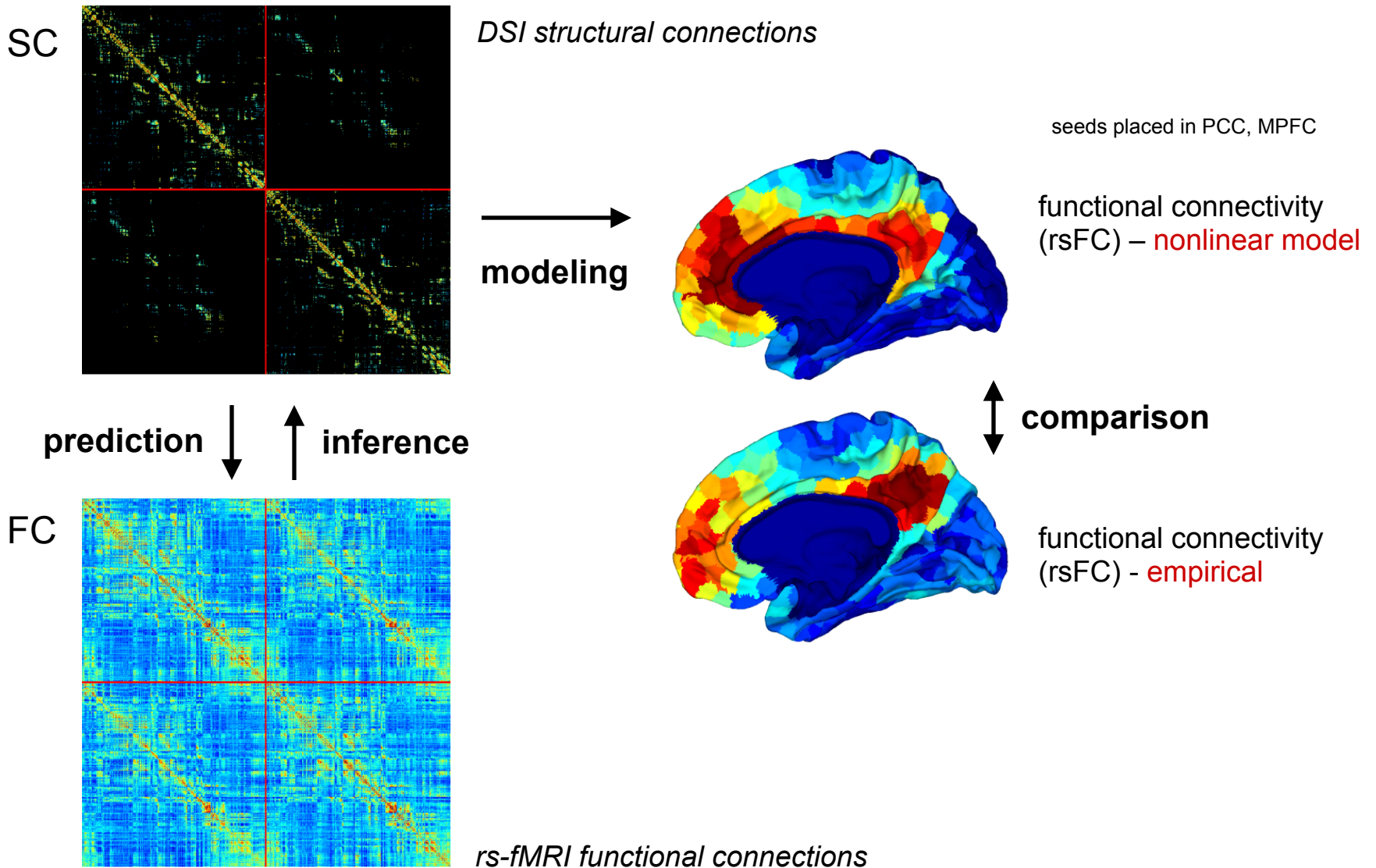


RC damage (node/edge deletion) has large effects on **network integrity and efficiency**.

