

# Mapping white matter neurodegeneration in the human connectome: a network science study of hereditary diffuse leukoencephalopathy with spheroids



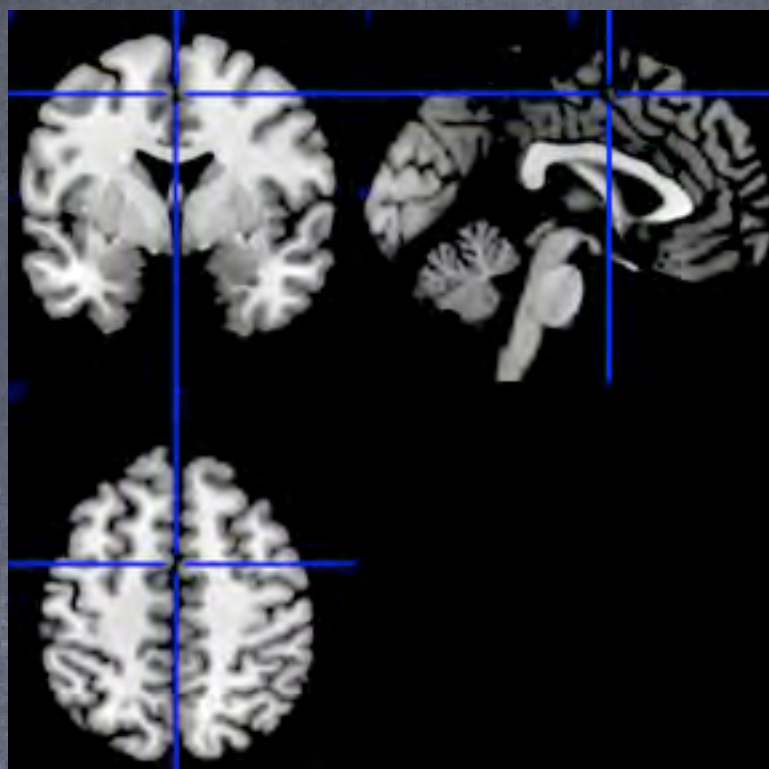
January 26, 2014  
Network Science Talks

Joaquín Goñi  
jgonicor@indiana.edu

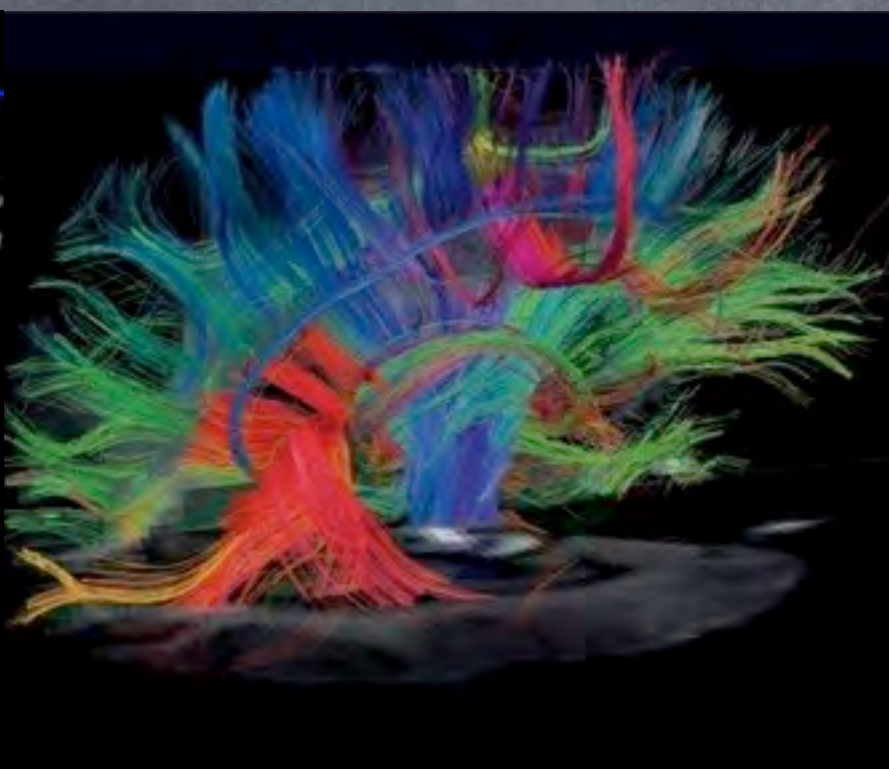
Indiana University Network Science Institute  
Dpt. of Radiological and Imaging Sciences. School of Medicine, IU





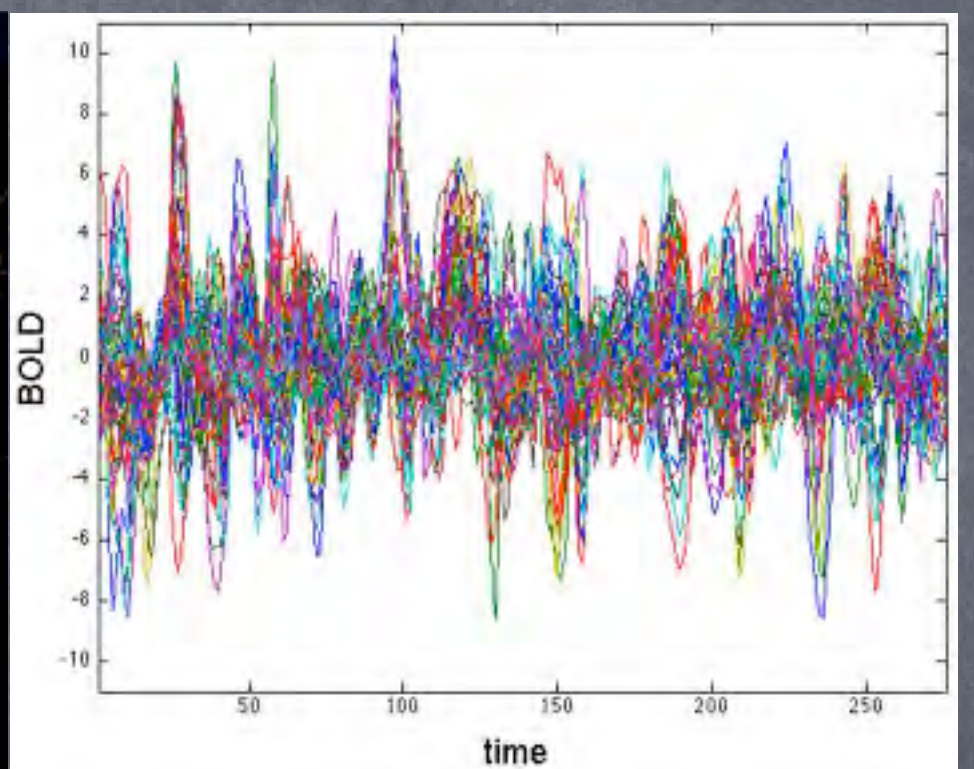


T1 MRI



diffusion weighted imaging, DSI,DTI

fibers detection



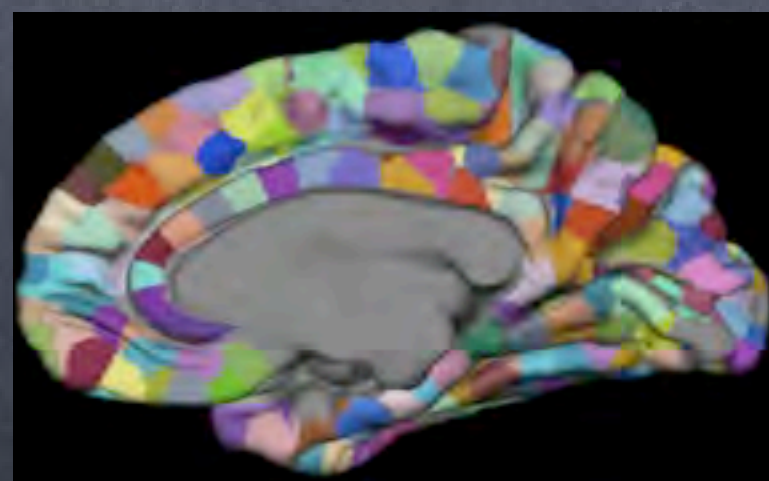
fMRI, resting-state time-series

functional coupling

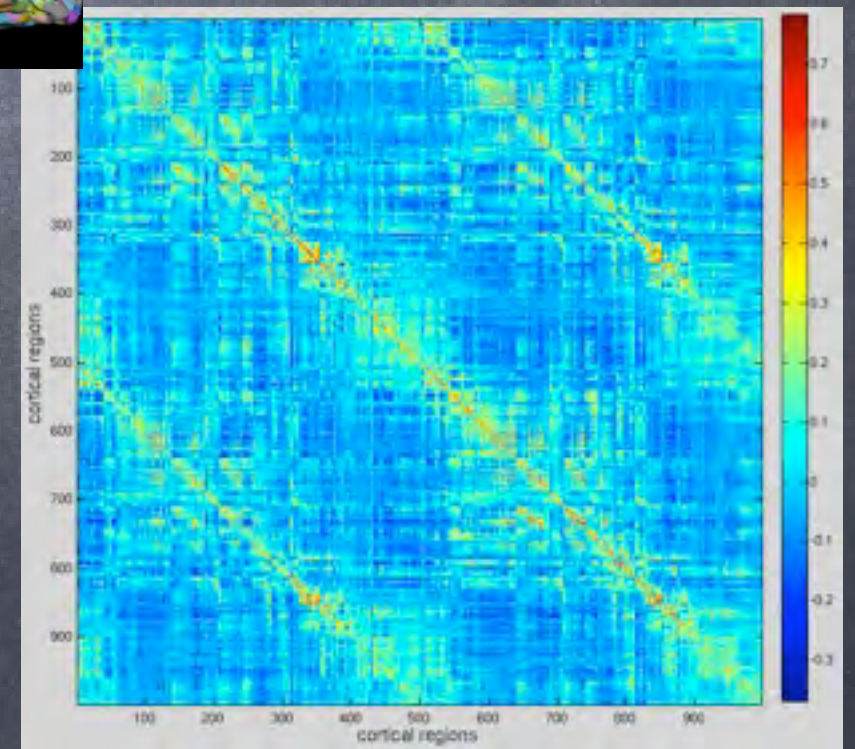
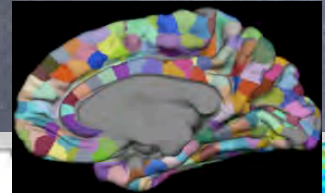
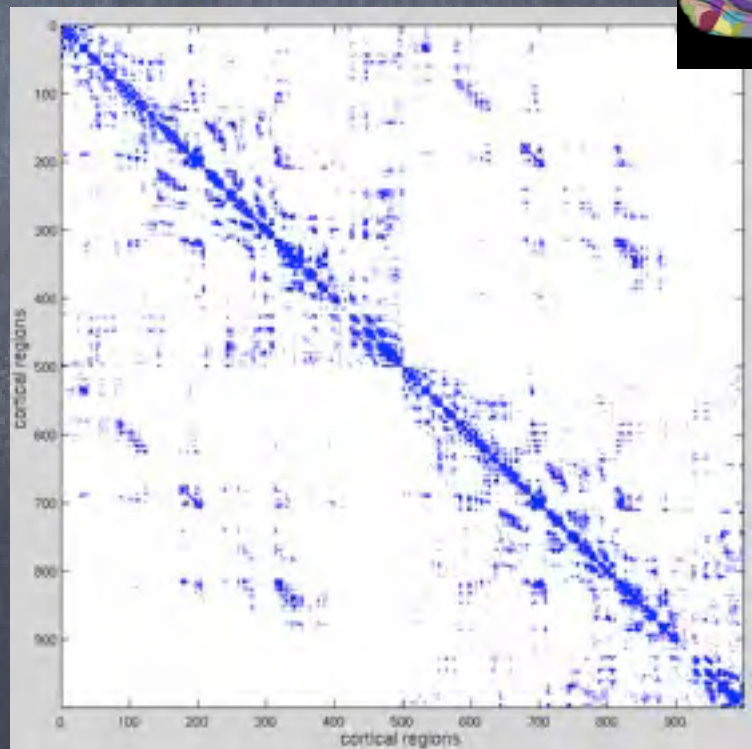
Grey matter segmentation  
Cortical partition

structural connectivity

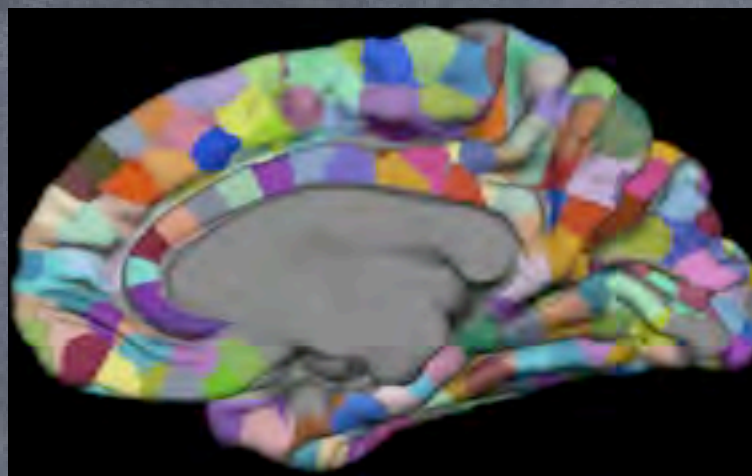
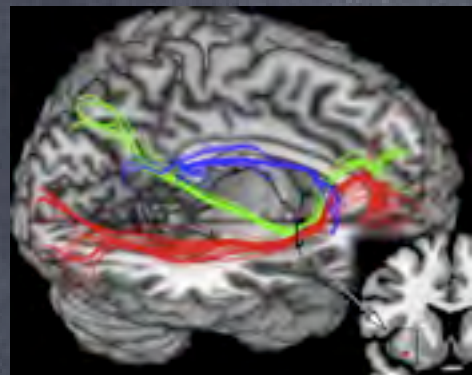
functional connectivity



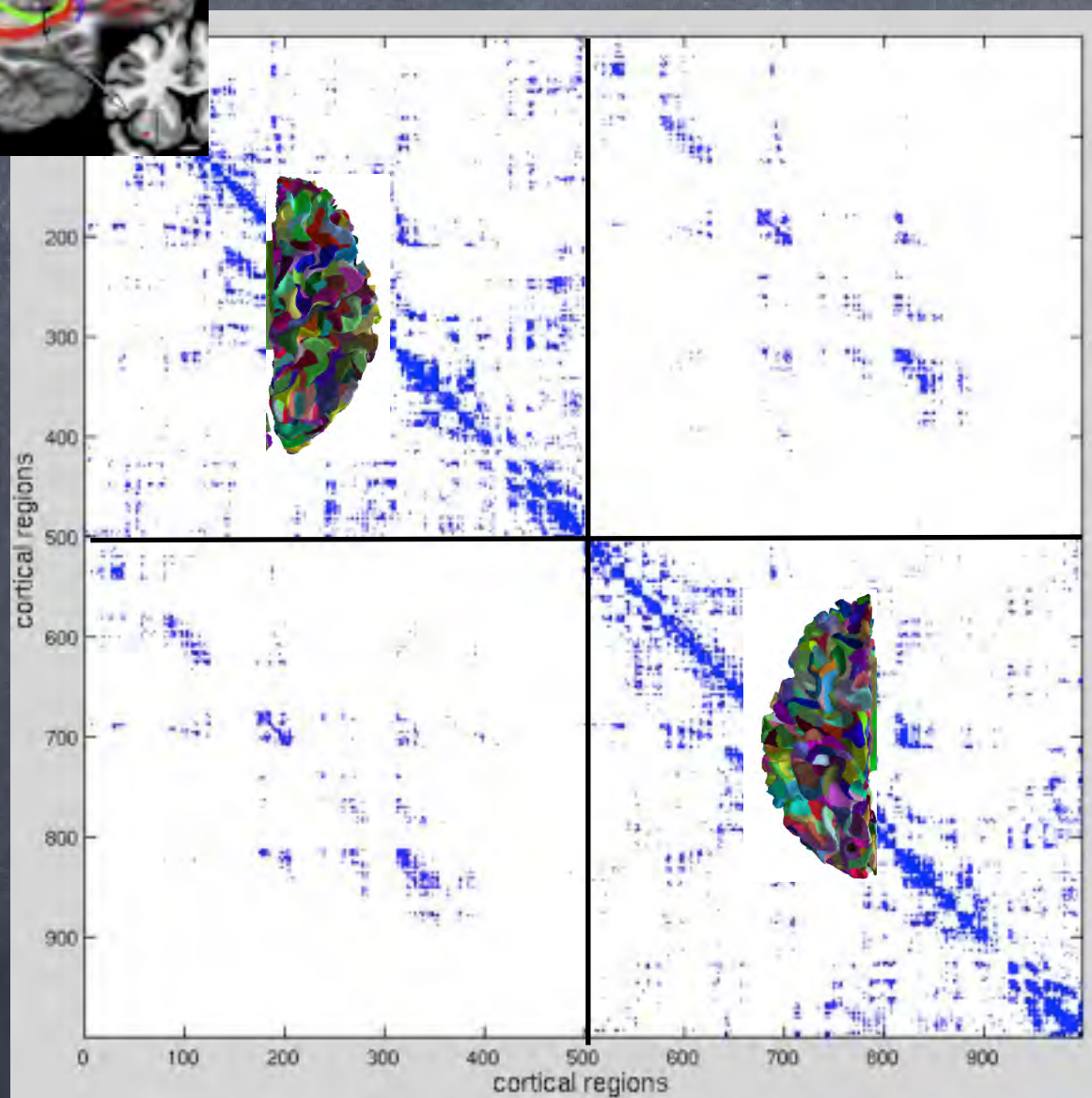
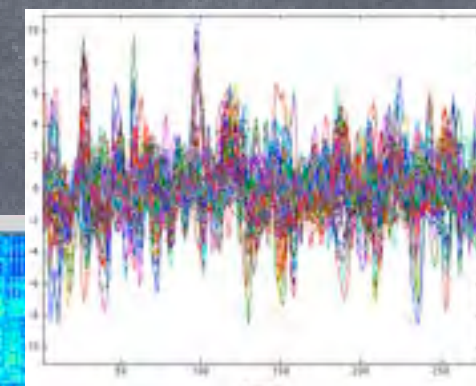
Hagmann et al. Plos Biol. 2008



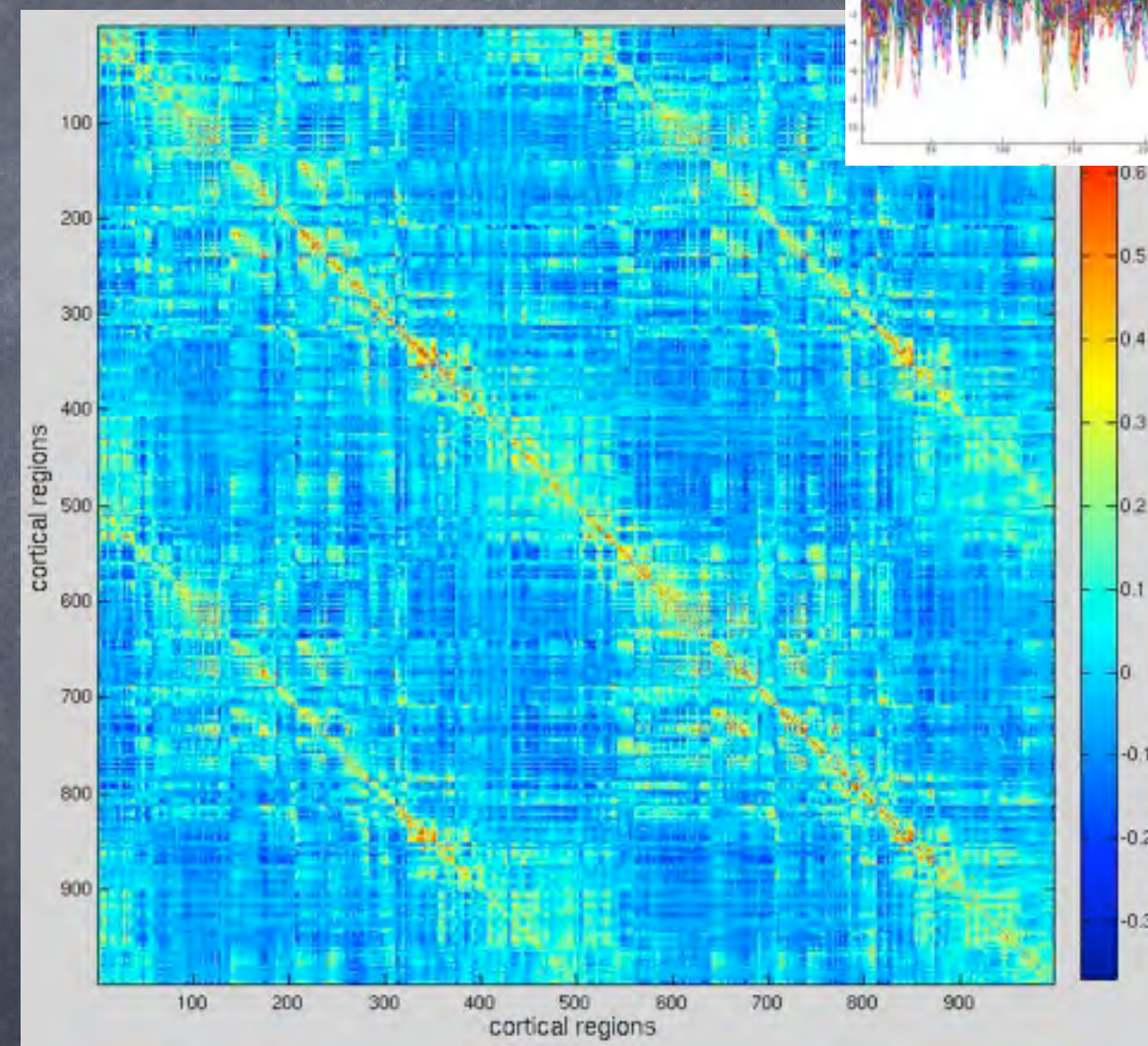
fiber-tracts (model)



neural activity (model)

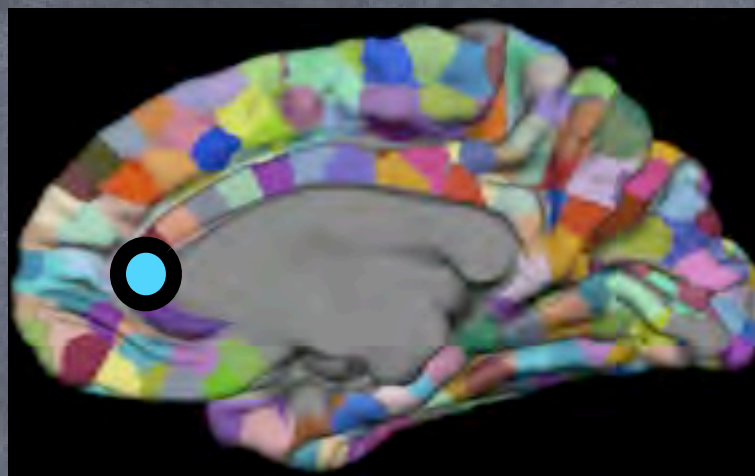


structural connectivity (SC)

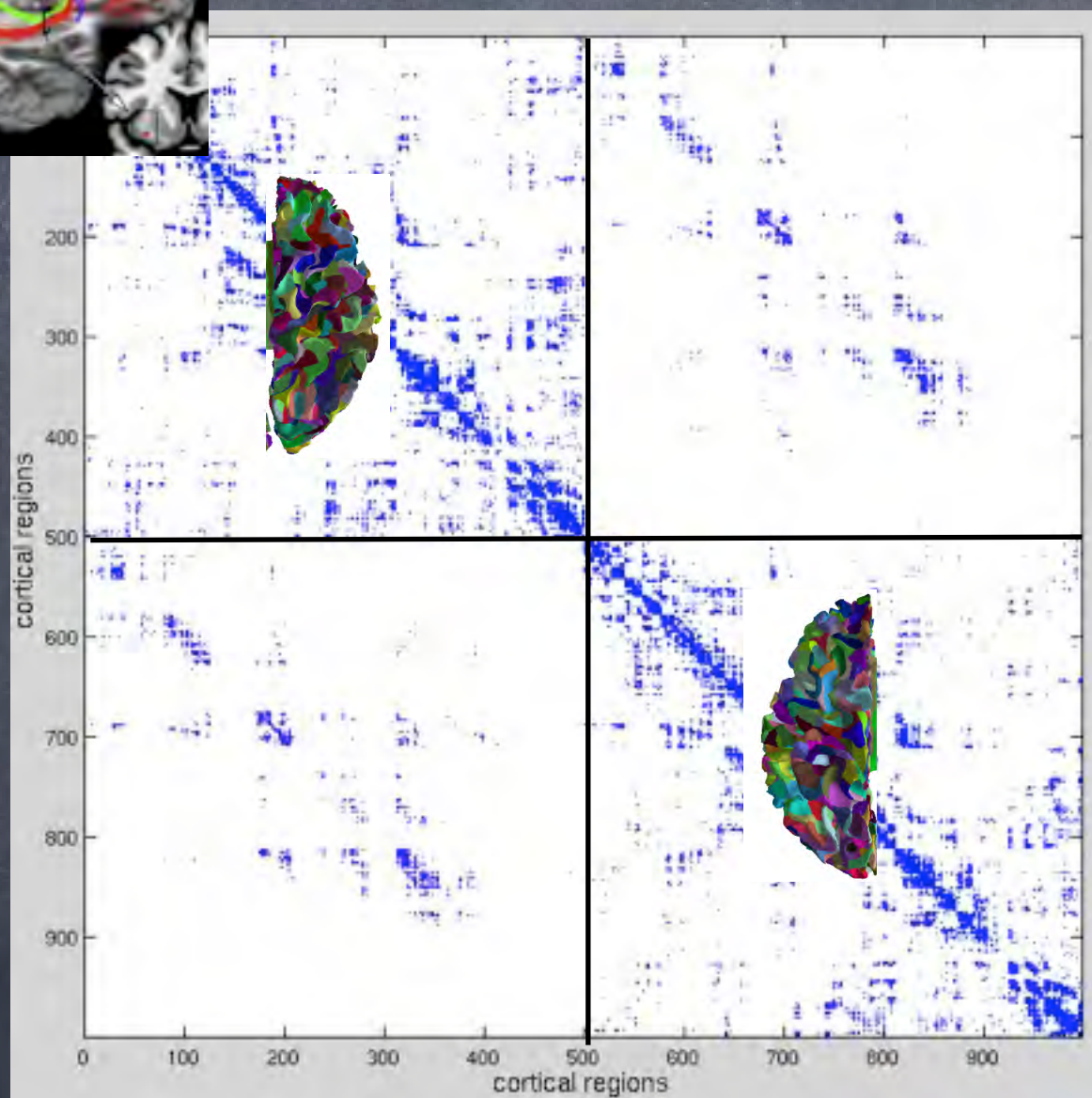
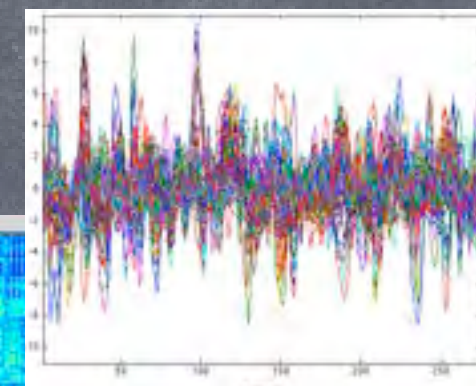


functional connectivity (FC)

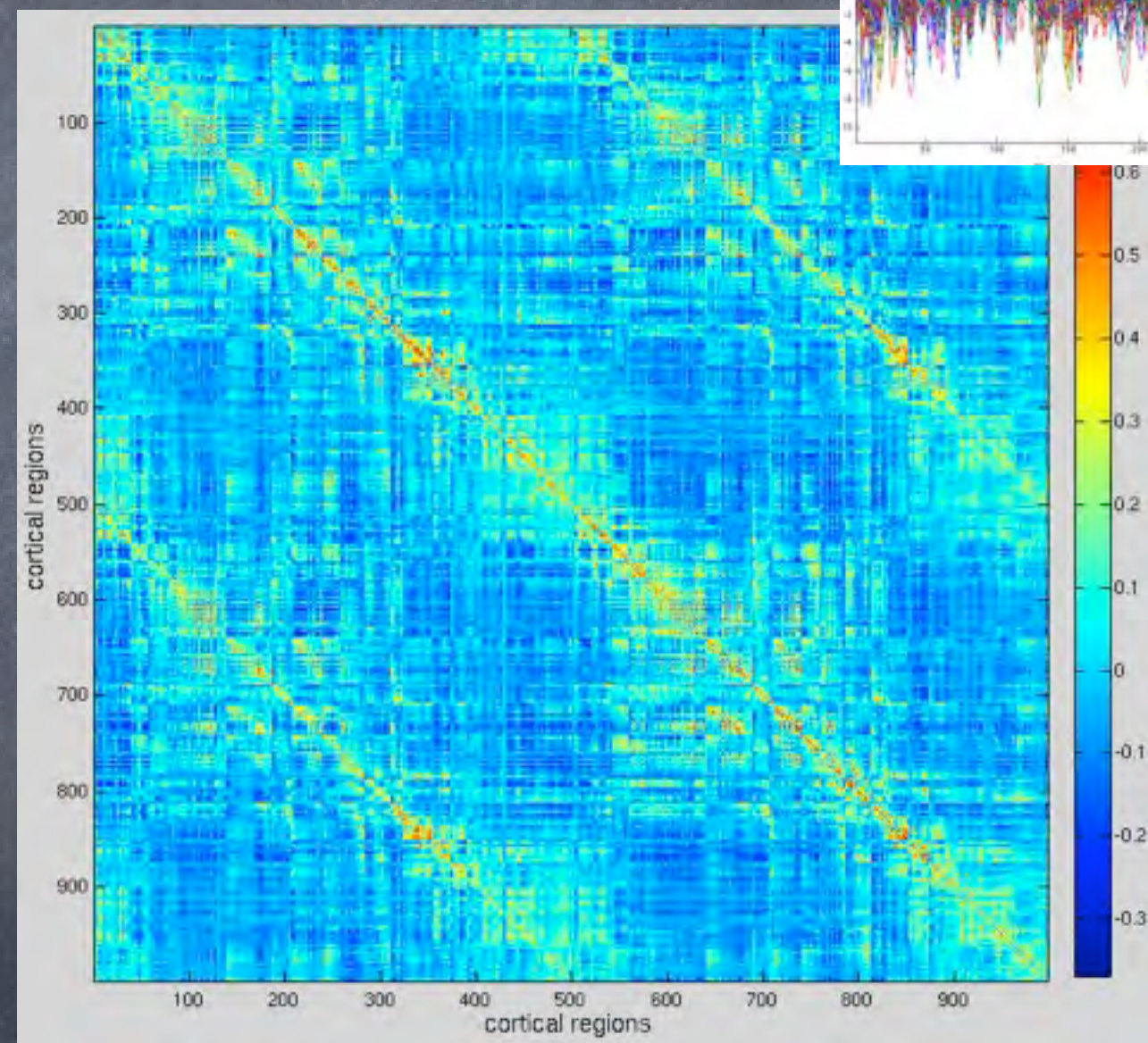
fiber-tracts (model)



neural activity (model)

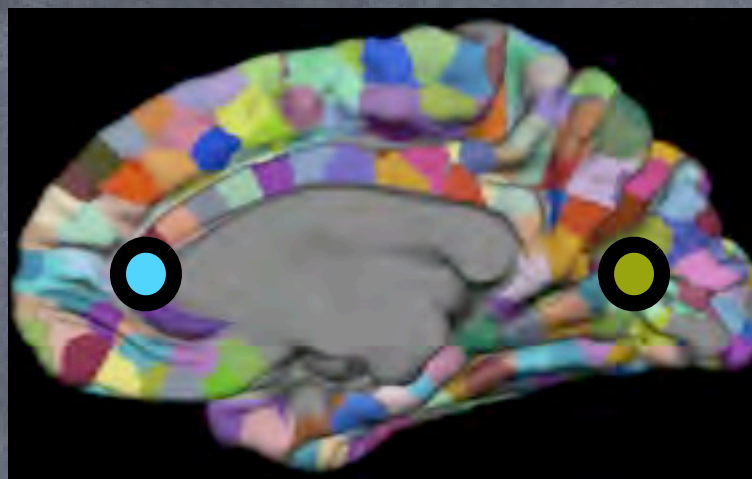
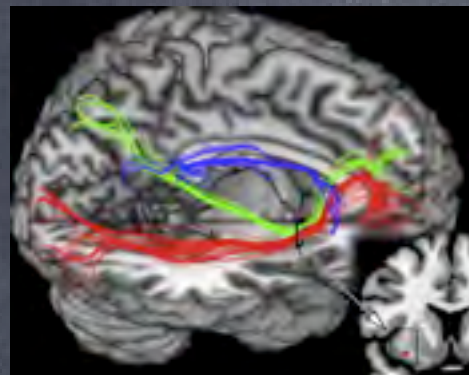


structural connectivity (SC)

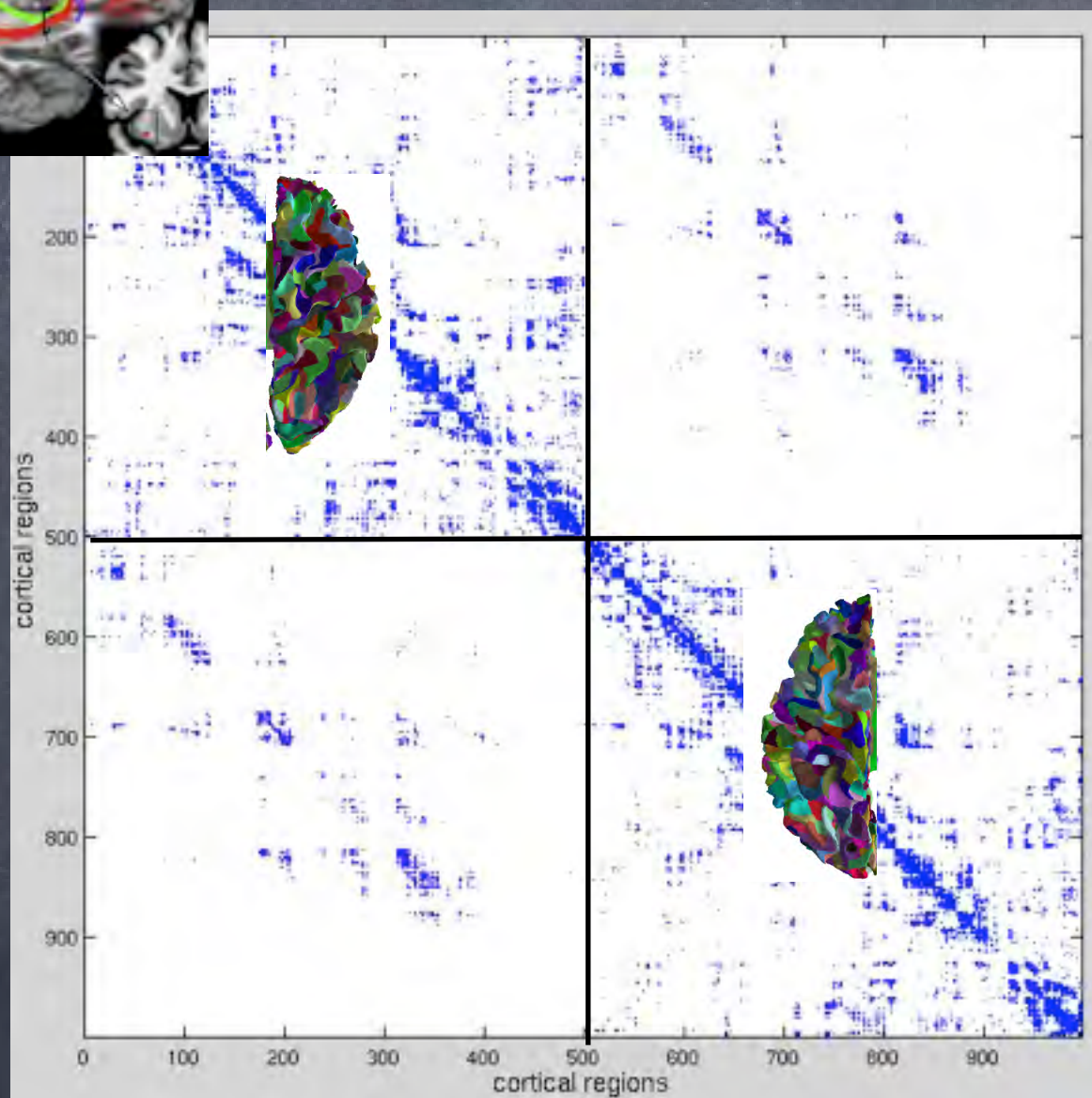
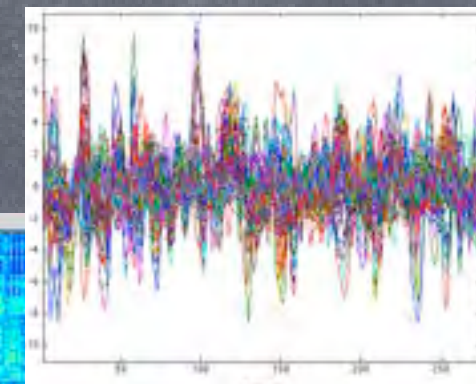


functional connectivity (FC)

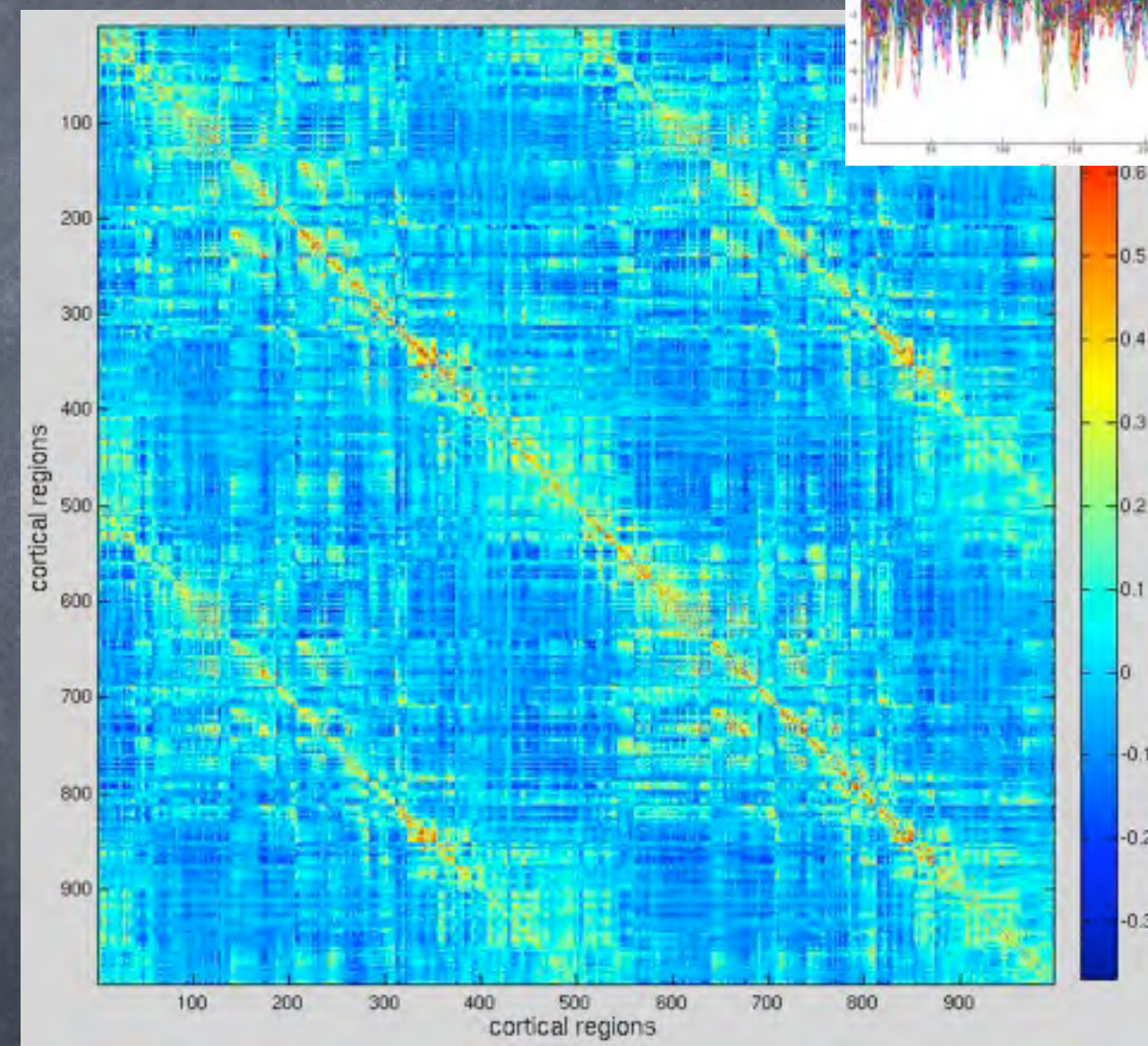
fiber-tracts (model)



neural activity (model)

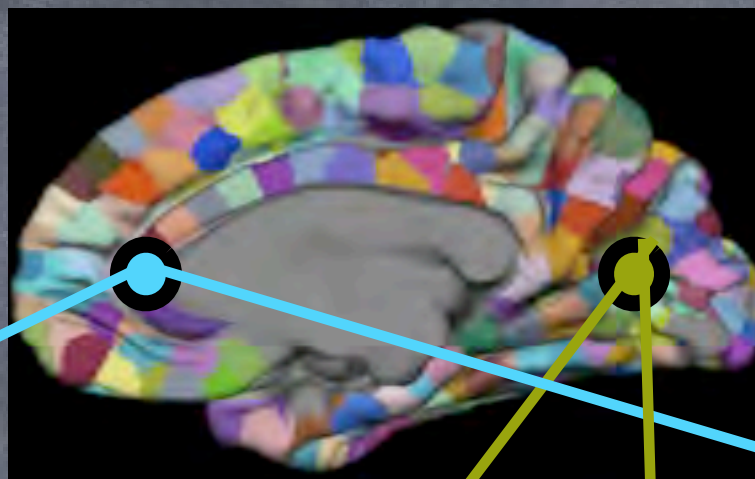


structural connectivity (SC)

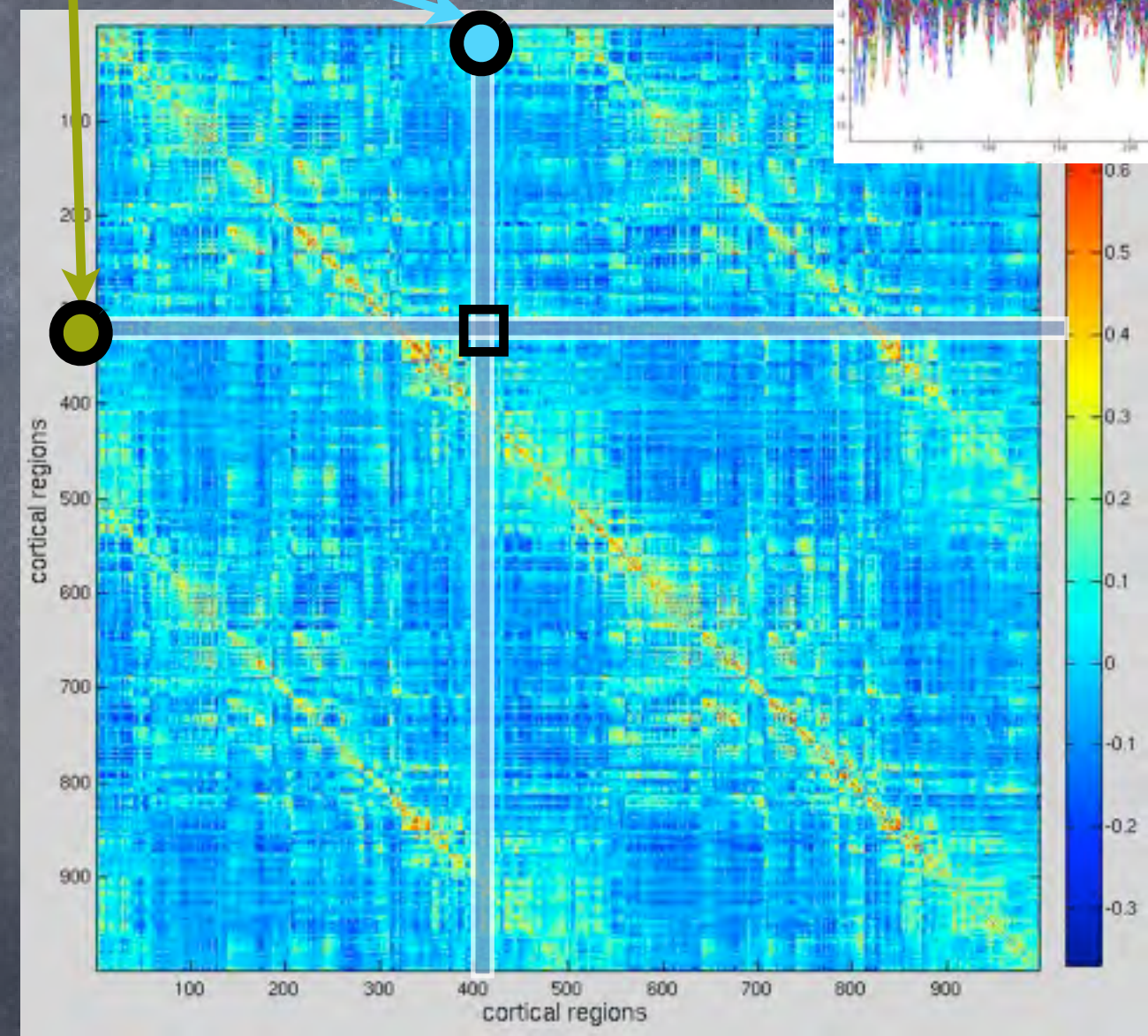
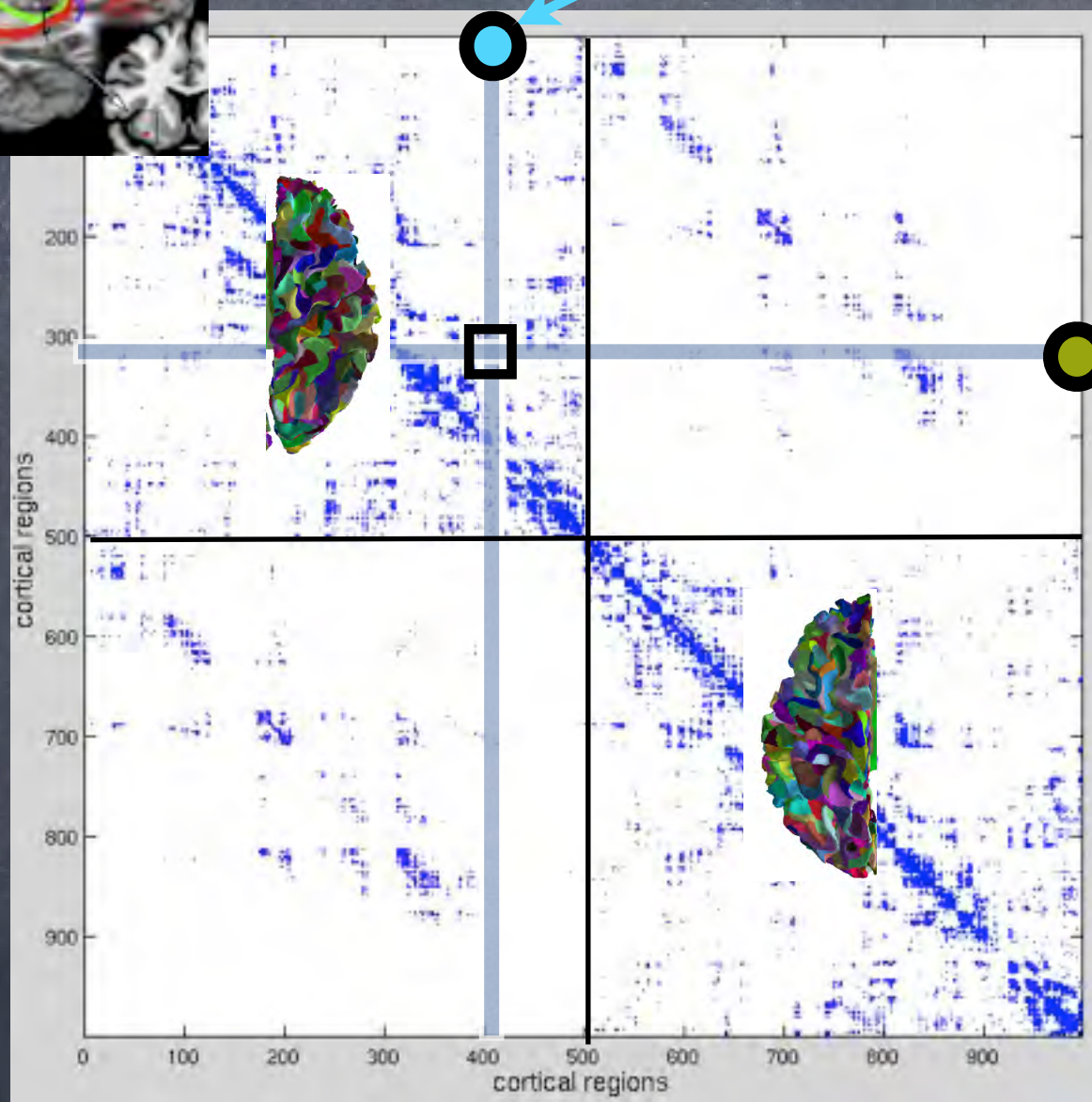
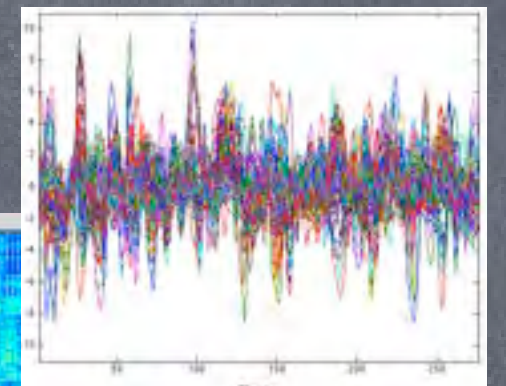


functional connectivity (FC)

fiber-tracts (model)

