The Waisman Laboratory for Brain Imaging and Behavior

University of Wisconsin
SCHOOL OF MEDICINE AND PUBLIC HEALTH

Topological Learning for Brain Networks

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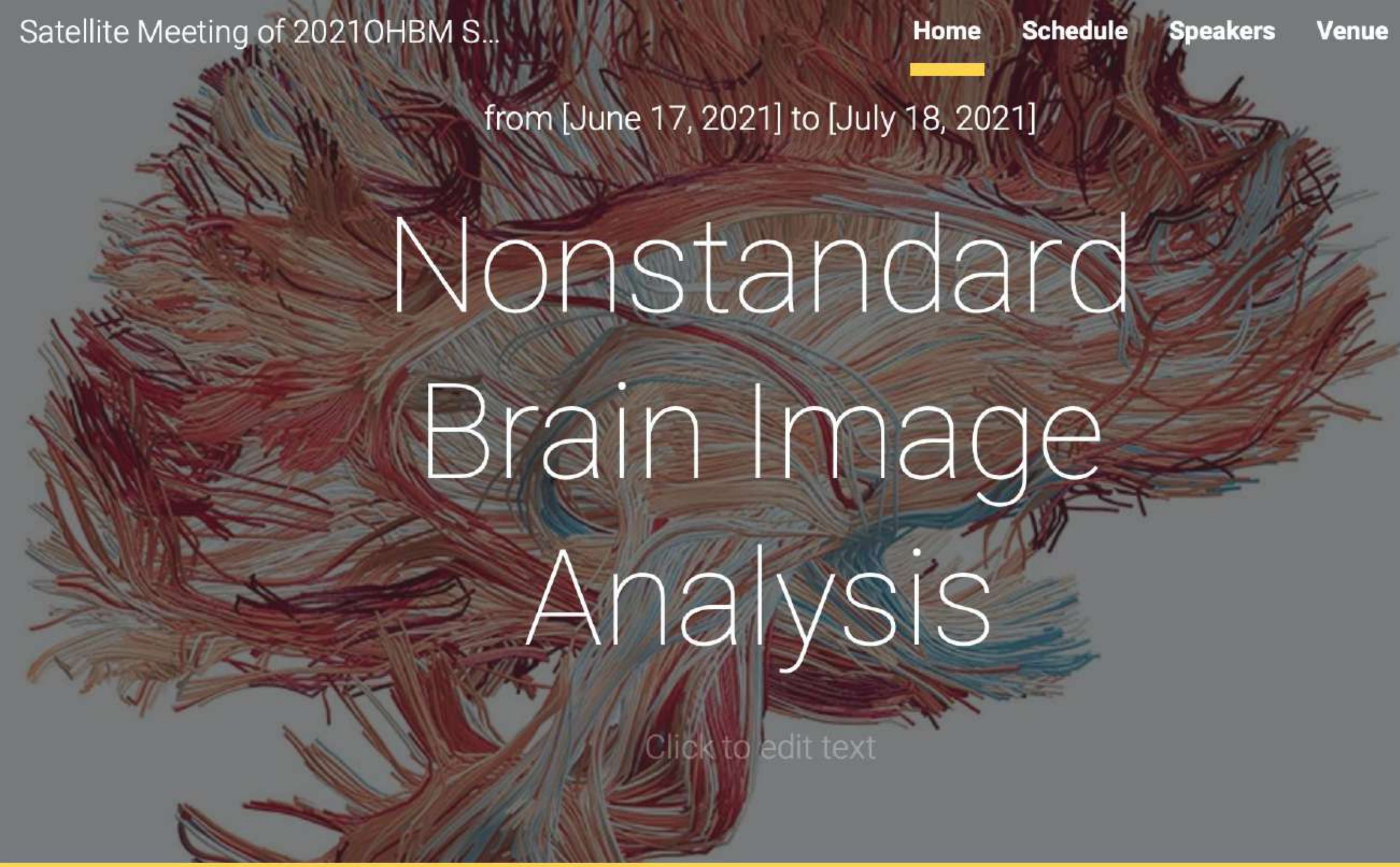


Satellite Meeting of 2021 OHBM

Date: June 17-18, 2021

Place: Virtual Zoom conference

Aim: Please join us in Seoul for the **Workshop on Nonstandard Brain Image Analysis (NBIA)**. This satellite meeting will be held after the Organization for Human Brain Mapping (OHBM) annual meeting. **NBIA 2021** will focus on showcasing various emerging nonstandard or experimental techniques in brain image processing and analysis. This workshop combines lectures by leaders in the field of processing and analysis, poster sessions and other opportunities to network. The workshop is meant to inform and educate students and researchers on emerging methods. The workshop follows the spirit of the previous succesful workshop NBIA 2018 in Singapore.

Satellite meeting of OHBM 2021

June 17-18, 2021
~~Seoul, Korea~~
Virtual Zoom

Organizers:
Vince Calhoun
Moo K. Chung
Yong Jeong
Martin Lindquist
Hea-Jeong Park
Anqi Qiu