Linking Networks across Levels



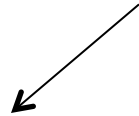
Connectome-Based Models of Functional Connectivity



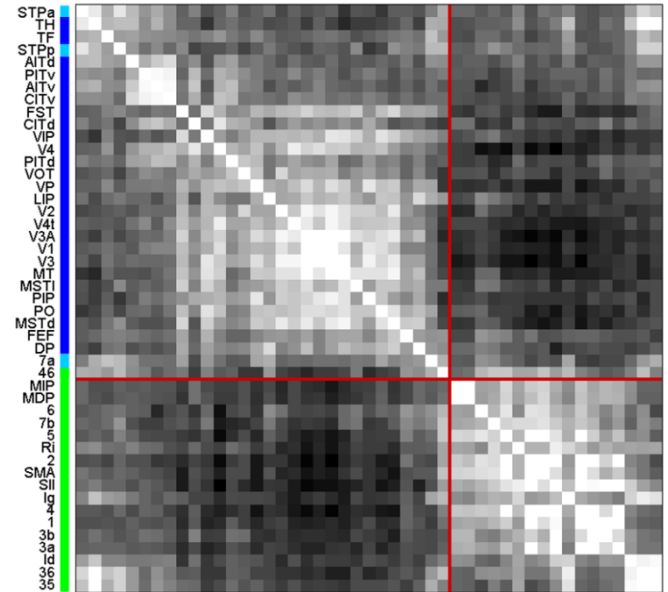
Connectome-Based Models of Functional Connectivity