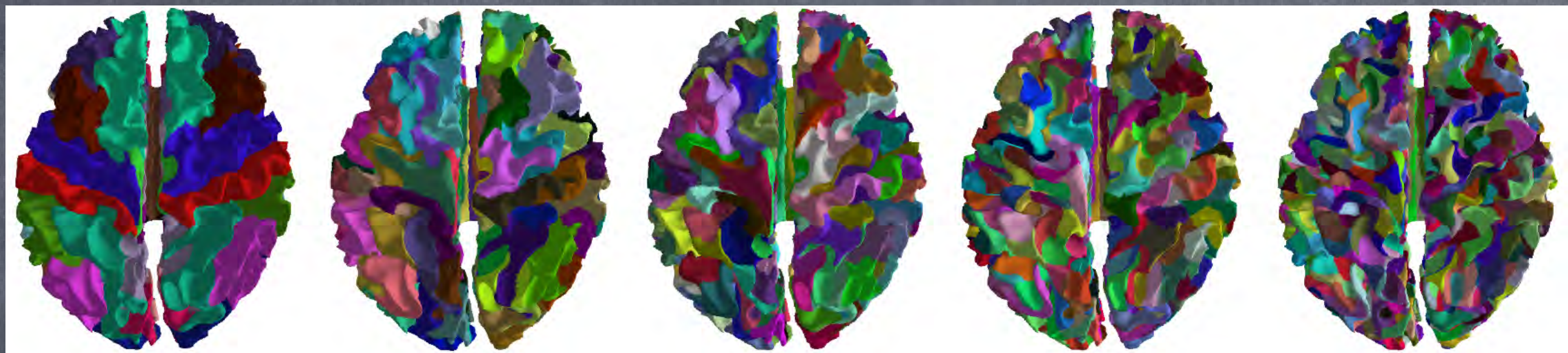


neural activity (model)



structural connectivity (SC)

functional connectivity (FC)



68

114

219

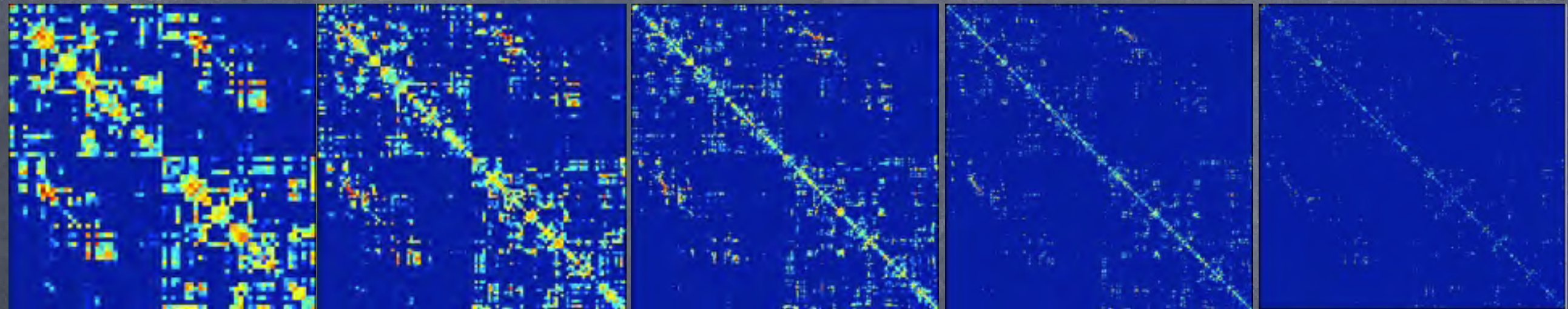
448

1000

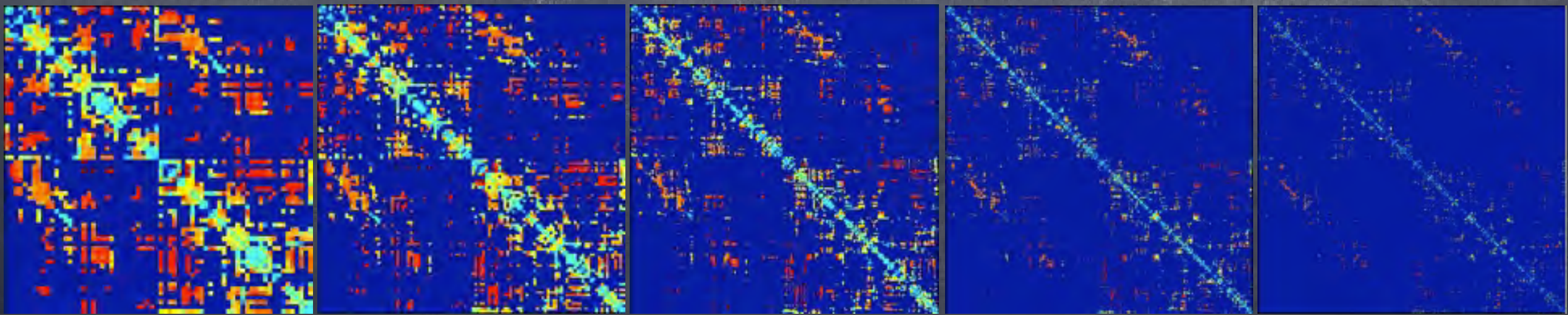
$\log_{10}(\#\text{fibers})$

RH

LH



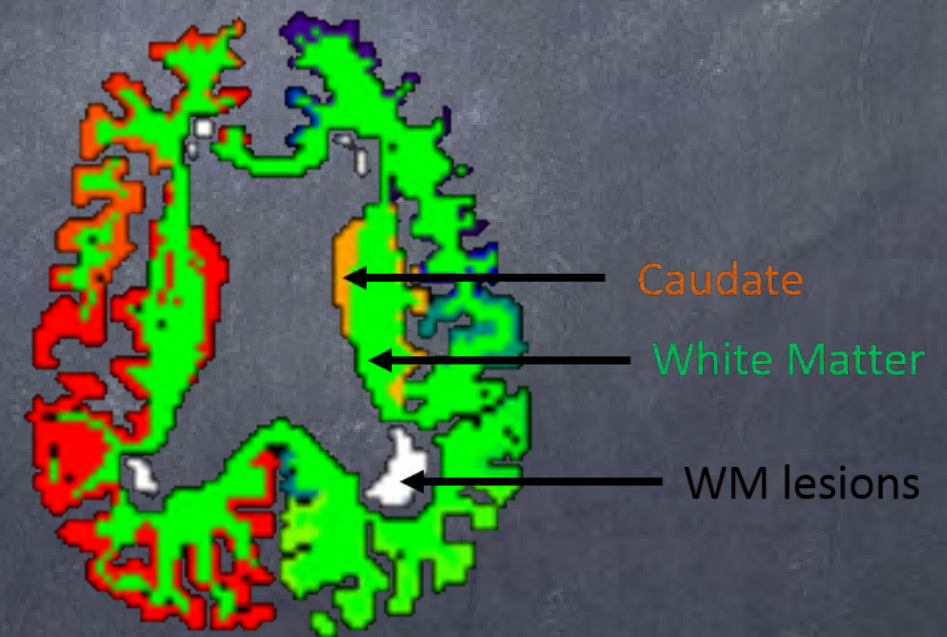
$\log_{10}(\text{fiber-length})$





# A case study of HDLS

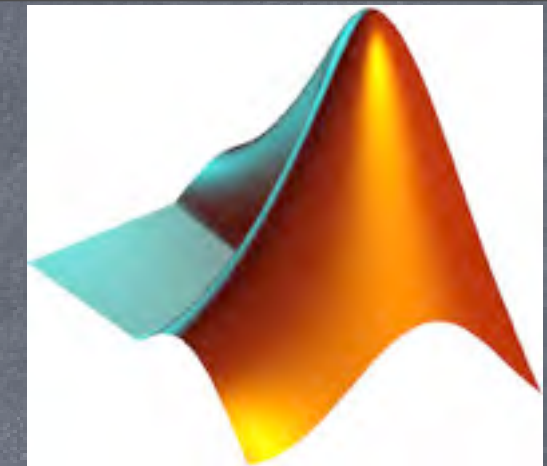
- Hereditary diffuse leukoencephalopathy with spheroids, (HDLS), is an autosomal dominant neurodegenerative disorder caused by mutations in the colony stimulating factor 1 receptor (CSF1R) gene.
- It is characterized by white matter damage and axonal swelling (spheroids) leading to subcortical lesions visualized using MRI1.
- Clinical symptoms include progressive motor problems and cognitive decline. Patients with HDLS can often be mistaken for other neurodegenerative diseases.
- two siblings, HC (female, 48) and HDLS (male, 46)
- HDLS mutation: three base deletion (TCT) in CSF1R




reliable  
individual  
connectomes




reliable  
individual  
connectomes



**UCL MICROSTRUCTURE IMAGING GROUP**

 **UCL**

UCL >> CMIC >> MIG >> CAMINO >> UCL Camino Diffusion MRI Toolkit



### UCL Camino Diffusion MRI Toolkit

Camino is an open-source software toolkit for diffusion MRI processing. The toolkit implements standard techniques, such as diffusion tensor fitting, mapping fractional anisotropy and mean diffusivity, deterministic and probabilistic tractography. It also contains more specialized and cutting-edge techniques, such as Monte-Carlo diffusion simulation, multi-fibre and HARDI reconstruction techniques, multi-fibre PICo, compartment models, and axon density and diameter estimation.

Camino has a modular design to enable construction of processing pipelines that include modules from other software packages. The toolkit is primarily designed for unix platforms and structured to enable simple scripting of processing pipelines for batch processing. Most users use linux, MacOS or a unix emulator like cygwin running under windows. However, the core code is written in Java and thus is simple to call from other platforms and programming environments, such as matlab running under unix or windows.

The microstructure imaging group at UCL lead development and maintenance of the toolkit. The **PICSL** group at the University of Pennsylvania also contribute heavily, as have Geoff Parker and colleagues at the University of Manchester. Many of the specialist modules arise from the research of the MIG and collaborating groups. However, the toolkit also includes implementations of many other techniques in the literature that we have found useful.

We hope you find Camino useful. We welcome any feedback, contributions or suggestions for additions to the toolkit.

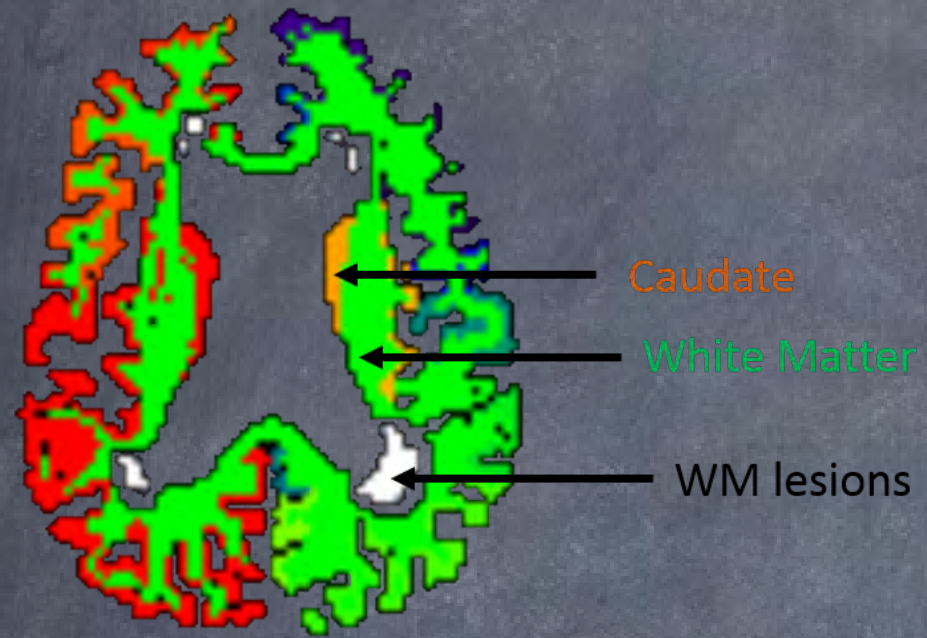
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If you use Camino in your research, please include the appropriate citations from the [citations page](#).

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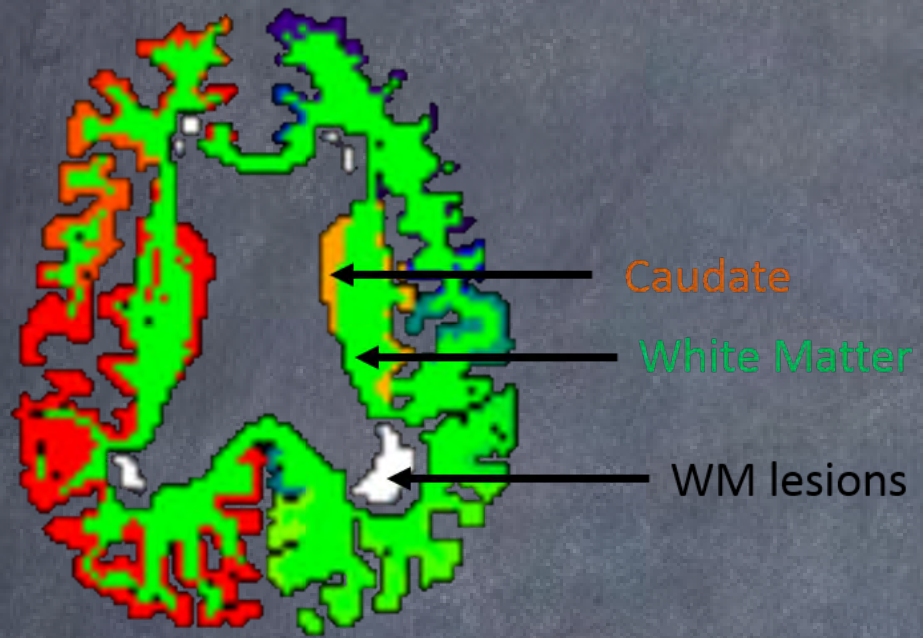
how to model an individual  
connectome?

# how to model an individual connectome?




tissue segmentation

# how to model an individual connectome?



tissue segmentation

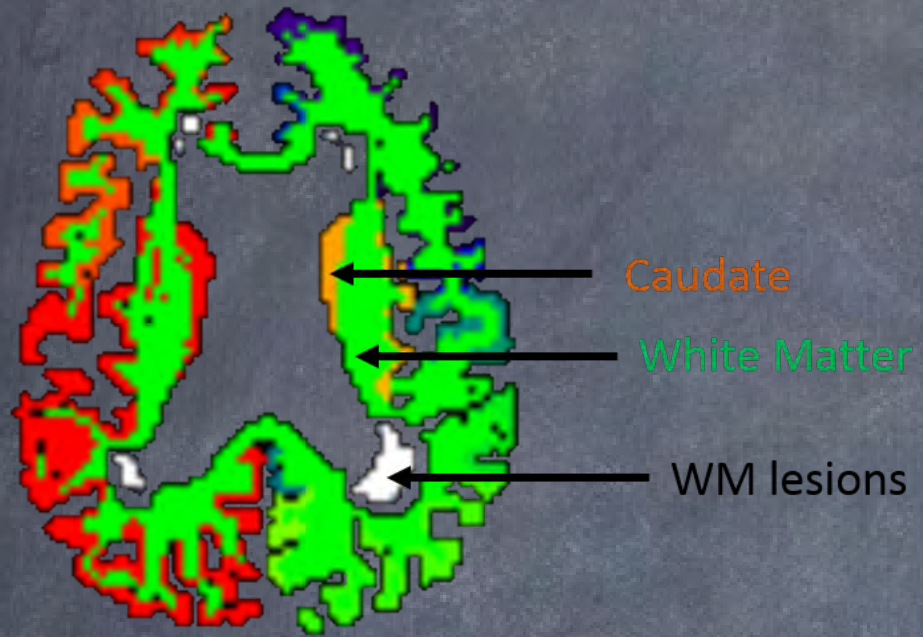


  
single-tensor

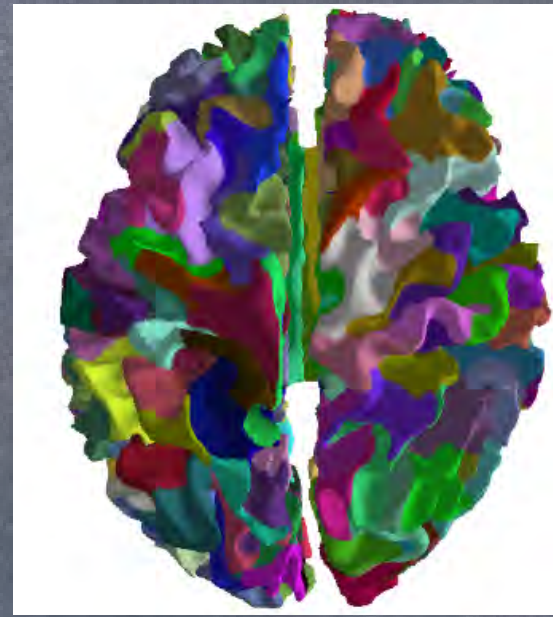
  
multi-tensor

multi-tensor modeling

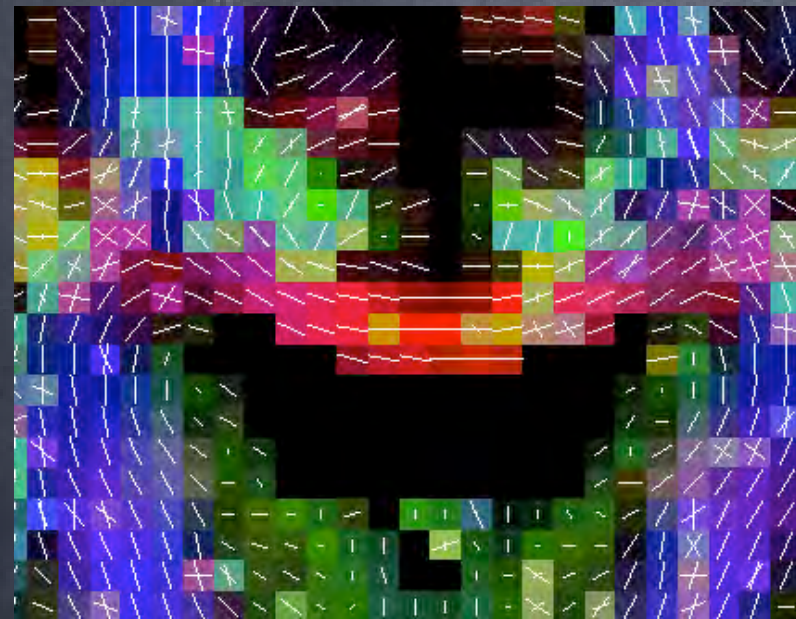
# how to model an individual connectome?



tissue segmentation



GM parcellation



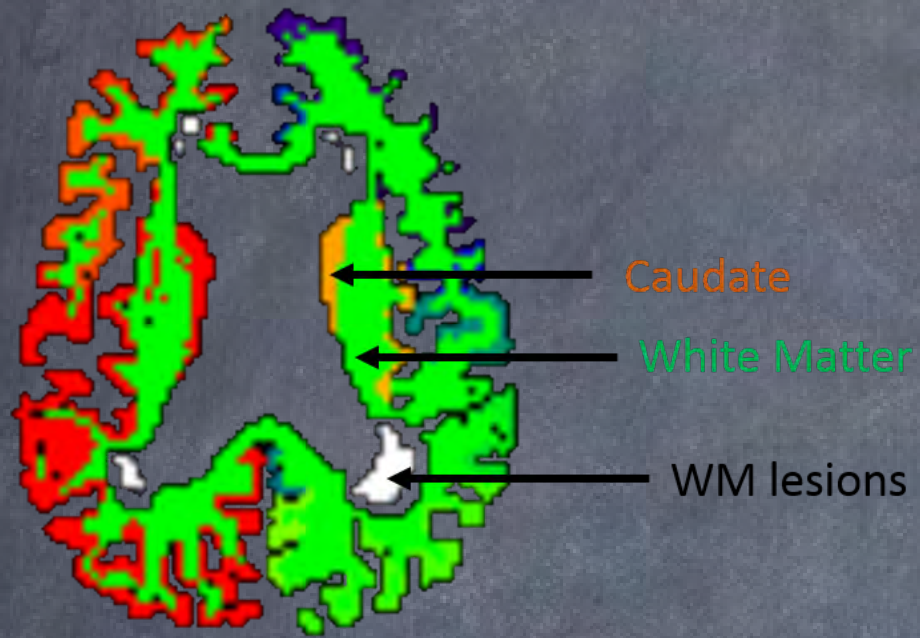
single-tensor



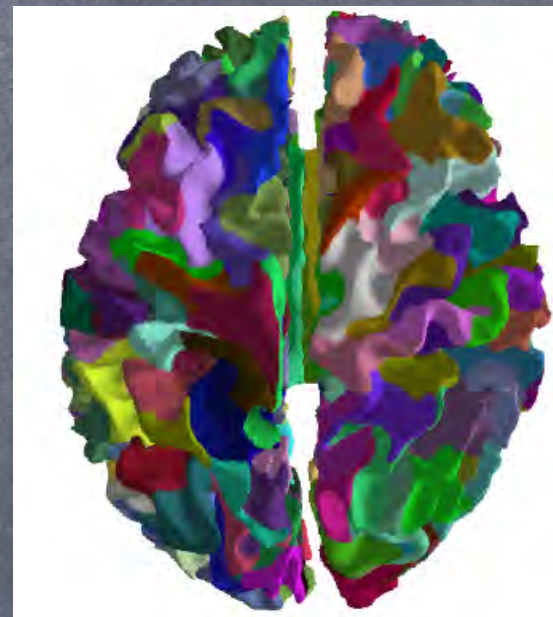
multi-tensor

multi-tensor modeling

# how to model an individual connectome?



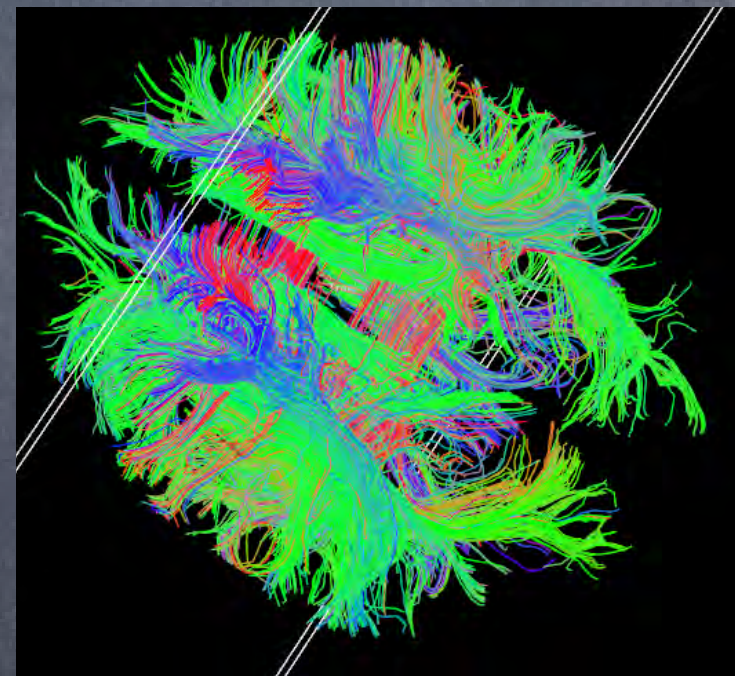
tissue segmentation



GM parcellation



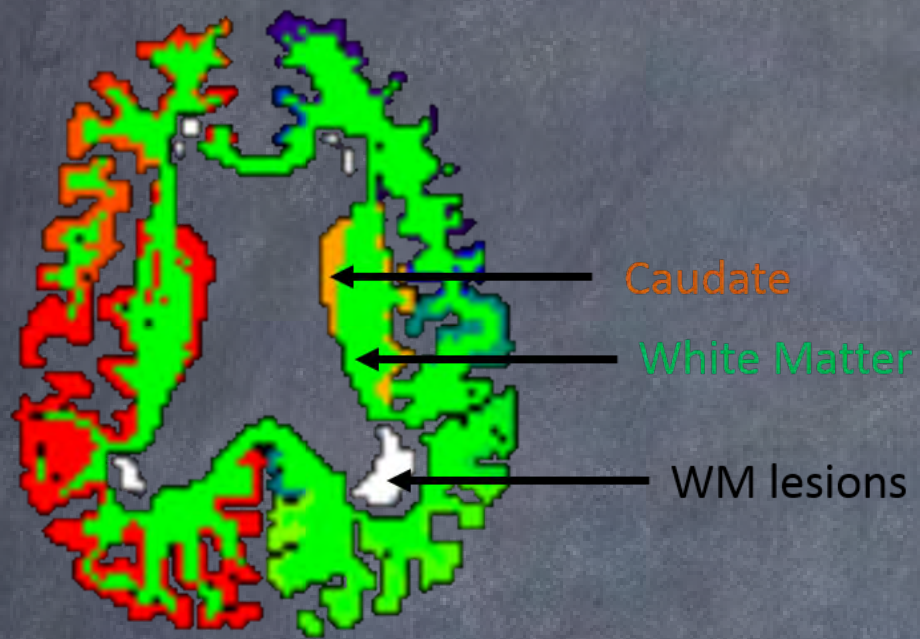
multi-tensor modeling



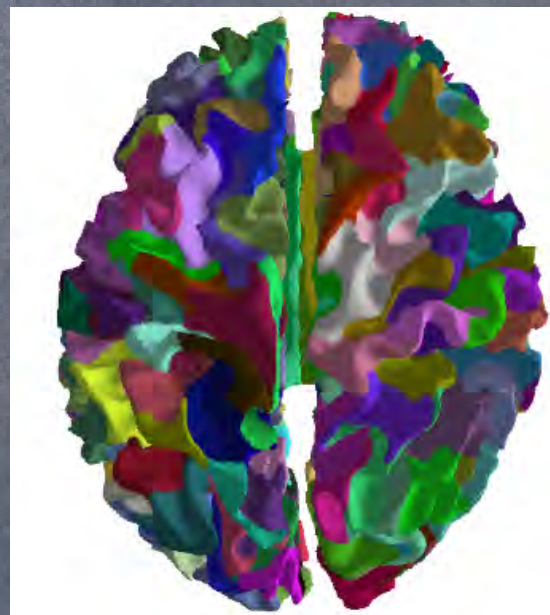
WM fiber-tracts



# how to model an individual connectome?



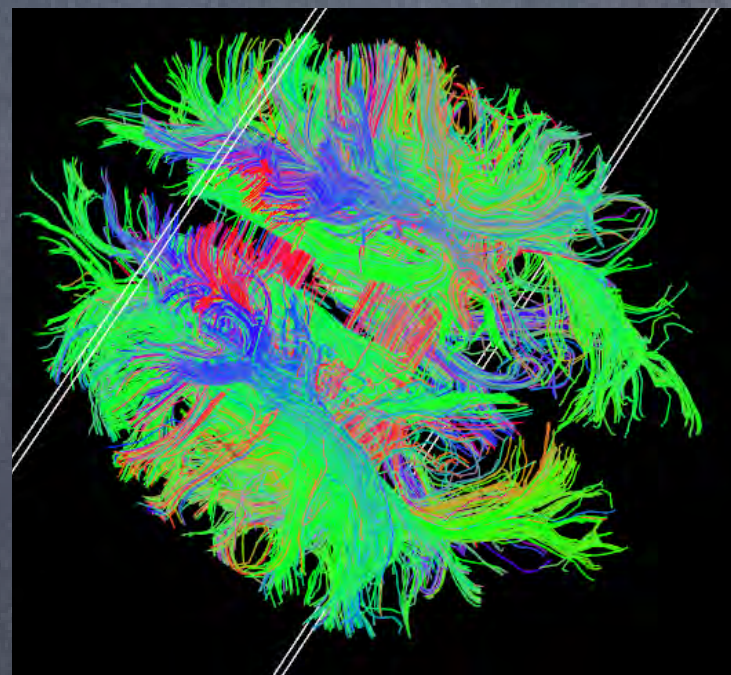
tissue segmentation



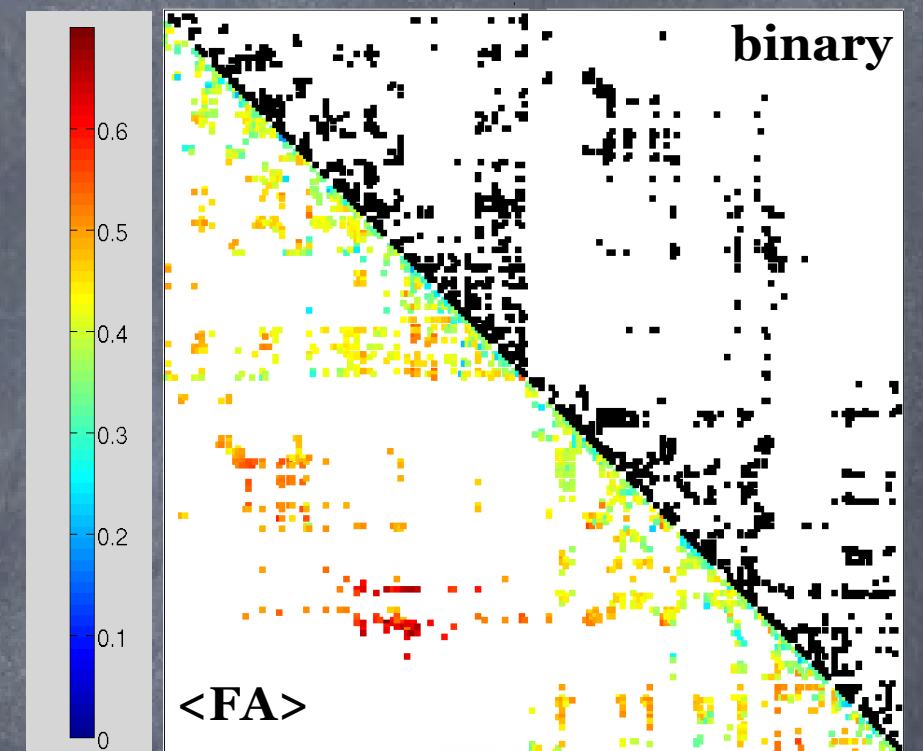
GM parcellation



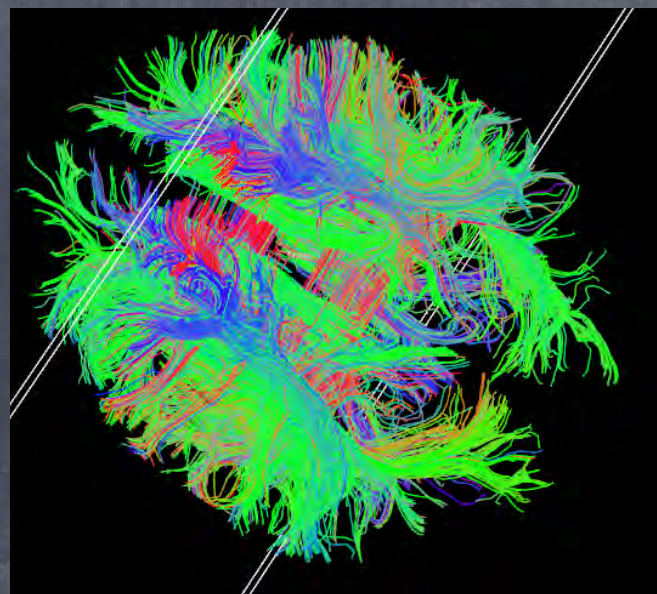
multi-tensor modeling



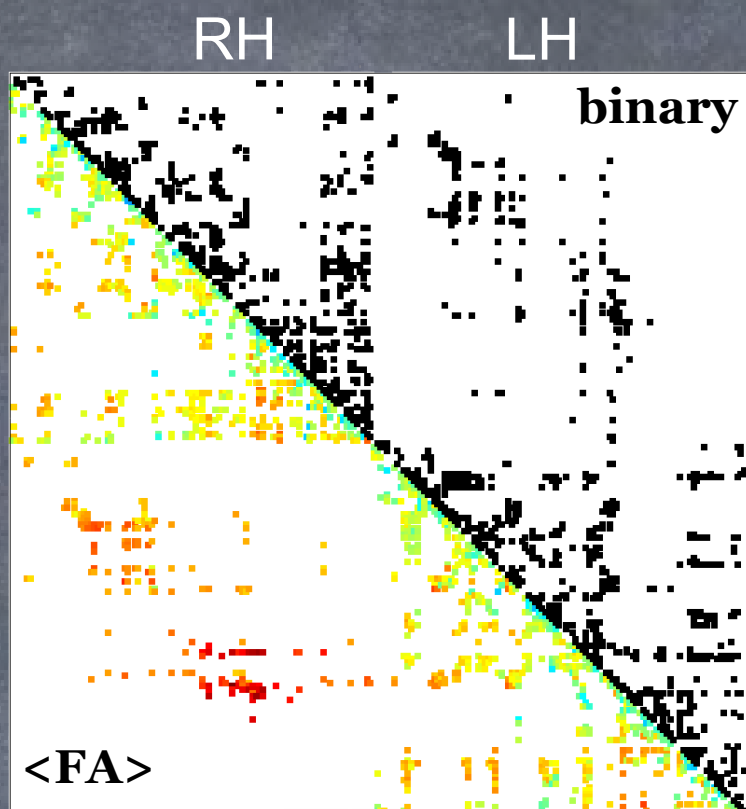
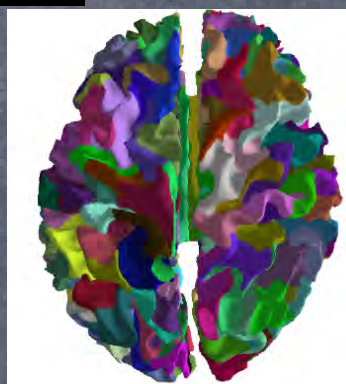
WM fiber-tracts



structural connectivity (SC)



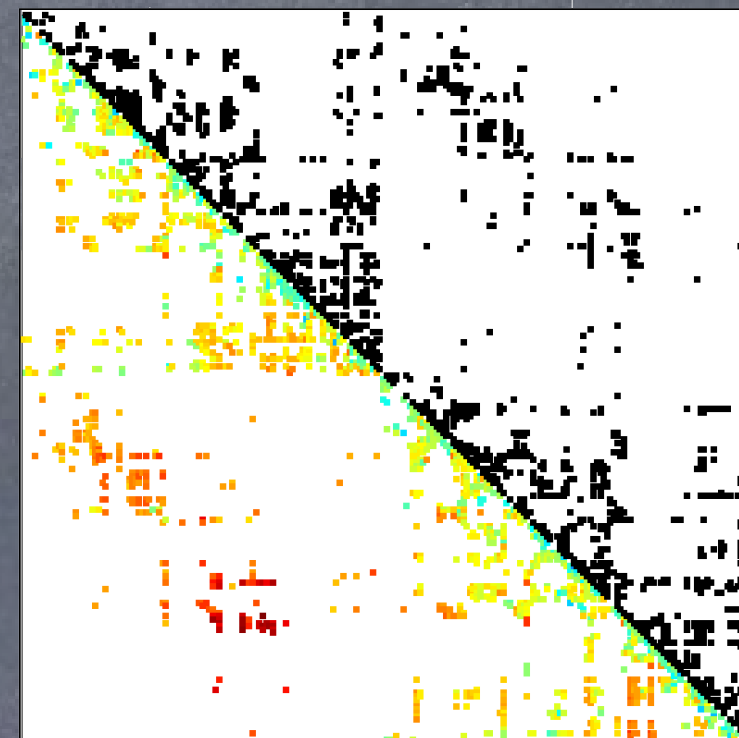
HC



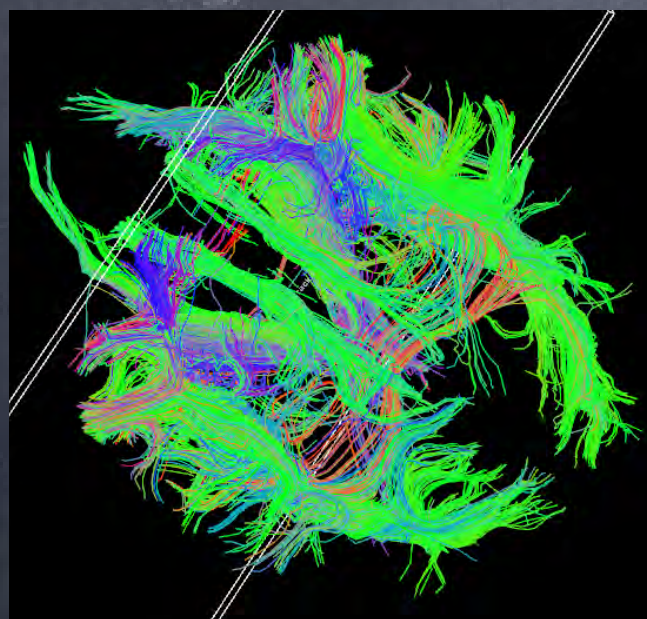
<FA>

visit 1

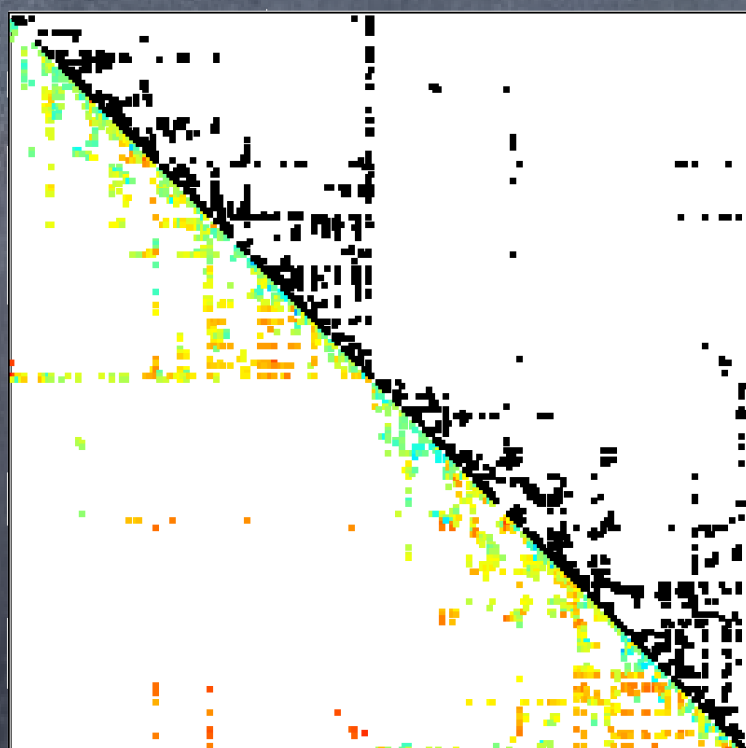
1.5 y  
→



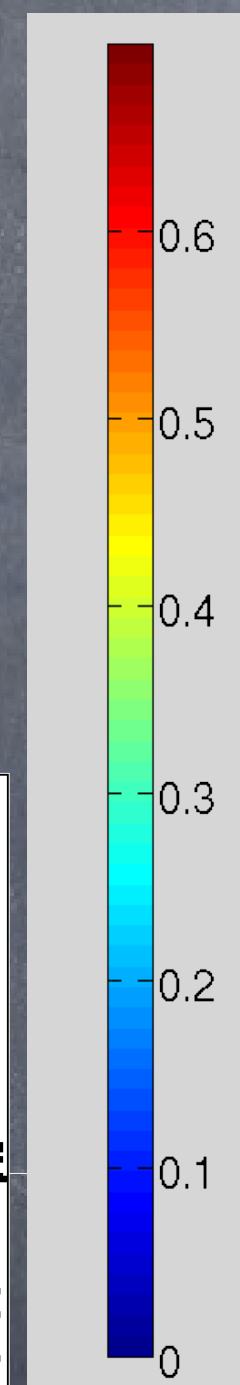
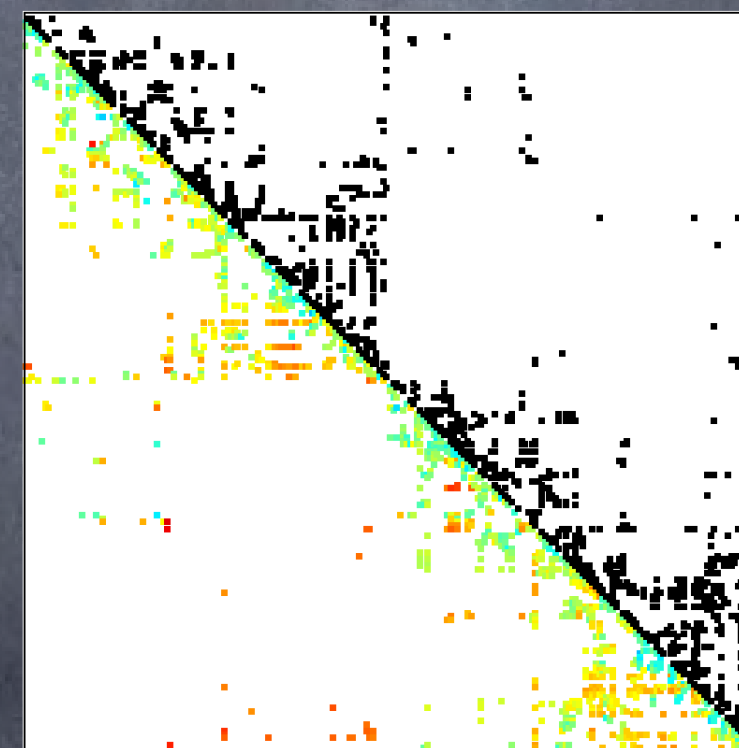
visit 2