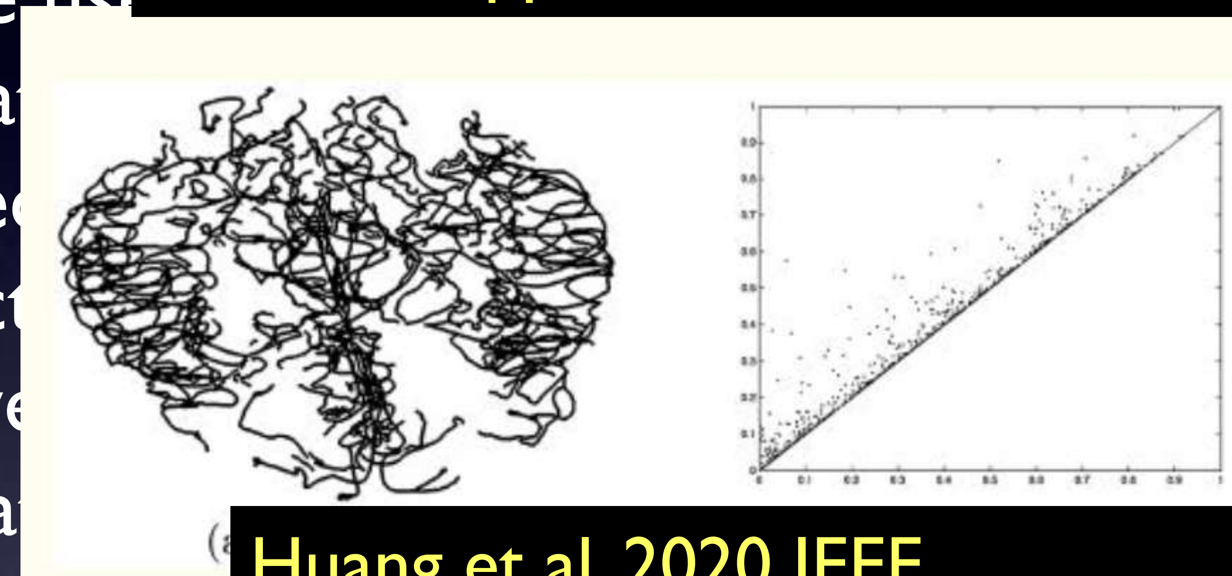
http://sites.google.com/view/nbia2021

Abstr

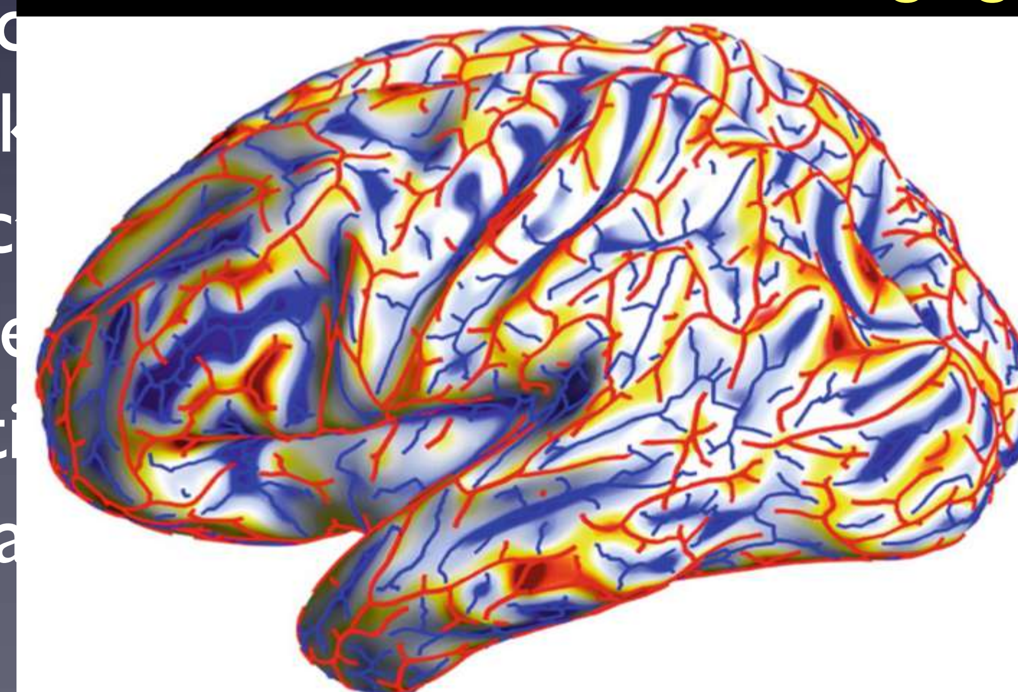
arXiv:2012.00675

We prese ... tegrate
... persistent homology.
... ction o
... llenging tasks. The use
... bypasses the intrinsic computa
matching networks. The method is effe
imaging study in determining if the func
heritable. The biggest challenge is in ove
networks obtained from the resting-sta
imaging (fMRI) onto the structural brain netw
... While the func
... work is tree-lik
... on top of struc
... We found the
... ar demonstrati
... terns. This is a
... iwut.