structural connections

perturbations



BOLD correlations



connectome

+

biophysical equations

rest

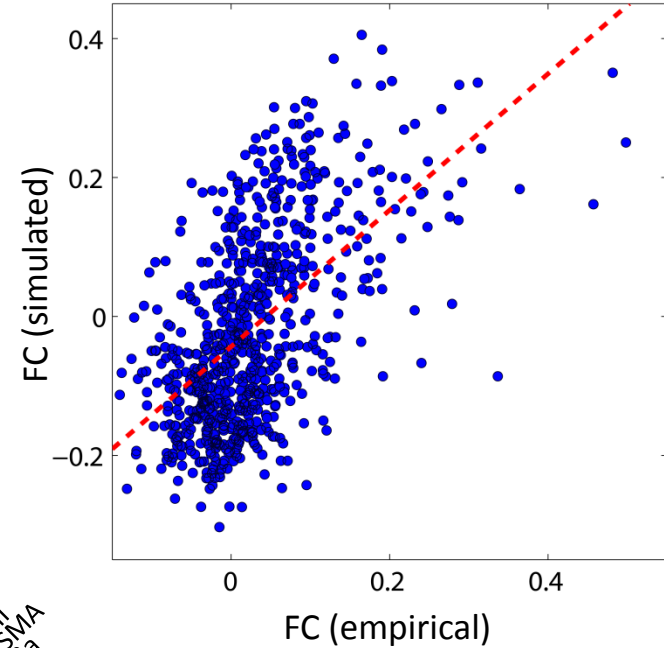
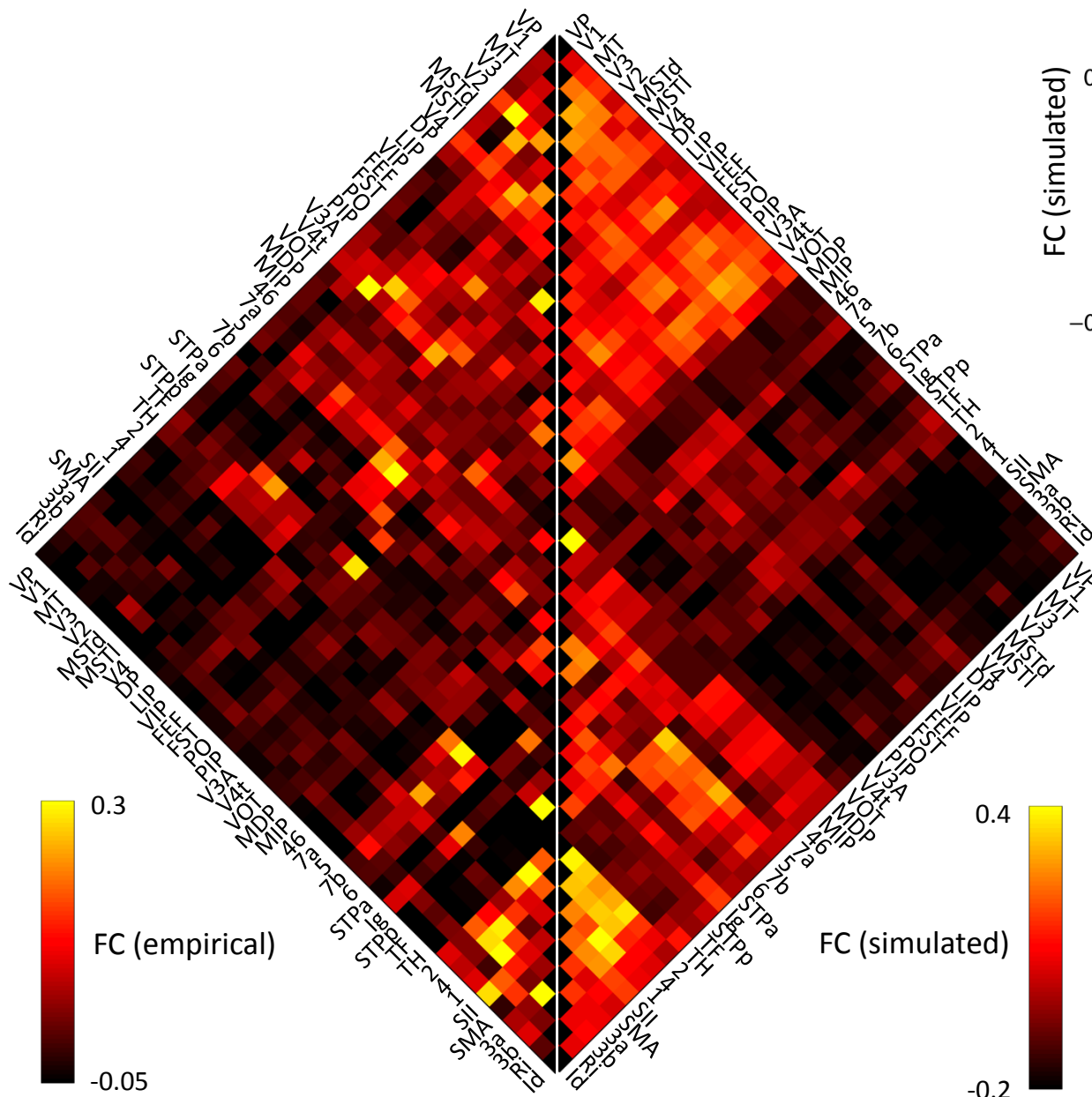
task