HDLS  
patient



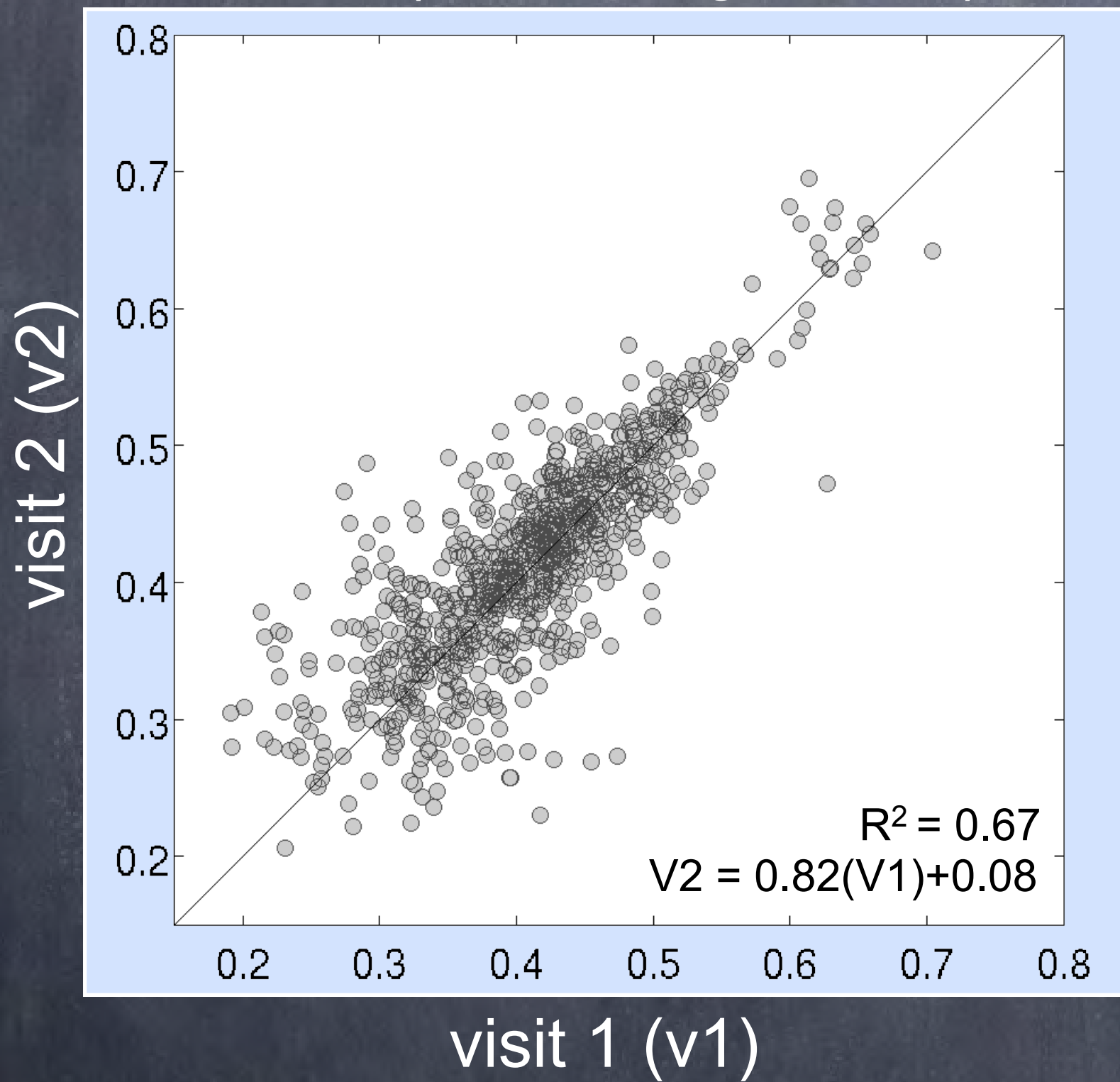
1.5 y  
→



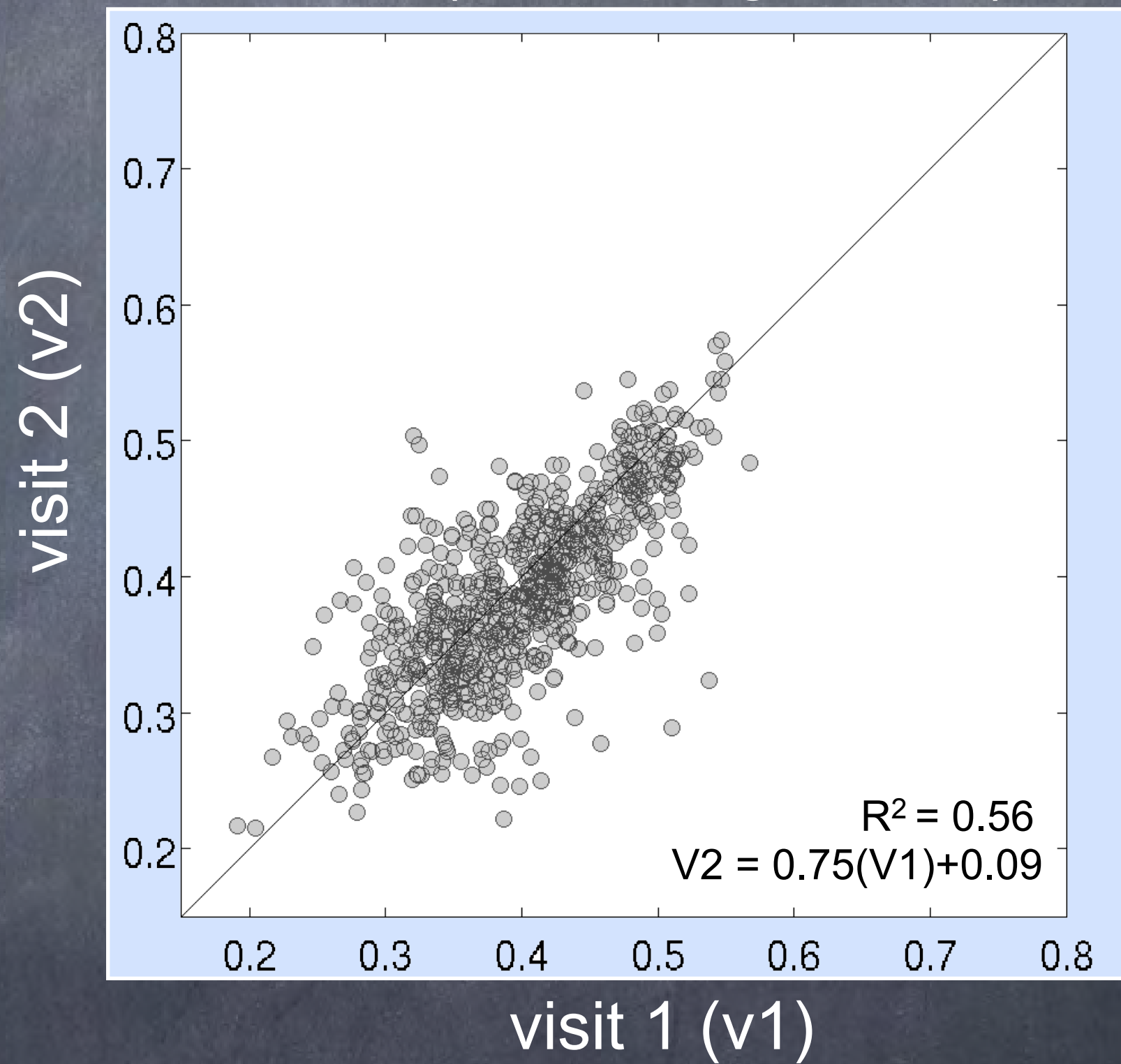
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Hereditary diffuse leukoencephalopathy with spheroids

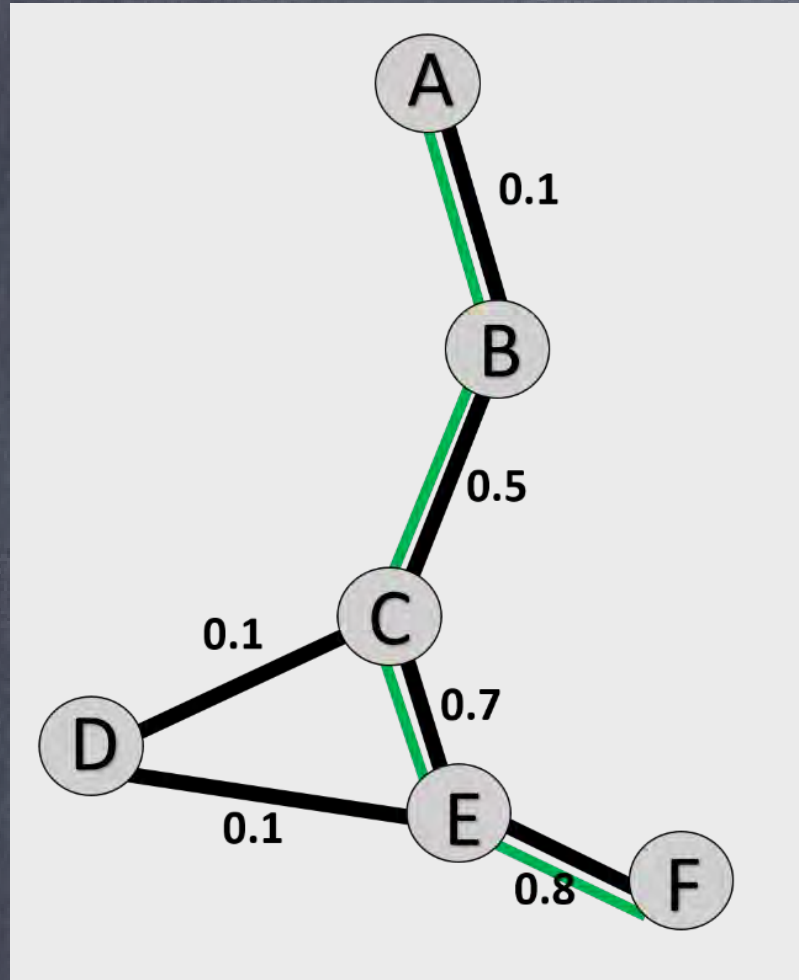
HC (<FA> progression)



HDLS (<FA> progression)



# shortest-paths on networks



$SP(A,B) = \{A,B,C,E,F\}$

adjacency matrix

	A	B	C	D	E	F
A	0	0.1	0	0	0	0
B	0.1	0	0.5	0	0	0
C	0	0.5	0	0.1	0.7	0
D	0	0	0.1	0	0.1	0
E	0	0	0.7	0.1	0	0.8
F	0	0	0	0	0.8	0

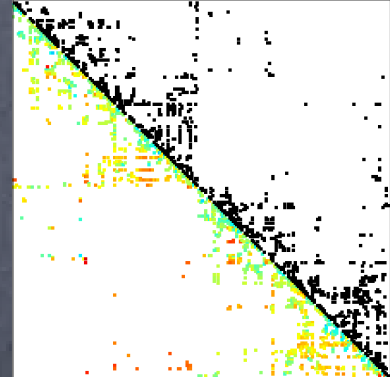
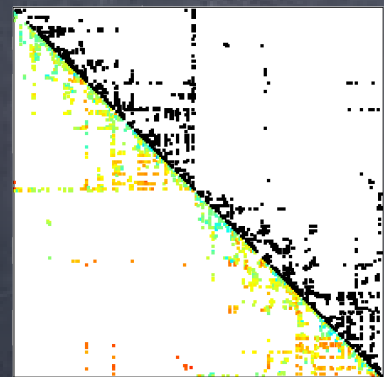
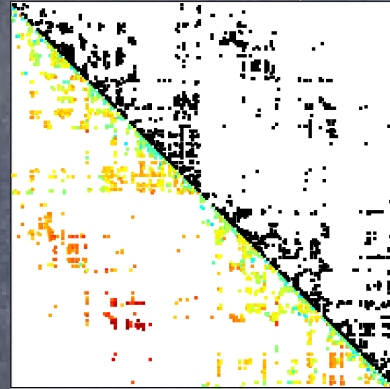
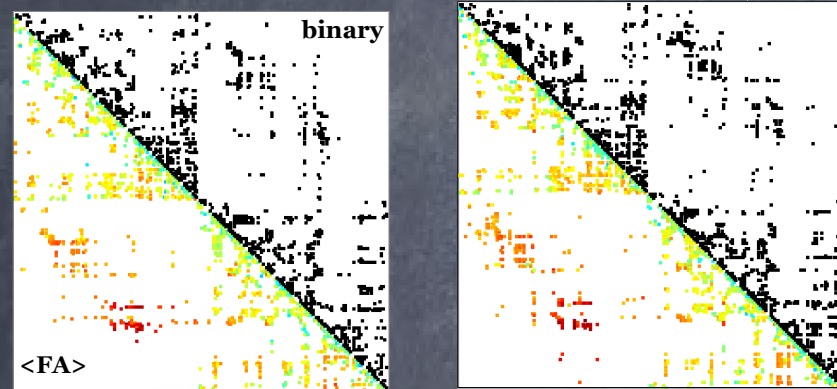
shortest-path distance (SPD)

	A	B	C	D	E	F
A	-	10	12	22	13.4	14.7
B	10	-	2	12	3.4	4.7
C	12	2	-	10	1.4	2.7
D	22	12	10	-	10	11.3
E	13.4	3.4	1.4	10	-	1.3
F	14.7	4.7	2.7	11.3	1.3	-

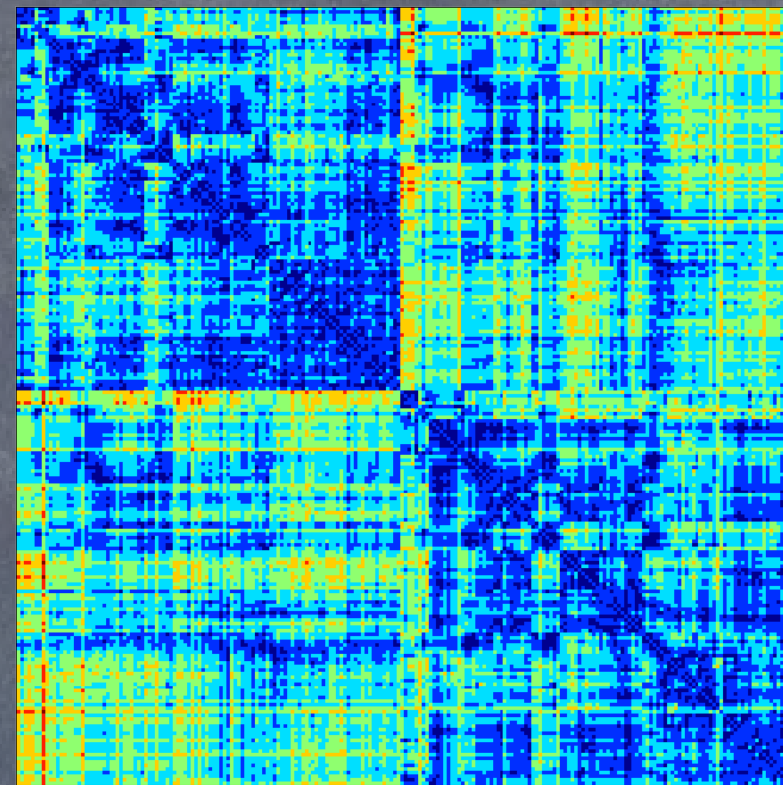
shortest-path #edges (SPE)

	A	B	C	D	E	F
A	-	1	2	3	3	4
B	1	-	1	2	2	3
C	2	1	-	1	1	2
D	3	2	1	-	1	2
E	3	2	1	1	-	1
F	4	3	2	2	1	-

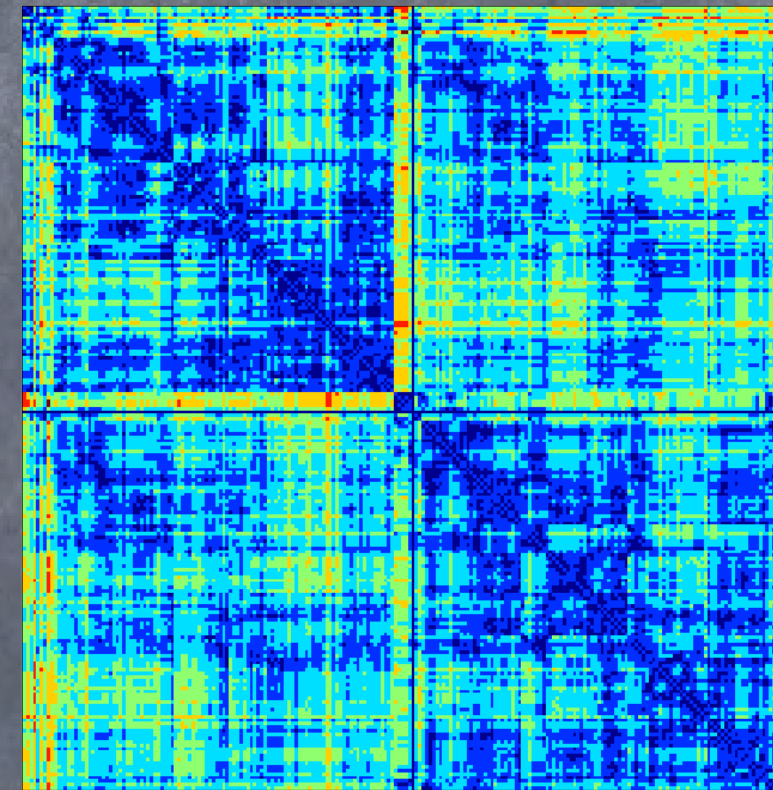
# Shortest-path # Edges (SPE)



HC

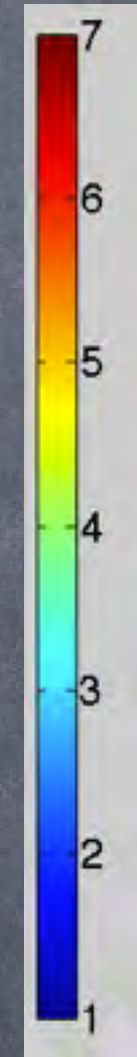
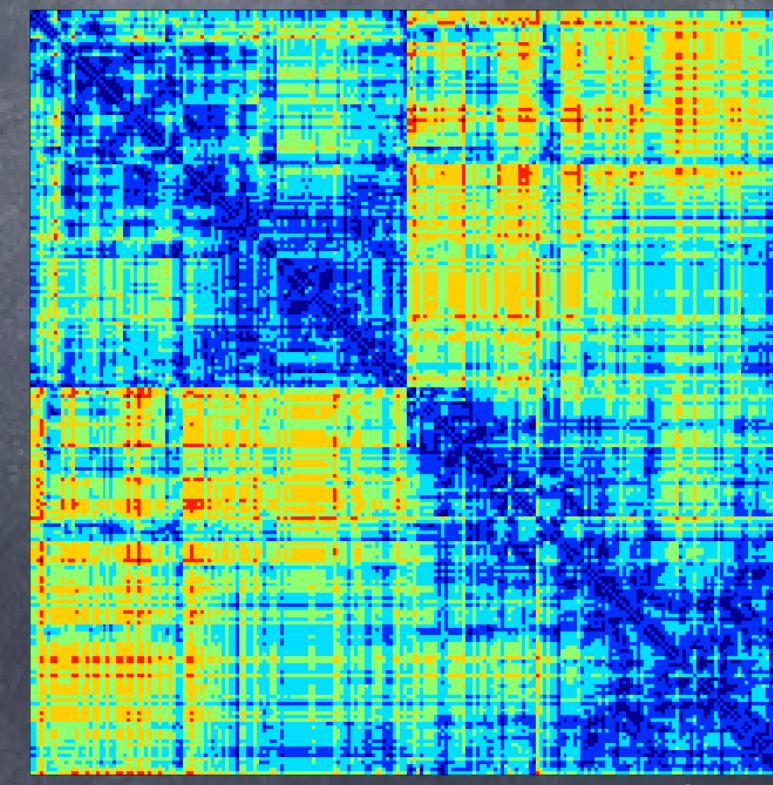
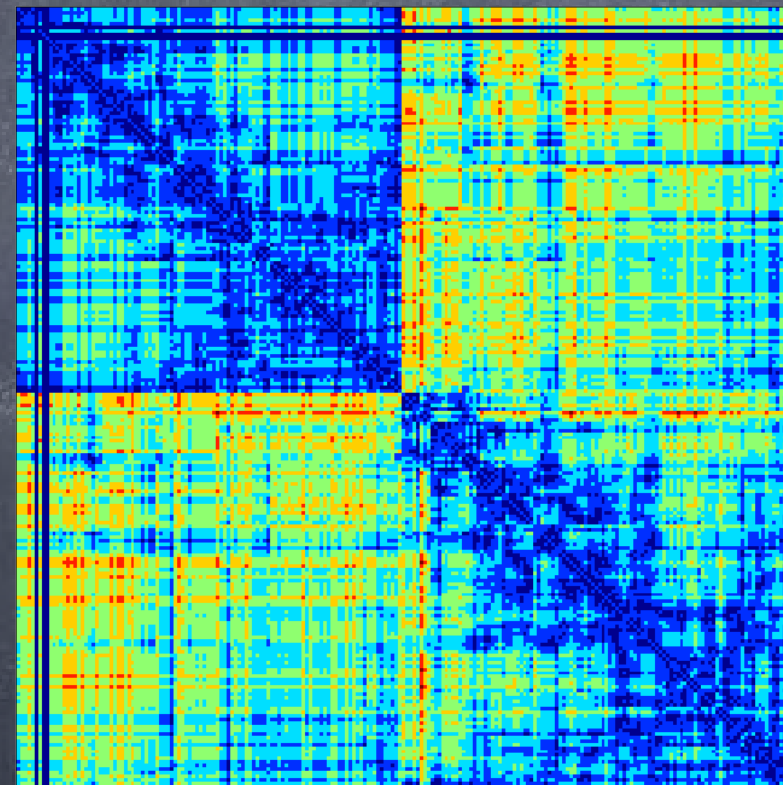


visit 1



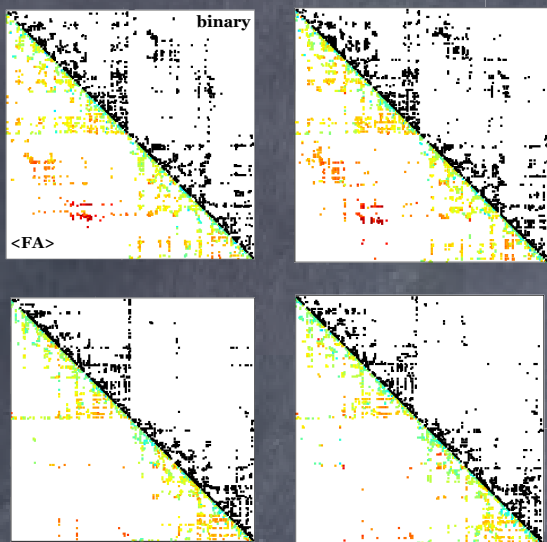
visit 2

HDLS

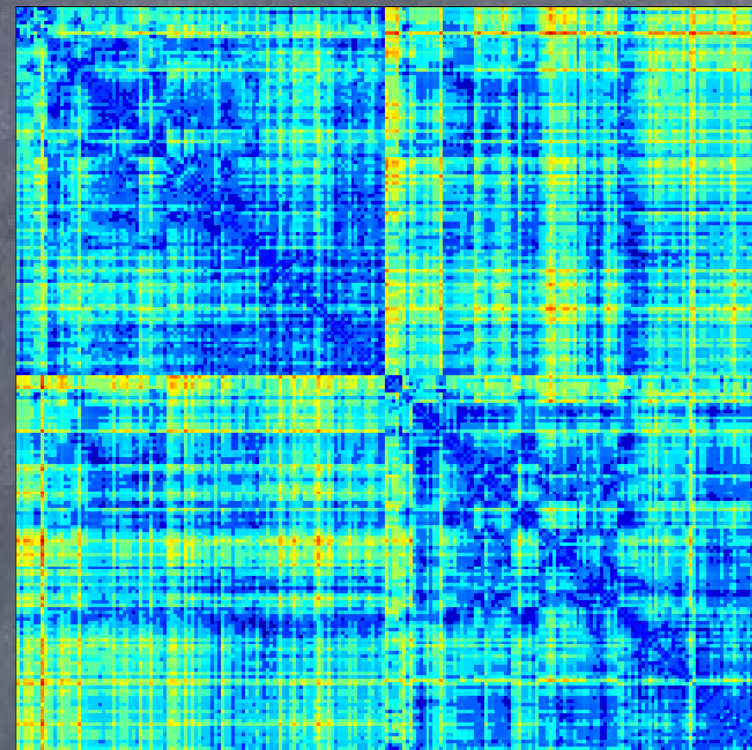


SPE

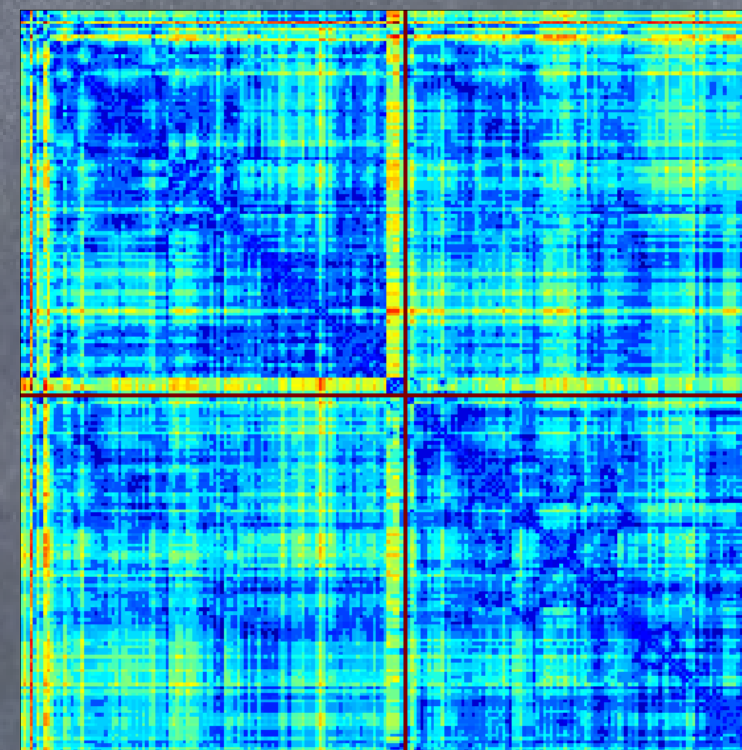
# Shortest-path # Distance (SPD)



HC

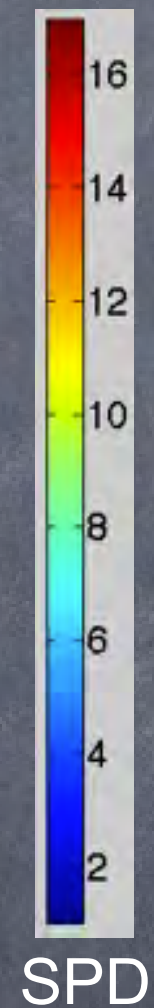
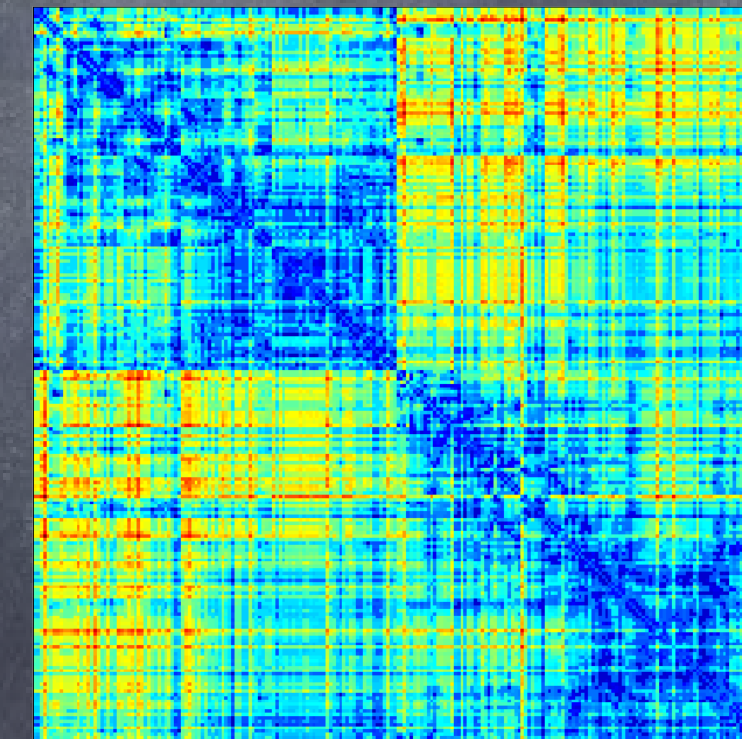
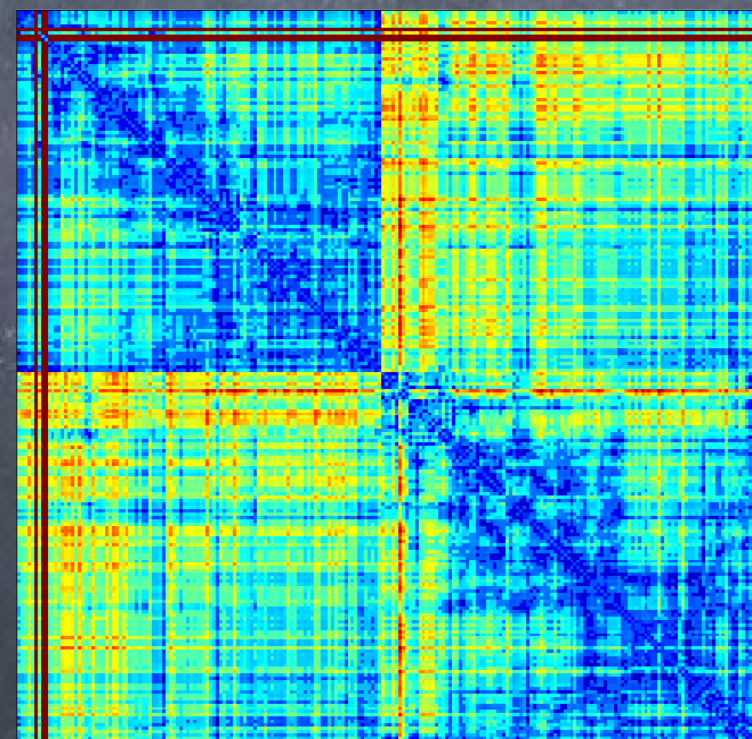


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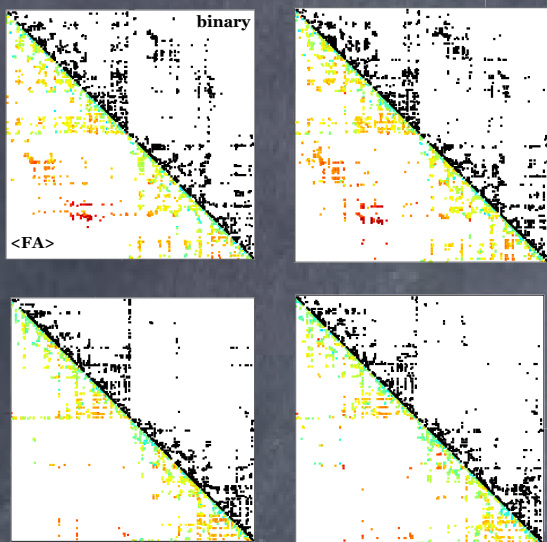
visit 2

HDLS

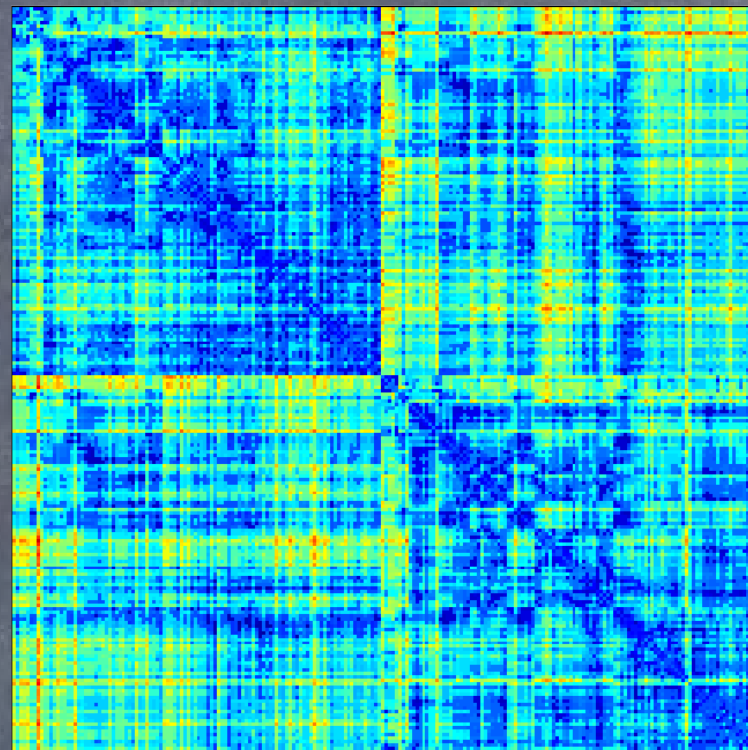


Brain regions ranked by integration impairment

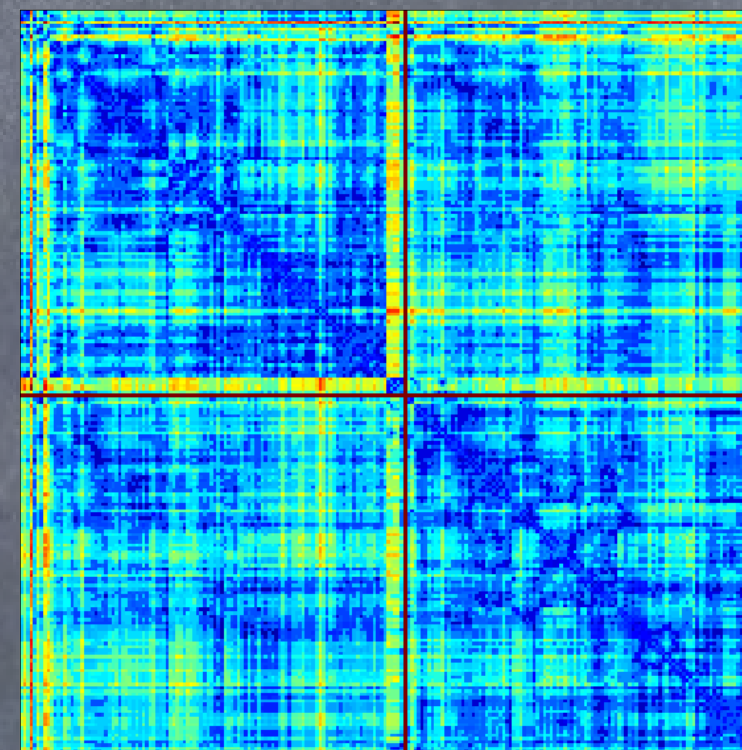
# Shortest-path # Distance (SPD)



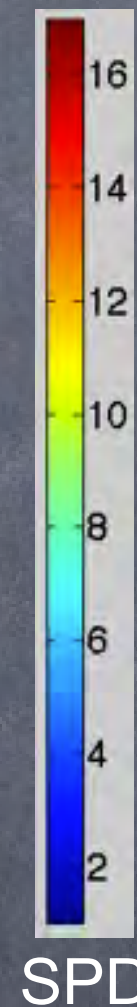
HC



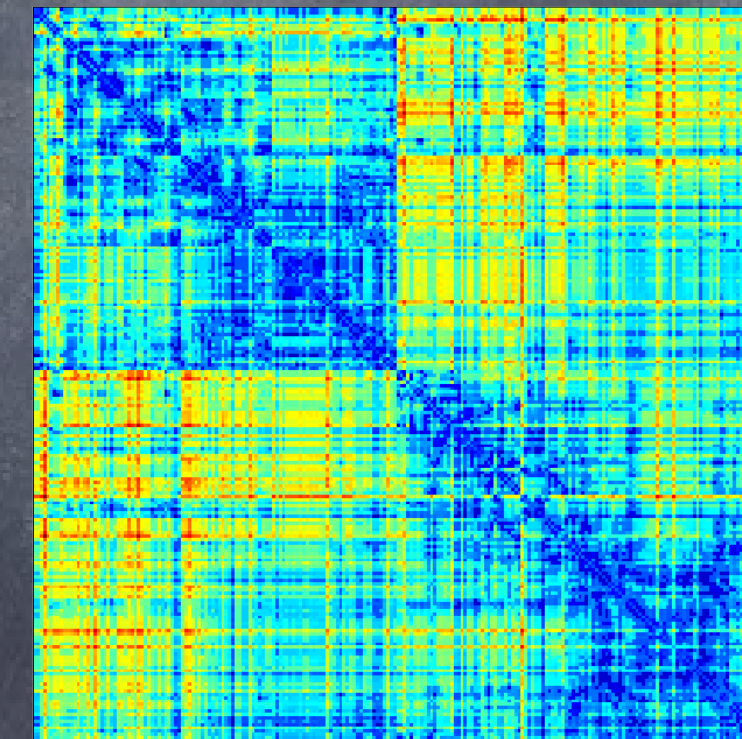
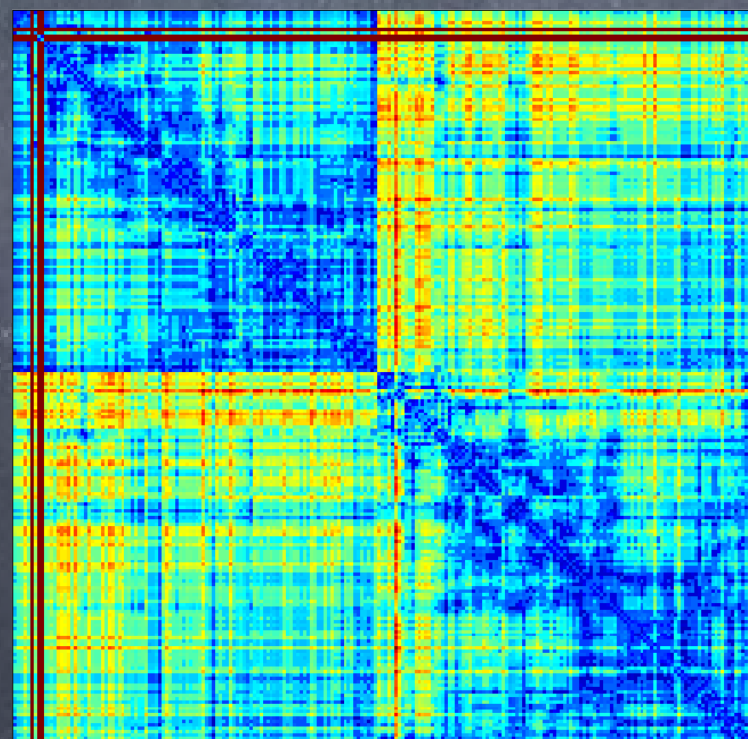
visit 1



visit 2



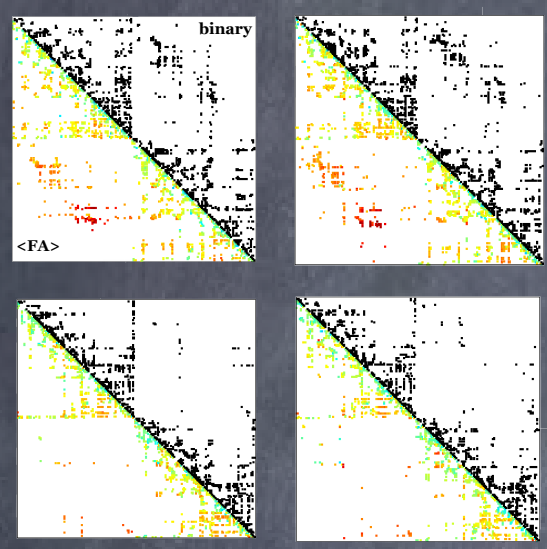
HDLS



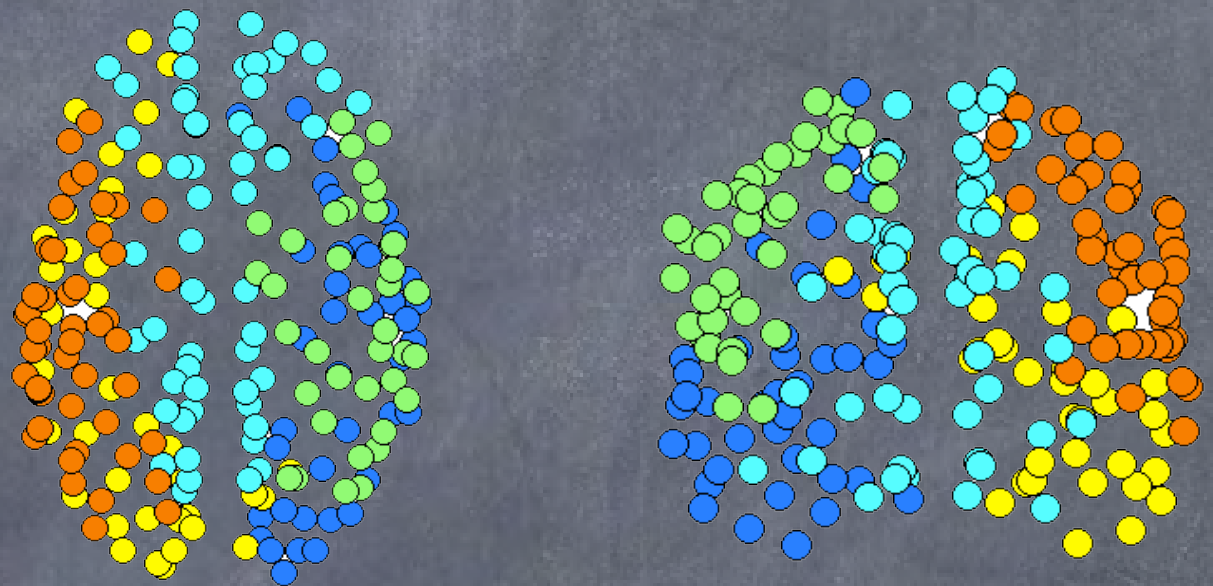
## Brain regions ranked by integration impairment

- superior frontal (L,R),
- caudal middle frontal (R)
- precentral (L,R),
- inferior parietal (R),
- insula (R)
- paracentral (L)

# Segregation: organization in communities

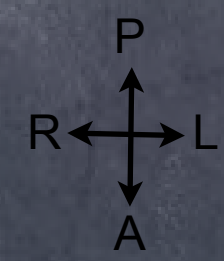
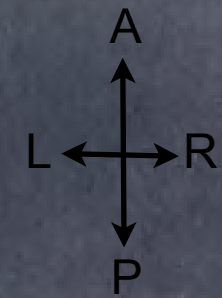
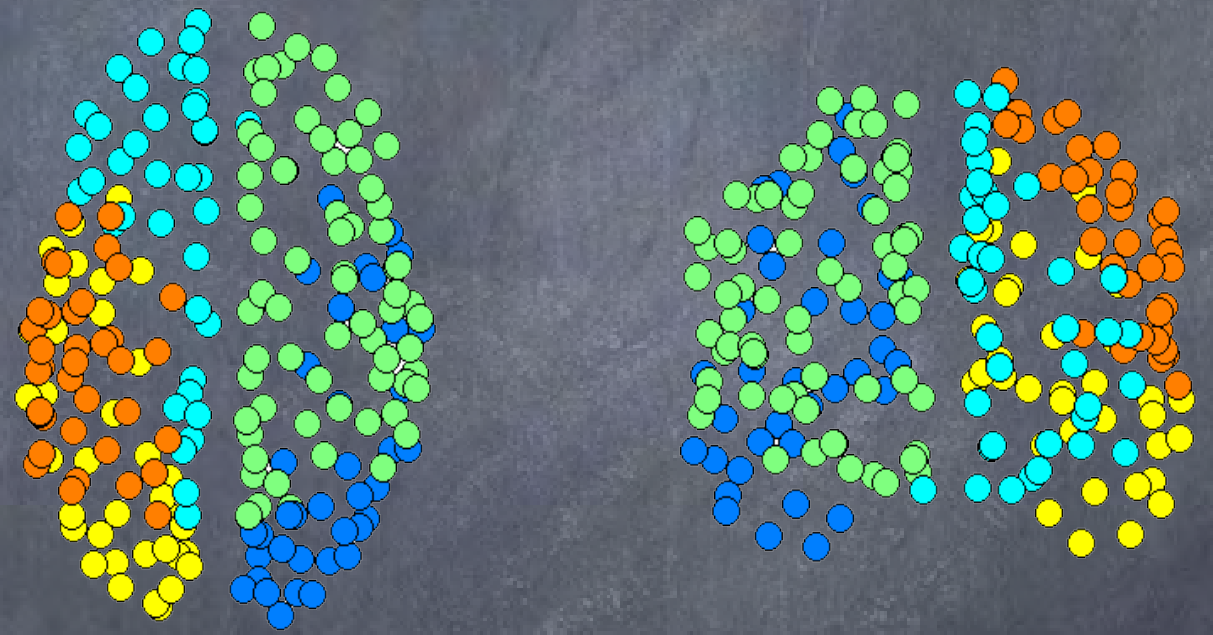


HC



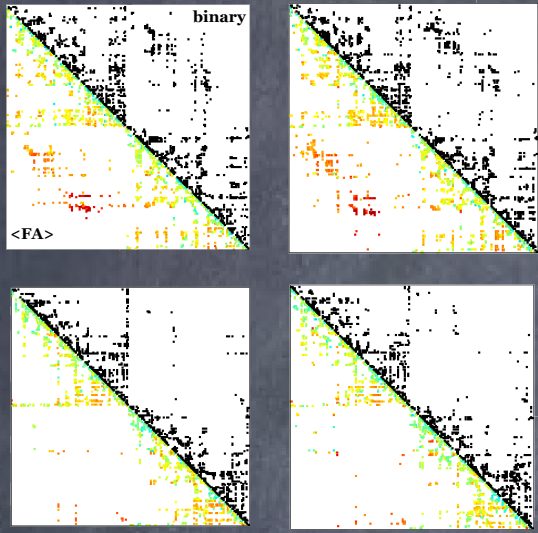
Main segregation changes

HDLS patient

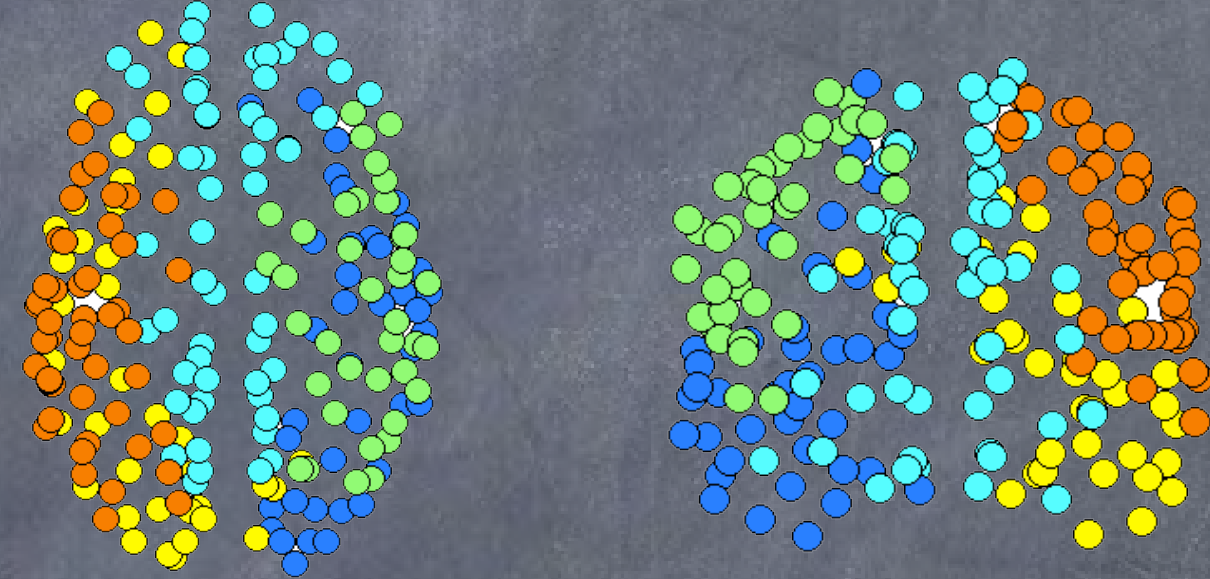




# Segregation: organization in communities



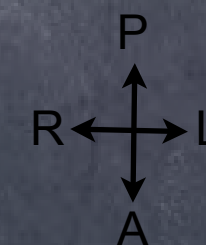
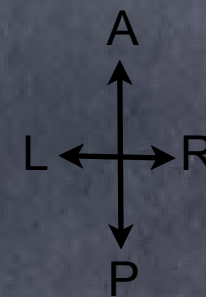
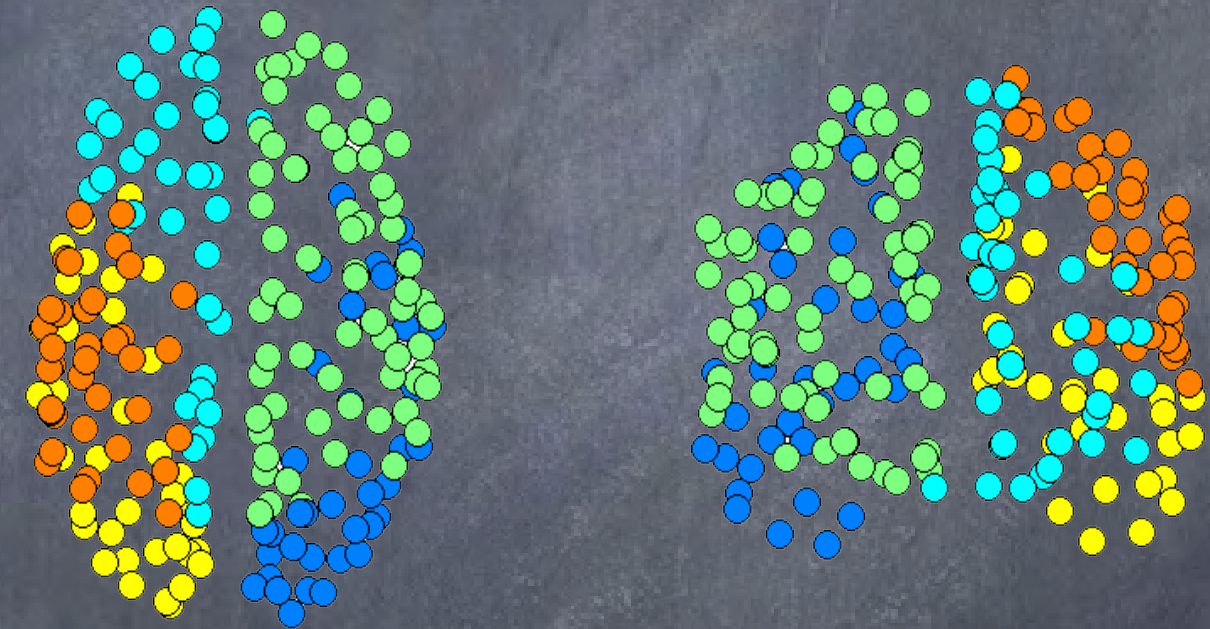
HC



## Main segregation changes

- HDLS patient a more segregated structural organization
- **Module 2** disruption involves bilateral portions of insula, superior frontal area, caudate and pre/paracentral areas

HDLS patient



# Information theoretical approaches to brain connectivity

# Information theoretical approaches to brain connectivity

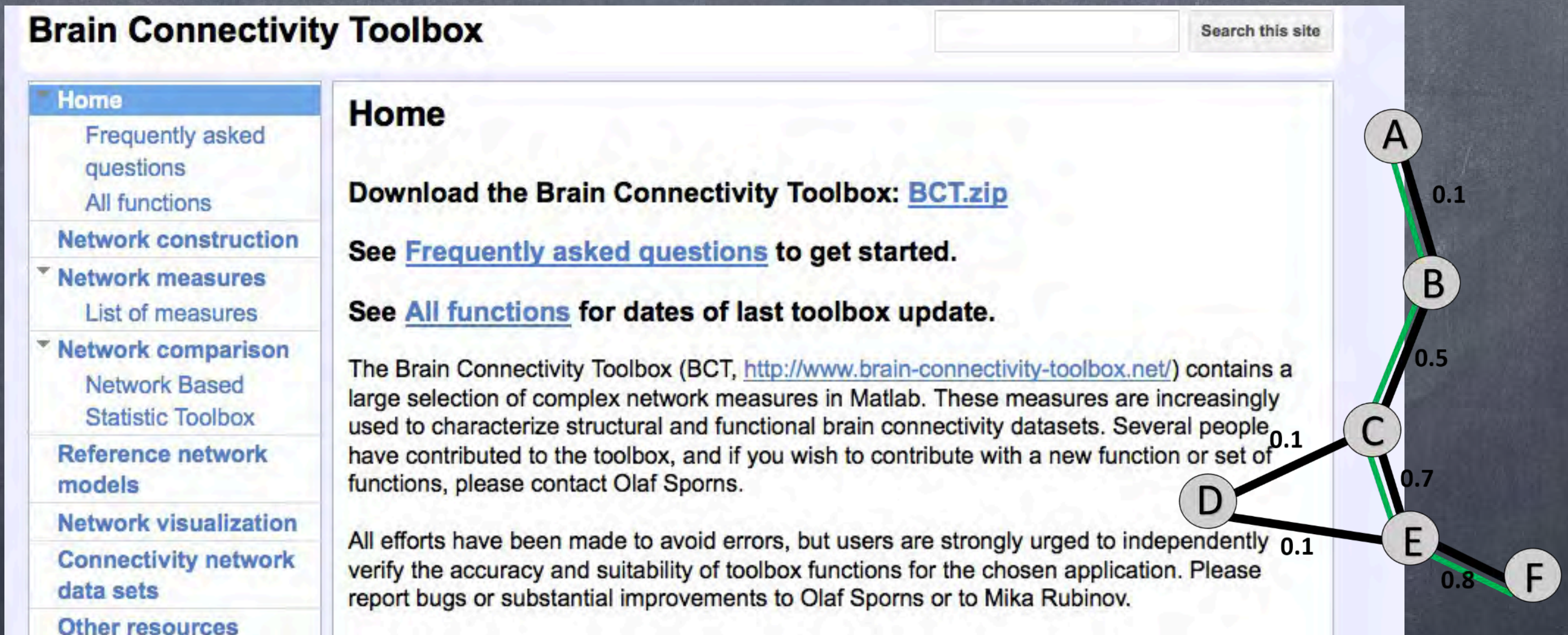
(making sense on network measurements, what they represent,  
and what the assumptions are when using them)

Information theoretical approaches to brain connectivity  
(making sense on network measurements, what they represent,  
and what the assumptions are when using them)

The image shows a screenshot of the Brain Connectivity Toolbox website. At the top left is the title "Brain Connectivity Toolbox". To its right is a search bar with the text "Search this site". Below the title is a navigation menu with the following items: "Home", "Frequently asked questions", "All functions", "Network construction", "Network measures" (with a dropdown arrow), "List of measures", "Network comparison" (with a dropdown arrow), "Network Based Statistic Toolbox", "Reference network models", "Network visualization", "Connectivity network data sets", and "Other resources". The main content area is titled "Home" and contains the following text: "Download the Brain Connectivity Toolbox: [BCT.zip](#)", "See [Frequently asked questions](#) to get started.", and "See [All functions](#) for dates of last toolbox update." Below this is a paragraph: "The Brain Connectivity Toolbox (BCT, <http://www.brain-connectivity-toolbox.net/>) contains a large selection of complex network measures in Matlab. These measures are increasingly used to characterize structural and functional brain connectivity datasets. Several people have contributed to the toolbox, and if you wish to contribute with a new function or set of functions, please contact Olaf Sporns." At the bottom is another paragraph: "All efforts have been made to avoid errors, but users are strongly urged to independently verify the accuracy and suitability of toolbox functions for the chosen application. Please report bugs or substantial improvements to Olaf Sporns or to Mika Rubinov."