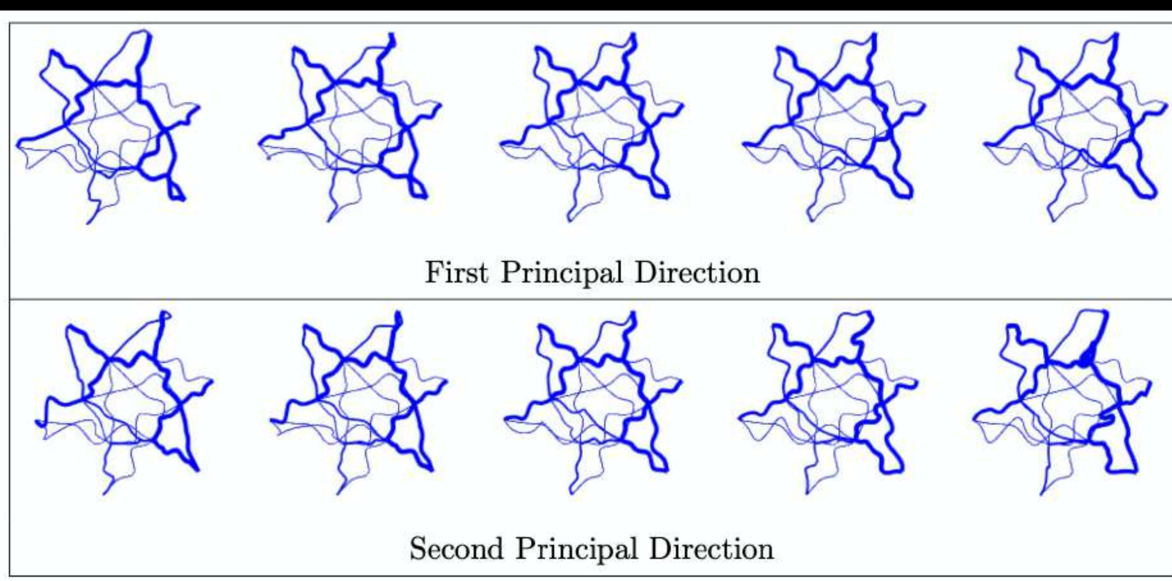
Steve Marron: persistent homology
Annals of applied statistics 2016



Huang et al. 2020 IEEE Transactions on Medical Imaging



Anuj Srivastava: elastic graph matching
arXiv: 2007.04793



Acknowledgement

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Seoul National University, Korea