inputs

$$\frac{dV}{dt} = -(g_{Ca} + r_{NMDA} a_{ee} Q_V) m_{Ca} (V - V_{Ca}) - (g_{na} m_{na} + a_{ee} Q_V) (V - V_{na}) - g_K W (V - V_K) - g_L (V - V_L) + a_{ie} Z Q_Z + a_{ne} I_\delta,$$

$$\frac{dZ}{dt} = b(a_{ni} I_\delta + a_{ei} V Q_V),$$

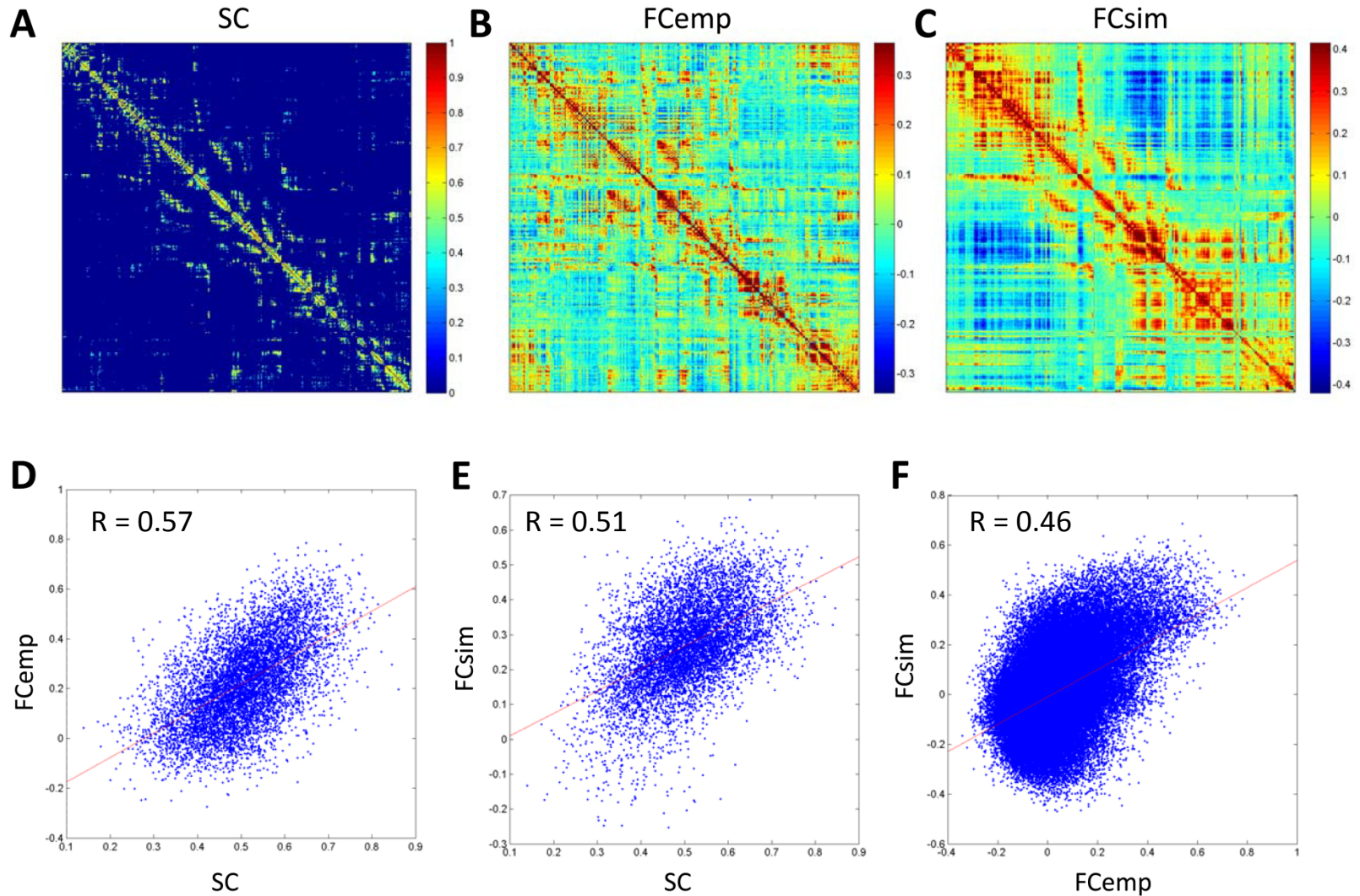
R = 0.55 correlation with empirical macaque rs-fMRI data
Adachi et al. (2012) *Cereb Cortex*



Adachi et al (2012) Cereb Cortex

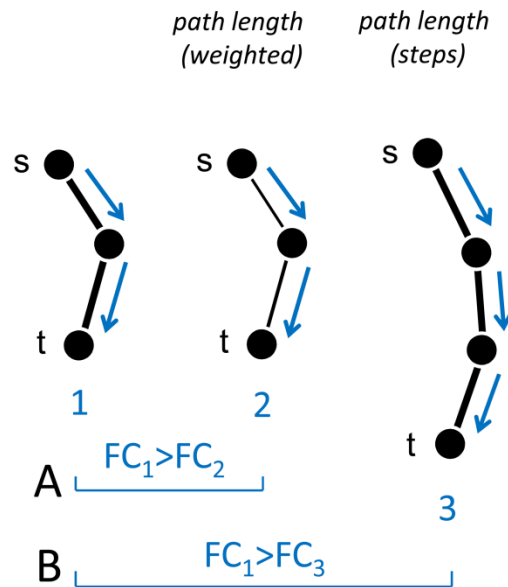
Connectome-Based Models for Functional Connectivity

A network model of **human resting-state fMRI functional connectivity**.



Connectome-Based Models for Functional Connectivity

Role of network topology in shaping patterns of **network communication**.



Search information quantifies the “hiddenness” of a path, i.e. the information needed to access it.

Path transitivity quantifies the density of “local detours” surrounding a given path.

Predictions:

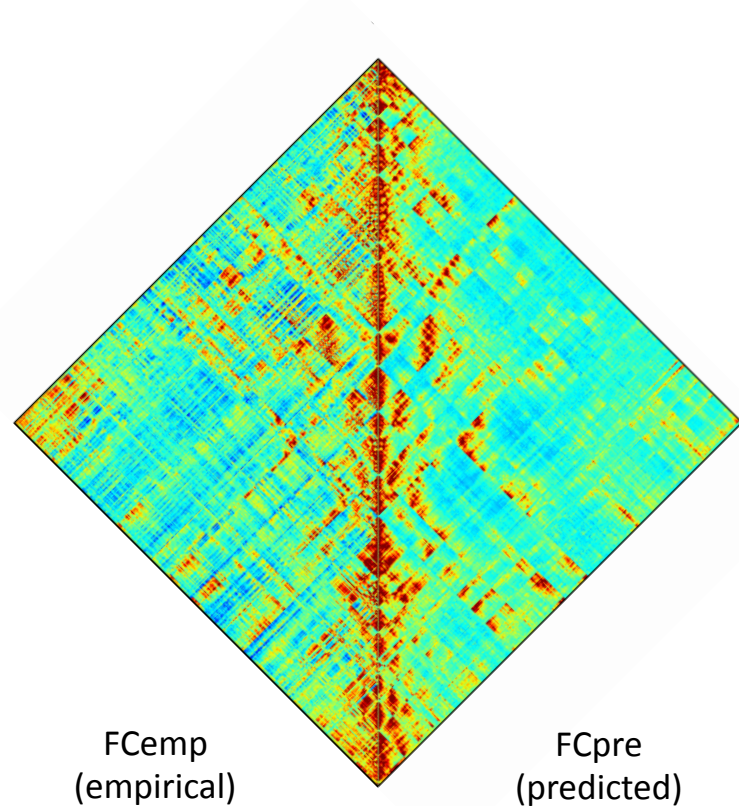
- [s,t] node pairs requiring greater search information exhibit **weaker FC***
- [s,t] node pairs with higher path transitivity exhibit **stronger FC****

* holding path length constant

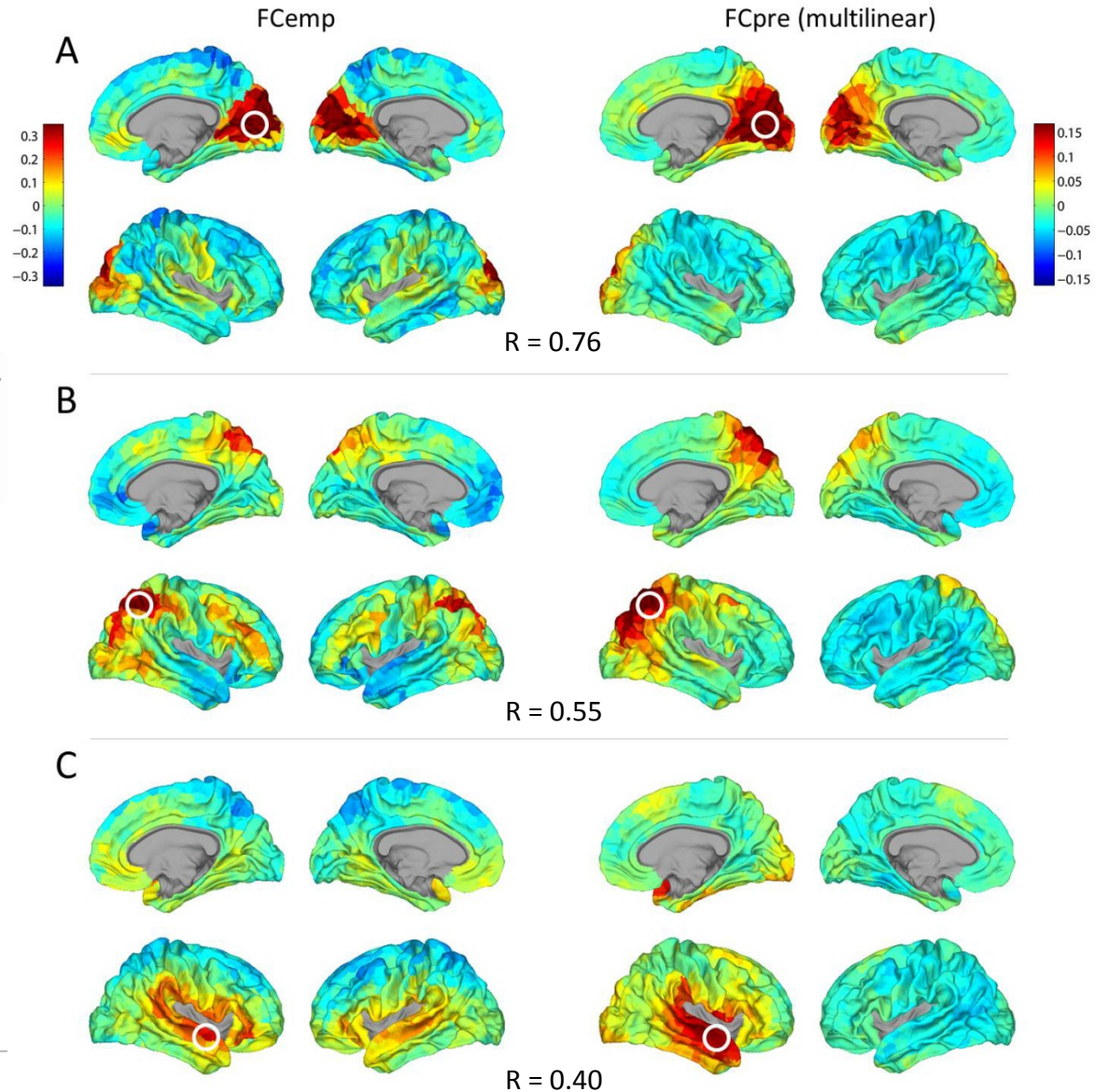
** holding path length and search information constant