# Information theoretical approaches to brain connectivity

(making sense on network measurements, what they represent, and what the assumptions are when using them)



The image shows a screenshot of the Brain Connectivity Toolbox website. The page title is "Brain Connectivity Toolbox". On the left, there is a navigation menu with the following items: Home, Frequently asked questions, All functions, Network construction, Network measures (List of measures), Network comparison (Network Based Statistic Toolbox), Reference network models, Network visualization, Connectivity network data sets, and Other resources. The main content area is titled "Home" and contains the following text:

**Download the Brain Connectivity Toolbox: [BCT.zip](#)**

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All efforts have been made to avoid errors, but users are strongly urged to independently verify the accuracy and suitability of toolbox functions for the chosen application. Please report bugs or substantial improvements to Olaf Sporns or to Mika Rubinov.

Overlaid on the right side of the screenshot is a network diagram with six nodes labeled A, B, C, D, E, and F. The nodes are arranged in a roughly vertical line from top to bottom. Node A is at the top, followed by B, C, D, E, and F at the bottom. The nodes are connected by edges with the following weights: A-B (0.1), B-C (0.5), C-D (0.1), C-E (0.7), D-E (0.1), and E-F (0.8). The edges between A-B, B-C, and E-F are highlighted in green.

## Shortest-paths vs random-walks : routing vs exploration

will be studied further elsewhere [14]. The random walk is also interesting since it could be a mechanism of transport and search on networks [15, 16, 17]. Those processes would be optimal if one follows the shortest path between two nodes under considerations. Among all paths connecting two nodes, the shortest path is given by the one with the smallest number of links [18]. However the shortest path can be found only after global connectivity is known at each node, which is improbable in practice.

J.D Noh and H.D. Rieger. Physical Review Letters 2004

# Shortest-paths vs random-walks : routing vs exploration

## Routing requires knowledge ...

will be studied further elsewhere [14]. The random walk is also interesting since it could be a mechanism of transport and search on networks [15, 16, 17]. Those processes would be optimal if one follows the shortest path between two nodes under considerations. Among all paths connecting two nodes, the shortest path is given by the one with the smallest number of links [18]. However the shortest path can be found only after global connectivity is known at each node, which is improbable in practice.

J.D Noh and H.D. Rieger. Physical Review Letters 2004

... but topologies may favor communication without such knowledge

# Navigability of complex networks

Marián Boguñá<sup>1\*</sup>, Dmitri Krioukov<sup>2</sup> and K. C. Claffy<sup>2</sup>

**Routing information through networks is a universal phenomenon in both natural and man-made complex systems. When each node has full knowledge of the global network connectivity, finding short communication paths is merely a matter of distributed computation. However, in many real networks, nodes communicate efficiently even without such global intelligence. Here, we show that the peculiar structural characteristics of many complex networks support efficient communication without global knowledge. We also describe a general mechanism that explains this connection between network structure and function.**

M. Boguñá et al. Nature Physics 2009



Get directions

My places

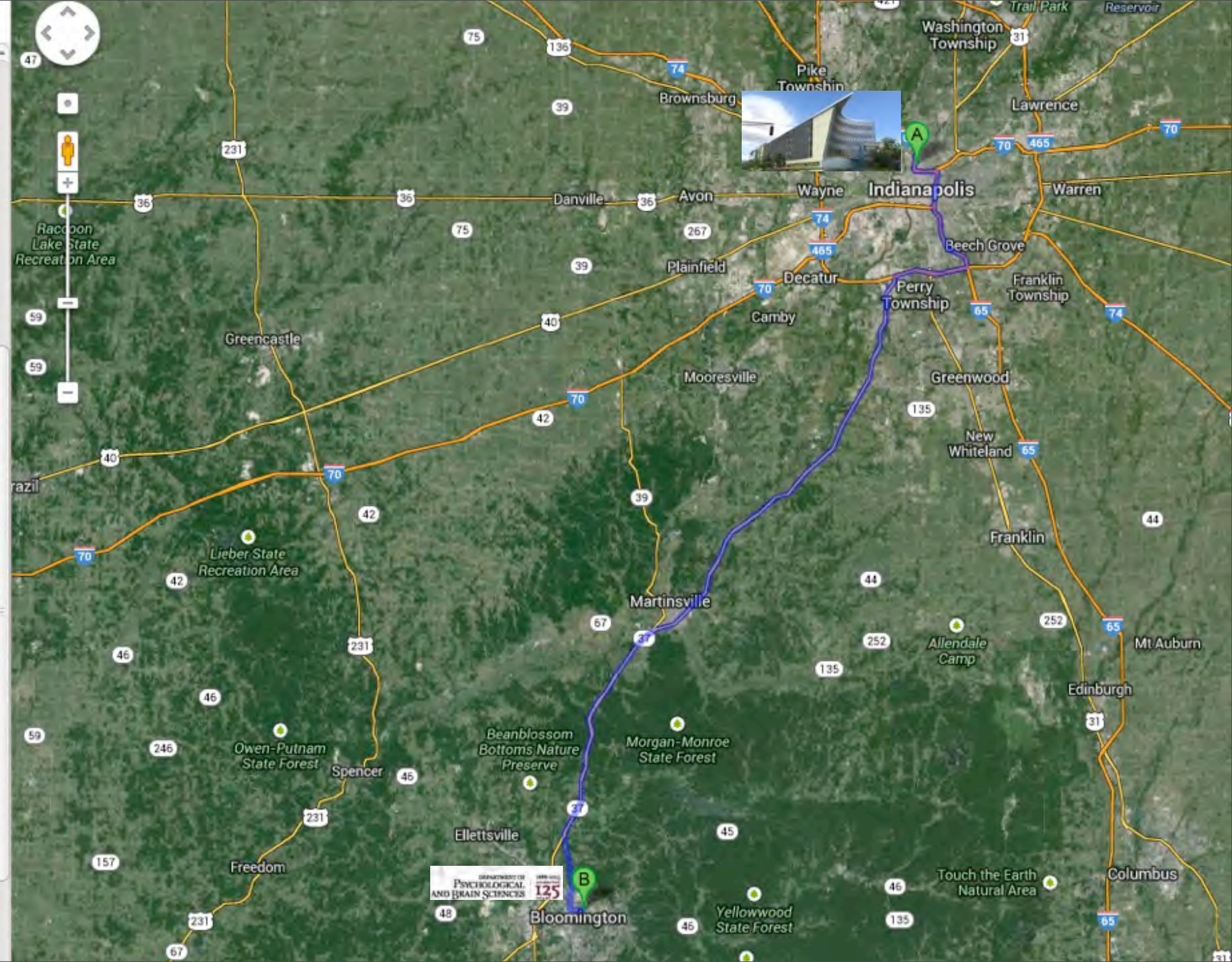


**355 W 16th St**  
Indianapolis, IN 46202

- 1. Head **west** on **W 16th St** toward **Senate Blvd**  
318 ft
- ➔ 2. Take the 1st right onto **Senate Blvd**  
0.5 mi
- ➔ 3. Turn left onto **W 21st St**  
0.1 mi
- ➔ 4. Take the ramp onto **I-65 S**  
4.3 mi
- ➔ 5. Keep left to stay on **I-65 S**  
4.2 mi
- ➔ 6. Take exit **106** for **I-465 E/I-74 E/I-465 W/I-74 W**  
0.1 mi
- ➔ 7. Keep right at the fork, follow signs for **Interstate 465 W/Interstate 74 W** and merge onto **I-465 W/I-74**  
4.1 mi
- ➔ 8. Take exit **4** for **Indiana 37 S/Harding St**  
0.2 mi
- ➔ 9. Turn left onto **IN-37 S/S Harding St**  
Continue to follow IN-37 S  
39.0 mi
- ➔ 10. Take the **Walnut St N** exit toward **College Ave**  
0.5 mi
- ➔ 11. Merge onto **N State Road 37 Business/N Walnut St**  
Continue to follow N Walnut St  
3.2 mi
- ➔ 12. Continue onto **N College Ave**  
1.0 mi
- ➔ 13. Turn left onto **W 10th St**  
Destination will be on the left  
0.8 mi



**1101 E 10th St**



Get directions

My places



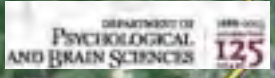
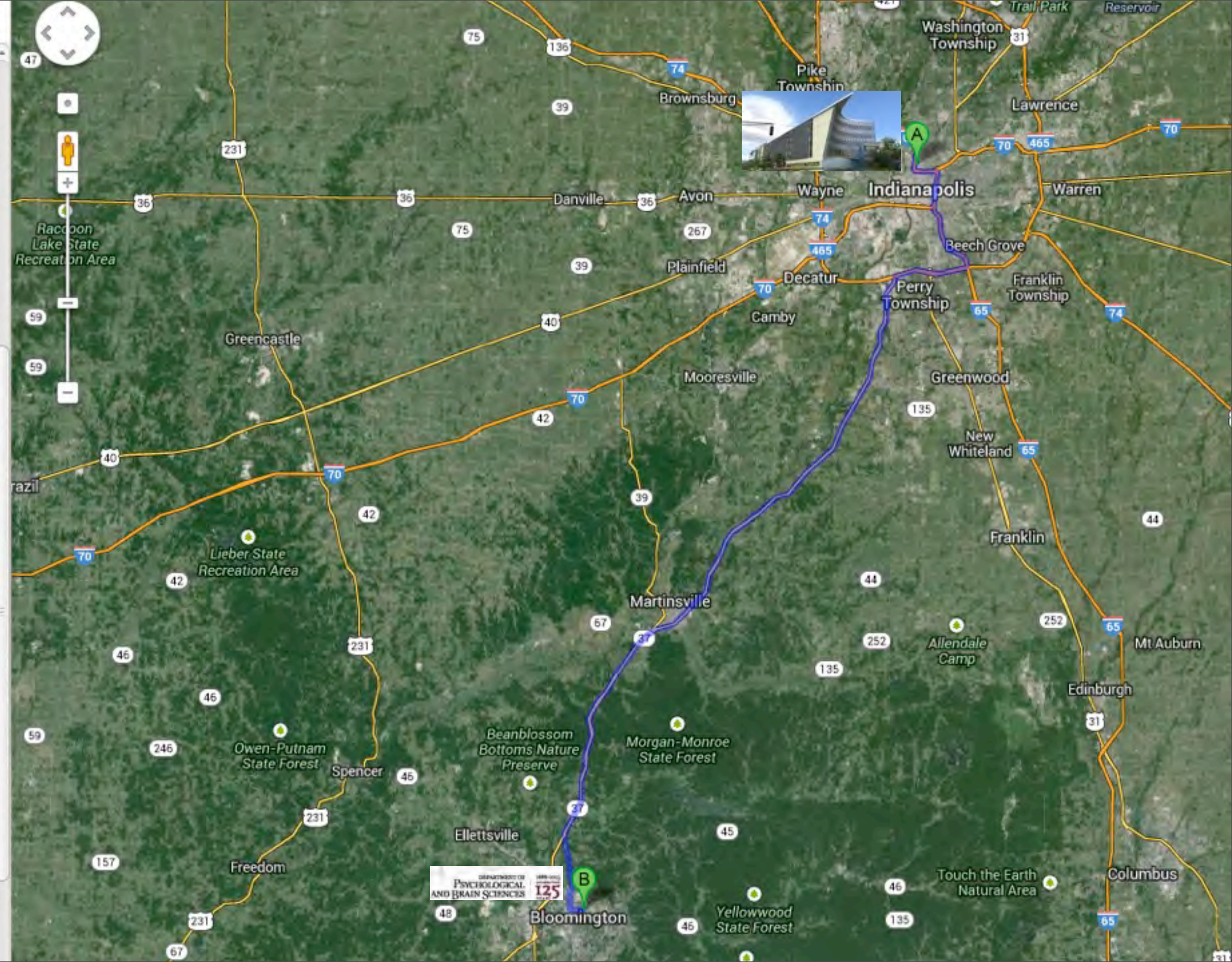
355 W 16th St  
Indianapolis, IN 46202

1. Head west on W 16th St toward Senate Blvd
2. Take the 1st right onto Senate Blvd
3. Turn left onto W 21st St
4. Take the ramp onto I-65 S
5. Keep left to stay on I-65 S
6. Take exit 106 for I-465 E/I-74 E/I-465 W/I-74 W
7. Keep right at the fork, follow signs for Interstate 465 W/Interstate 74 W and merge onto I-465 W/I-74
8. Take exit 4 for Indiana 37 S/Harding St
9. Turn left onto IN-37 S/S Harding St  
Continue to follow IN-37 S
10. Take the Walnut St N exit toward College Ave
11. Merge onto N State Road 37 Business/N Walnut St  
Continue to follow N Walnut St
12. Continue onto N College Ave

58 mi, 13 decisions



1101 E 10th St





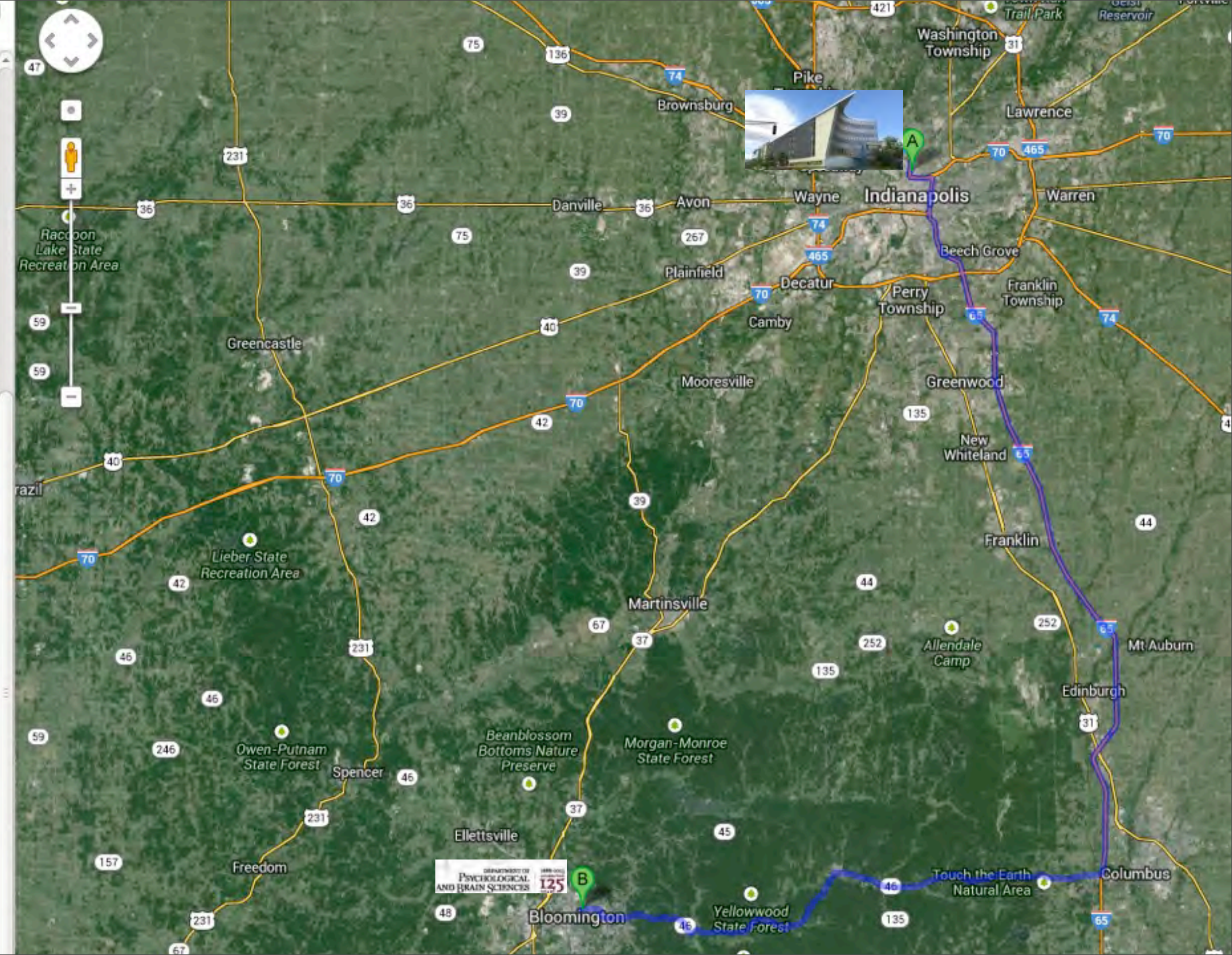
**A** 355 W 16th St  
Indianapolis, IN 46202

- 1. Head west on W 16th St toward Senate Blvd 318 ft
- 2. Take the 1st right onto Senate Blvd 0.5 mi
- 3. Turn left onto W 21st St 0.1 mi
- 4. Take the ramp onto I-65 S 4.3 mi
- 5. Keep left to stay on I-65 S 42.0 mi
- 6. Take exit 68 for IN-46 toward Columbus/Nashville/Bloomington 0.3 mi
- 7. Turn right onto IN-46 W/Jonathan Moore Pike 15.9 mi  
Continue to follow IN-46 W
- 8. Turn left onto IN-46 W/Van Buren St 16.6 mi  
Continue to follow IN-46 W
- 9. Turn right to stay on IN-46 W 0.5 mi
- 10. Turn left onto E 10th St 1.0 mi  
Destination will be on the right

**B** 1101 E 10th St  
Bloomington, IN 47405

Save to My Maps

These directions are for planning purposes only. You may find that construction projects, traffic, weather, or other events may cause conditions to differ from the map results, and you should plan your route accordingly. You must obey all signs or notices regarding your route.



**A** 355 W 16th St  
Indianapolis, IN 46202

1. Head west on W 16th St toward Senate Blvd

318 ft

2. Take the 1st right onto Senate Blvd

0.5 mi

3. Turn left onto W 21st St

0.1 mi

4. Take the ramp onto I-65 S

4.3 mi

5. Keep left to stay on I-65 S

42.0 mi

6. Take exit 68 for IN-46 toward Columbus/  
Nashville/Bloomington

0.3 mi

7. Turn right onto IN-46 W/Jonathan Moore  
Pike  
Continue to follow IN-46 W

15.9 mi

8. Turn left onto IN-46 W/Van Buren St  
Continue to follow IN-46 W

16.6 mi

9. Turn right to stay on IN-46 W

0.5 mi

10. Turn left onto E 10th St  
Destination will be on the right

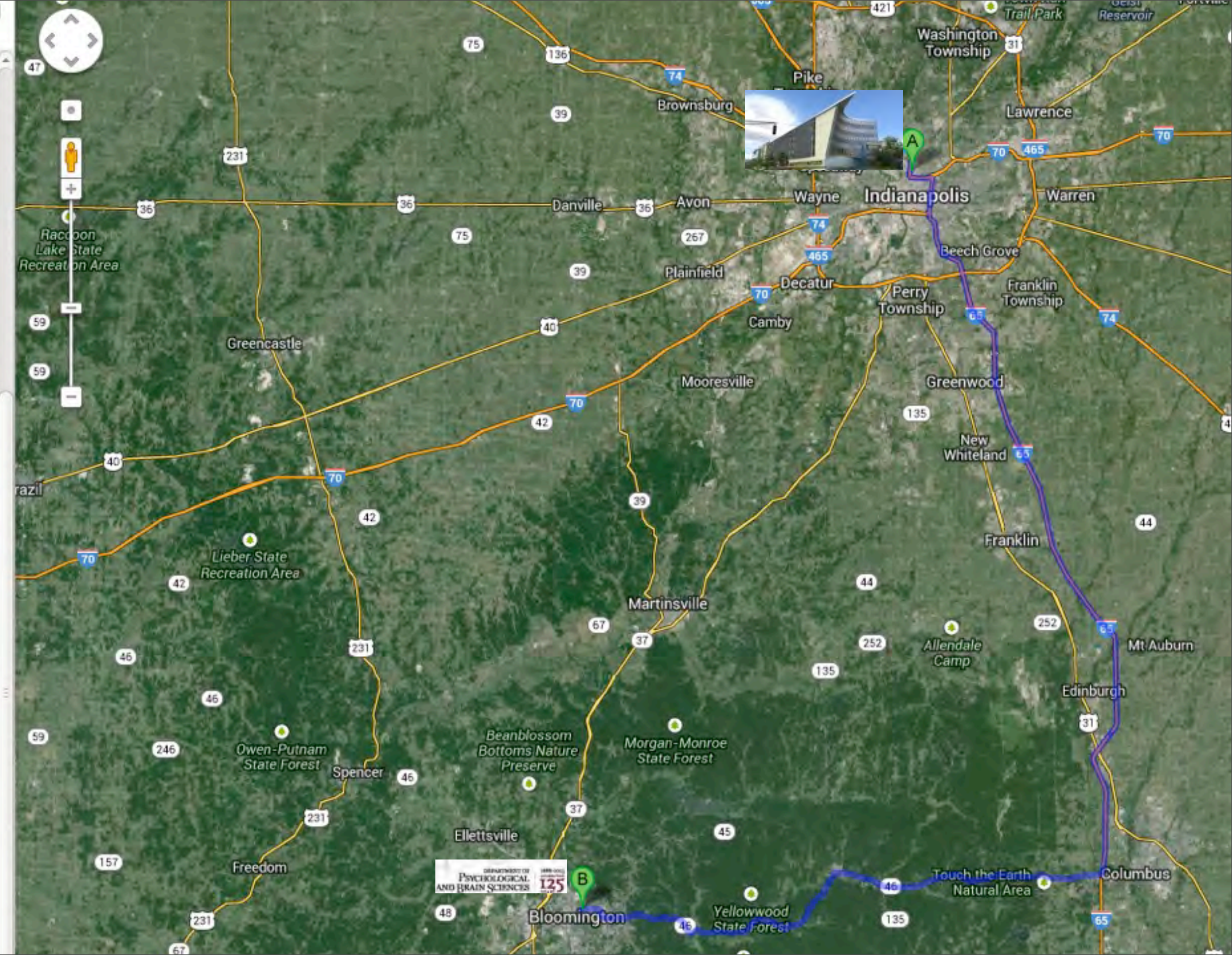
1.0 mi

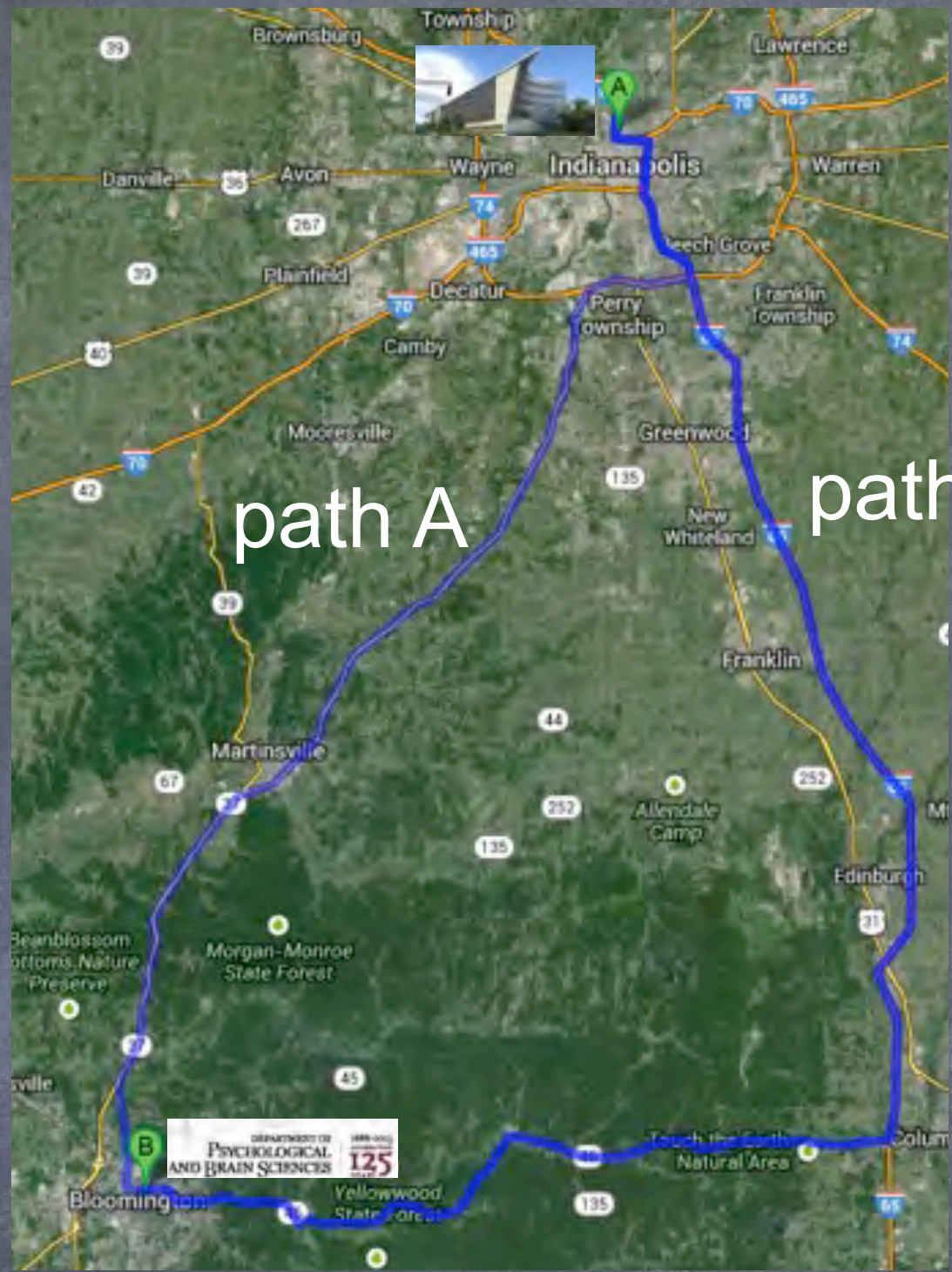
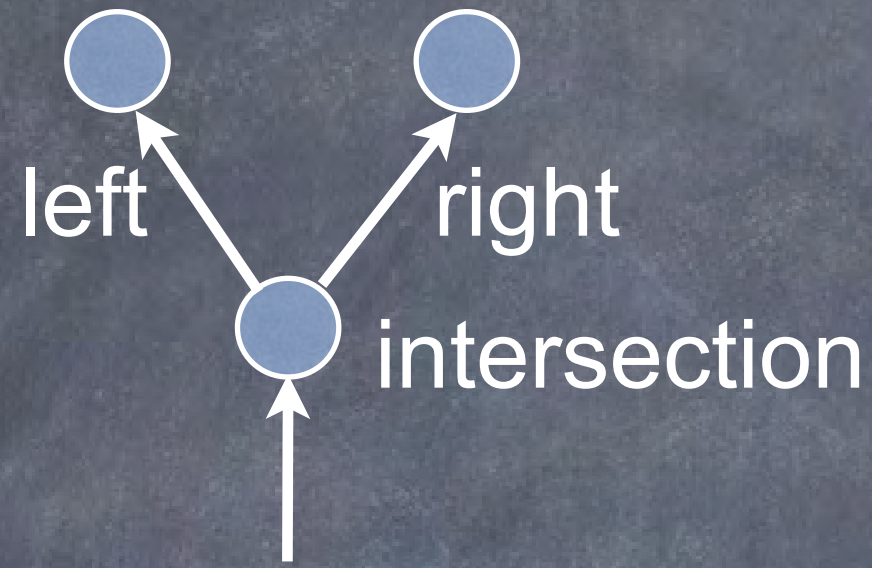
**B** 1101 E 10th St  
Bloomington, IN 47405

[Save to My Maps](#)

81mi, 10 decisions

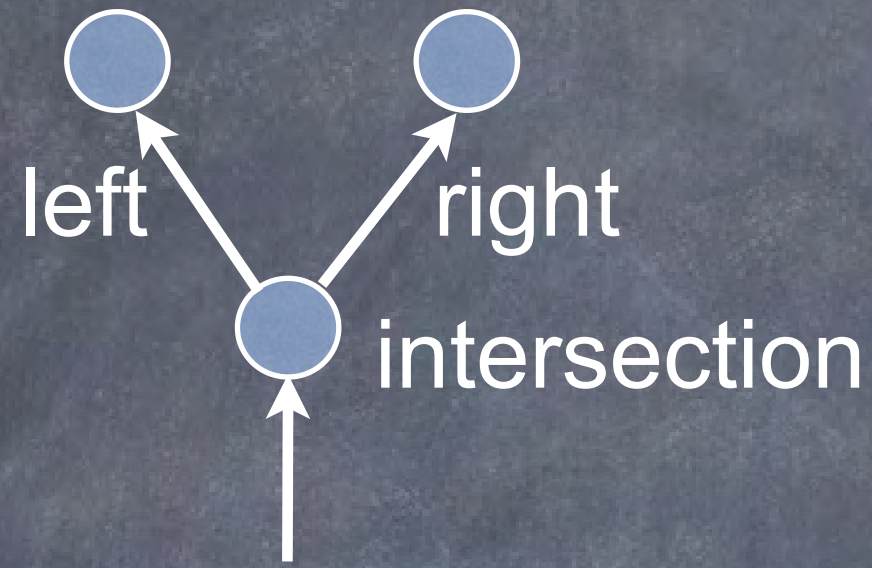
regarding your route.