Shih-Gu Huang, Anqi Qiu National University of Singapore
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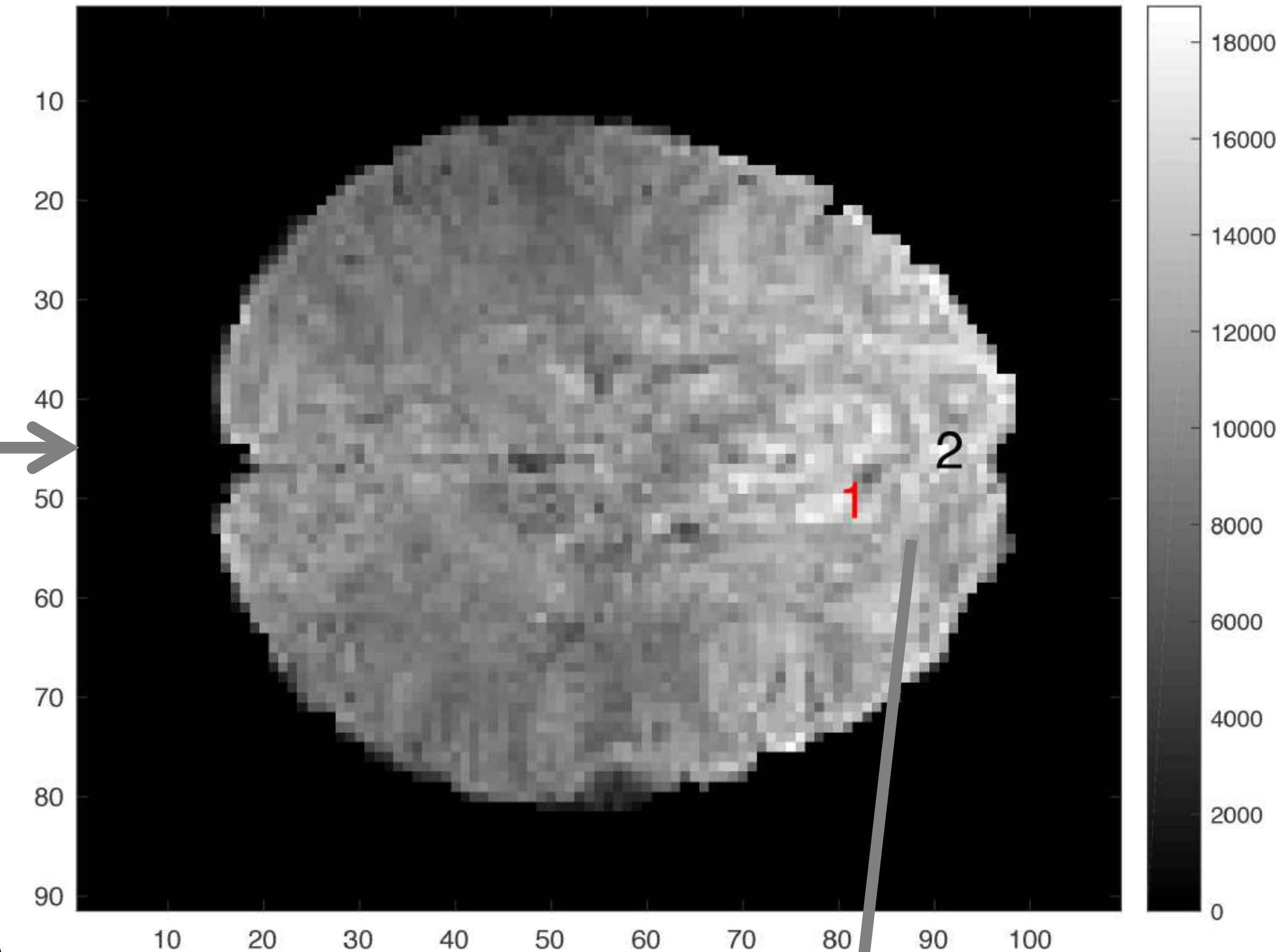
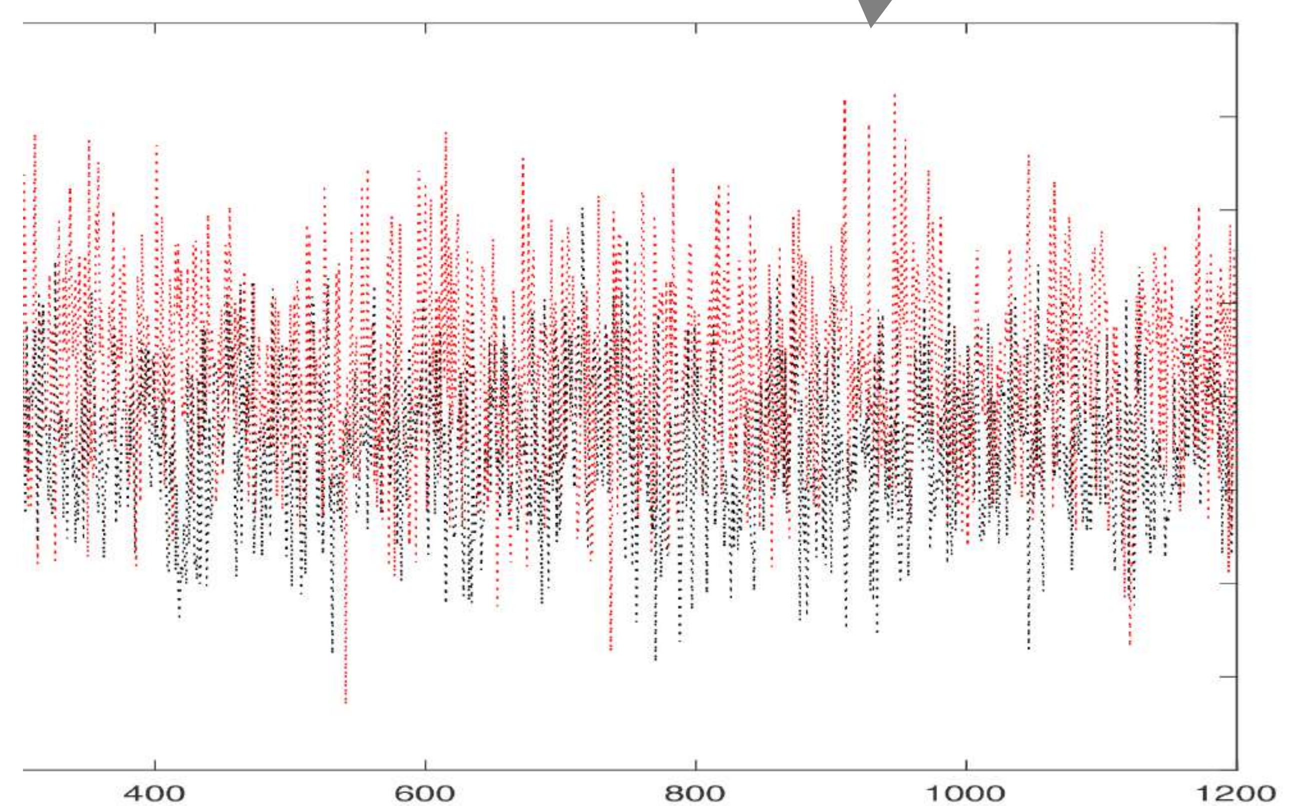
NIH R01 Brain Initiative EB022856, R01 EB028753, NSF DMS-2010778