Connectome-Based Models for Functional Connectivity

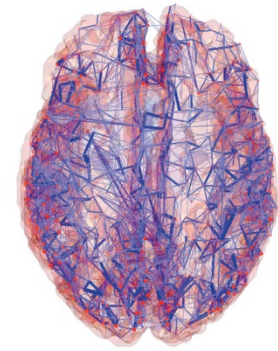
Analytic measures of **network communication** can predict functional connectivity.



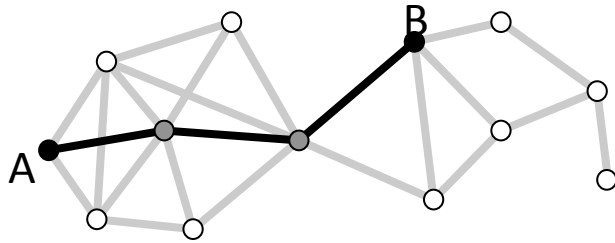
$R = 0.60$



Summary and Conclusion

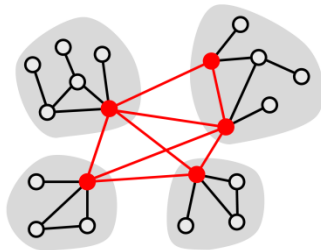


Connectomics is beginning to reveal the network architecture of the human brain.



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:

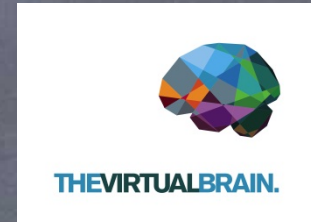
- van den Heuvel MP, Sporns O (2013) Network hubs in the human brain. *Trends Cogn Sci* 17, 683.
- Bullmore ET, Sporns O (2012) The economy of brain network organization. *Nature Rev Neurosci* 13, 336-349.
- Behrens TEJ, Sporns O (2012) Human connectomics. *Curr Opin Neurobiol* 22, 144-153.
- Rubinov M, Sporns O (2010) Complex network measures of brain connectivity: Uses and interpretations. *Neuroimage* 52, 1059-1069.
- Bullmore, ET, Sporns, O (2009) Complex brain networks: Graph-theoretical analysis of structural and functional systems. *Nature Rev Neurosci* 10, 186-198.

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- **Patric Hagmann**, Alessandra Griffa (EPFL Lausanne)
- **Martijn van den Heuvel**, Rene Kahn (Utrecht Medical Center)
- Yusuke Adachi, Yasushi Miyashita (Univ. Tokyo)
- AR McIntosh (Toronto), V Jirsa (Marseille), P Ritter (Charité Berlin), G Deco (Barcelona), M Breakspear (Brisbane)
- Ed Bullmore, Mika Rubinov (Cambridge)
- CT Shih, AS Chiang (Taiwan), Ralph Greenspan (UCSD)
- Xinian Zuo (Beijing)
- Bill Hetrick, Bernice Pescosolido (IU)
- Andy Saykin, Yang Wang (IUPUI)
- Nieves Velez de Mendizabal (IUPUI)

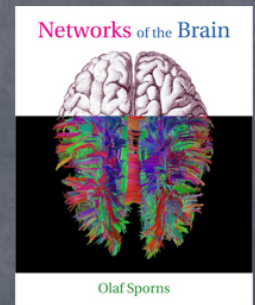
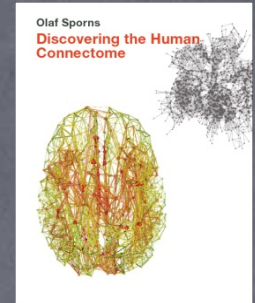


Lab: www.indiana.edu/~cortex

NIH Human Connectome Project:
www.humanconnectome.org

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

Network Analysis Toolbox (Matlab):
www.brain-connectivity-toolbox.net



Funded by the James S. McDonnell Foundation, NIH Human Connectome Project