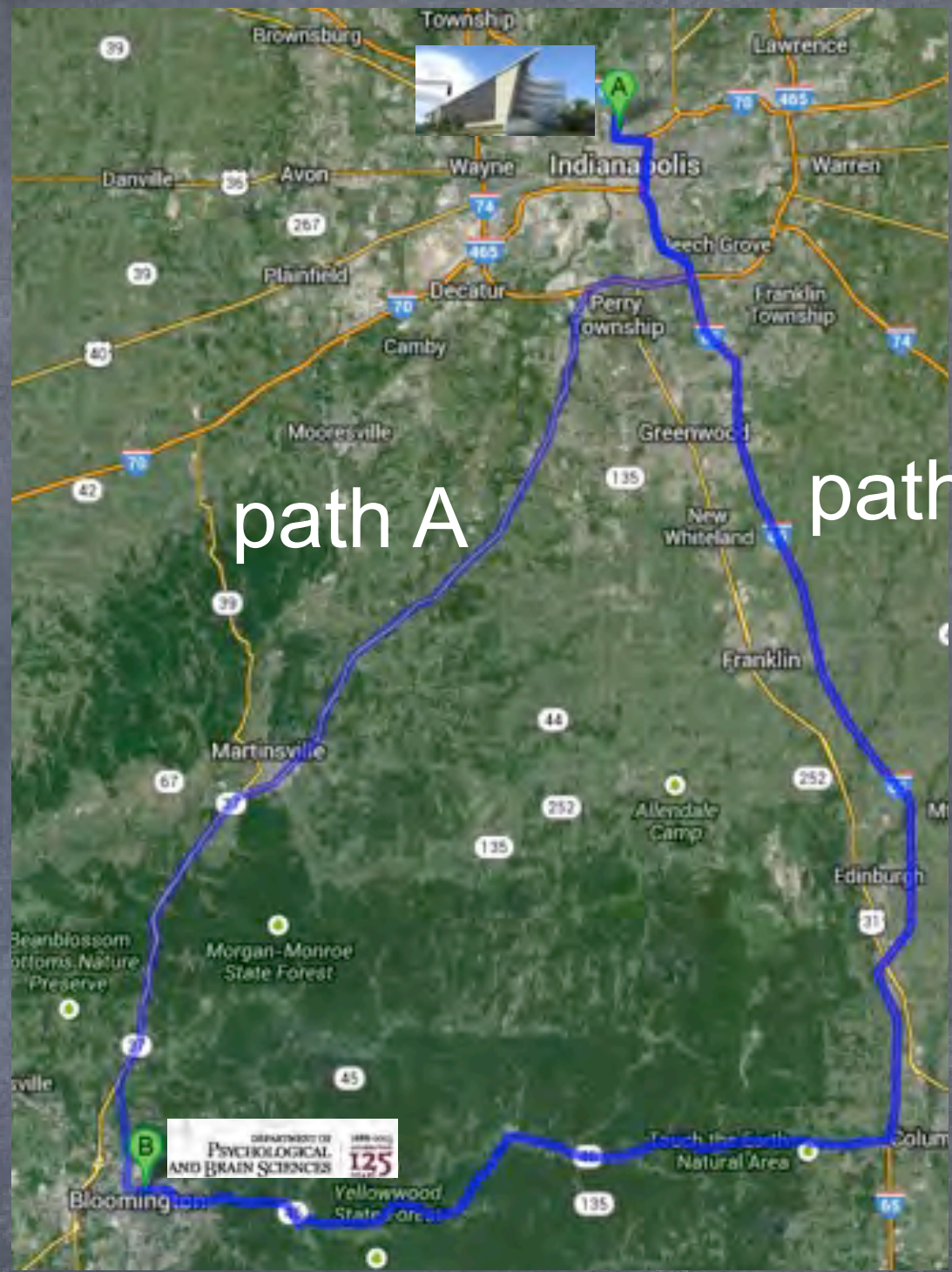


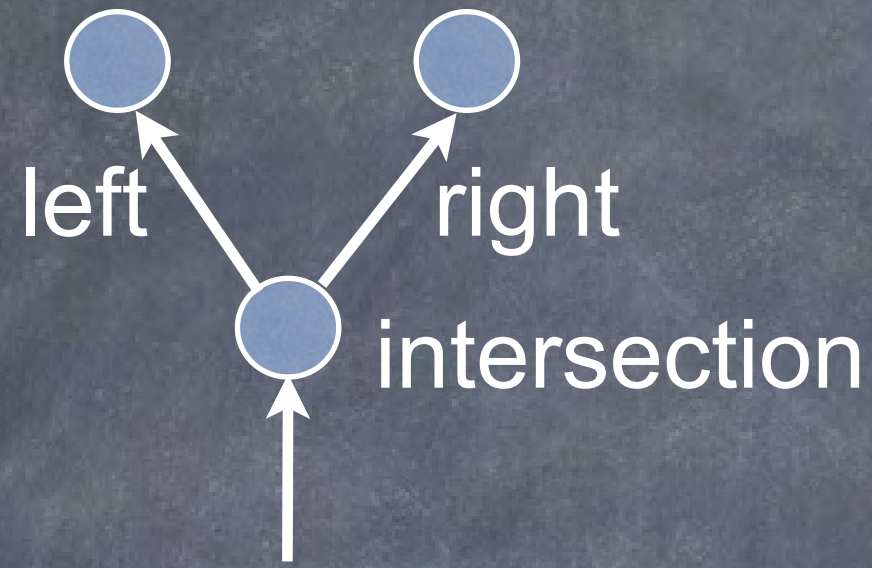
path A

path B



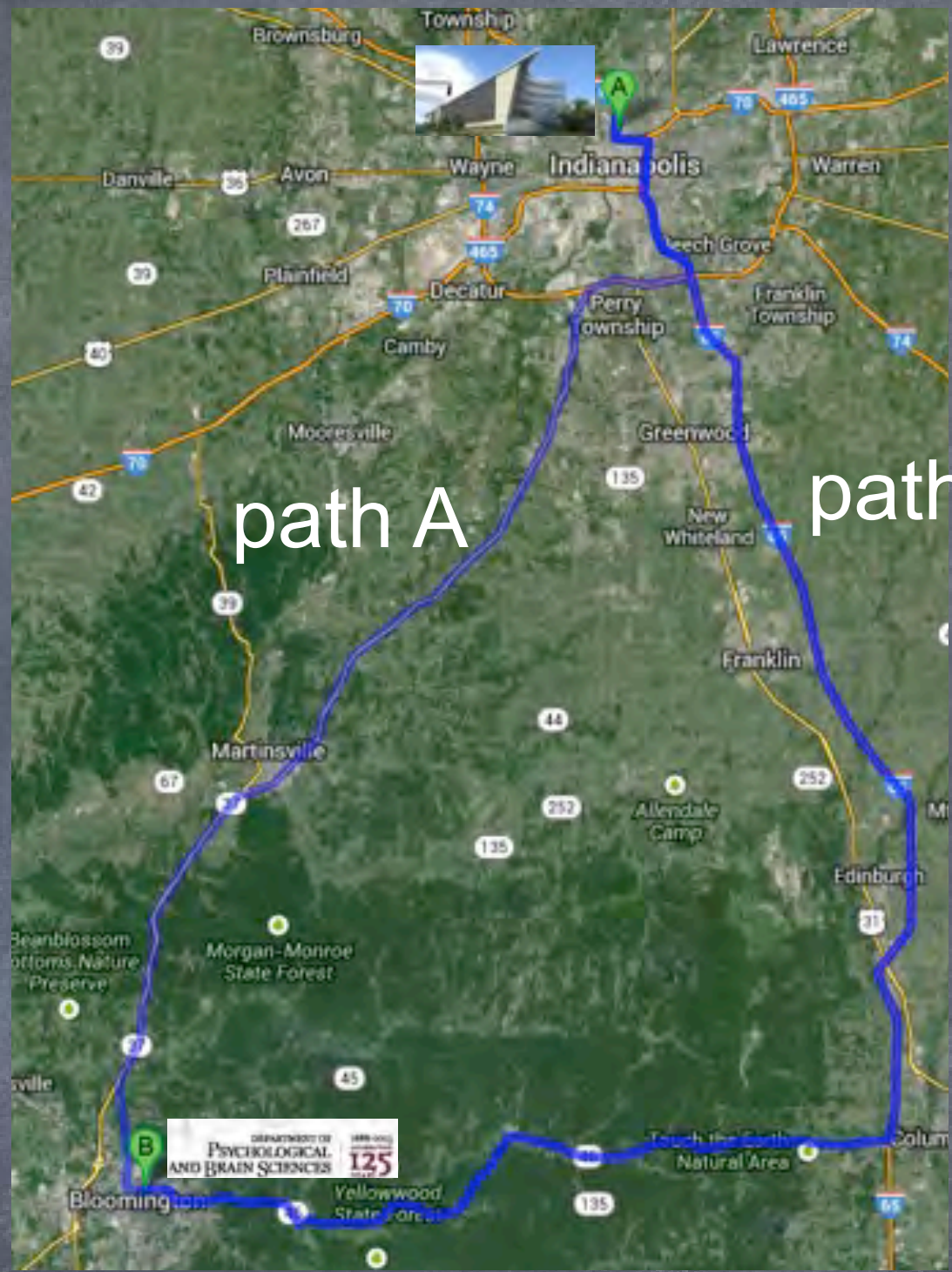
$p(\text{choice}) = .5$





$$p(\text{choice}) = .5$$

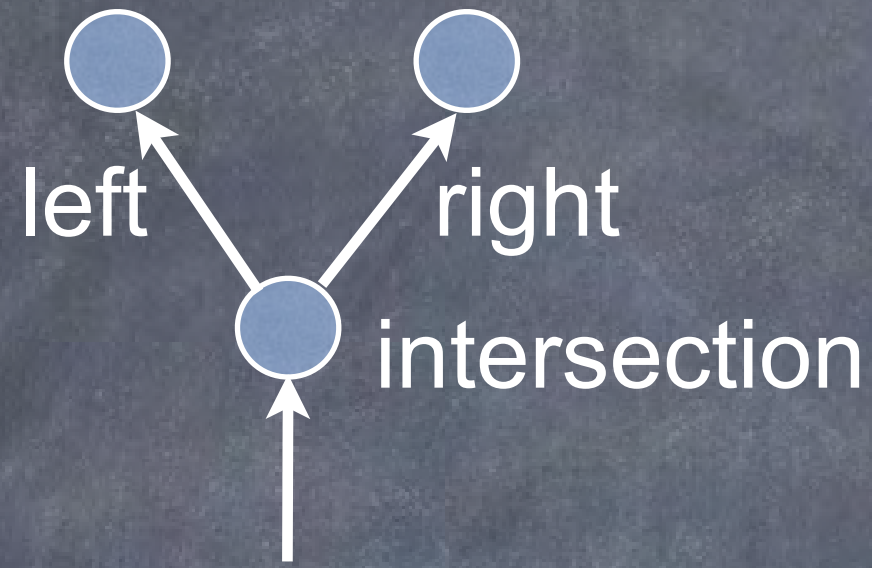
$$p(\text{path}) = (.5)^{\#d}$$



path A

path B

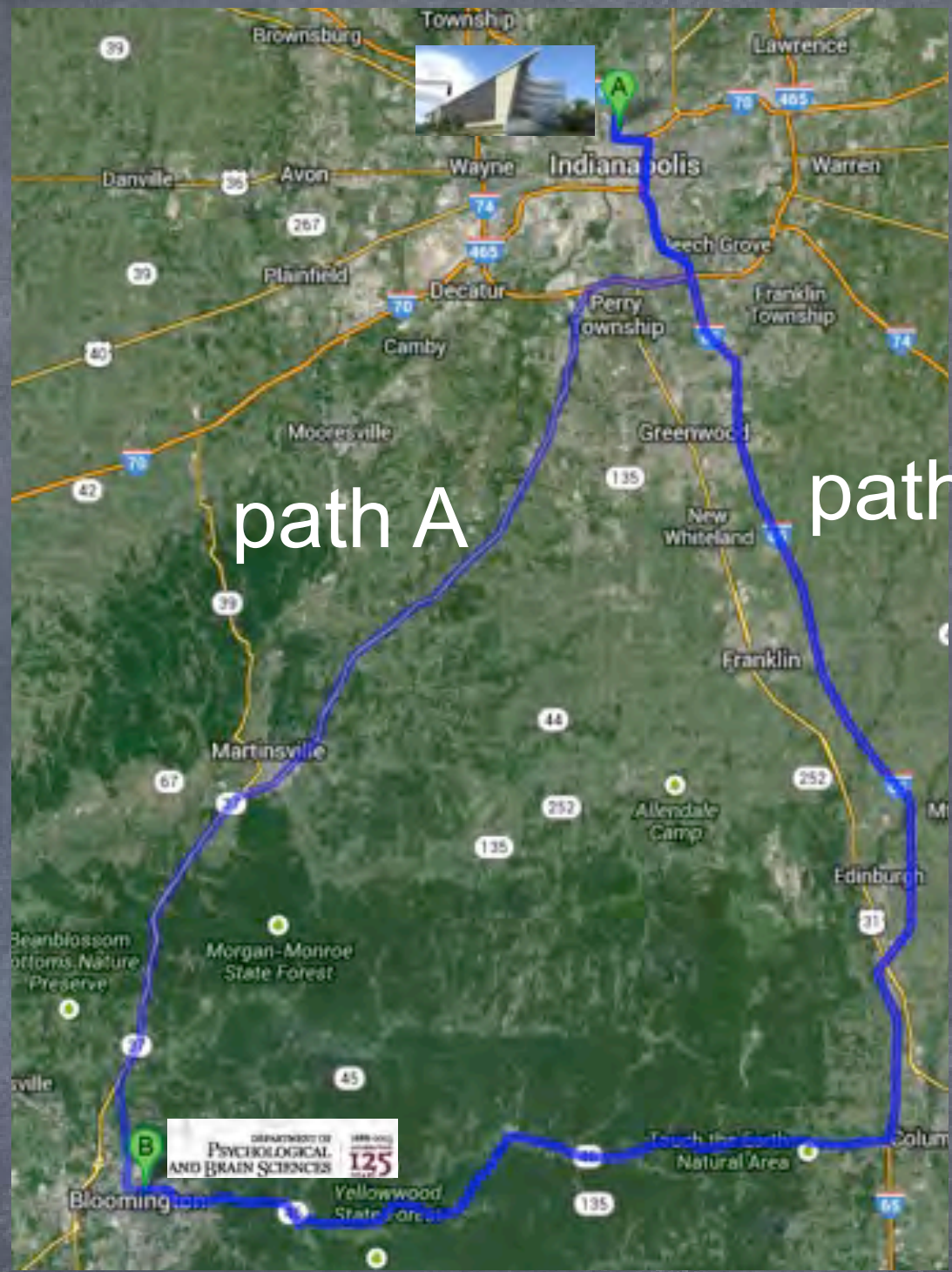
DEPARTMENT OF  
PSYCHOLOGICAL  
AND BRAIN SCIENCES  
135



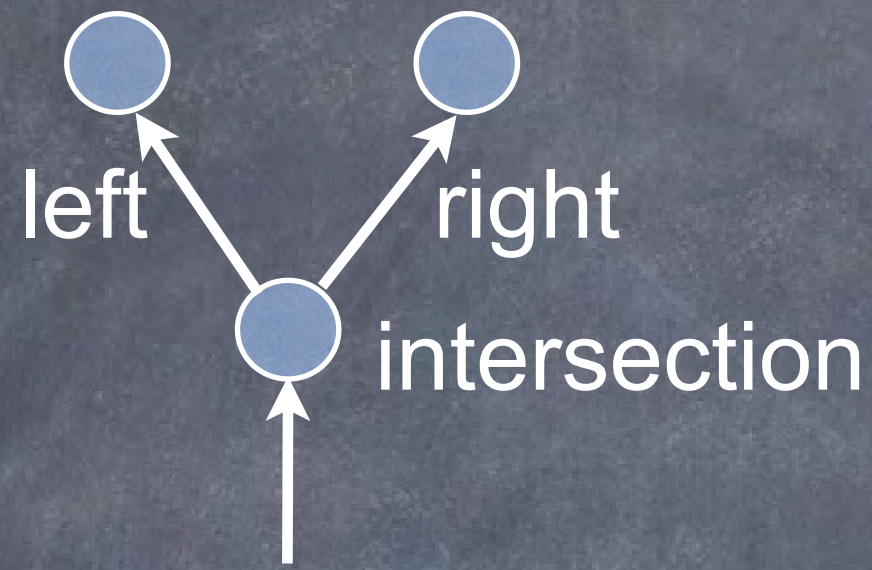
$$p(\text{choice}) = .5$$

$$p(\text{path}) = (.5)^{\#d}$$

search information:  $-\log(.5^{\#d})$



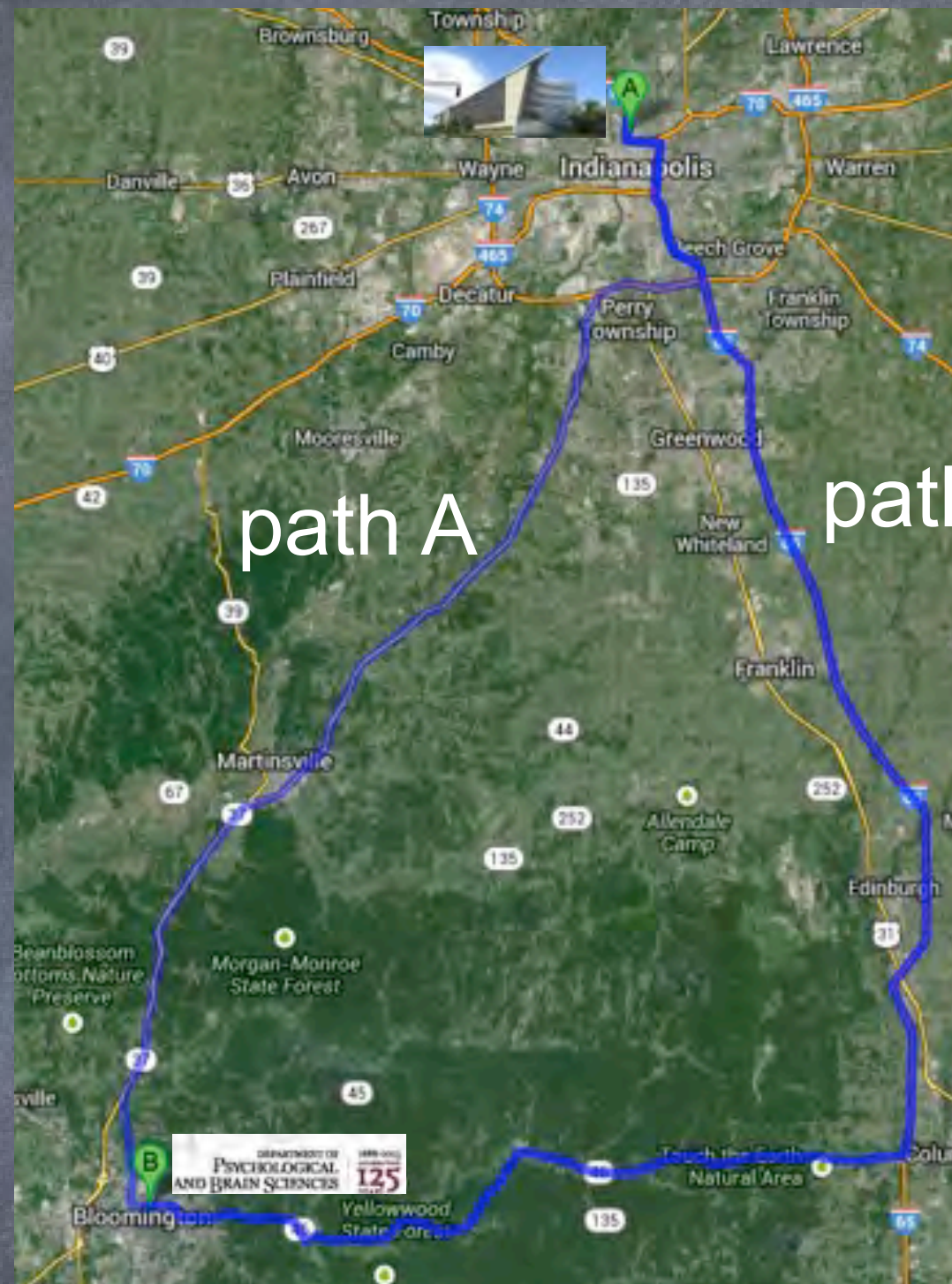




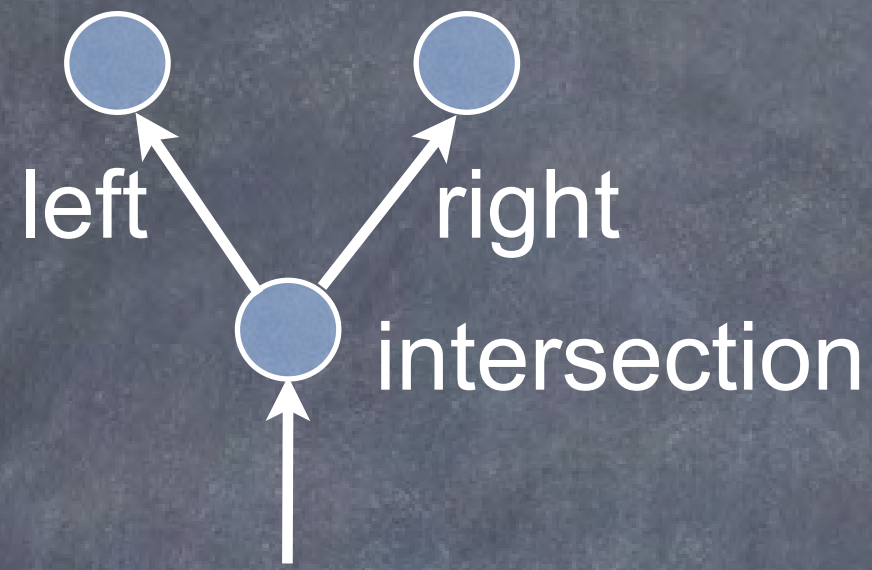
$$p(\text{choice}) = .5$$

$$p(\text{path}) = (.5)^{\#d}$$

search information:  $-\log(.5^{\#d})$



	length	#d	S
path A	58 mi	13	9.01 bits
path B	81 mi	10	6.93 bits

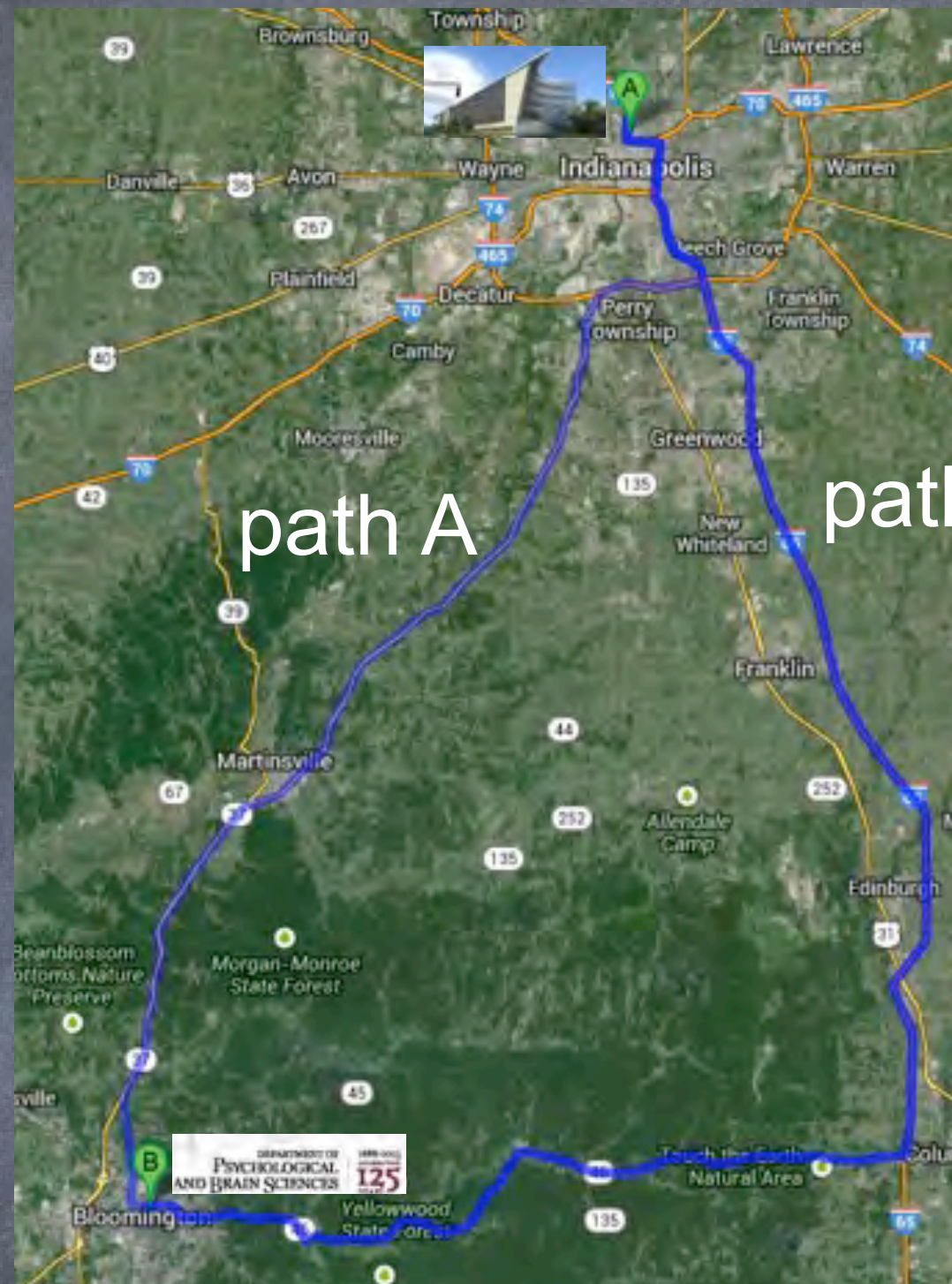


$$p(\text{choice}) = .5$$

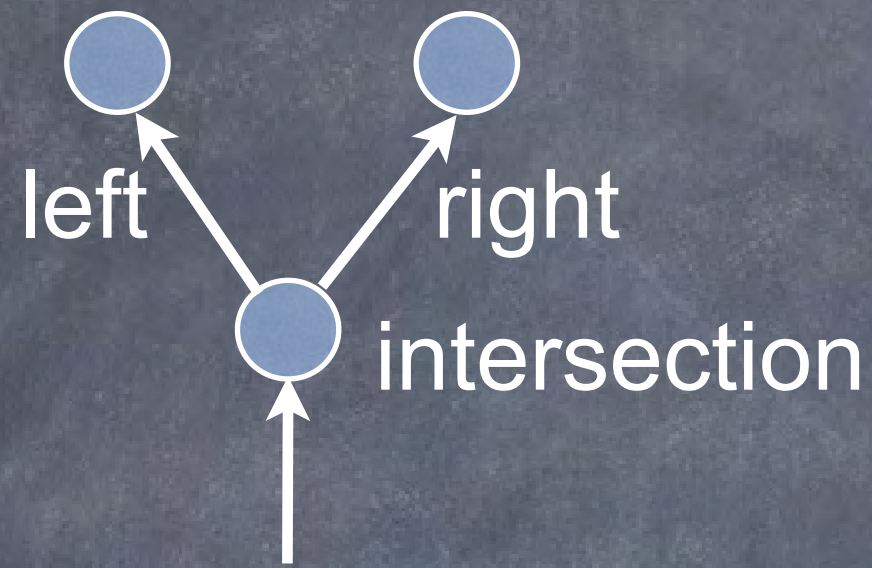
$$p(\text{path}) = (.5)^{\#d}$$

search information:  $-\log(.5^{\#d})$

	length	#d	S
path A	58 mi	13	9.01 bits
path B	81 mi	10	6.93 bits



path A is **shorter** than path B

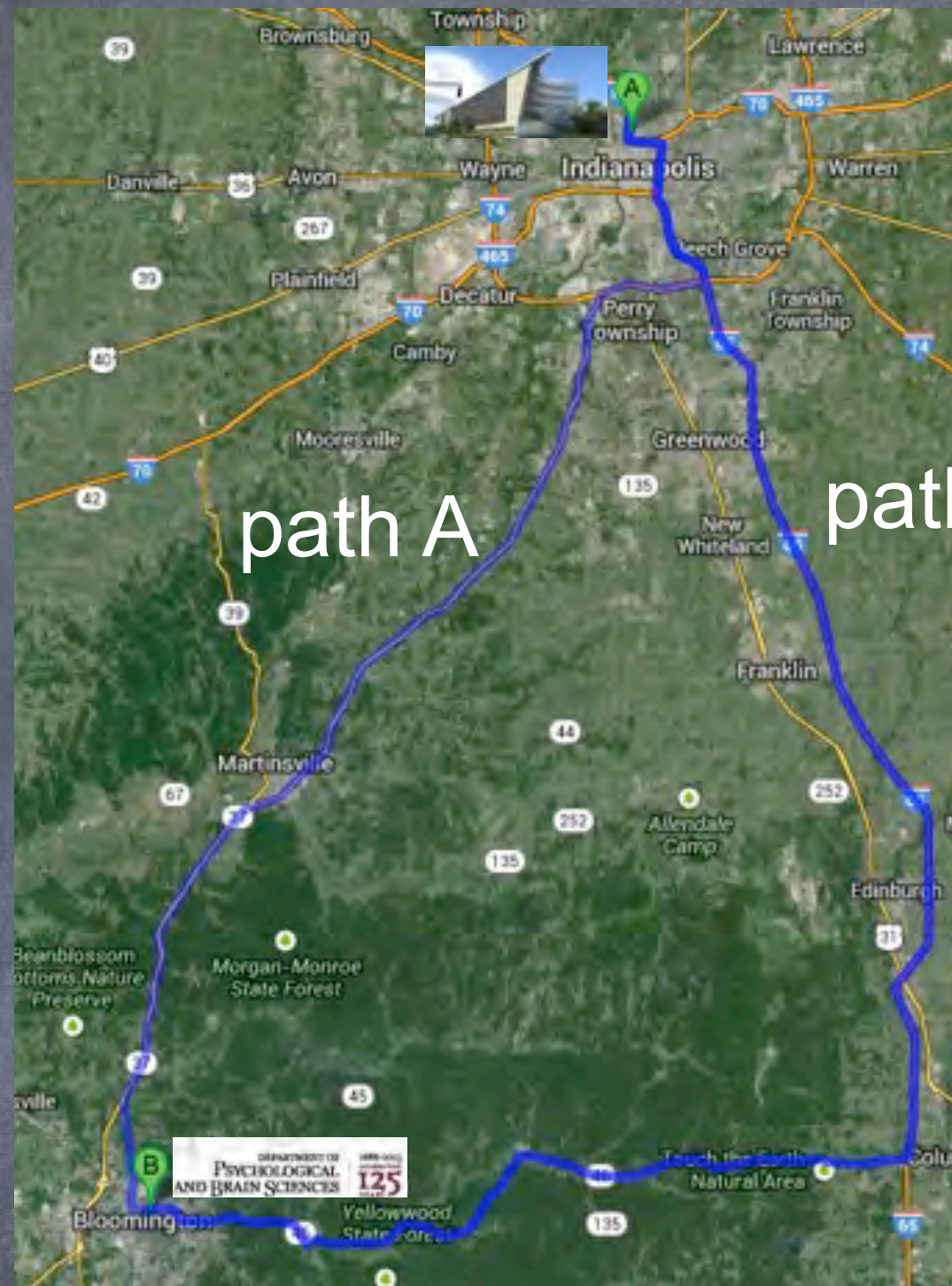


$$p(\text{choice}) = .5$$

$$p(\text{path}) = (.5)^{\#d}$$

search information:  $-\log(.5^{\#d})$

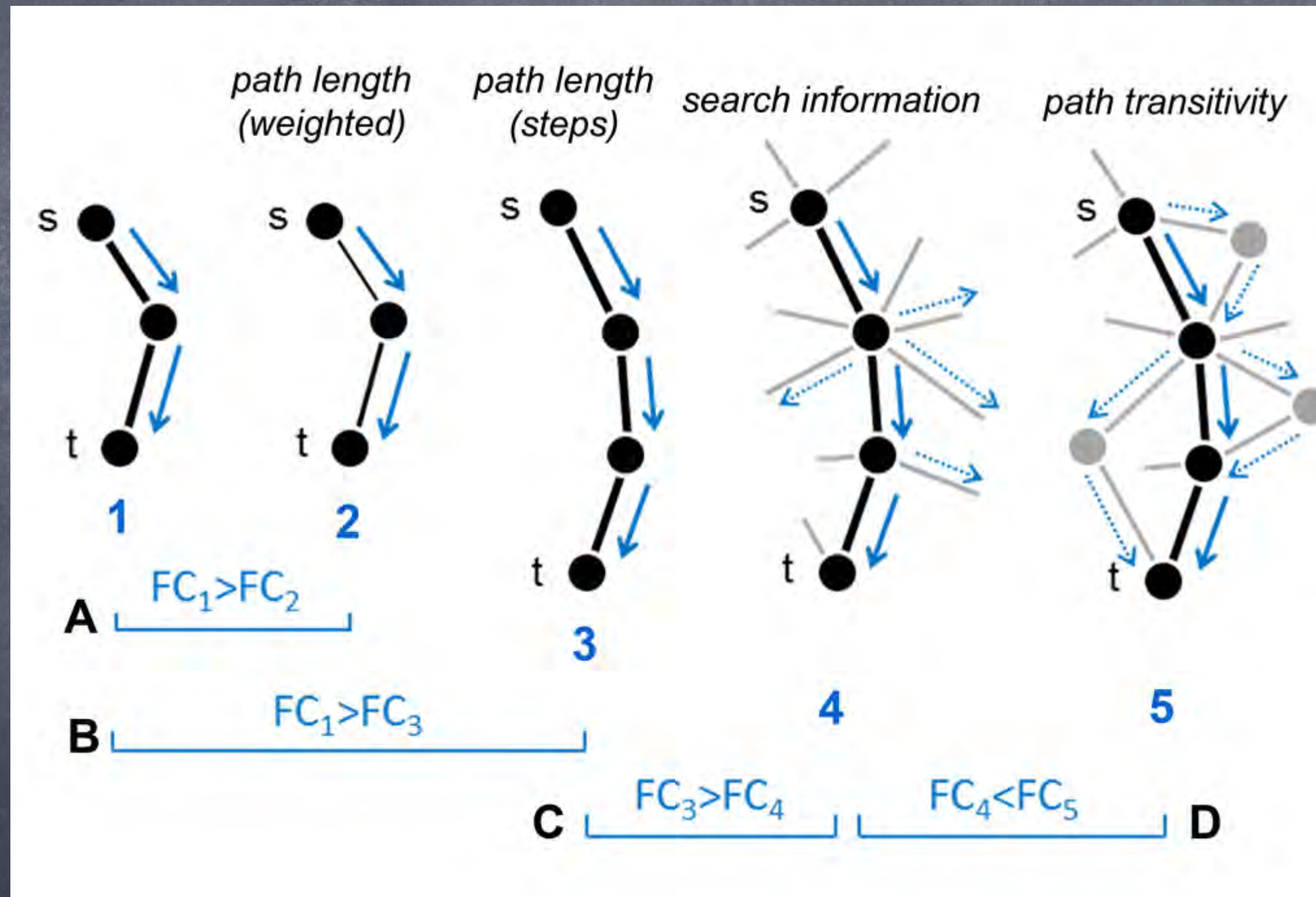
	length	#d	S
path A	58 mi	13	9.01 bits
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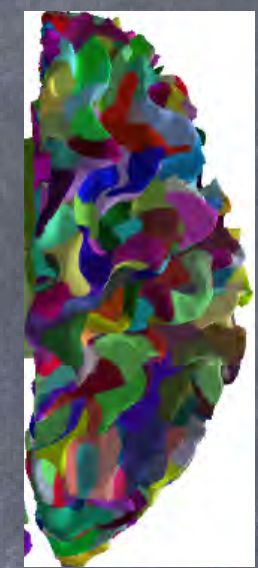
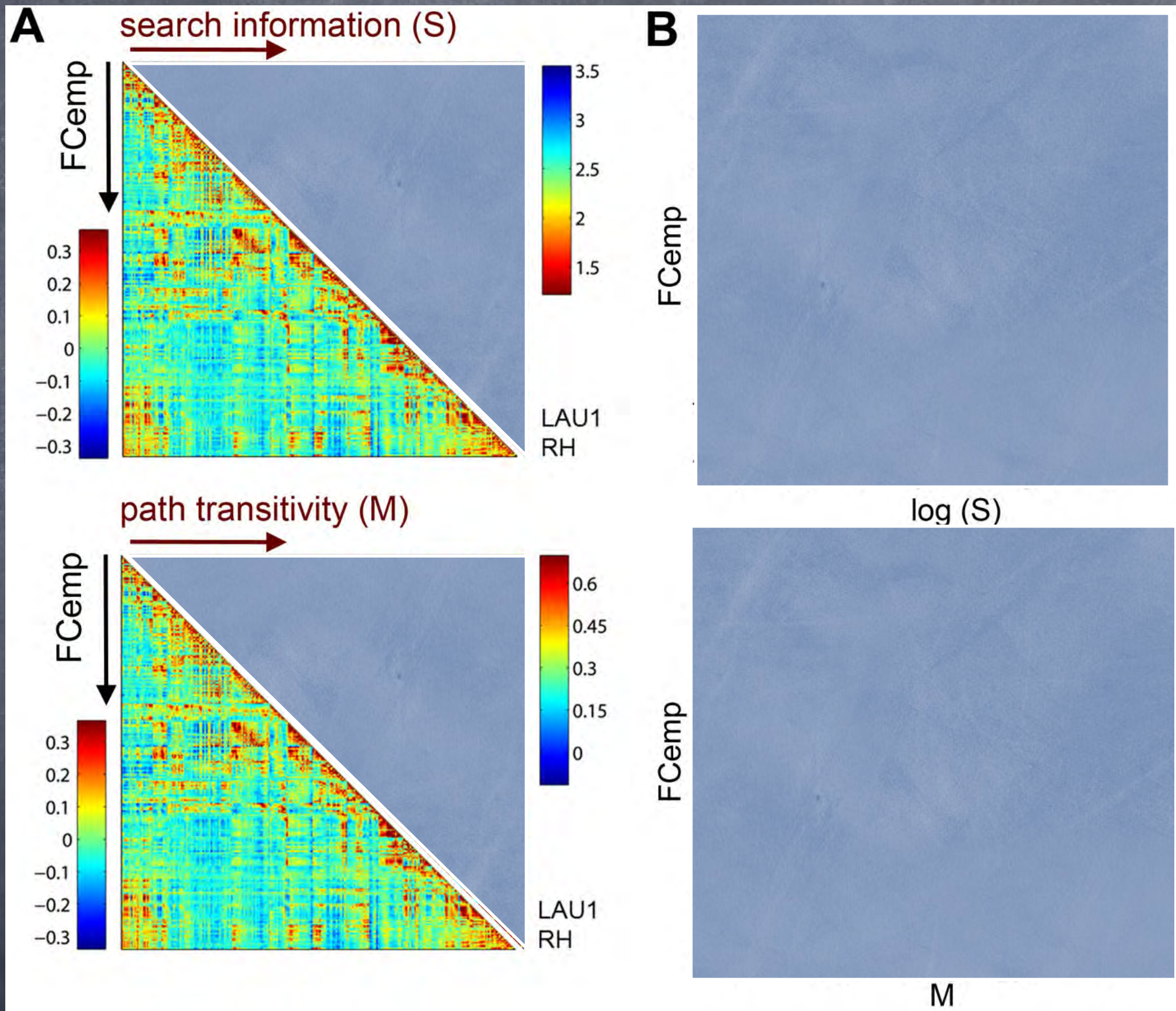


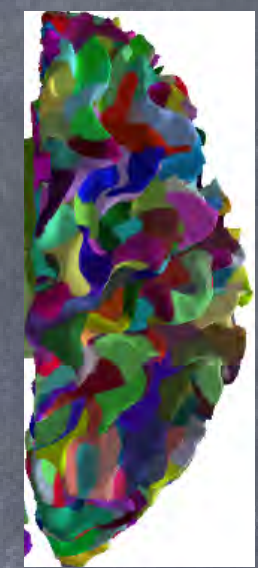
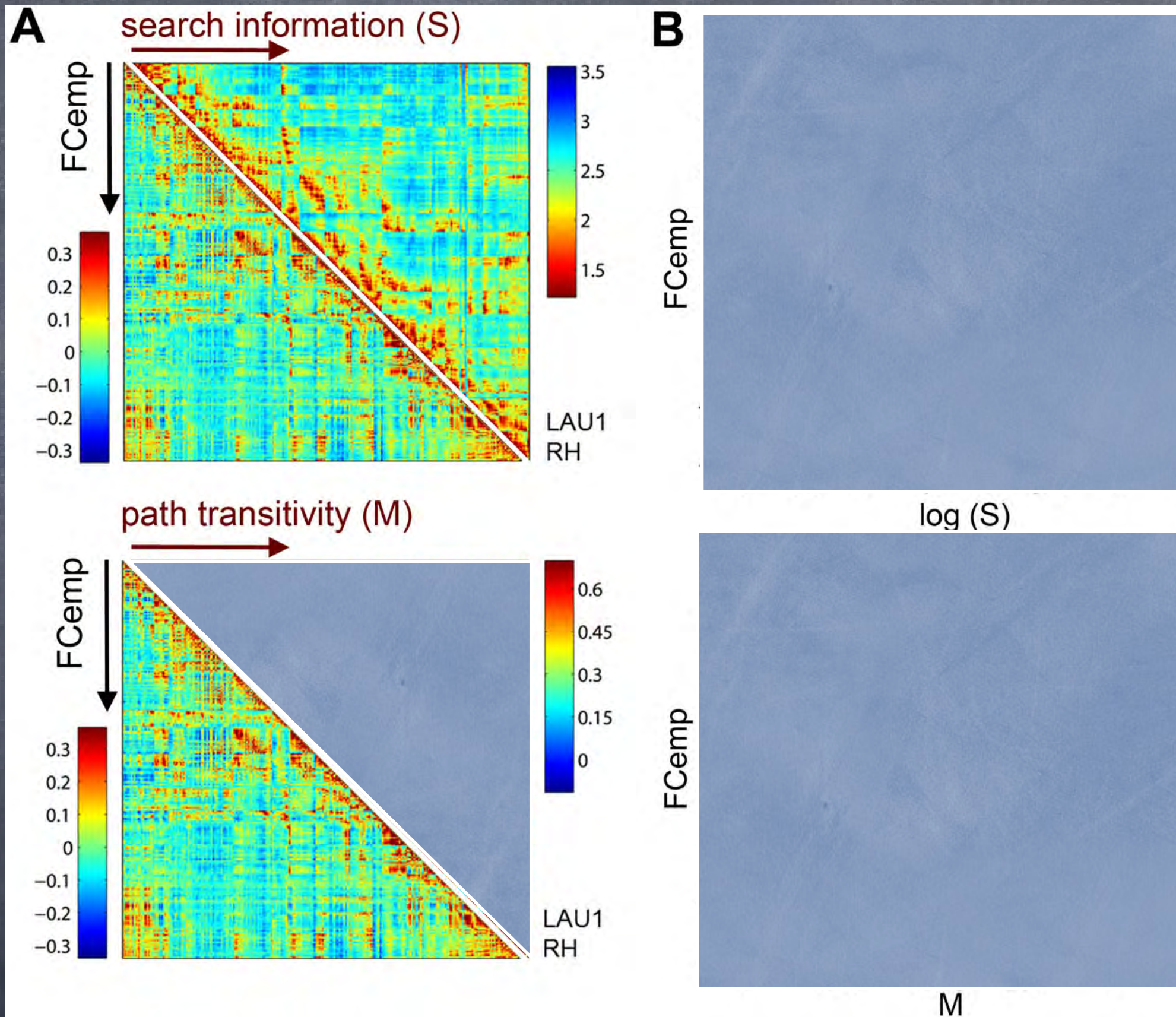
path A is **shorter** than path B  
 path A is more **hidden** than path B

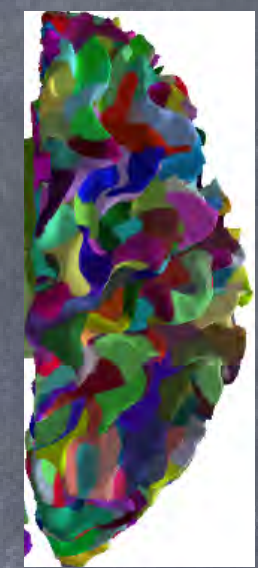
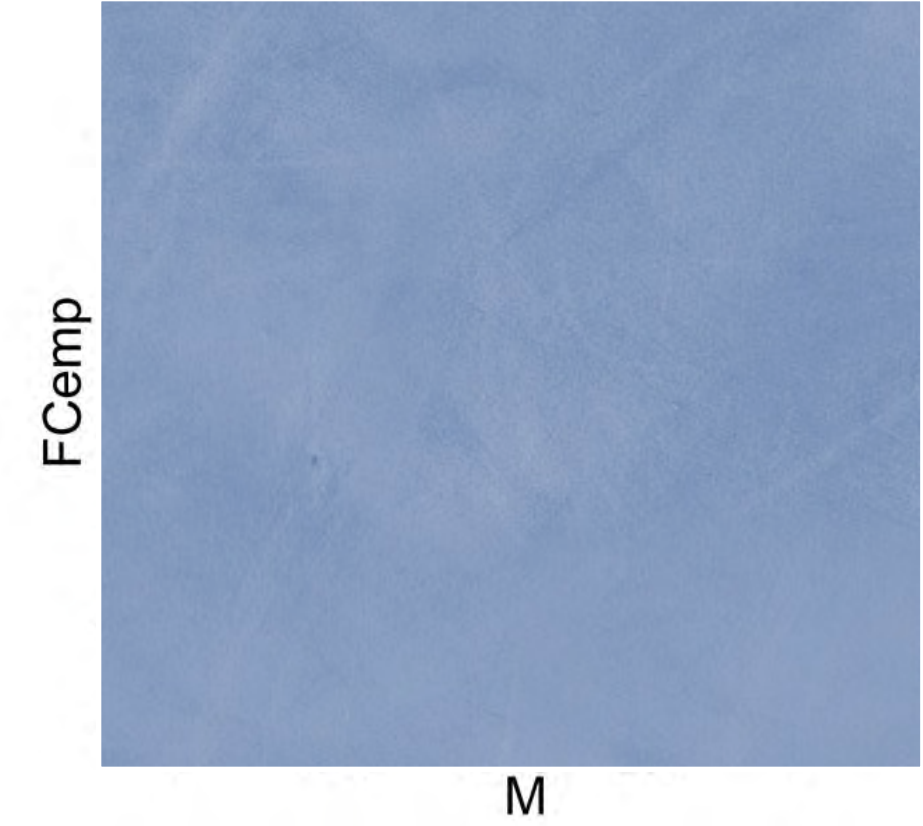
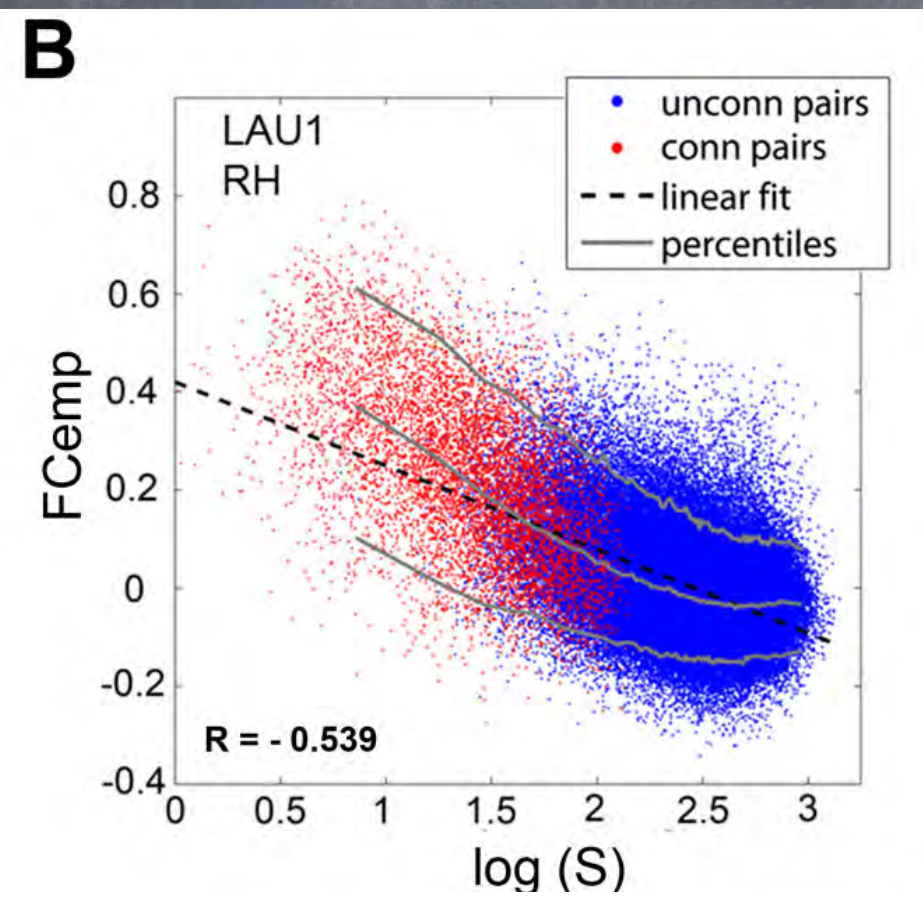
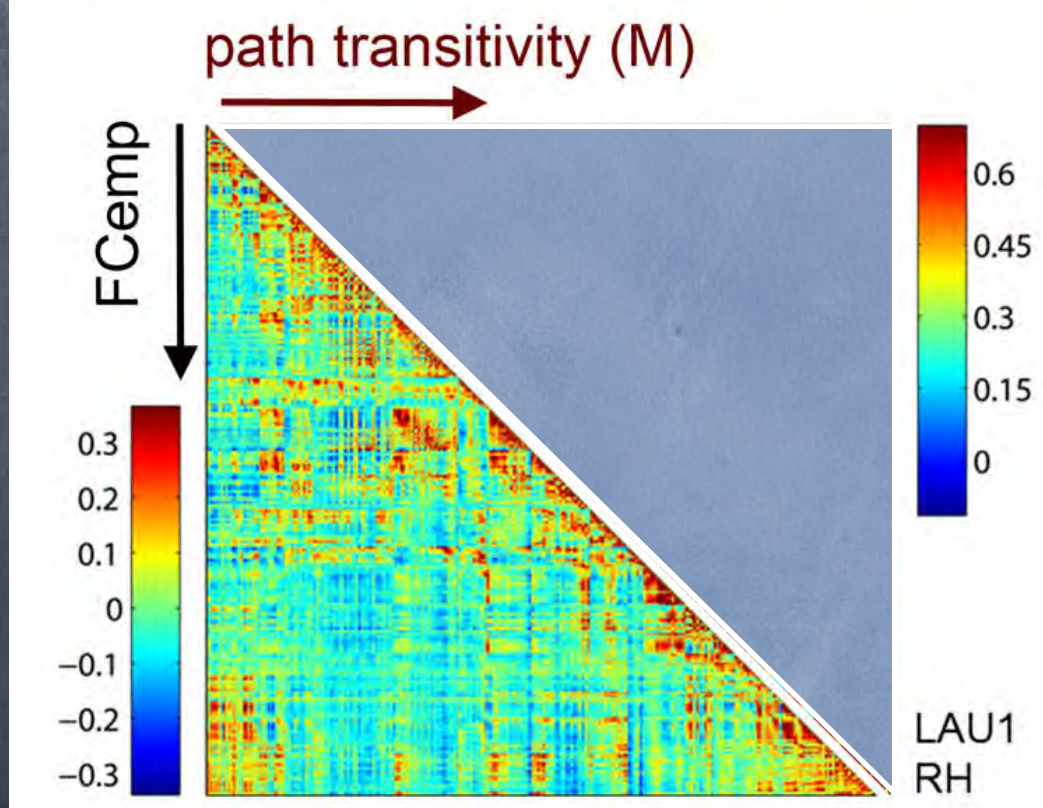
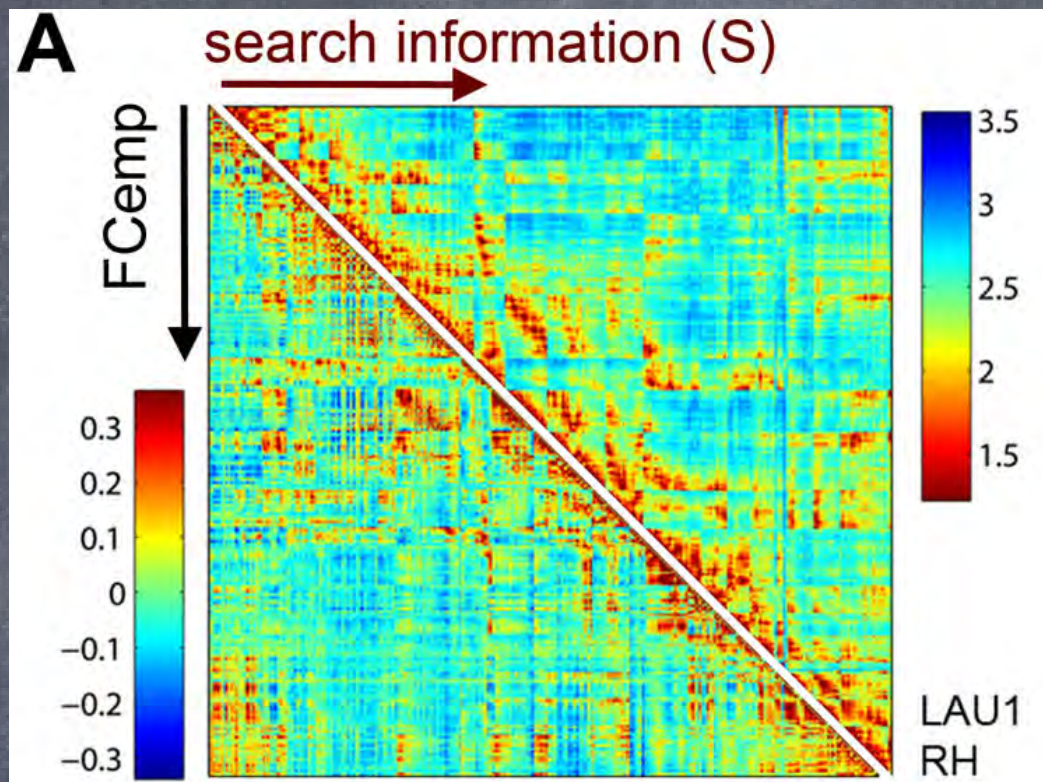
# Which hypotheses are we aiming to test?