Resting-state functional magnetic resonance imaging (rs-fMRI)

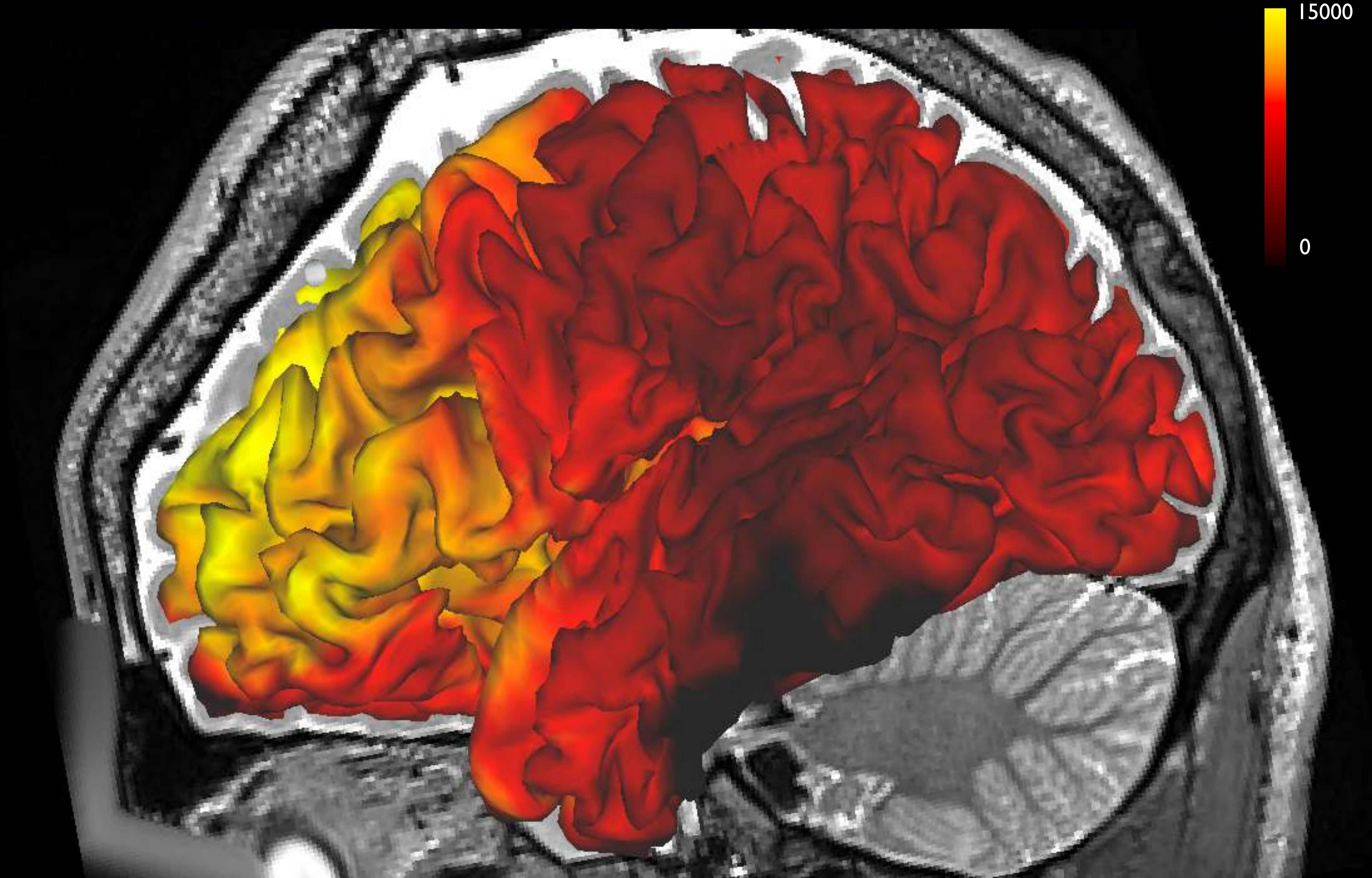




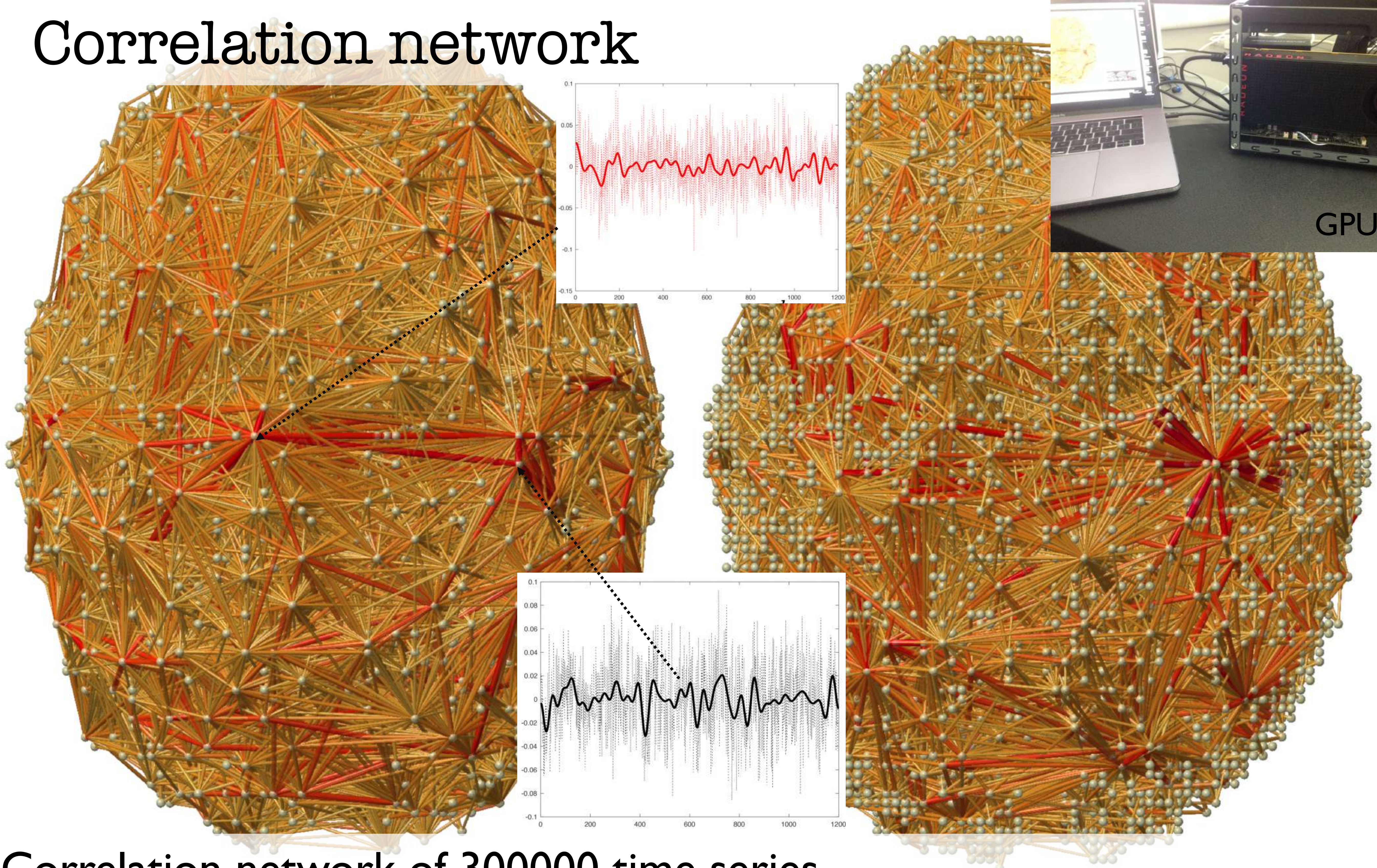
1200 time points and 300000 voxels per subject over 14min 33 seconds inside a 3T scanner at rest