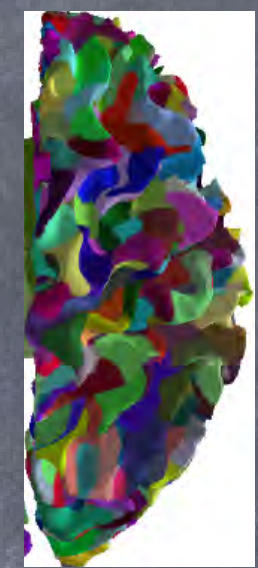
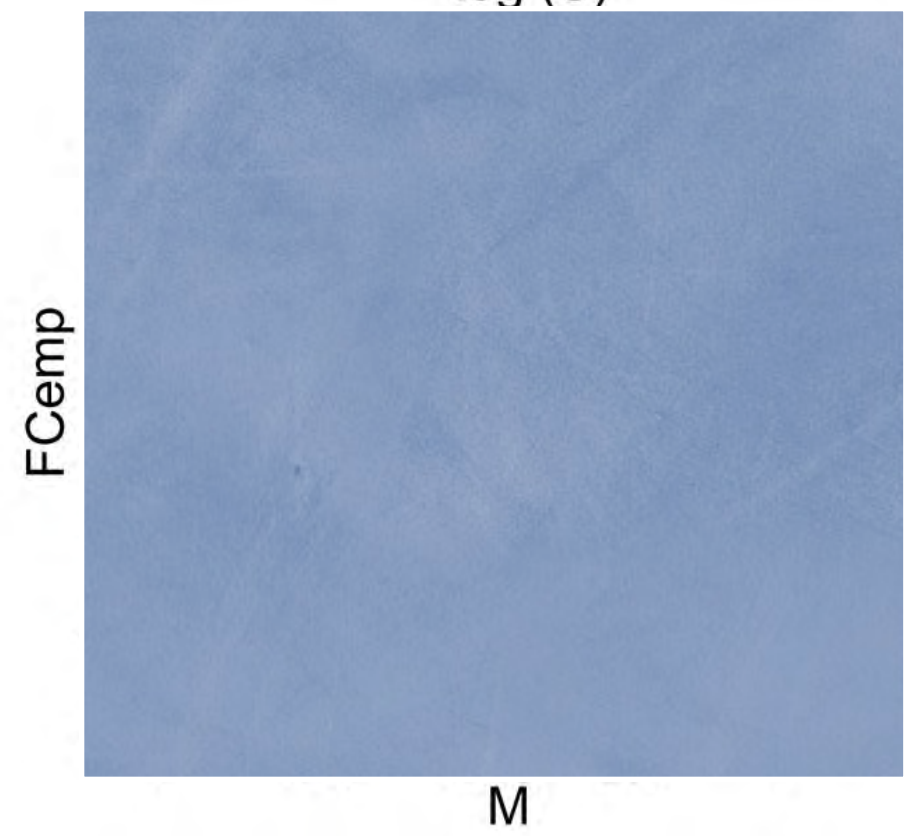
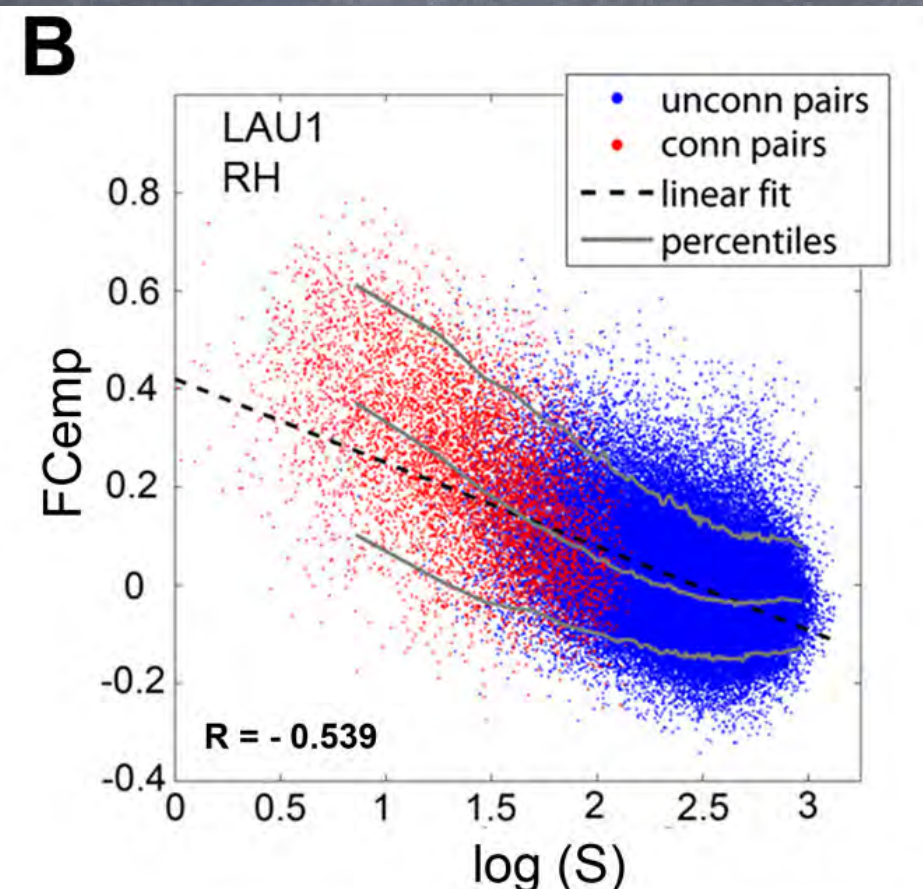
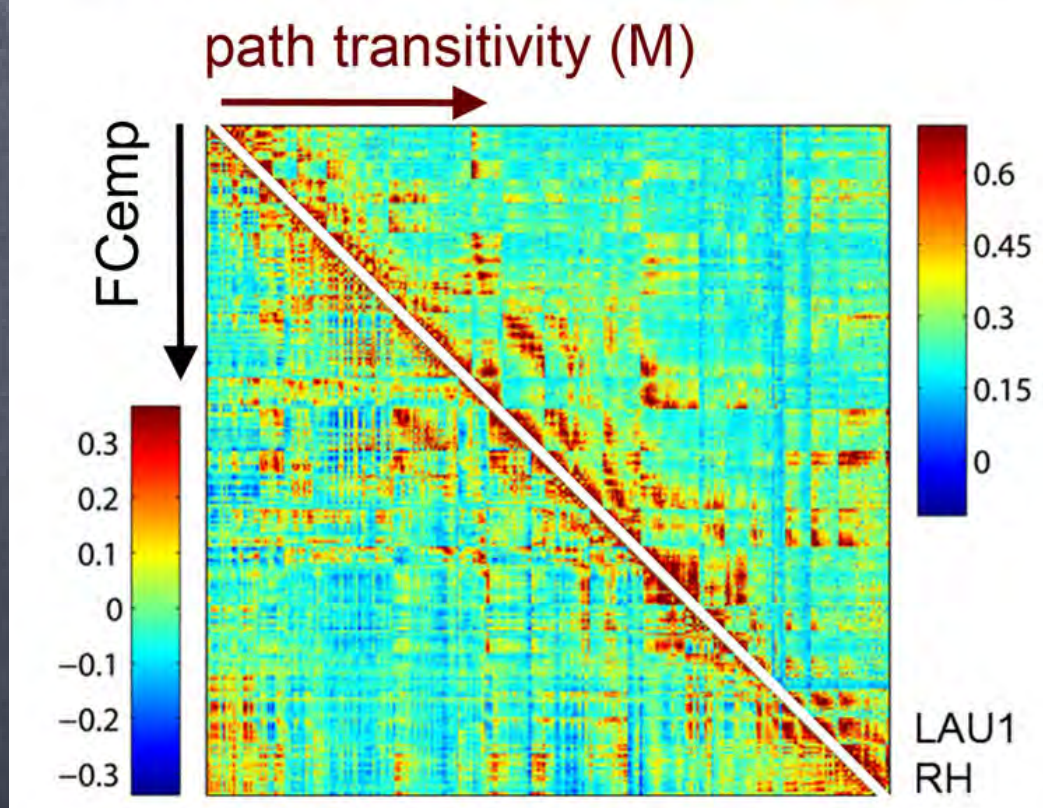
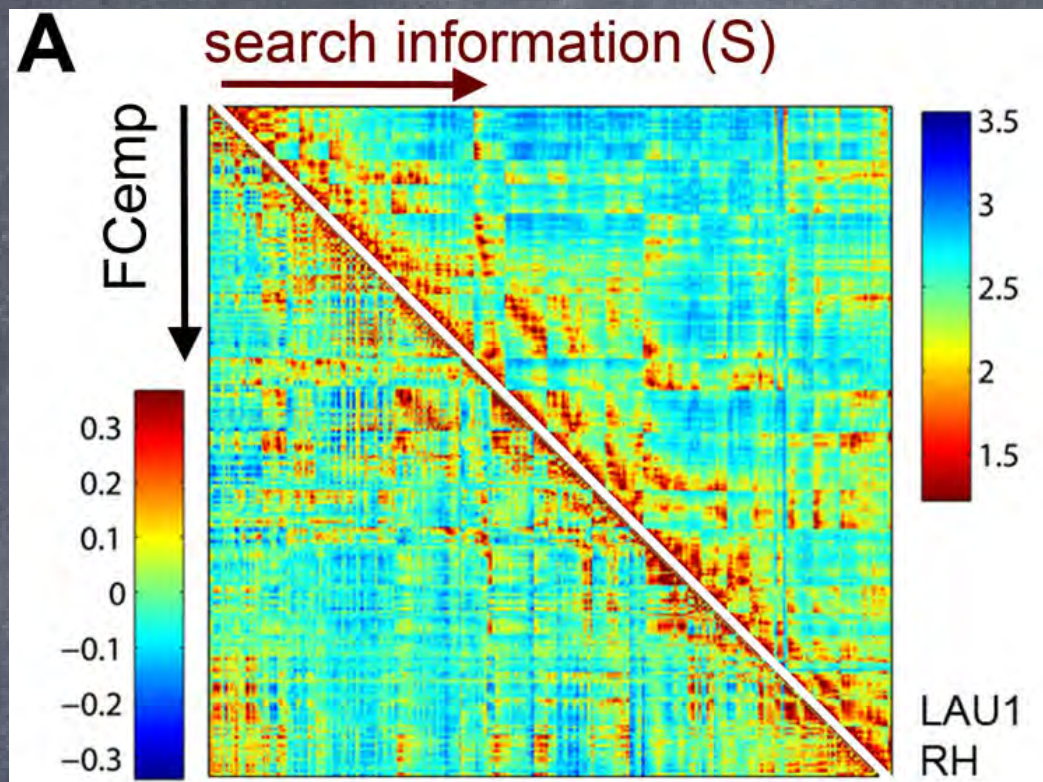
shortest-path communication measures



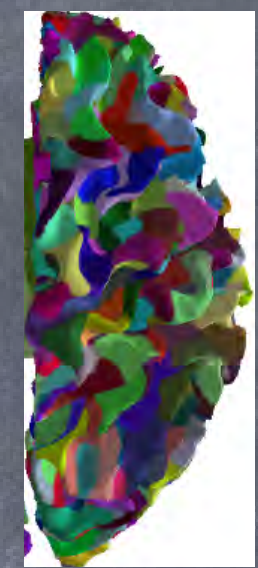
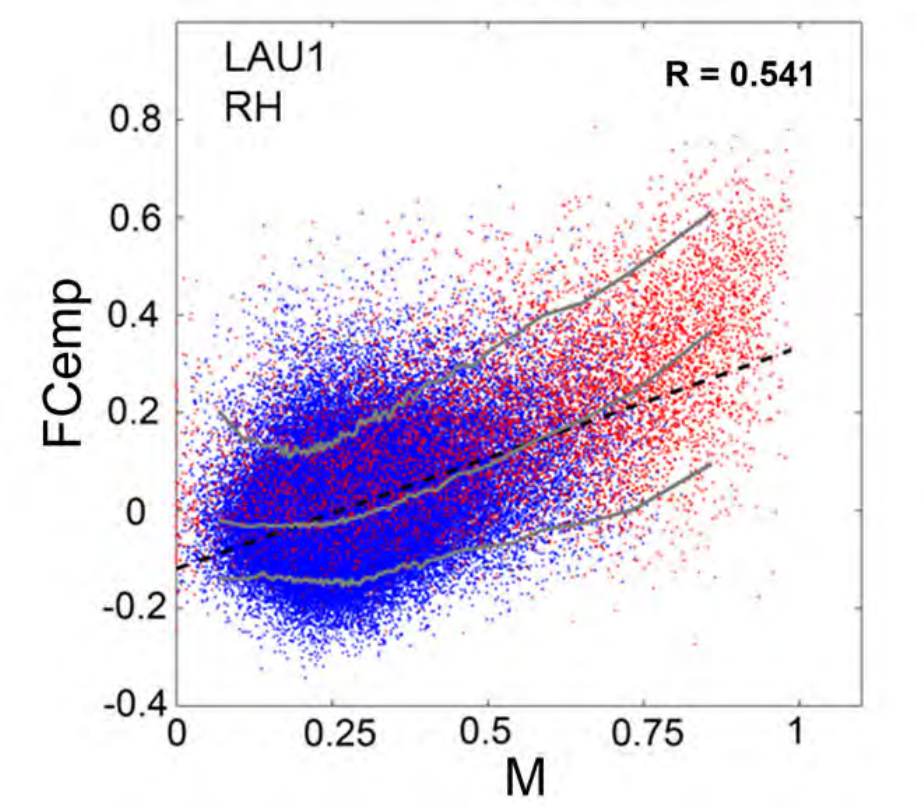
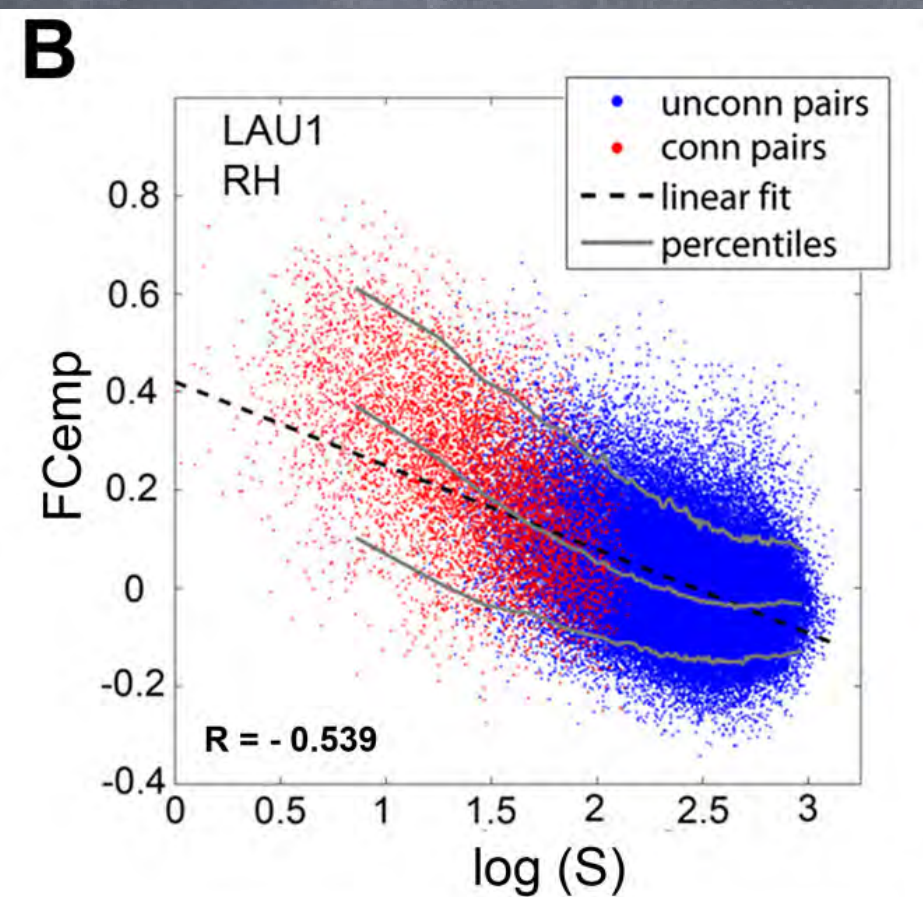
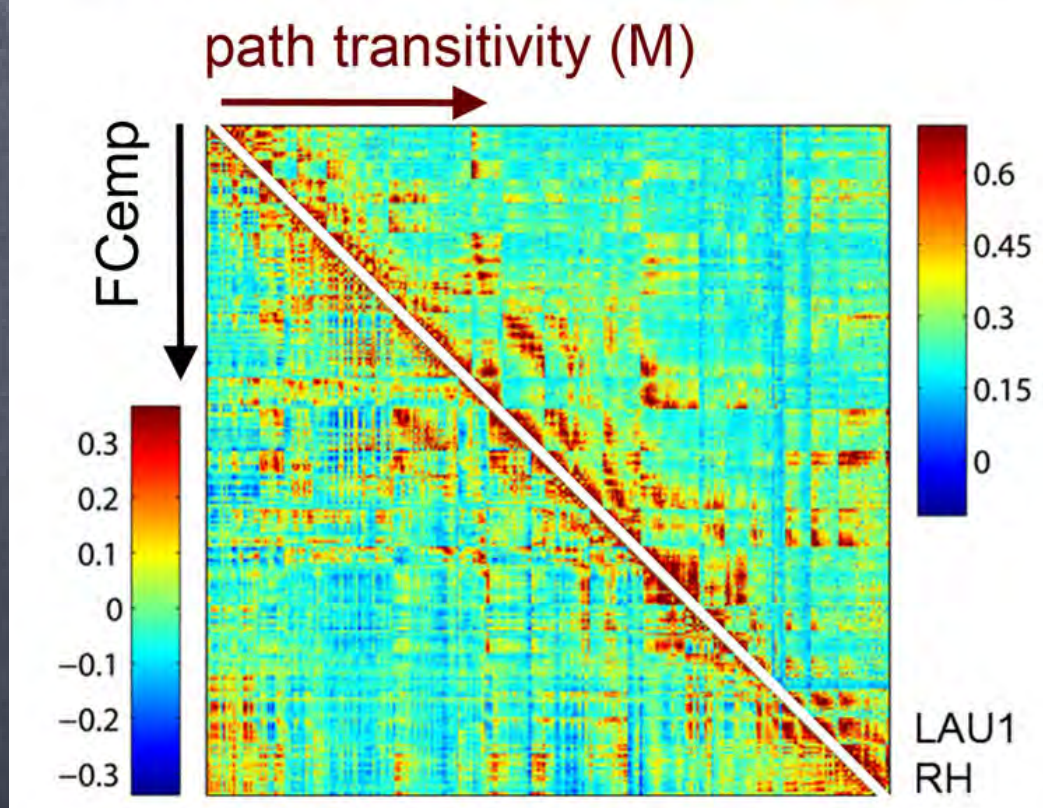
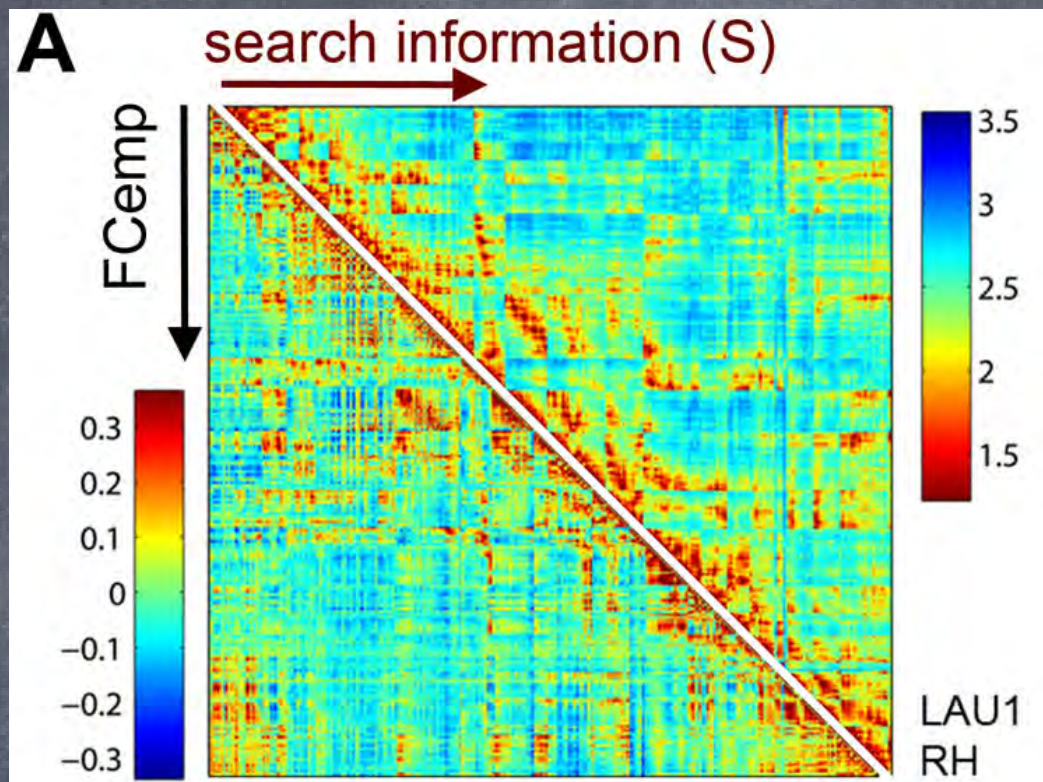






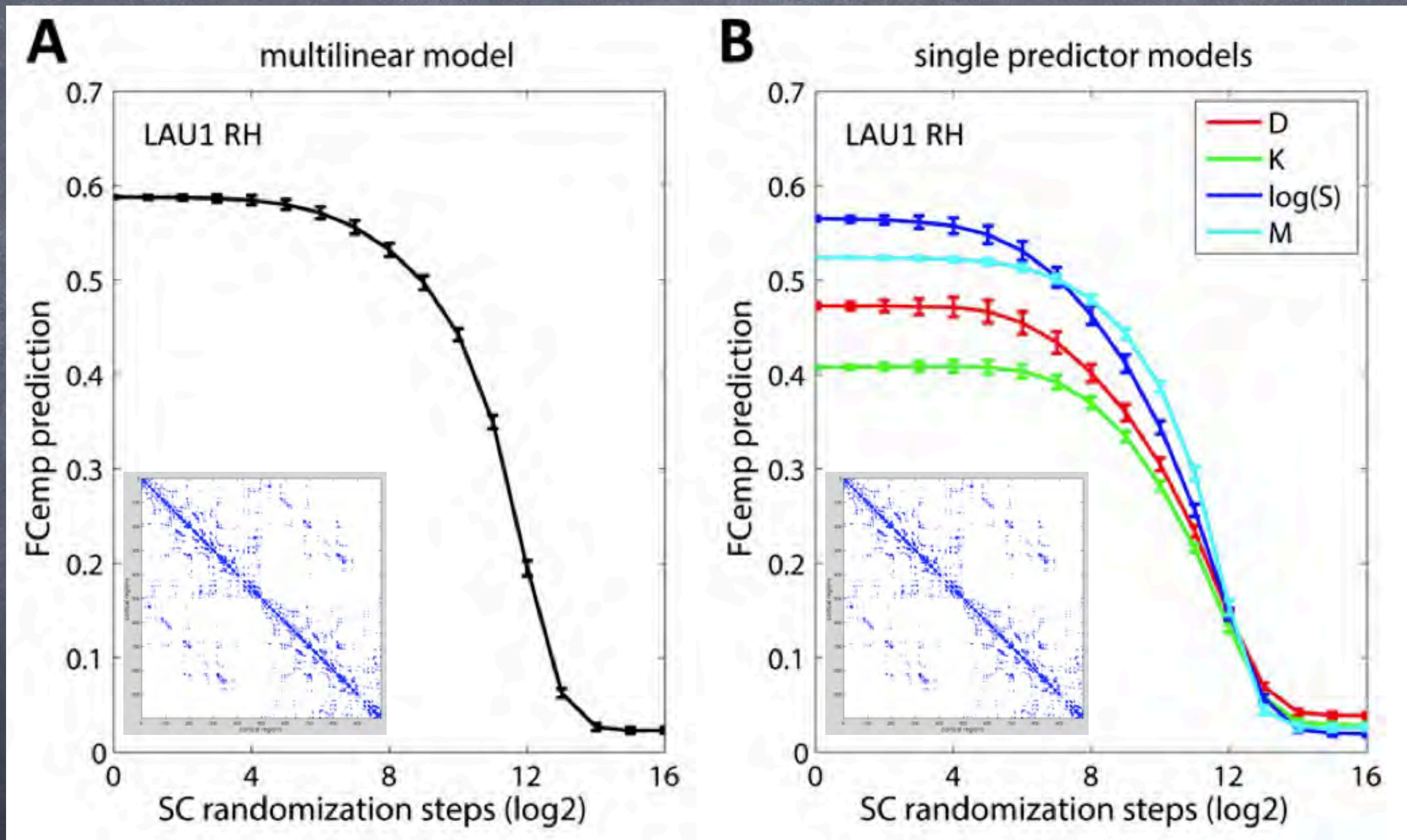
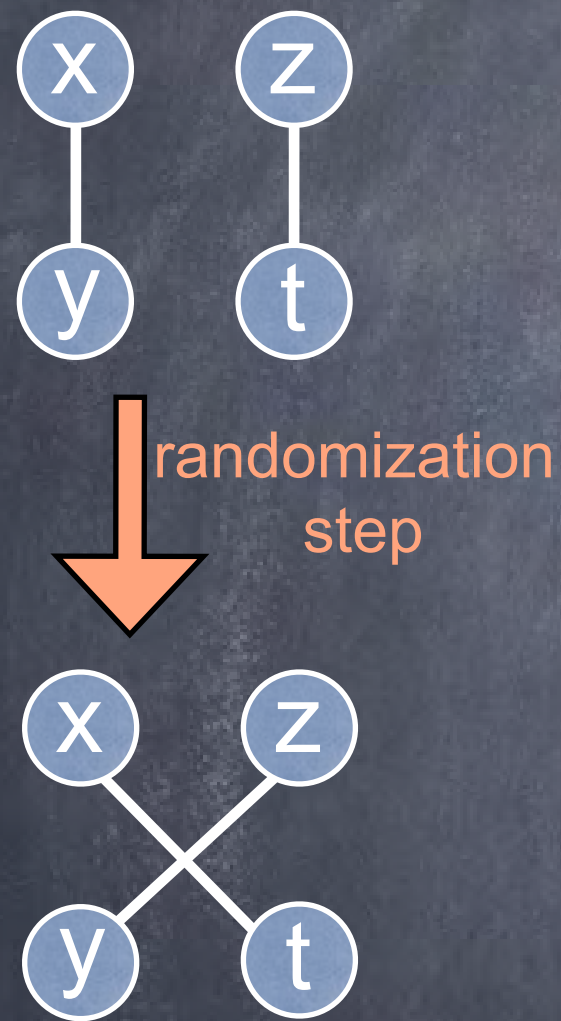






# Network randomization test

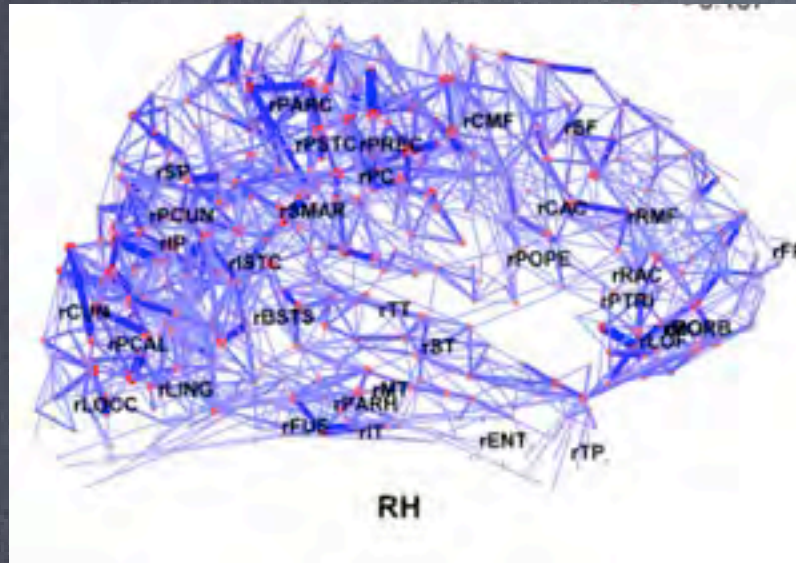
Goñi et al. PNAS 2014



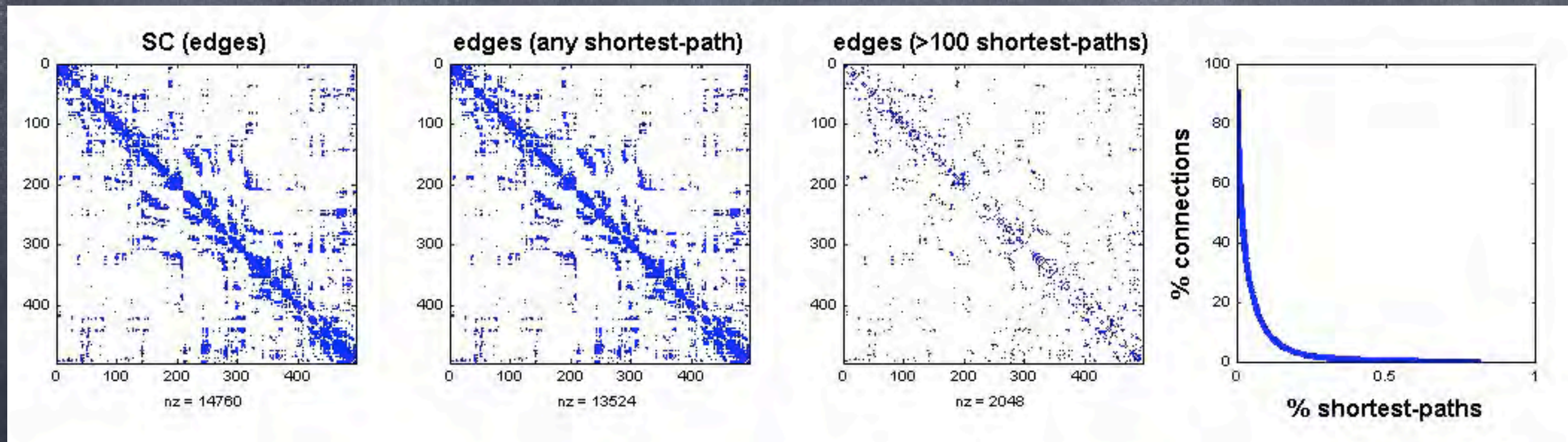
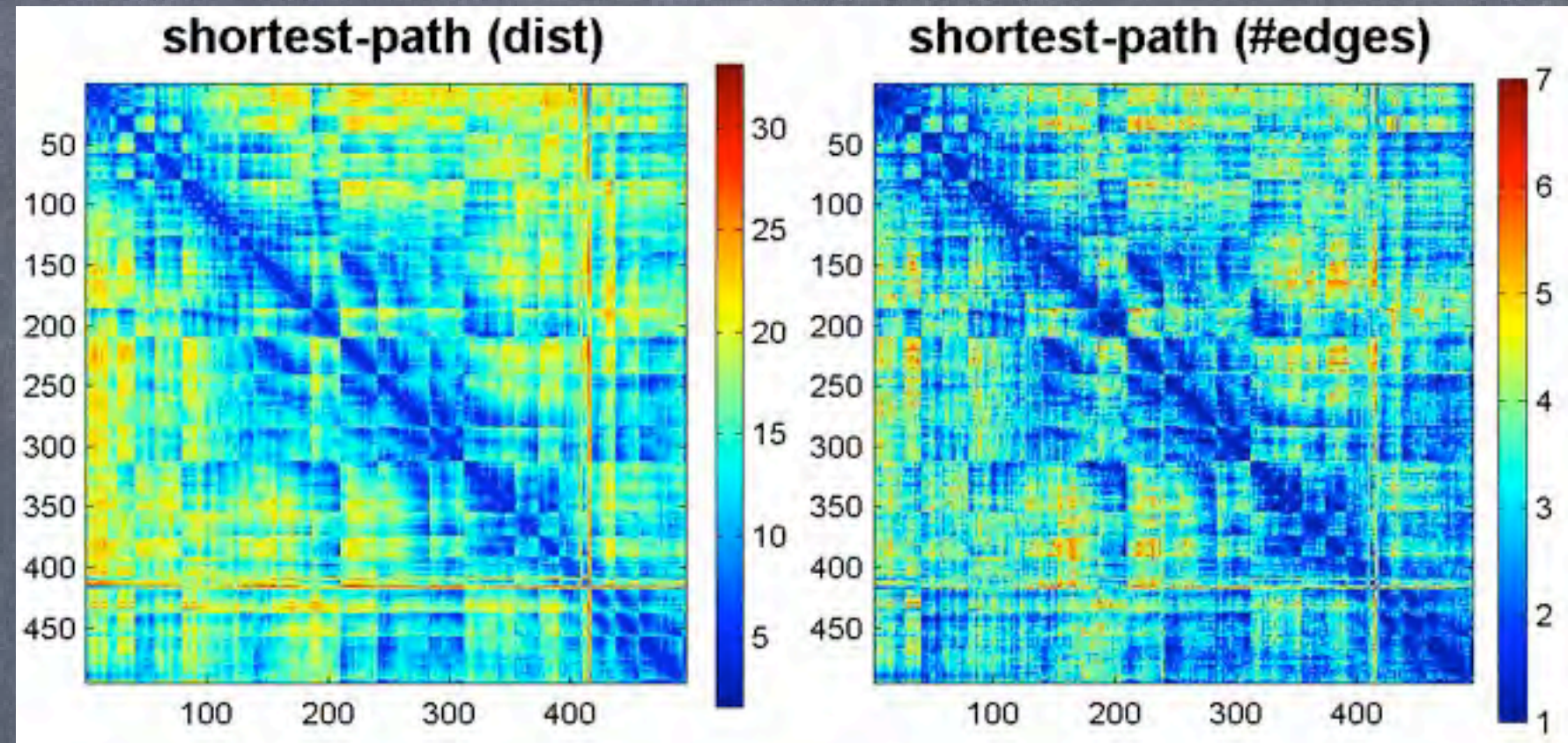
# Summary

- network theory is a useful framework to better understand the human brain and how its connectivity gets affected by diseases
- communication model(s) based on SC can predict resting-state FC
- the way shortest-paths are embedded (hidden) in the network is a strong predictor of resting-state FC.
- evidence of SC driving / shaping collective dynamics and fluctuations of neural activity during resting-state
- analytical, almost immediate computation.

# the shortest-path 'paradox'



Hagmann et al. Plos Biol. 2008







*“all roads lead to Rome”*





*“all roads lead to Rome”*

understanding the human connectome from an  
information theoretical perspective





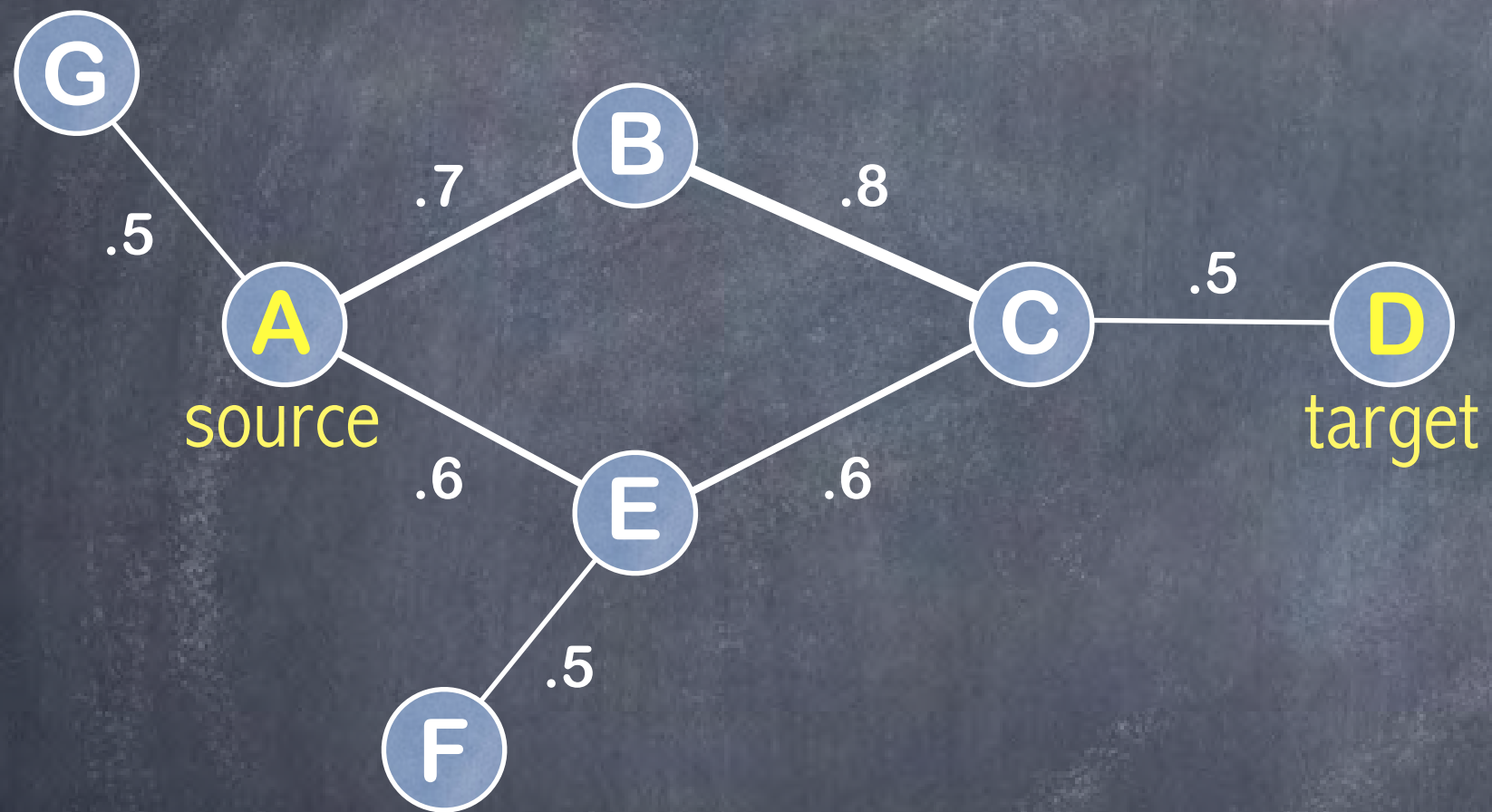
*“I promise you I’ll reach the destination. But I cannot really tell you which path I will take. Hopefully a good one among a set of possible ones.”*







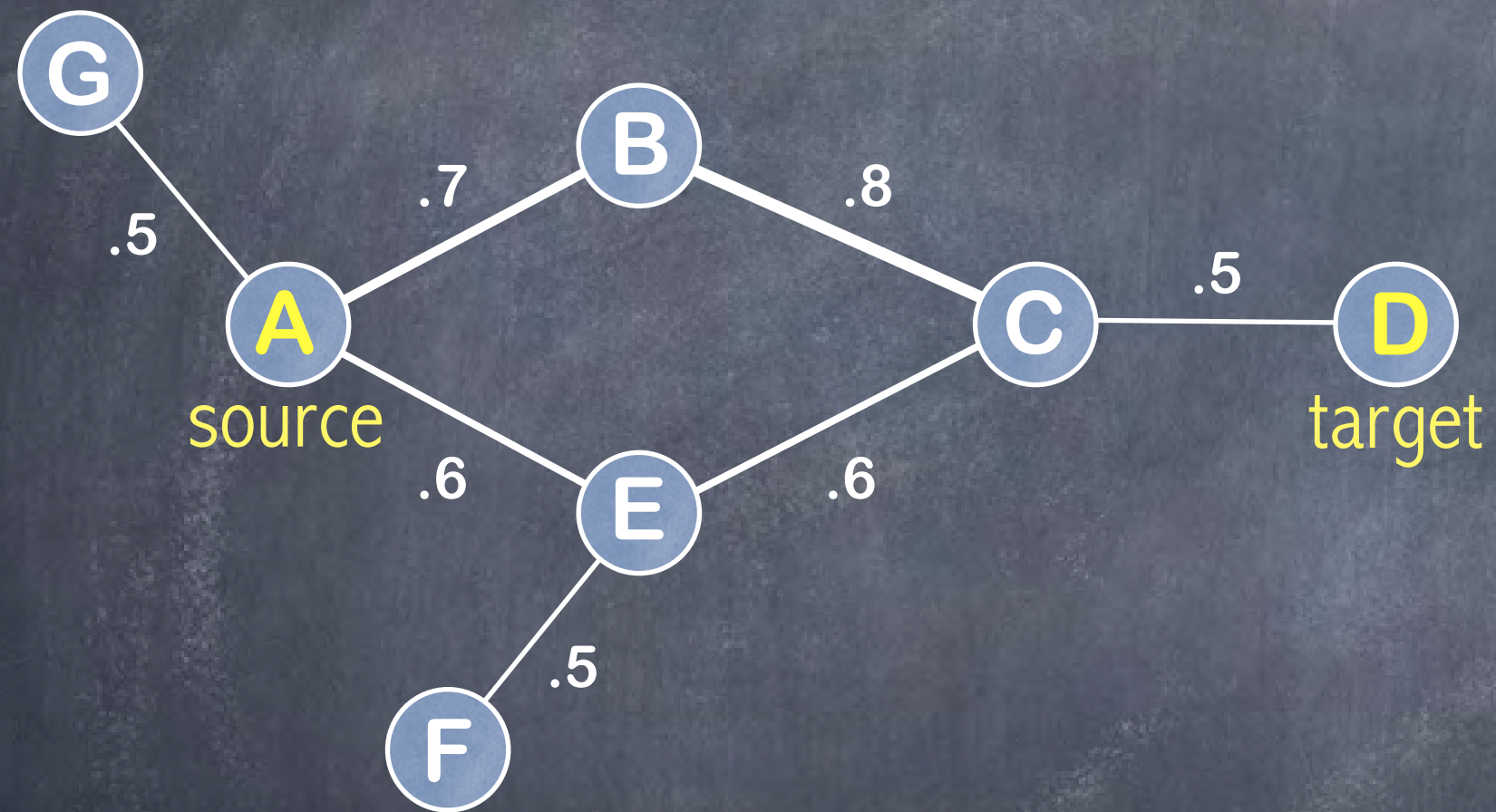
# generalized k-search-information. Example A





# generalized k-search-information. Example A

$$\Pi_1 = \{A, B, C, D\}$$

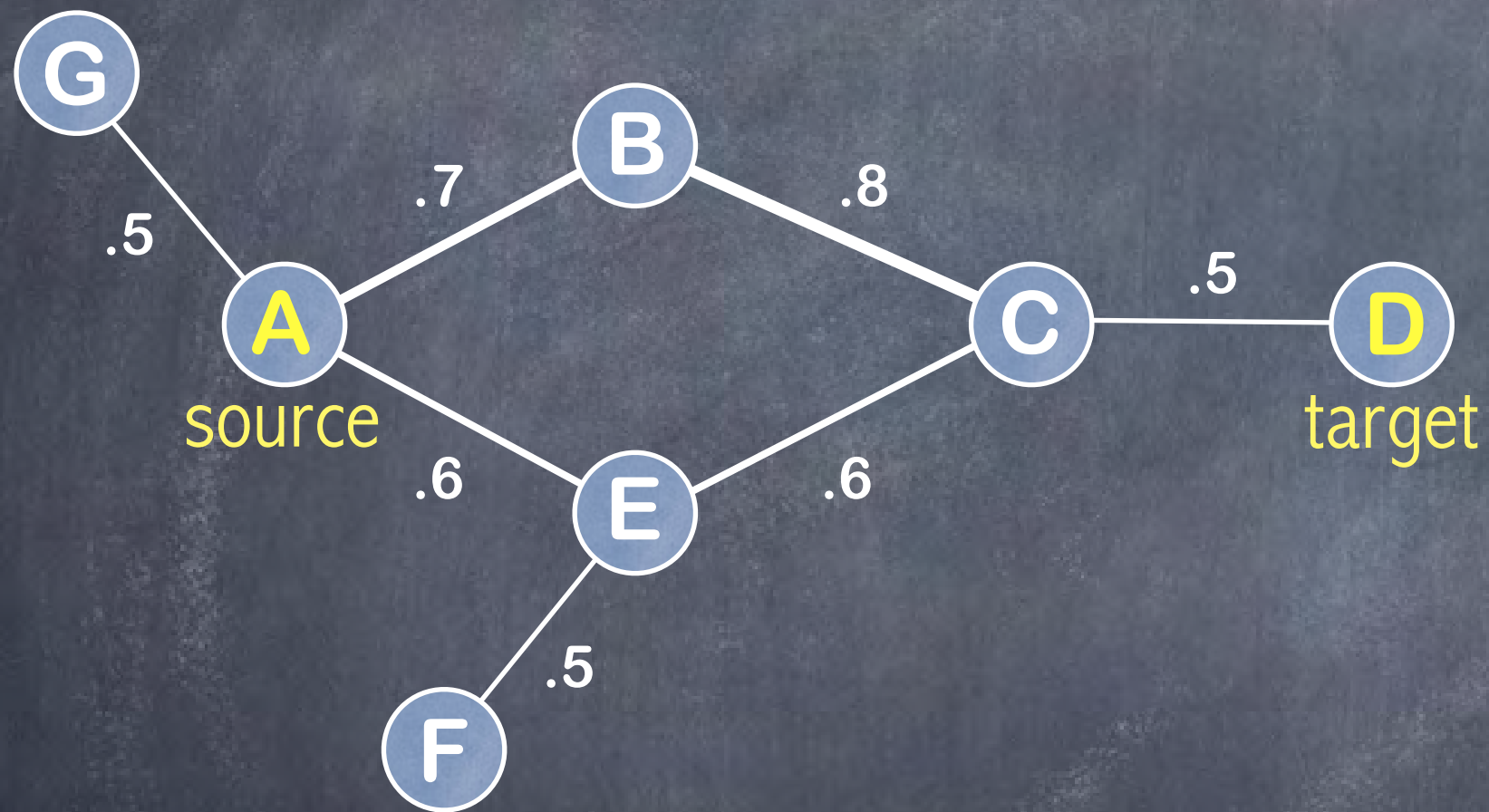




# generalized k-search-information. Example A

$$\Pi_1 = \{A, B, C, D\}$$

$$SI(\Pi_1) = -\log(.7/1.8 \cdot 1 \cdot .5/1.1) = 1.73 \text{ bits}$$



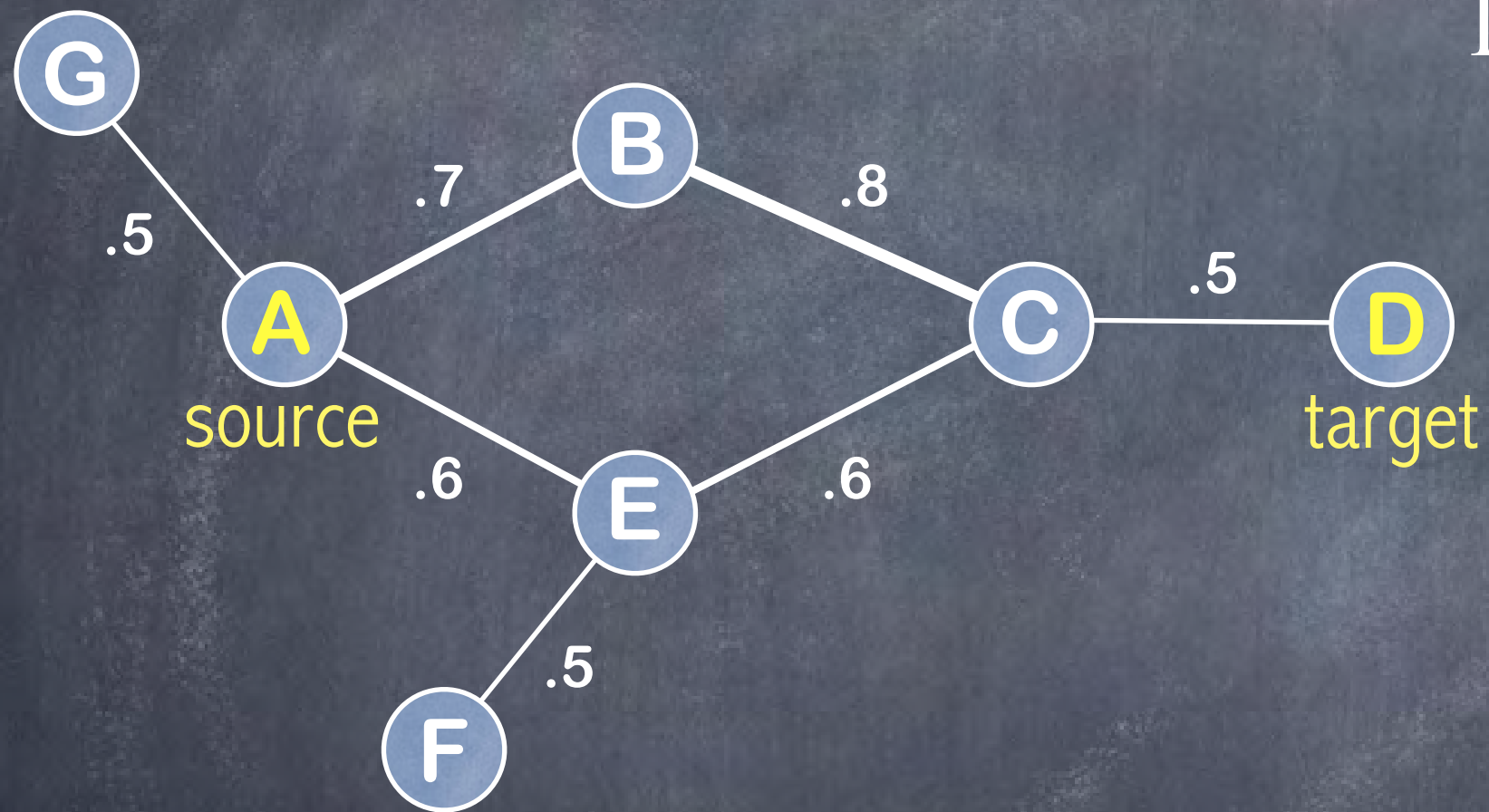


# generalized k-search-information. Example A

$$\Pi_1 = \{A, B, C, D\}$$

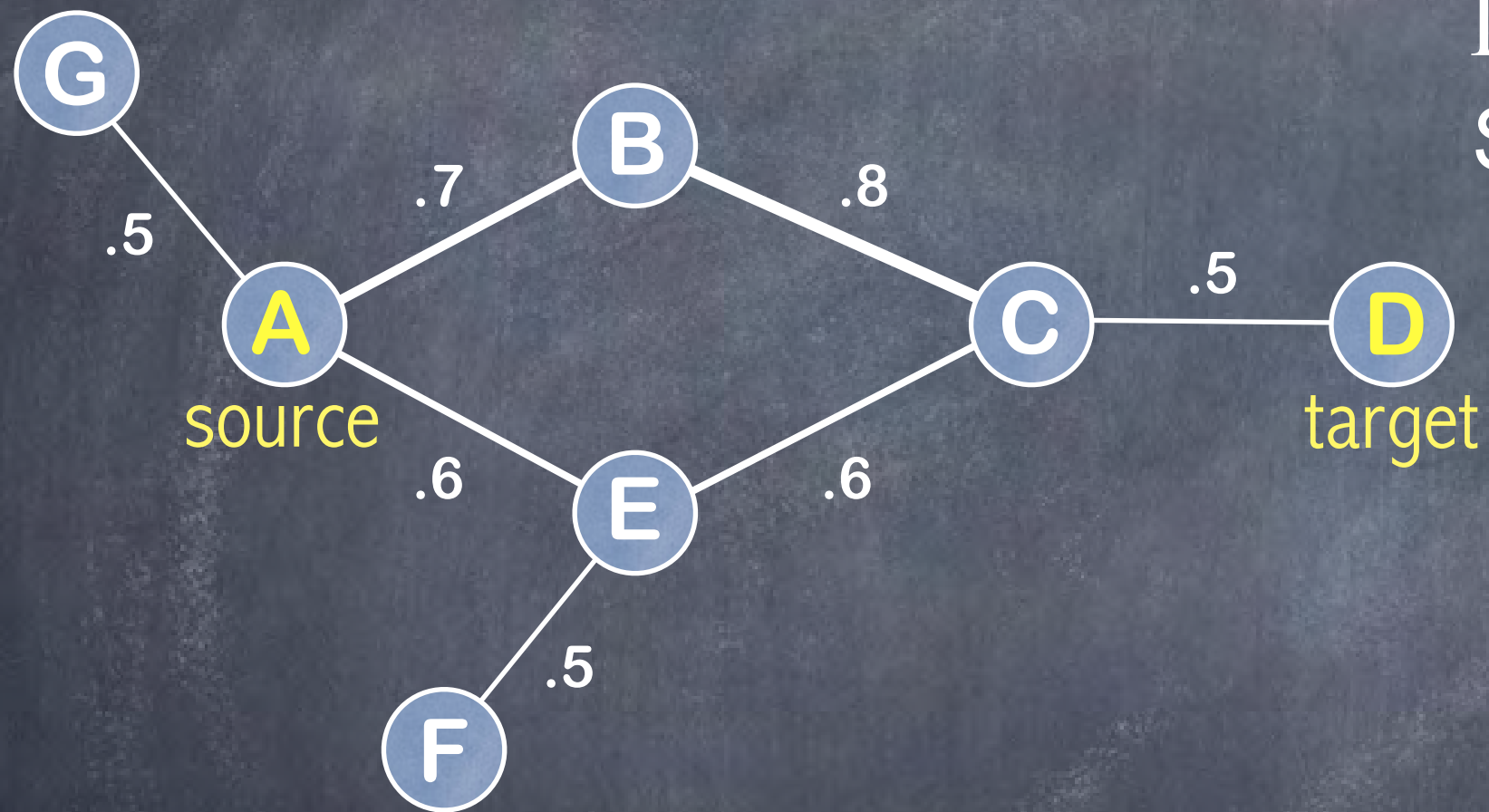
$$SI(\Pi_1) = -\log(.7/1.8 \cdot 1 \cdot .5/1.1) = 1.73 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$





# generalized k-search-information. Example A



$$\Pi_1 = \{A, B, C, D\}$$

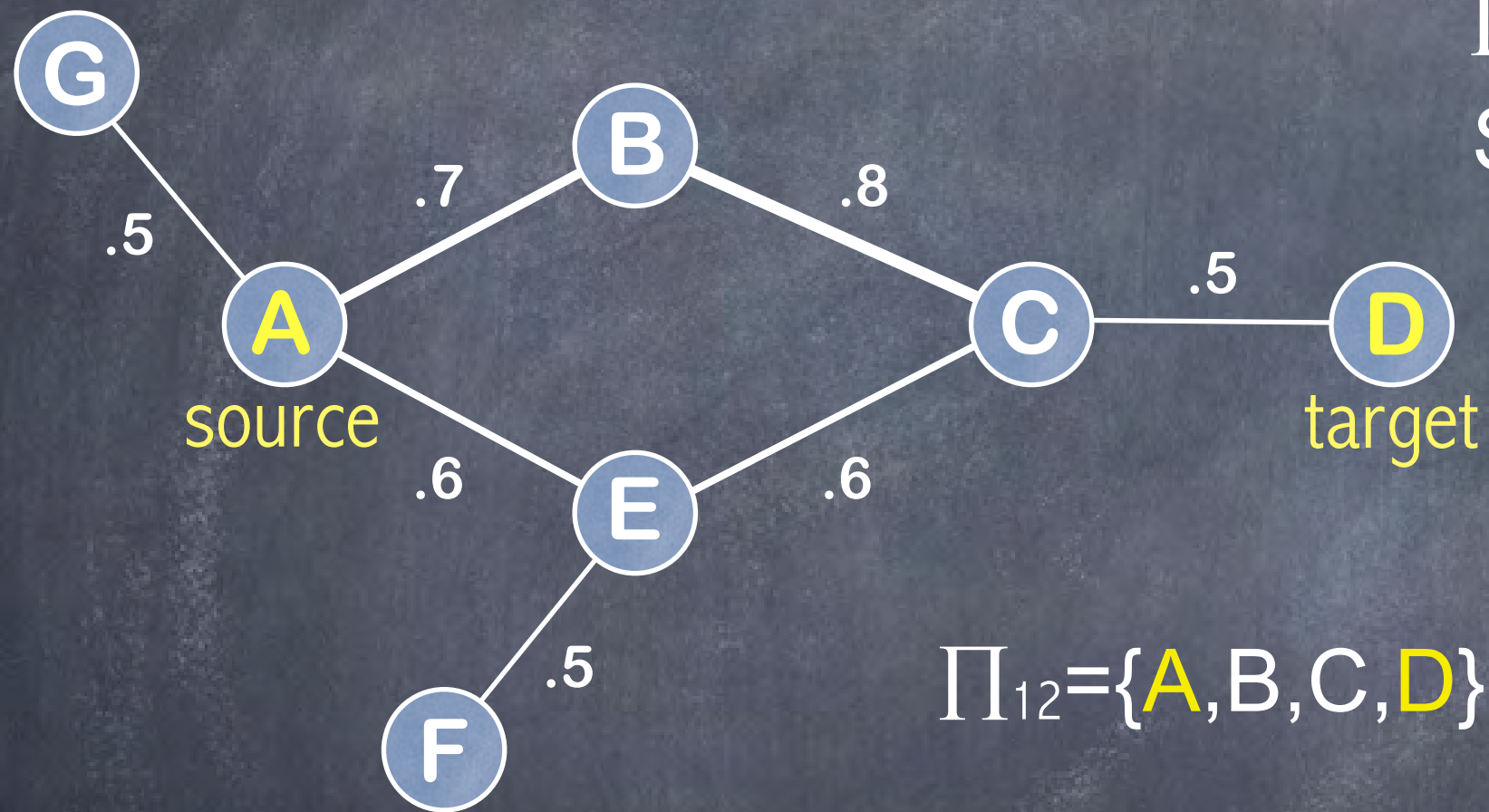
$$SI(\Pi_1) = -\log(.7/1.8 \cdot 1 \cdot .5/1.1) = 1.73 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = -\log(.6/1.8 \cdot .6/1.1 \cdot .5/1.3) = 2.66 \text{ bits}$$



# generalized k-search-information. Example A



$$\Pi_1 = \{A, B, C, D\}$$

$$SI(\Pi_1) = -\log(.7/1.8 \cdot 1 \cdot .5/1.1) = 1.73 \text{ bits}$$

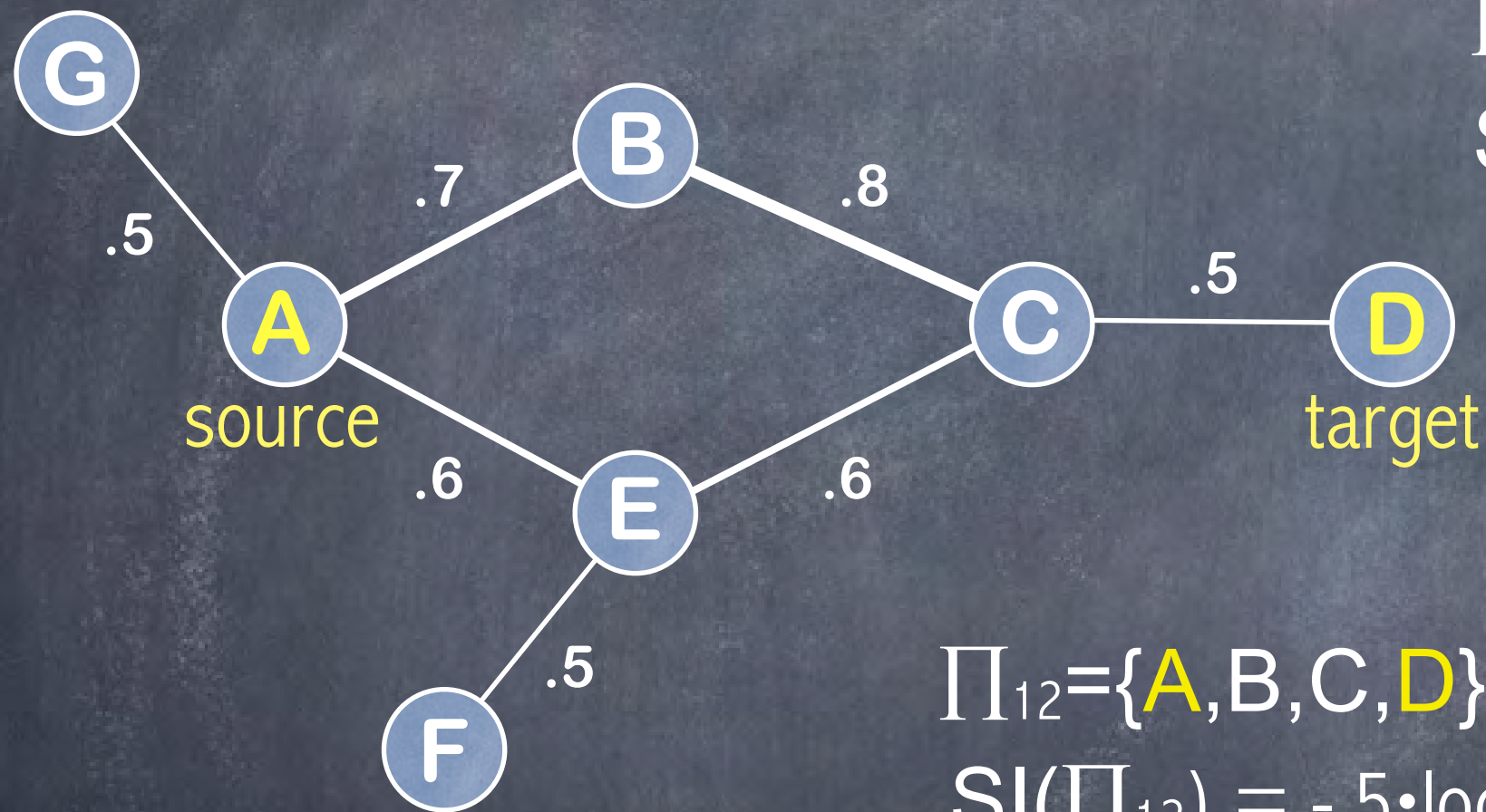
$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = -\log(.6/1.8 \cdot .6/1.1 \cdot .5/1.3) = 2.66 \text{ bits}$$

$$\Pi_{12} = \{A, B, C, D\} \parallel \{A, E, C, D\}$$



# generalized k-search-information. Example A



$$\Pi_1 = \{A, B, C, D\}$$

$$SI(\Pi_1) = -\log(.7/1.8 \cdot 1 \cdot .5/1.1) = 1.73 \text{ bits}$$

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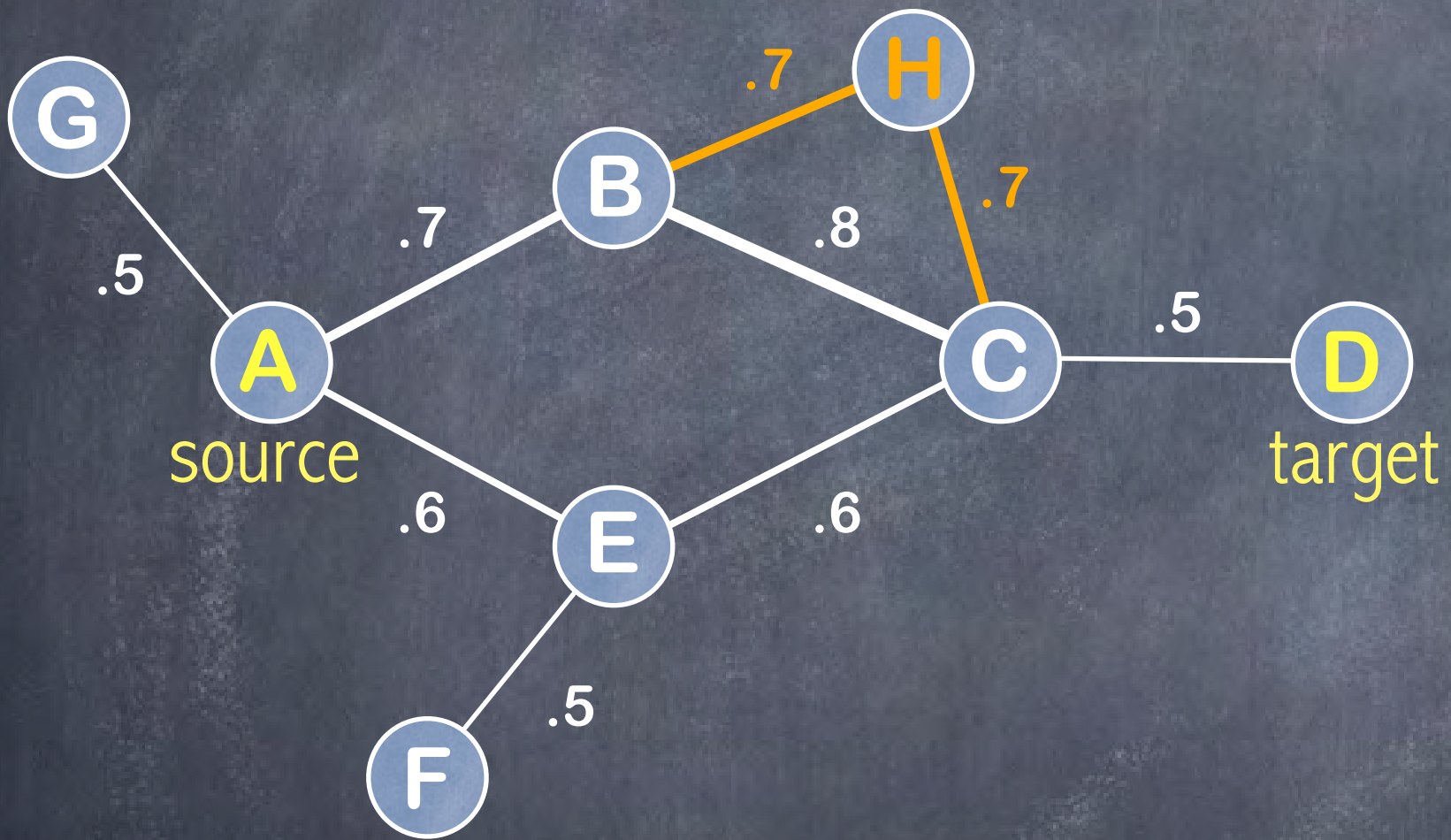
$$SI(\Pi_2) = -\log(.6/1.8 \cdot .6/1.1 \cdot .5/1.3) = 2.66 \text{ bits}$$

$$\Pi_{12} = \{A, B, C, D\} \parallel \{A, E, C, D\}$$

$$\begin{aligned} SI(\Pi_{12}) &= -.5 \cdot \log(1.3/1.8) - \log(1 \cdot .5/1.1) \\ &\quad -.5 \cdot \log(1.3/1.8) - \log(.6/1.1 \cdot .5/1.3) \\ &= 1.5 \text{ bits} \end{aligned}$$



# generalized k-search-information. Example B

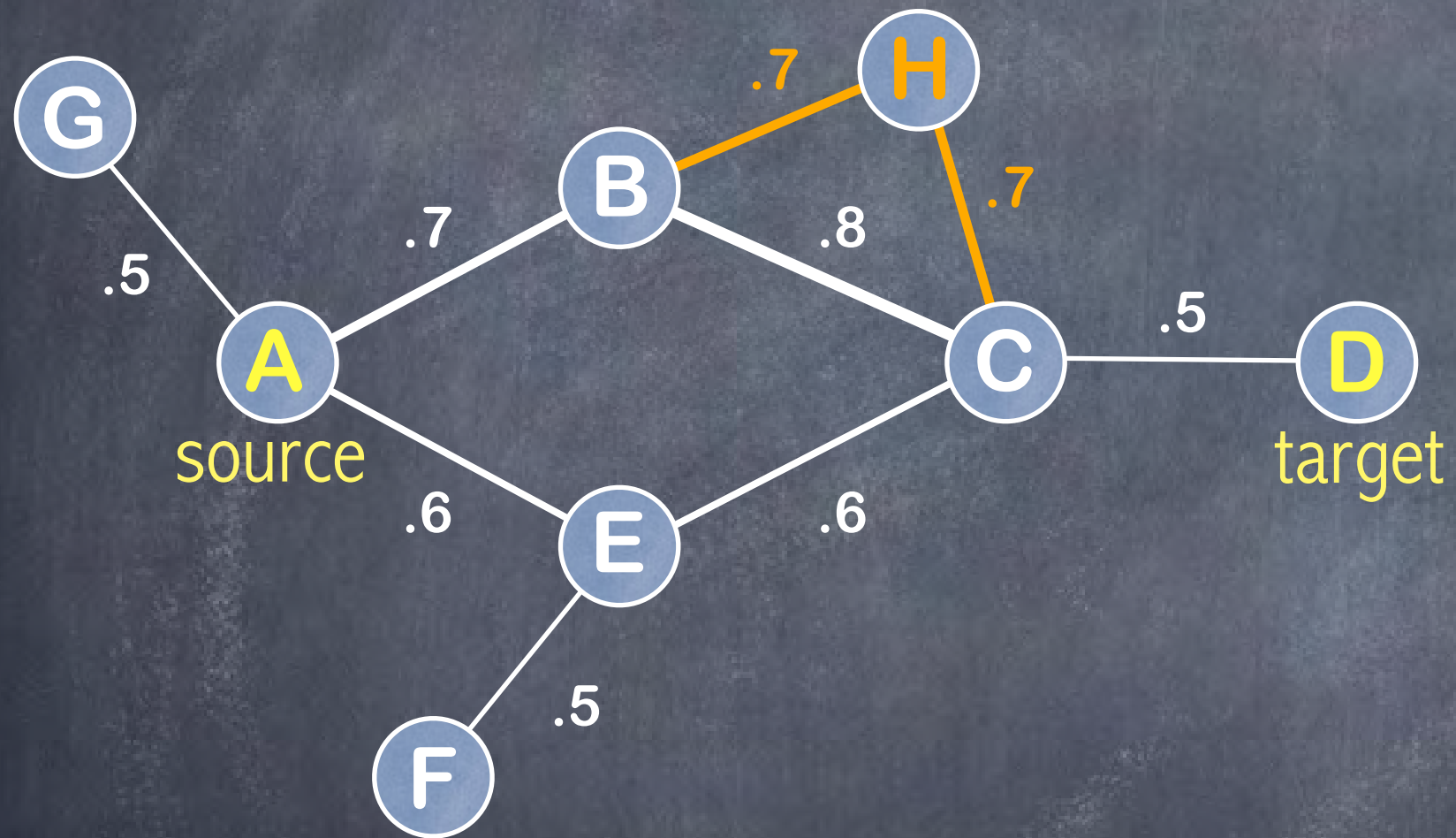






# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

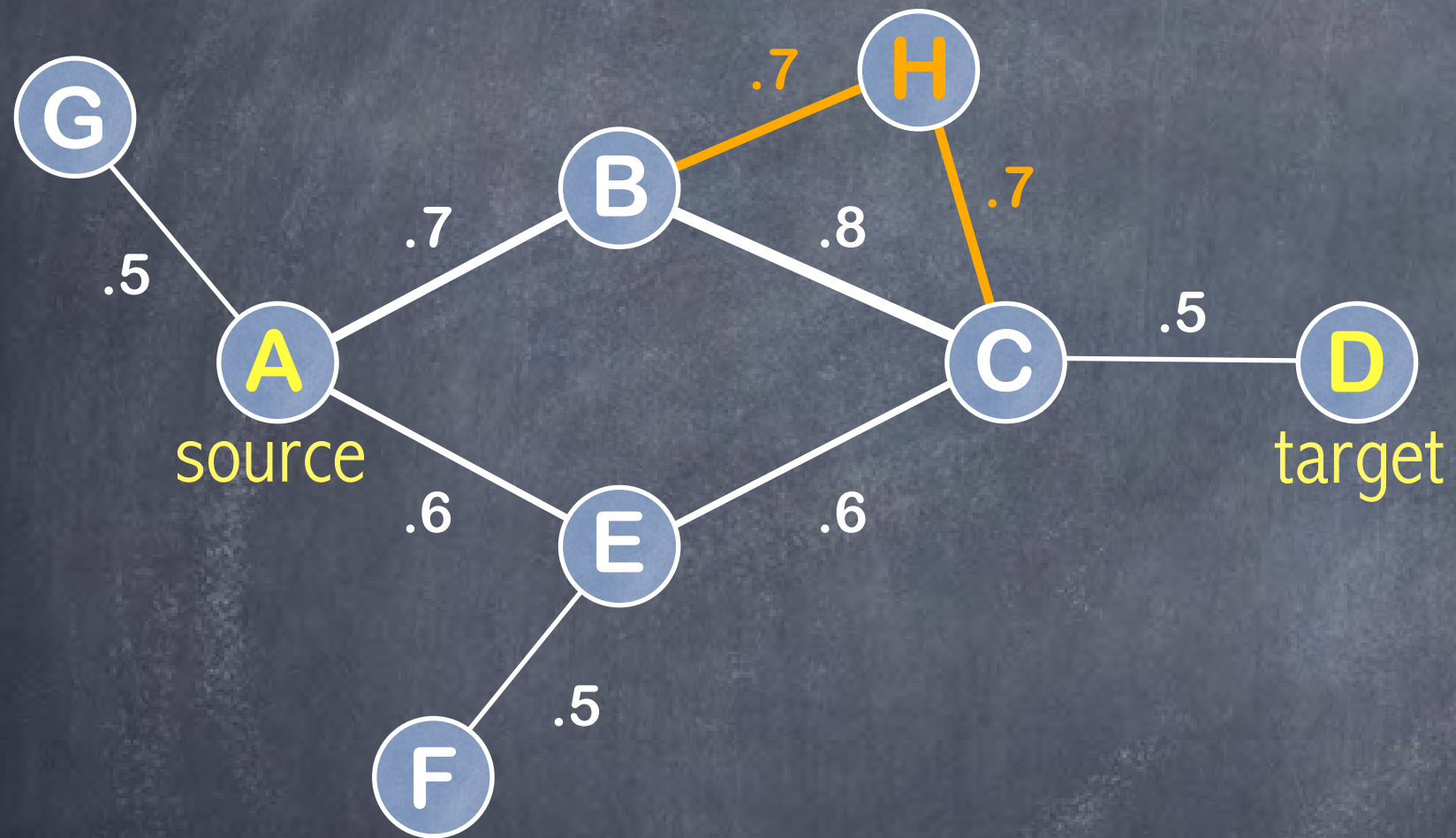




# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

$$SI(\Pi_1) = 2.85 \text{ bits}$$



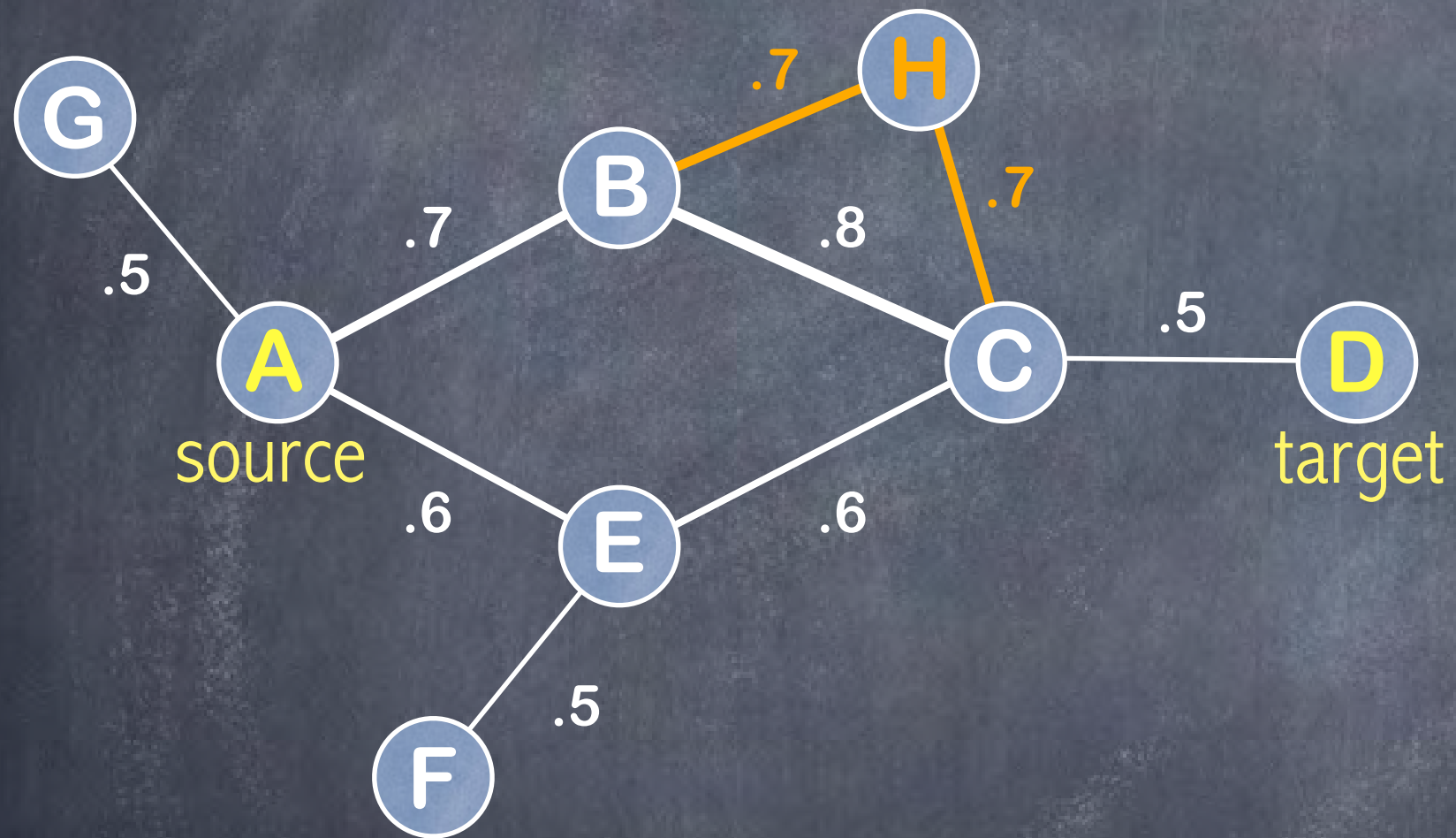


# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$





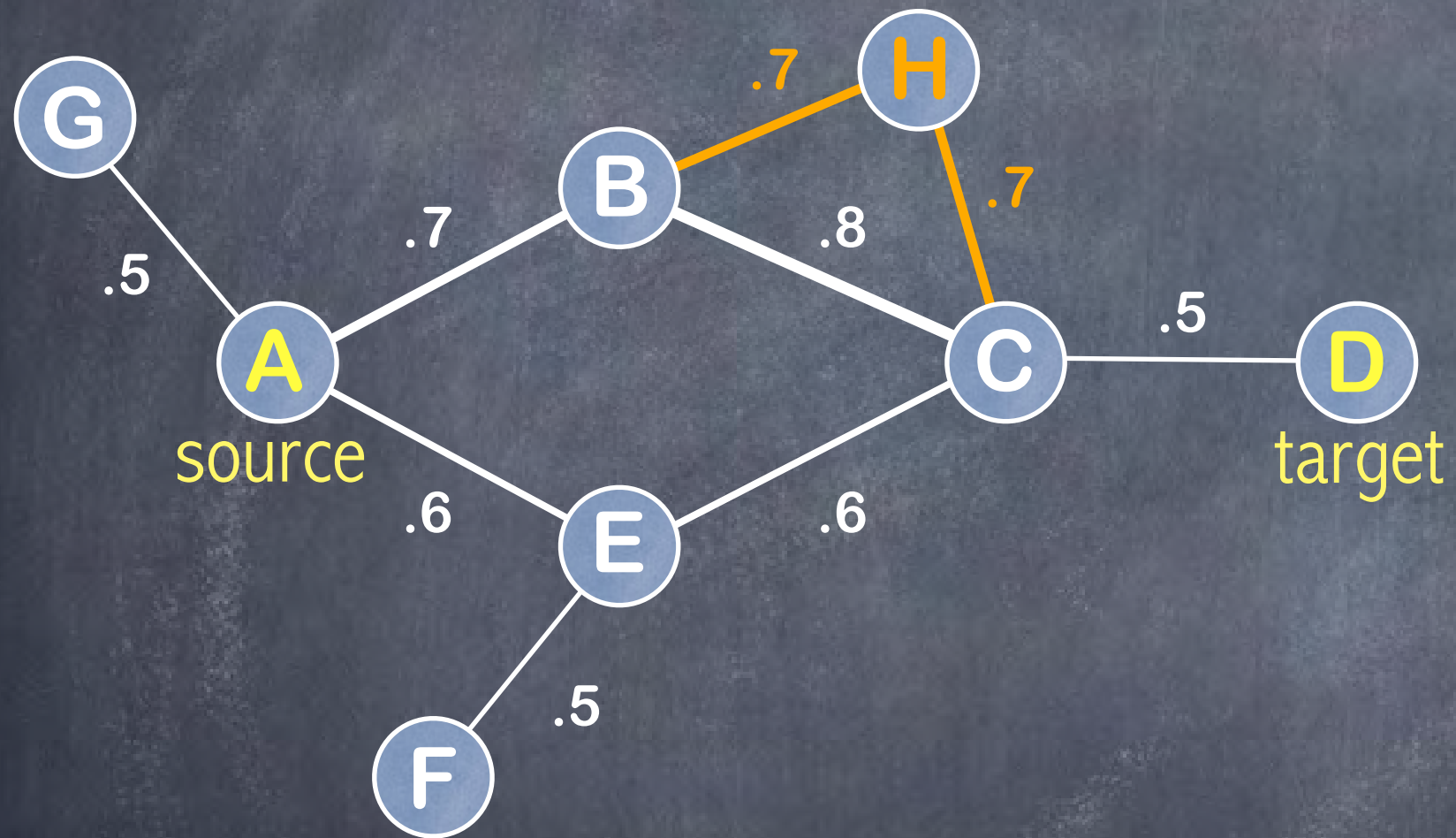
# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = 3.09 \text{ bits}$$





# generalized k-search-information. Example B

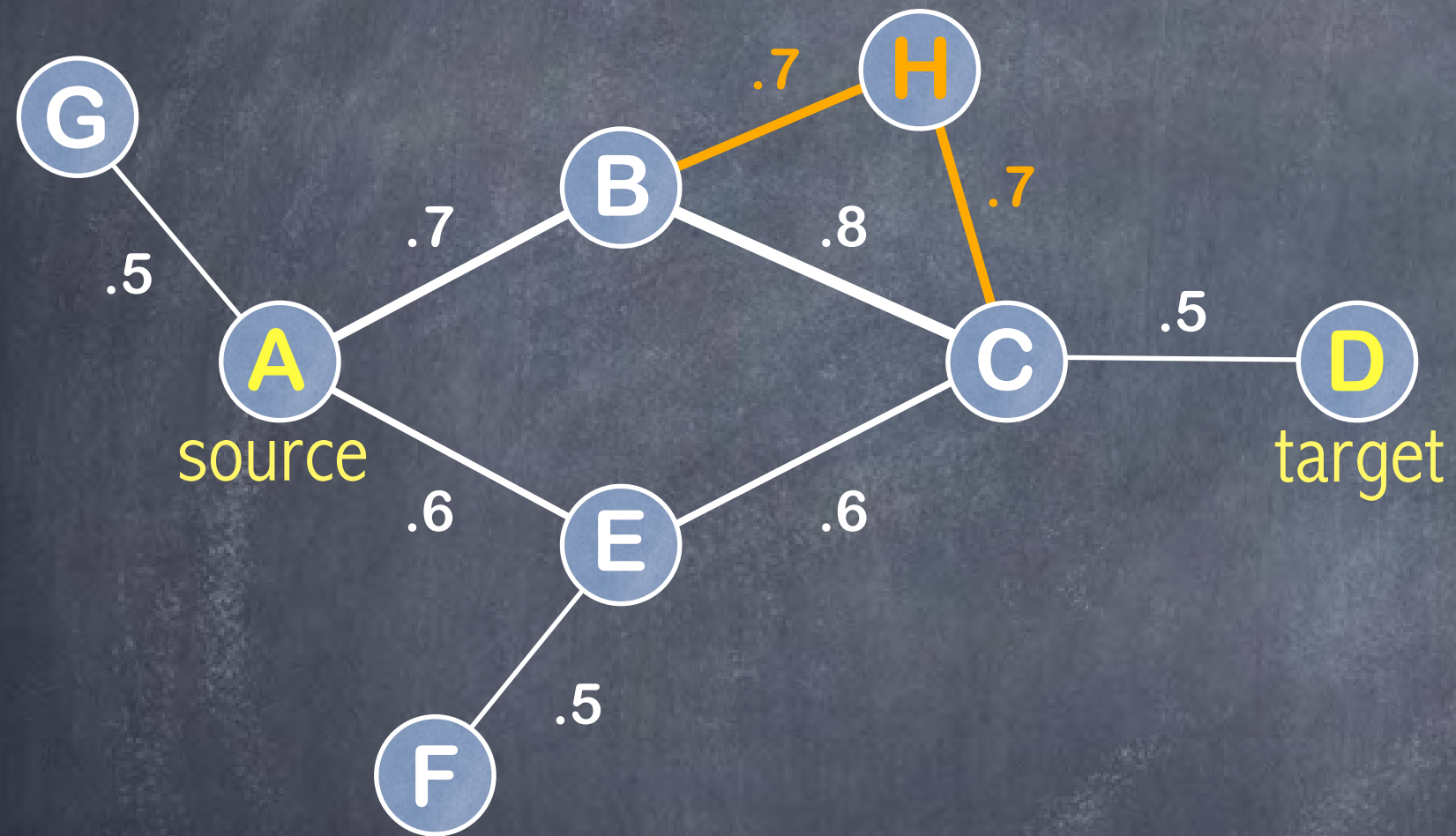
$$\Pi_1 = \{A, B, C, D\}$$

$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = 3.09 \text{ bits}$$

$$\Pi_3 = \{A, B, H, C, D\}$$





# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

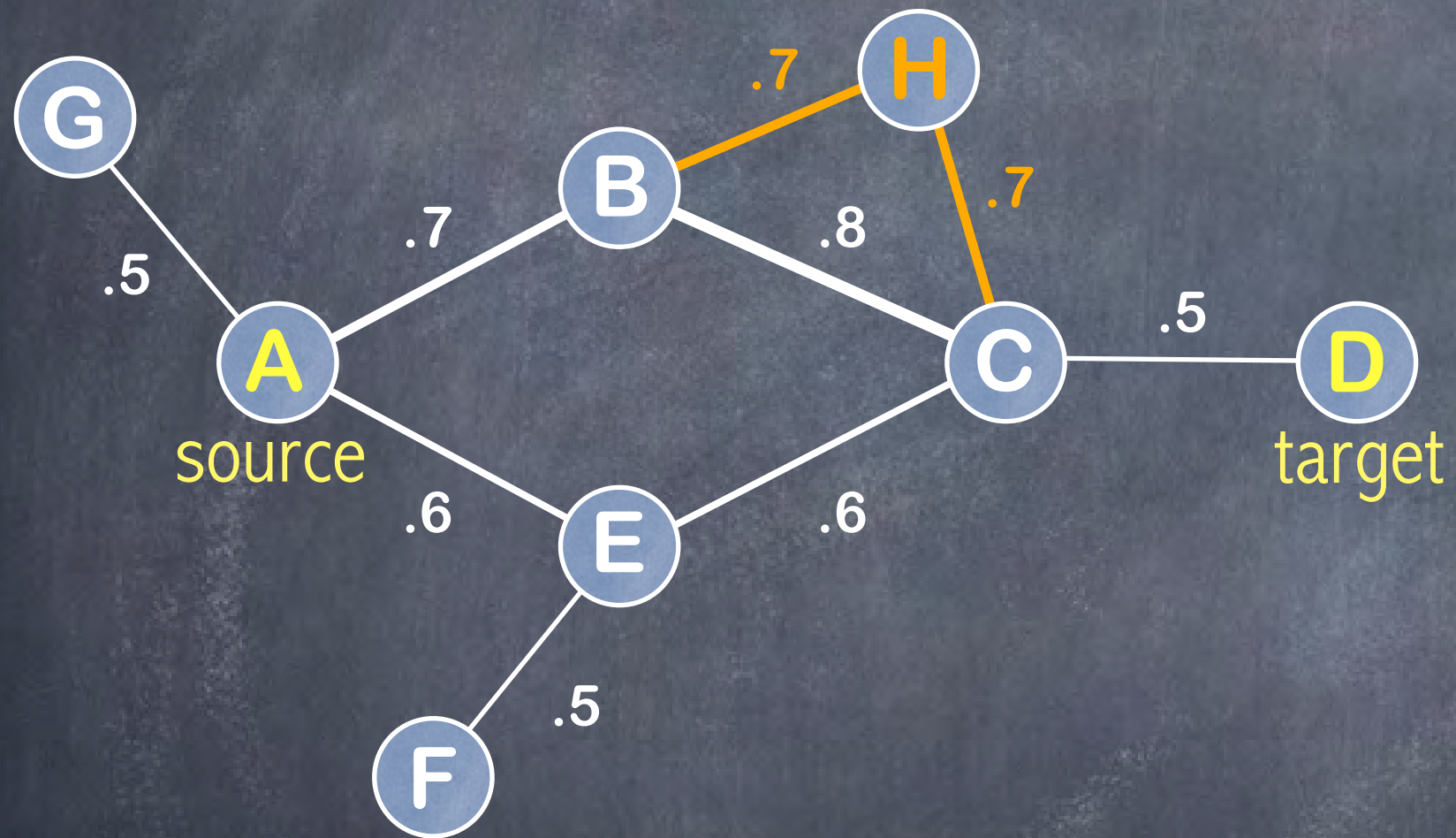
$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = 3.09 \text{ bits}$$

$$\Pi_3 = \{A, B, H, C, D\}$$

$$SI(\Pi_3) = 3.04 \text{ bits}$$





# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

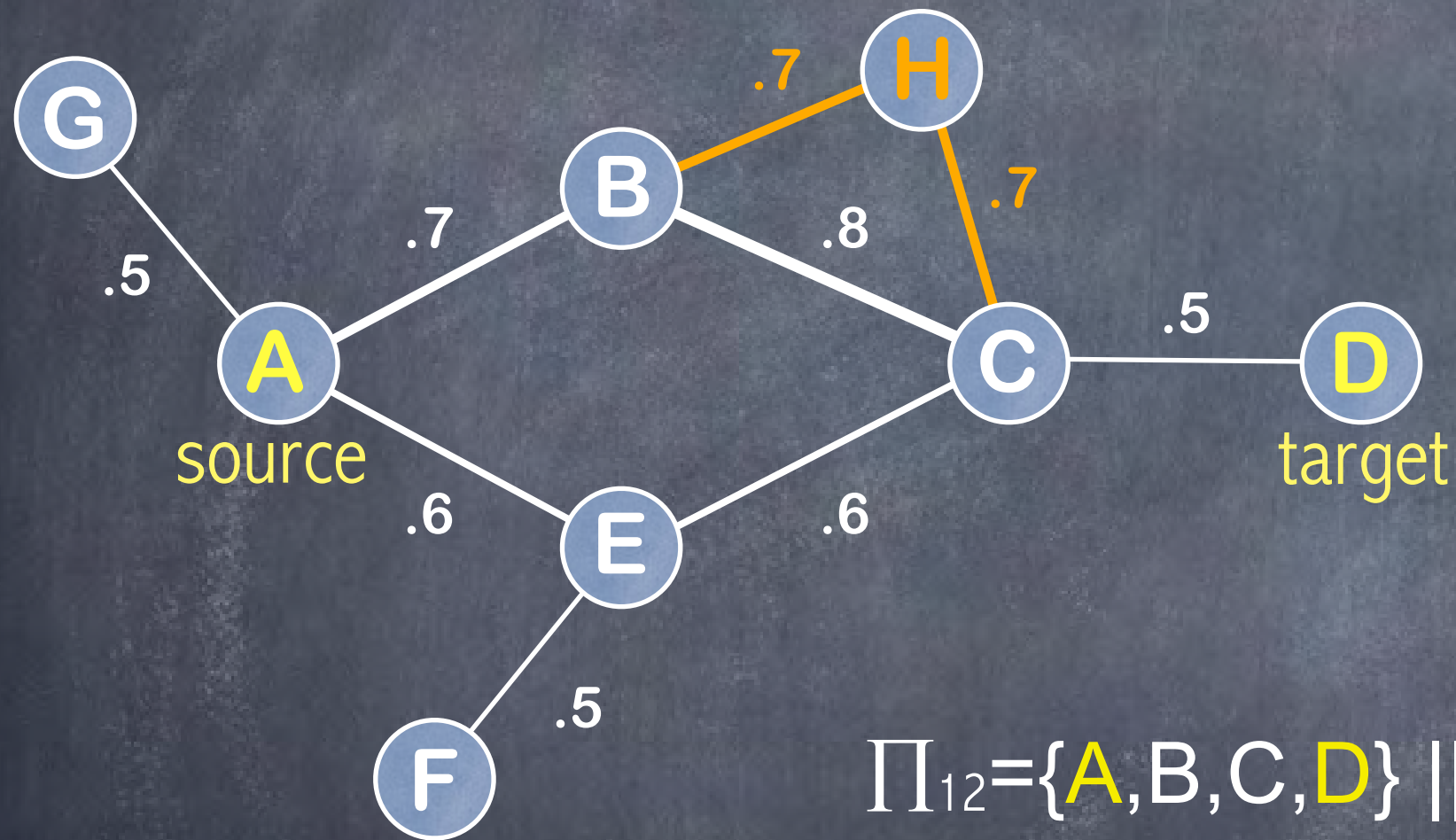
$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = 3.09 \text{ bits}$$

$$\Pi_3 = \{A, B, H, C, D\}$$

$$SI(\Pi_3) = 3.04 \text{ bits}$$



$$\Pi_{12} = \{A, B, C, D\} \parallel \{A, E, C, D\}$$



# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

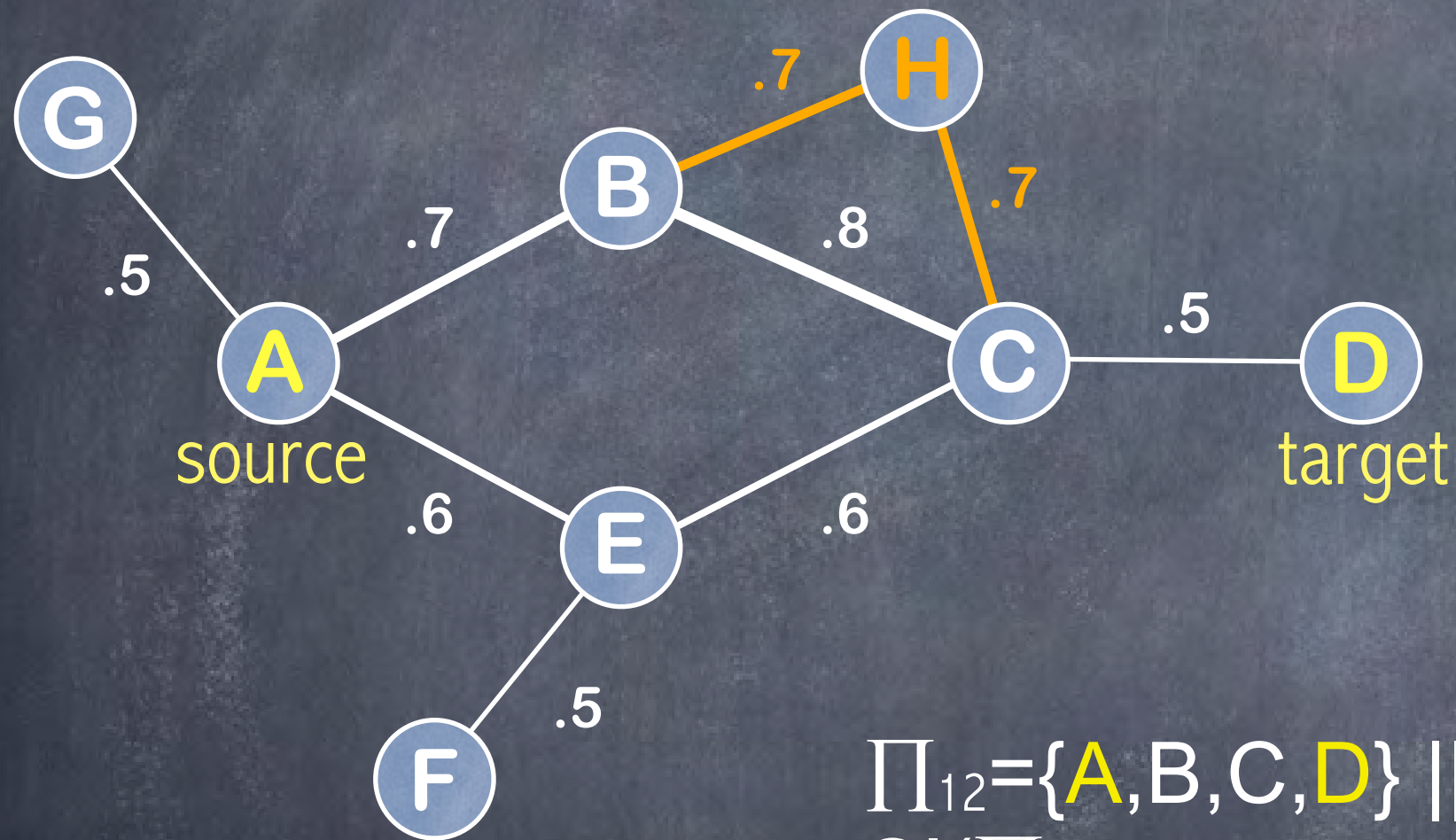
$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = 3.09 \text{ bits}$$

$$\Pi_3 = \{A, B, H, C, D\}$$

$$SI(\Pi_3) = 3.04 \text{ bits}$$



$$\Pi_{12} = \{A, B, C, D\} \parallel \{A, E, C, D\}$$

$$SI(\Pi_{12}) = 2.27 \text{ bits}$$





# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

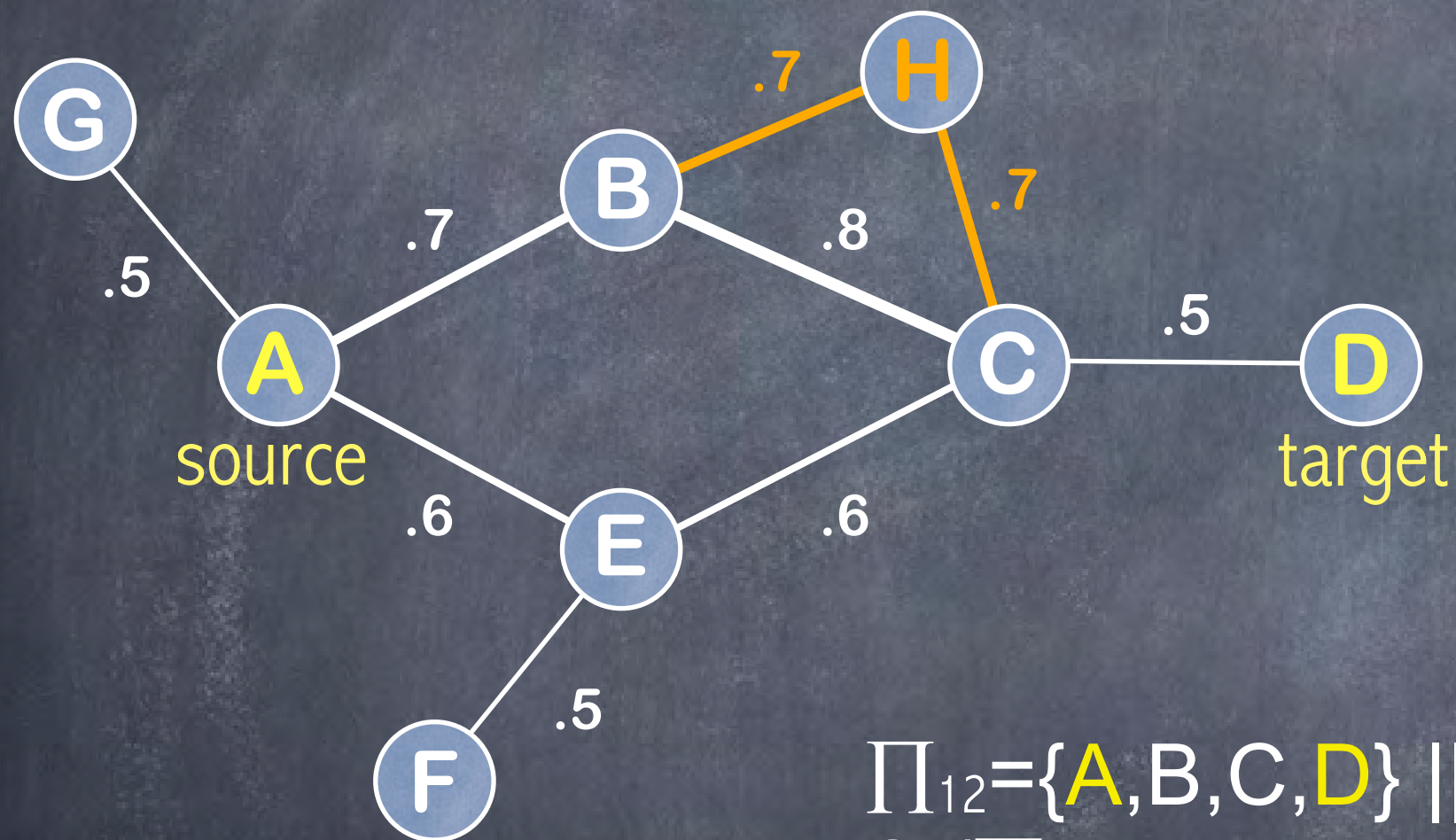
$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = 3.09 \text{ bits}$$

$$\Pi_3 = \{A, B, H, C, D\}$$

$$SI(\Pi_3) = 3.04 \text{ bits}$$



$$\Pi_{12} = \{A, B, C, D\} \parallel \{A, E, C, D\}$$

$$SI(\Pi_{12}) = 2.27 \text{ bits}$$

$$\Pi_{123} = \{A, B, C, D\} \parallel \{A, E, C, D\} \parallel \{A, B, H, C, D\}$$