After motion correction, scrubbing….
400 subjects (124 MZ twins
70 same-sex DZ twins)
x 2GB = 800GB data

Resting state fMRI (every 30 second)



Correlation network

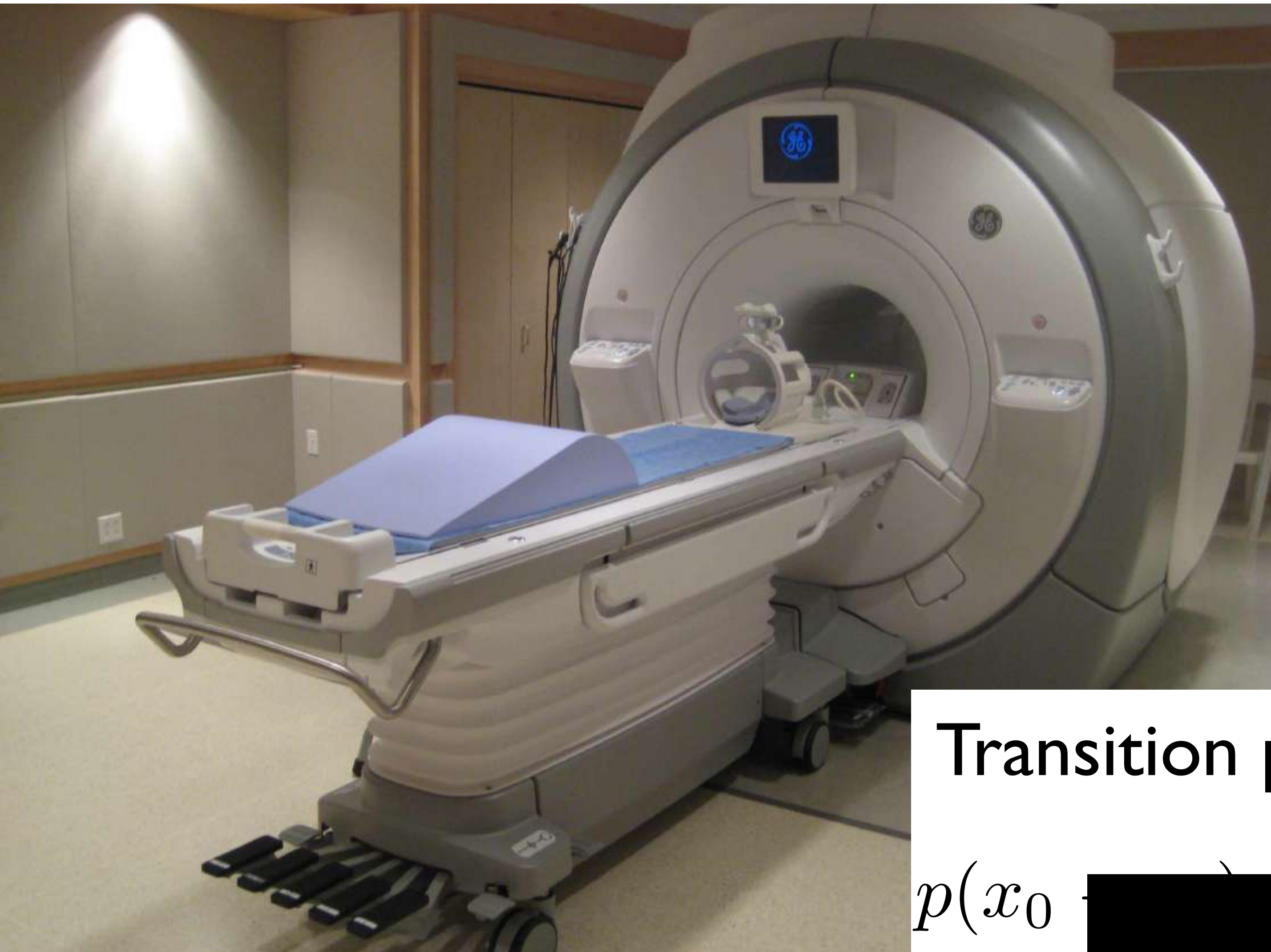


Correlation network of 300000 time series

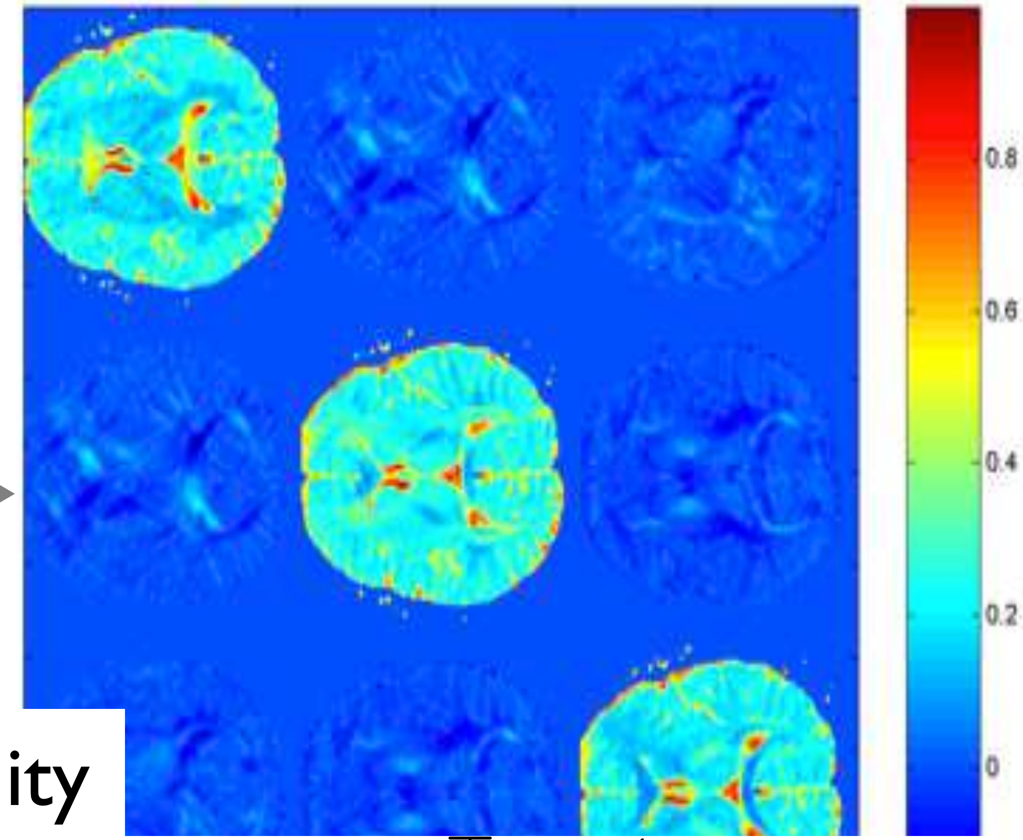
Complete graph with many cycles.