# generalized k-search-information. Example B

$$\Pi_1 = \{A, B, C, D\}$$

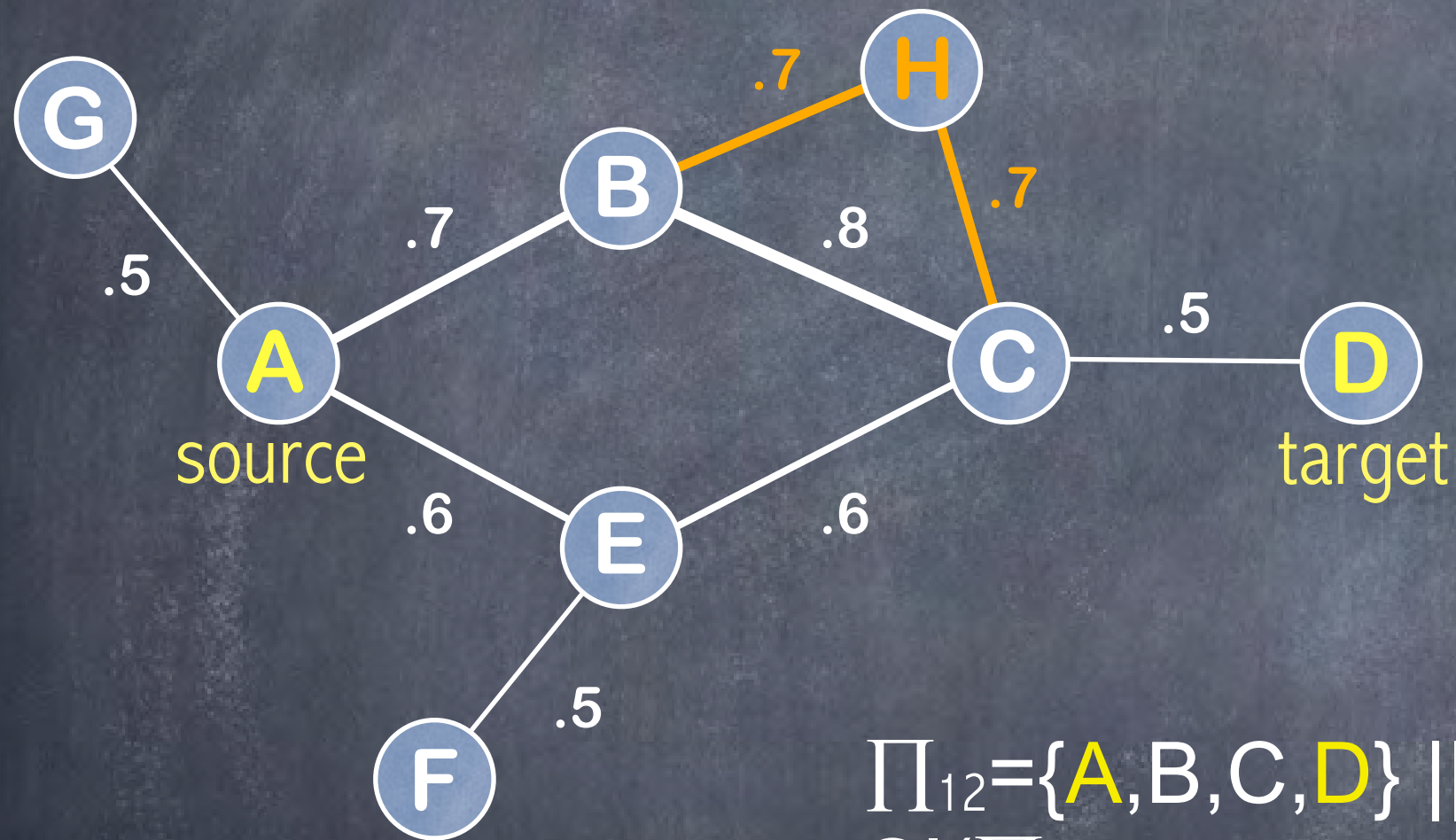
$$SI(\Pi_1) = 2.85 \text{ bits}$$

$$\Pi_2 = \{A, E, C, D\}$$

$$SI(\Pi_2) = 3.09 \text{ bits}$$

$$\Pi_3 = \{A, B, H, C, D\}$$

$$SI(\Pi_3) = 3.04 \text{ bits}$$



$$\Pi_{12} = \{A, B, C, D\} \parallel \{A, E, C, D\}$$

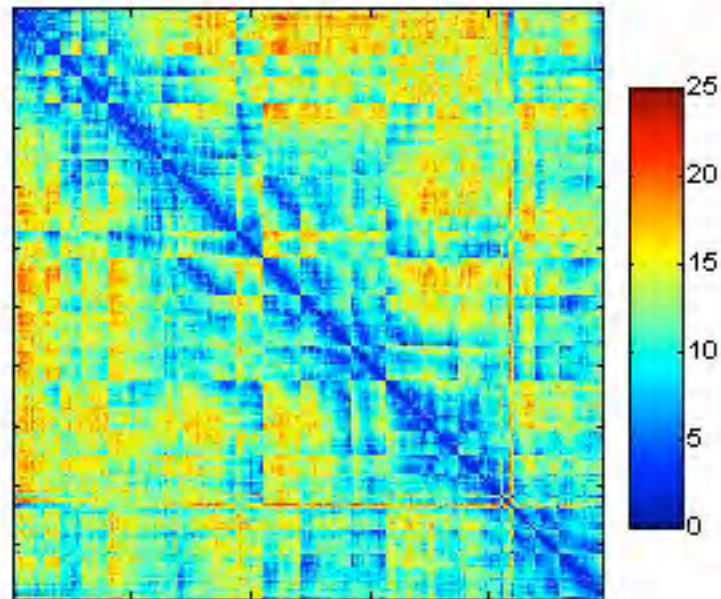
$$SI(\Pi_{12}) = 2.27 \text{ bits}$$

$$\Pi_{123} = \{A, B, C, D\} \parallel \{A, E, C, D\} \parallel \{A, B, H, C, D\}$$

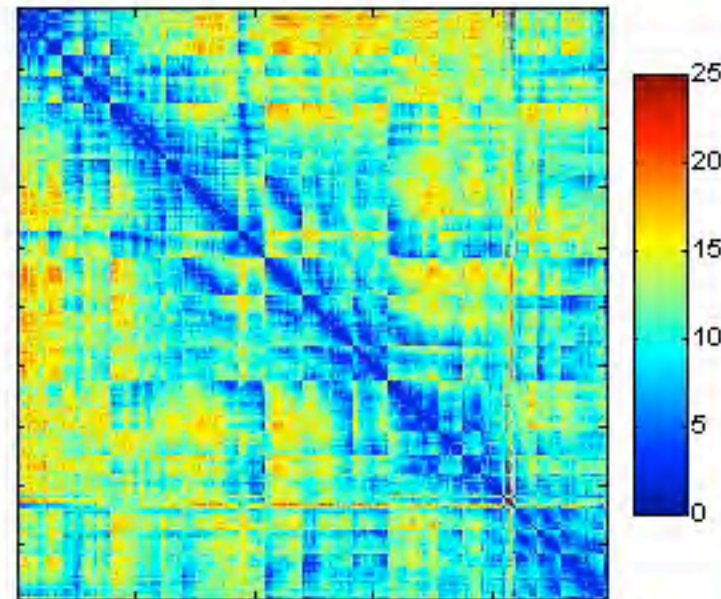
$$SI(\Pi_{123}) = 1.97 \text{ bits}$$



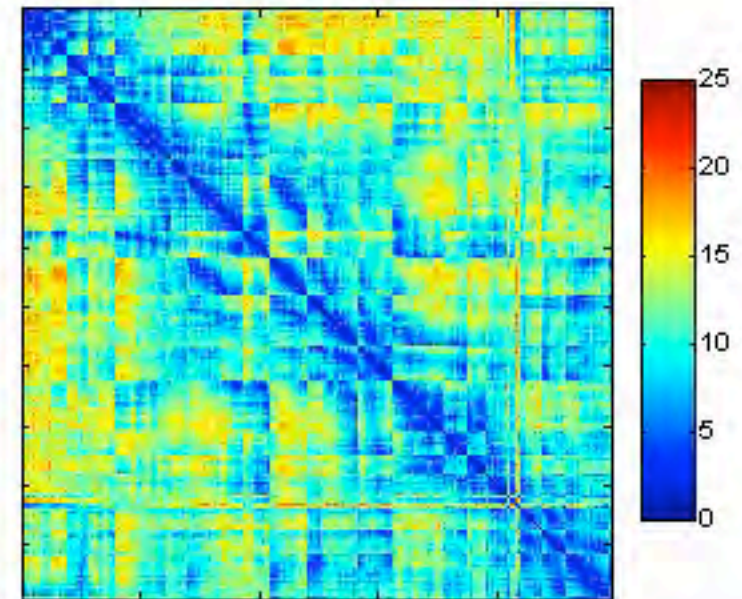
SI(k=1)



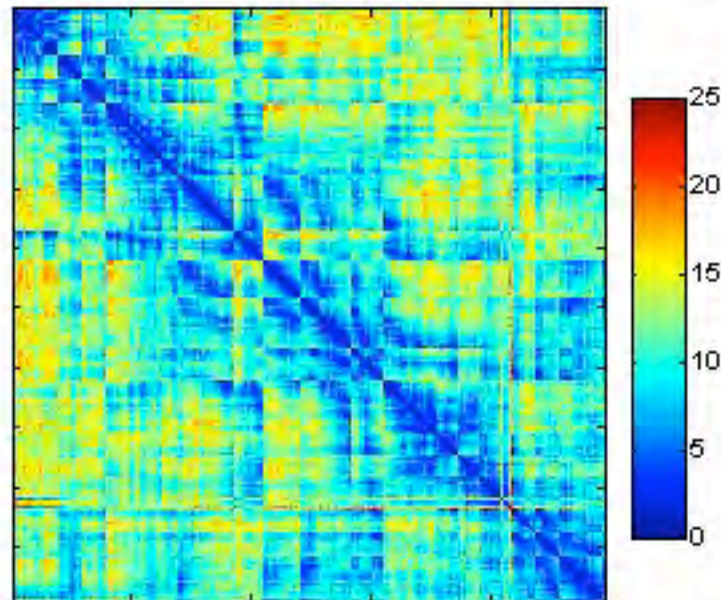
SI(k=2)



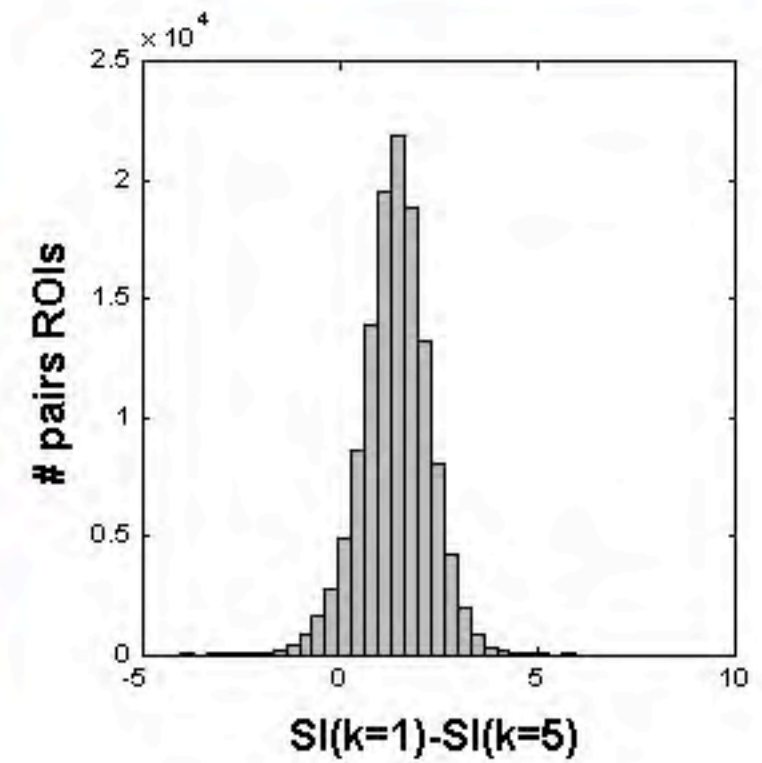
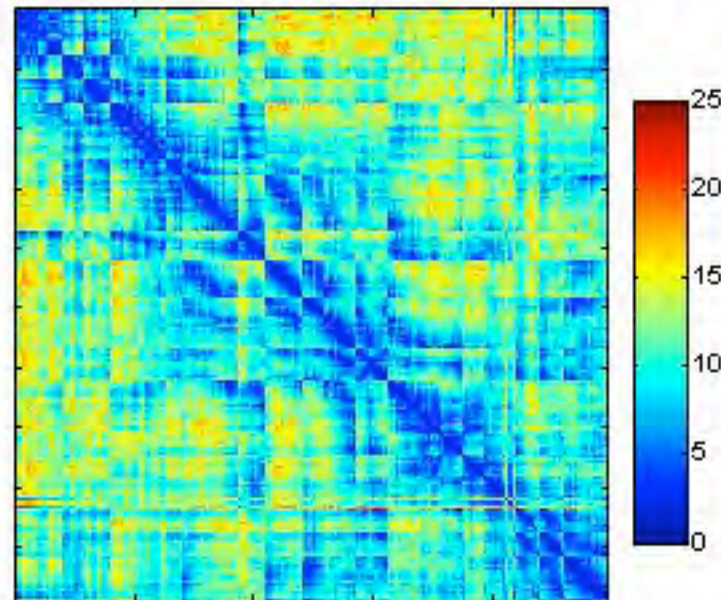
SI(k=3)



SI(k=4)



SI(k=5)

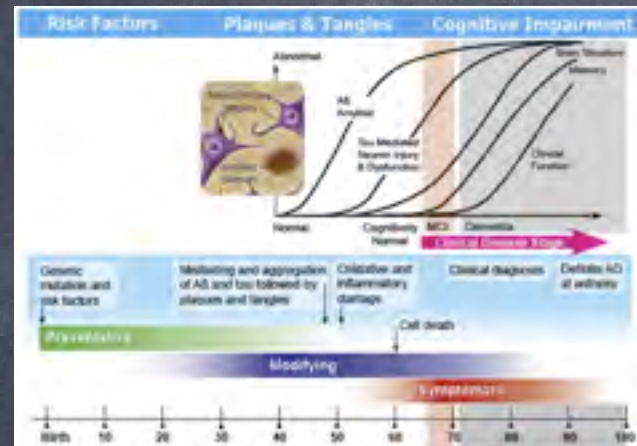


# generalized k-search-information

- Framework that permits to introduce the concept of information along the first k-shortest-paths within a system
- It represents a generalization on integration of information (by allowing local segregation).
- It permits to evaluate how a system may operate under different amounts of information.
- Challenging questions:
  - Is resting-state 'parsimonious' with respect to k-search-information?
  - Are task-specific FCs related to particular k-shortest-paths?
  - Are there k-values for which SI is particularly affected in neurodegeneration?



# Brain network disruption in neurodegeneration



- What are the network features and parcellation resolution that better characterize WM disruption in neurodegeneration?
- Mapping episodic memory into connectome neurodegeneration
- Impaired relationship between SC and FC in neurodegeneration
- Approaches based on multiplex networks

# neurodegeneration: a disconnection syndrome in “the” human connectome?

## literature summary

resolution of  
GM parcellation

definition of  
weights

article	diagnostics	# subjects	#regions	parcellation	subcortical	connectome
Daianu et al. 2013	HC,eMCI,IMCI,AD	111	68	Freesurfer	no	relative #fibers
Reijmer et al. 2013	HC,eAD	30	90	AAL	yes	relative #fibers
Bai et al. 2012	HC,aMCI,RGD	103	90	AAL	yes	#fibers
Lo et al. 2010	HC,AD	55	78	AAL	no	#fibers * FA

# Evidence of white matter disruption in MCI

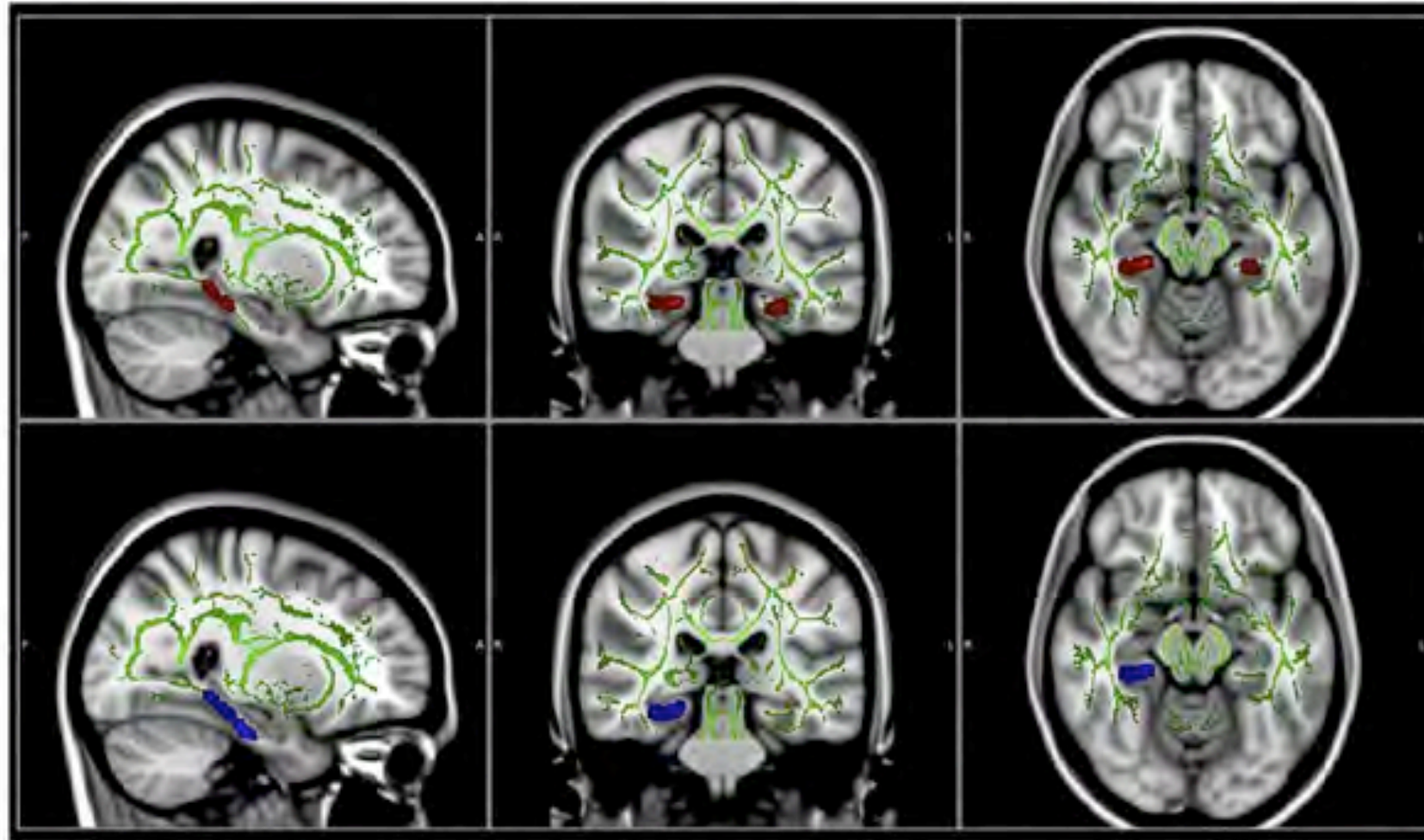
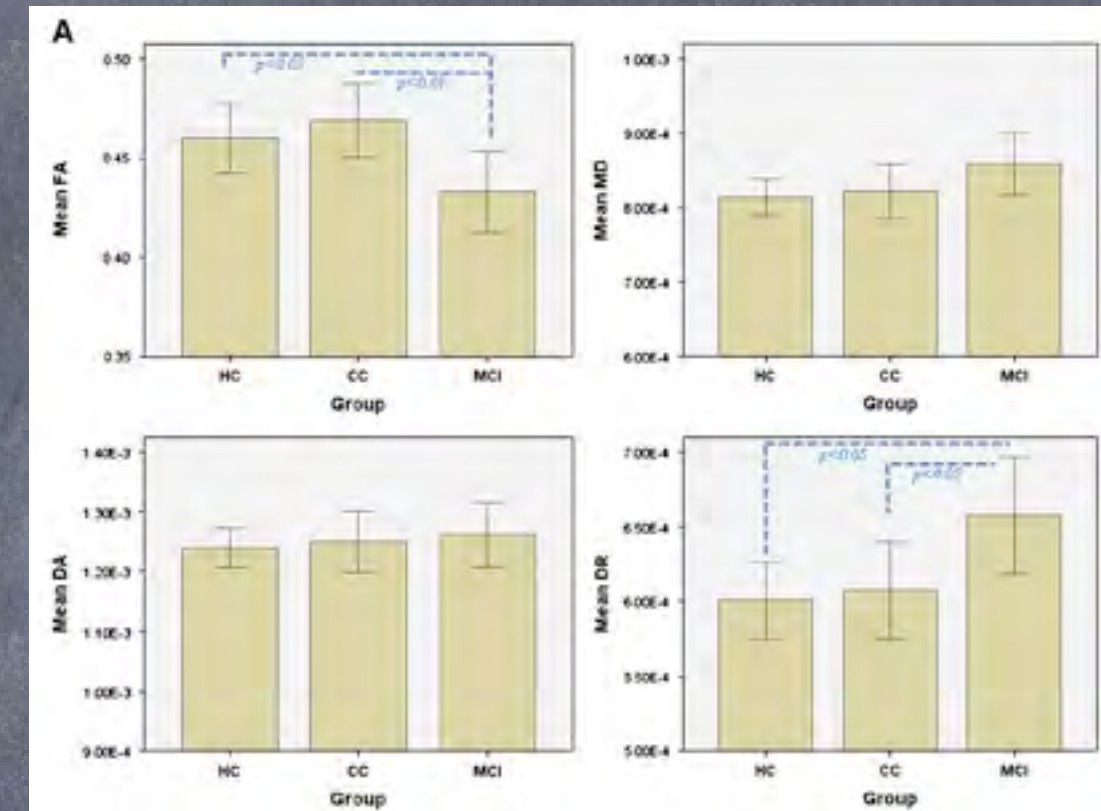


Fig. 1. Voxel-wise DTI comparison using tract-based spatial statistics analysis. The brain images showing underlying standard Montreal Neurological Institute (MNI) atlas MNI152 1-mm brain template and white matter skeleton derived from tract-based spatial statistics (TBSS) analysis (shown in green). Red color indicates tracts with reduced fractional anisotropy (FA) in bilateral parahippocampal white matter in patients with MCI vs. controls; Blue color indicates region with increased radial diffusivity (DR) in right parahippocampal white matter in MCI vs. controls. Only clusters surviving correction for multiple comparisons of voxel-wise whole brain analysis are shown on brain images ( $p < 0.01$ ). Statistical maps were dilated from the TBSS skeleton for visualization purposes.

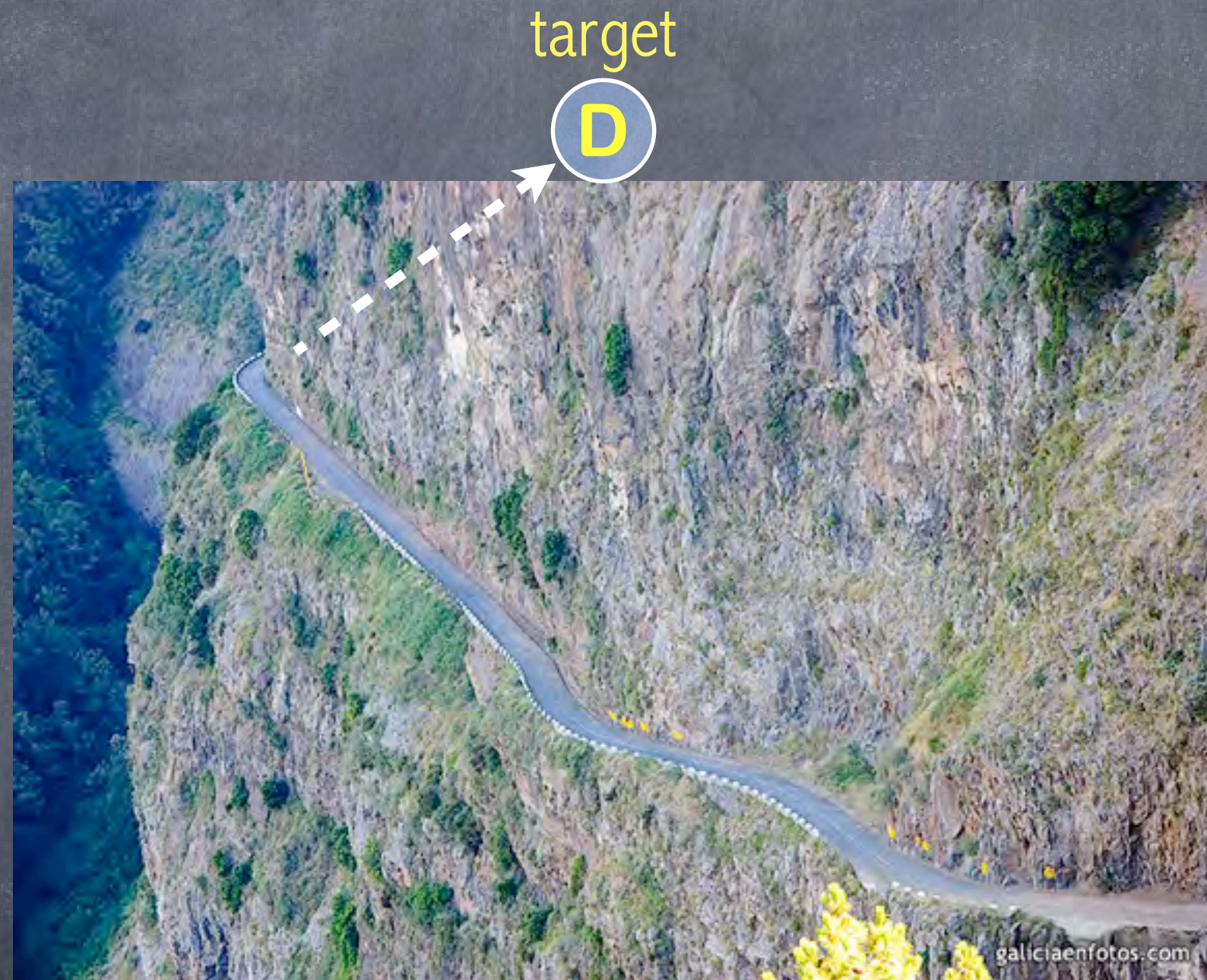


Wang et al. (2012)

Wang et al. (2012)

Reduced FA in parahippocampal WM (bilateral)  
Increased RD in parahippocampal WM (right hemisphere)

# interpretations on fractional anisotropy **along fibers**



target

D

A

source



# interpretations on fractional anisotropy **along fibers**



target

D

A

source

# interpretations on fractional anisotropy **along fibers**



source

# Evidence of white matter disruption in MCI

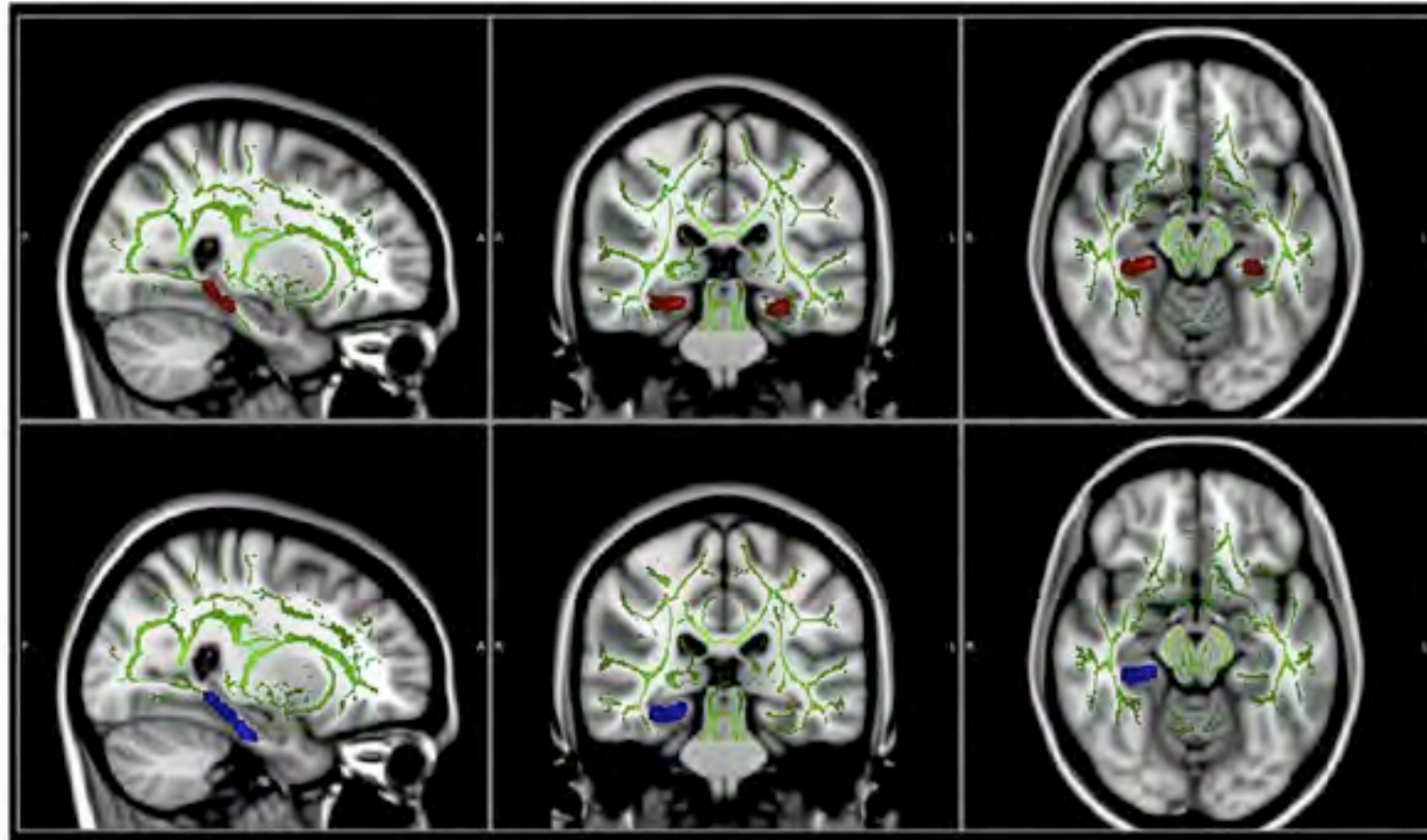
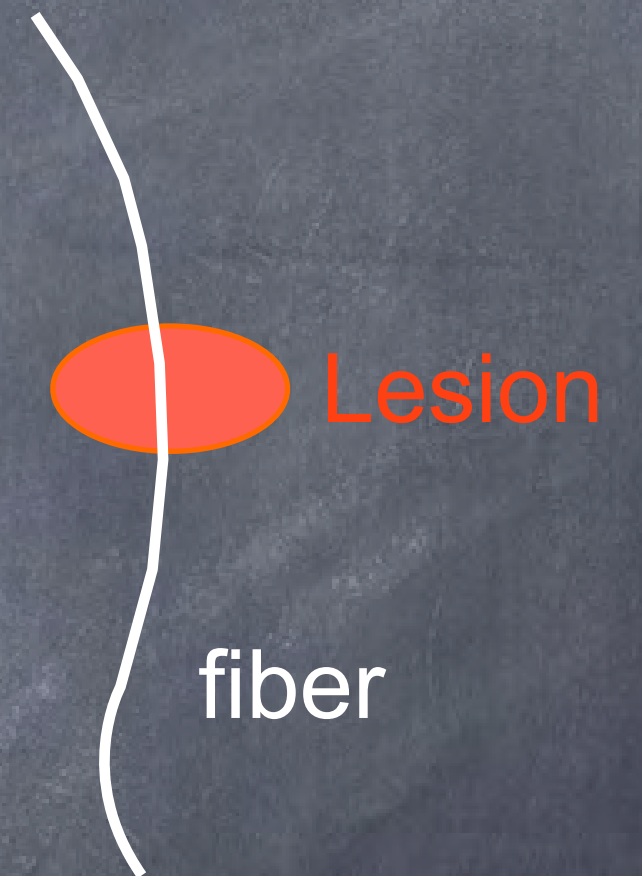


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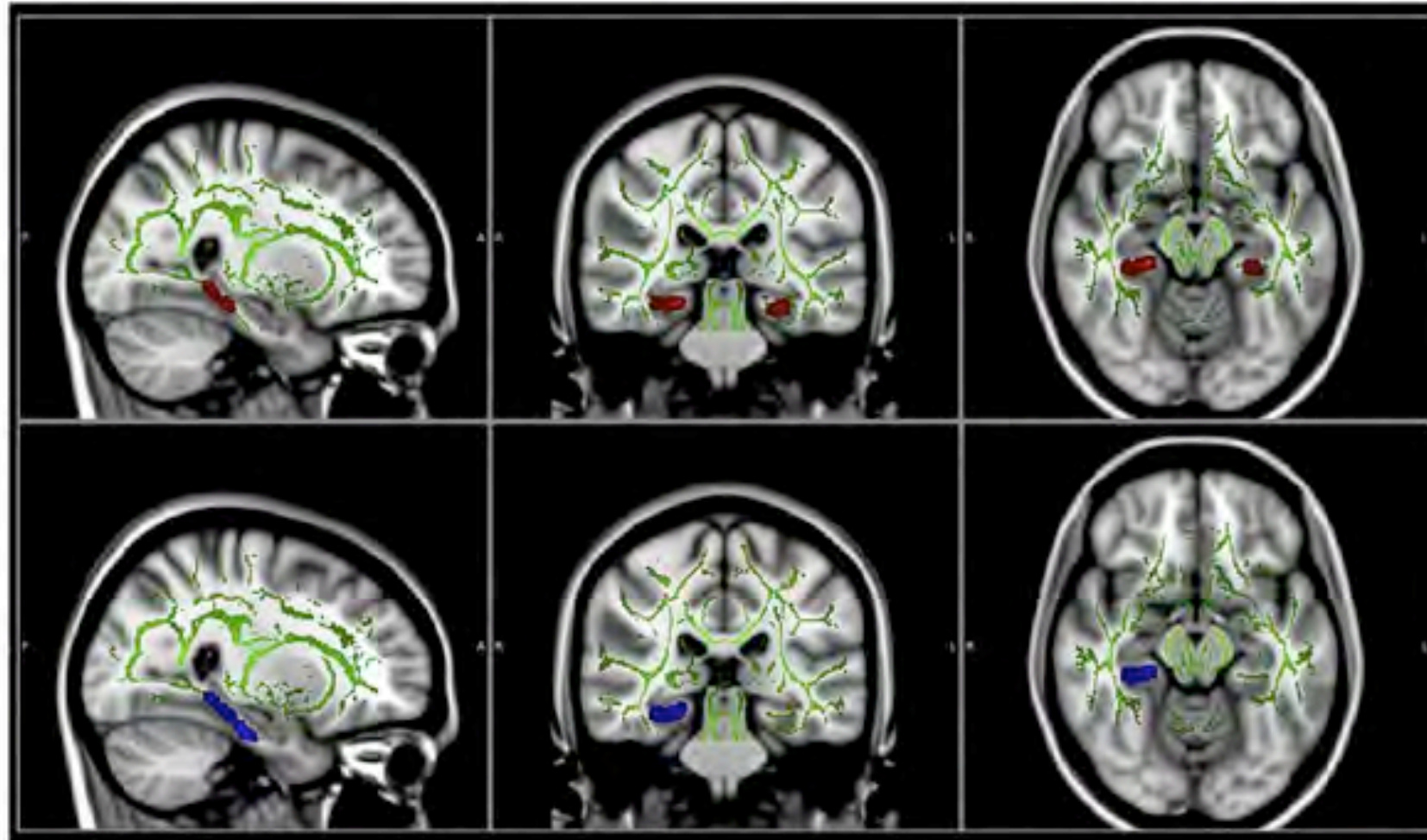
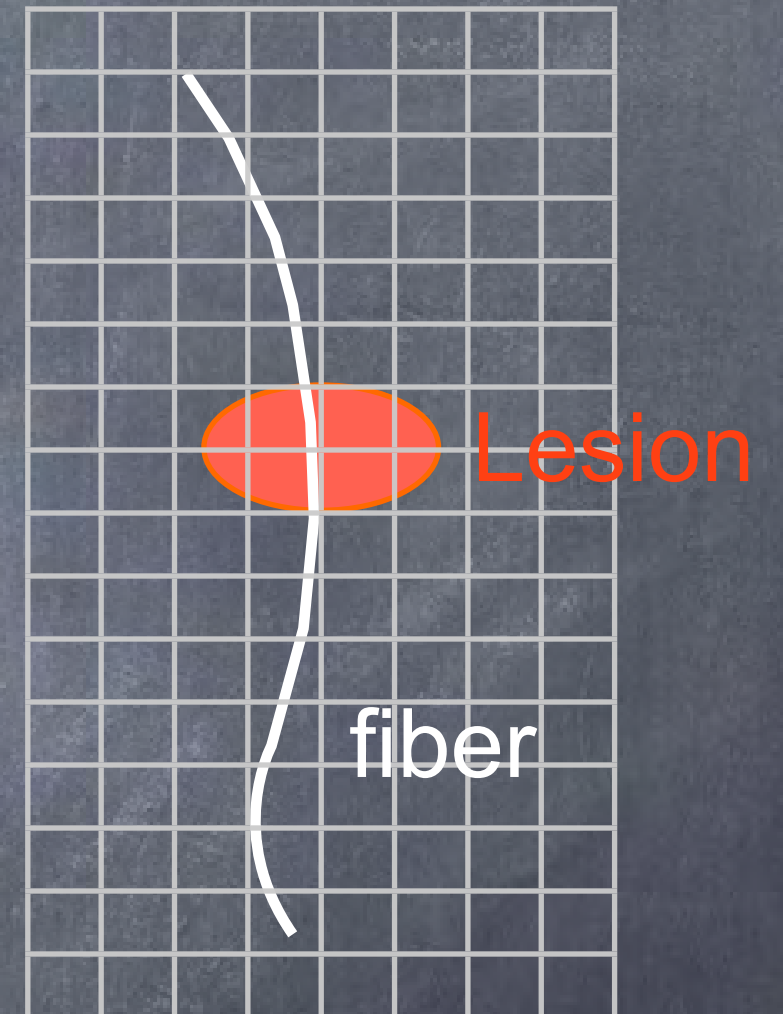


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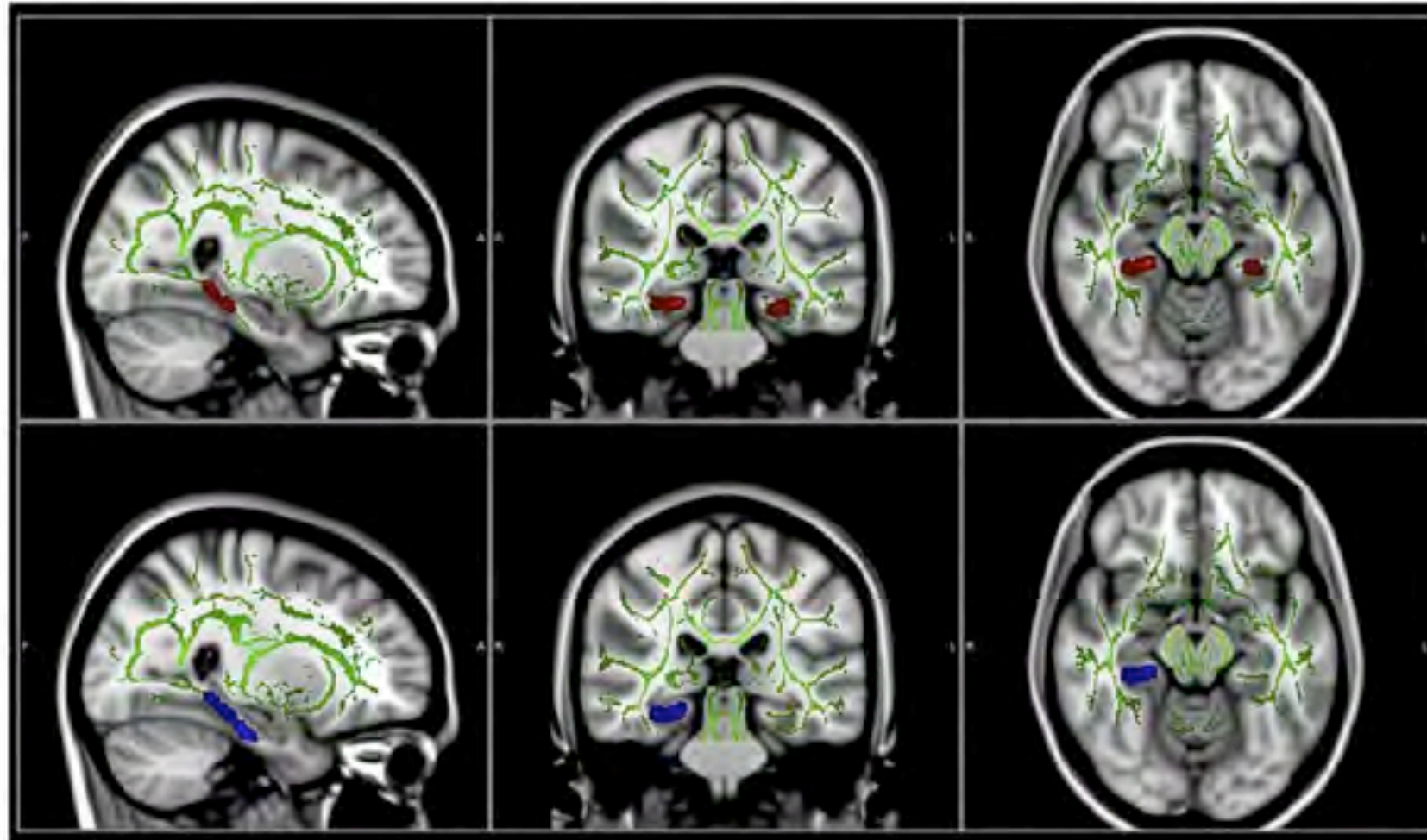
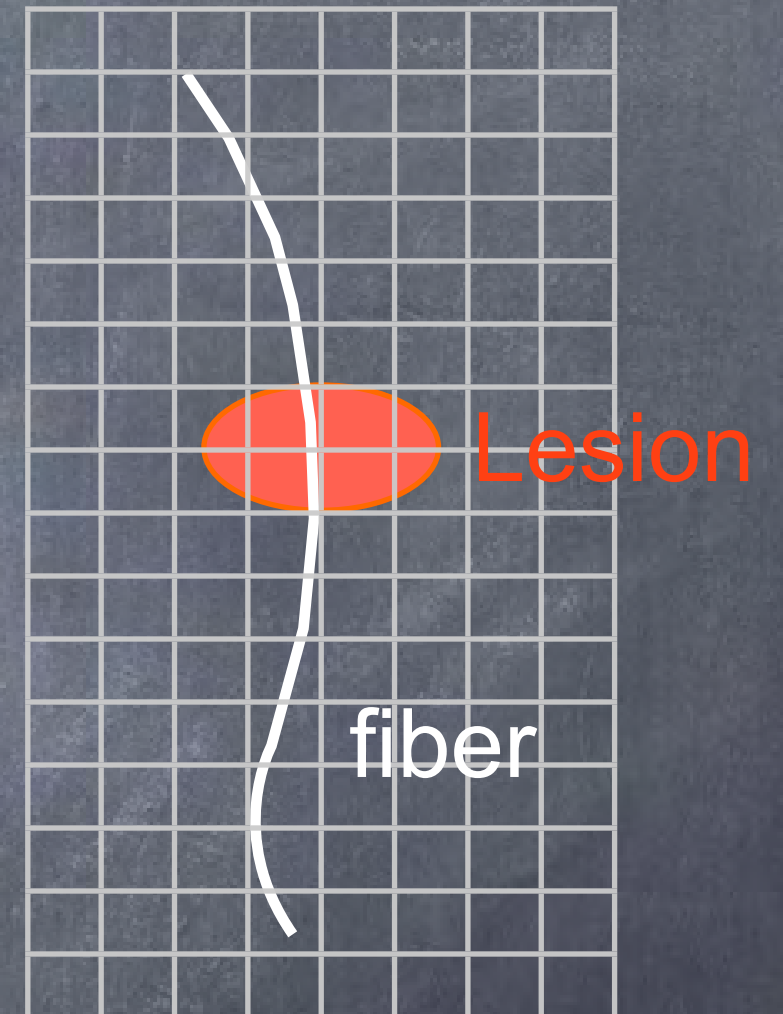


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Wang et al. (2012)

Reduced FA in parahippocampal WM (bilateral)  
Increased RD in parahippocampal WM (right hemisphere)



2 out of 15 voxels  
go through the lesion

thank you for your attention



Joaquín Goñi  
jgonicor@indiana.edu

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Dpt. of Radiological and Imaging Sciences. School of Medicine, IU