Chung et al. 2019 Network Neuroscience

Diffusion tensor Imaging (DTI)

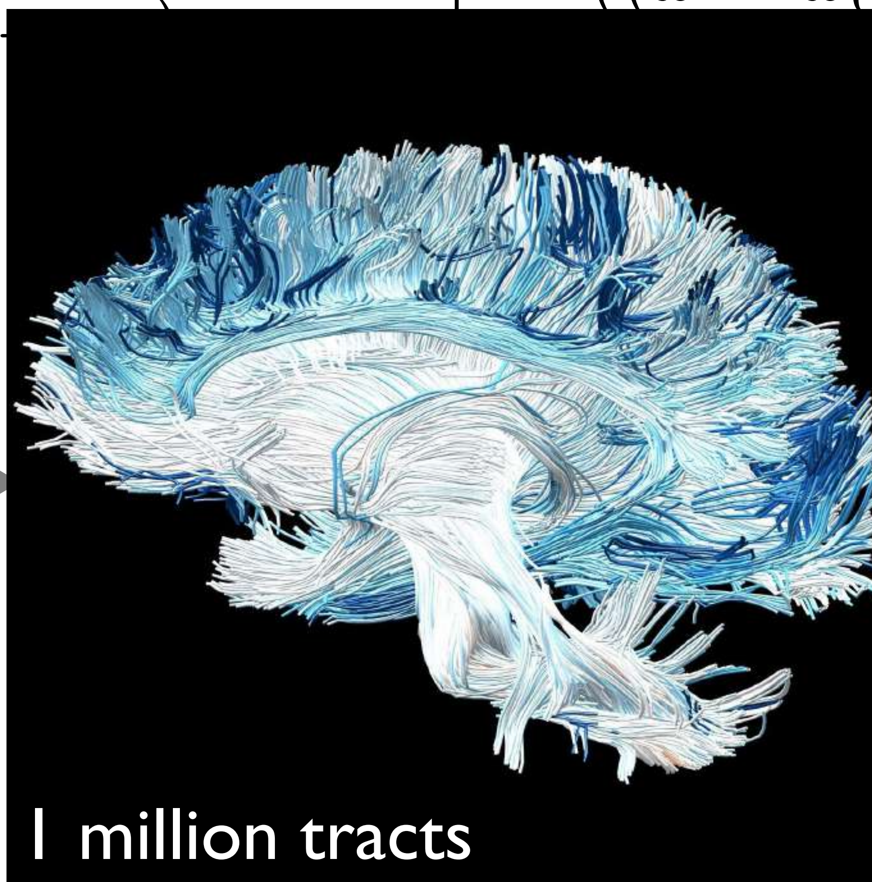


Diffusion tensor *D*



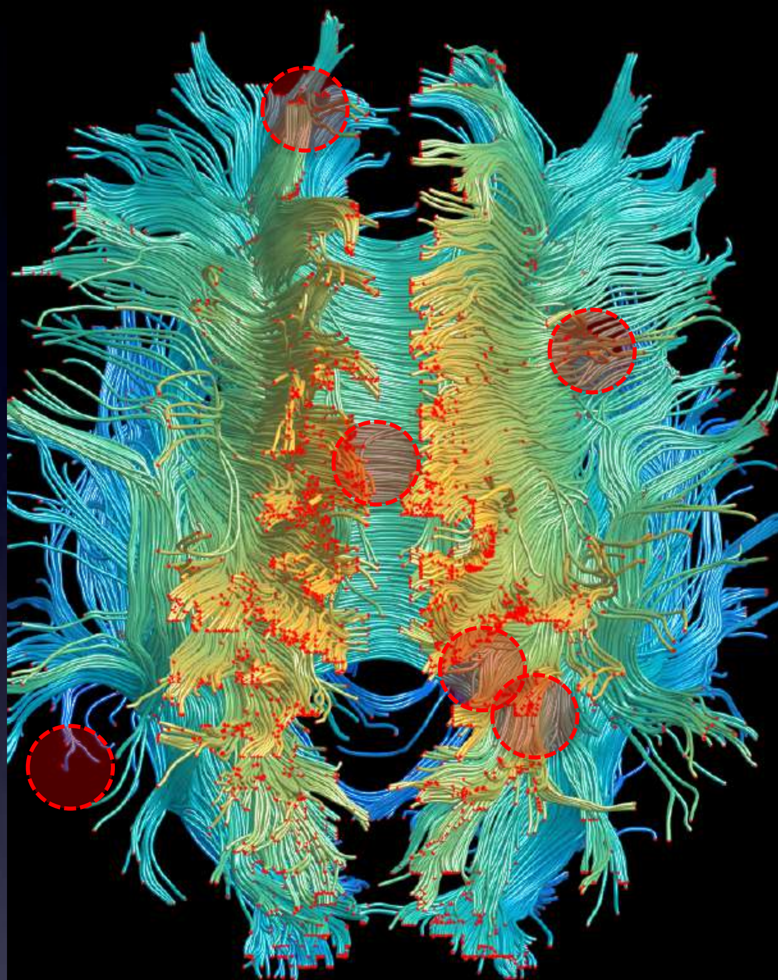
Transition probability

$p(x_0$ … $\left[\frac{((x-x_0)^\top D^{-1}(x-x_0)}{4\tau} \right]$



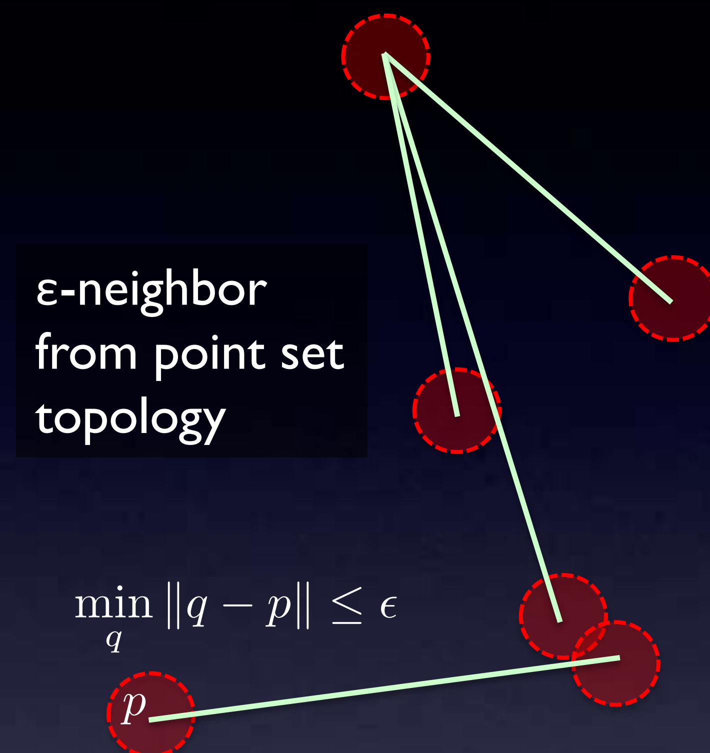
Epsilon-neighbor network construction

Parcellation free brain network construction



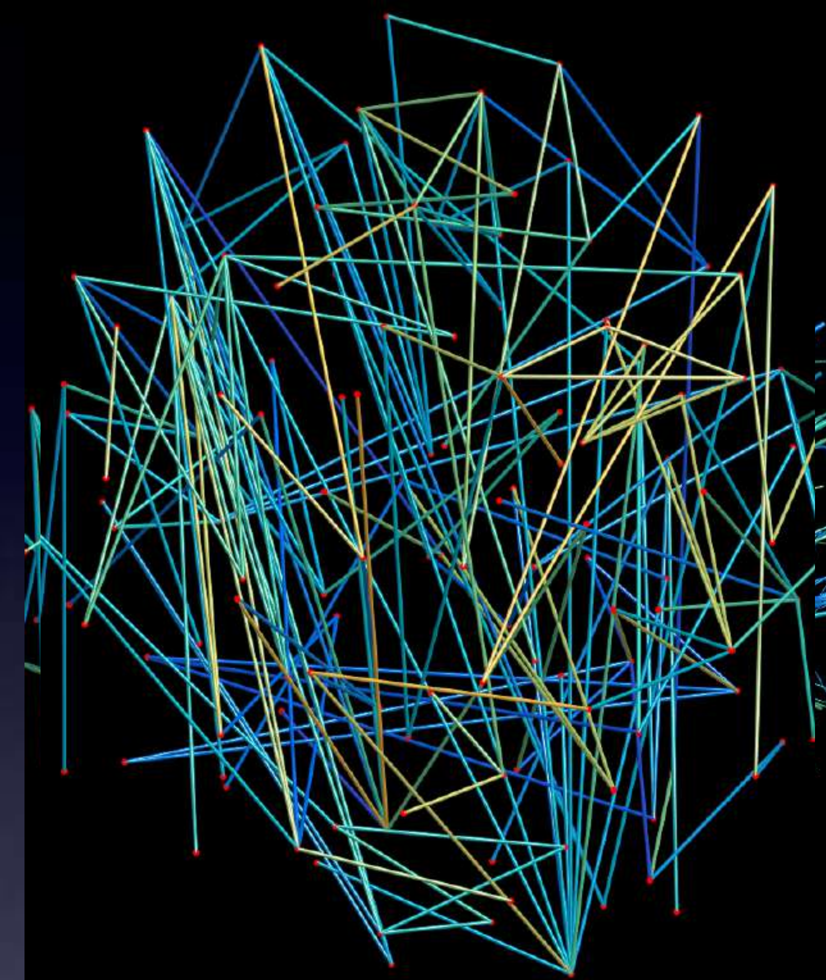
White matter fibers

Part I: Fiber tractography



Iteratively add one edge at a time

Part II: ε-neighbor construction



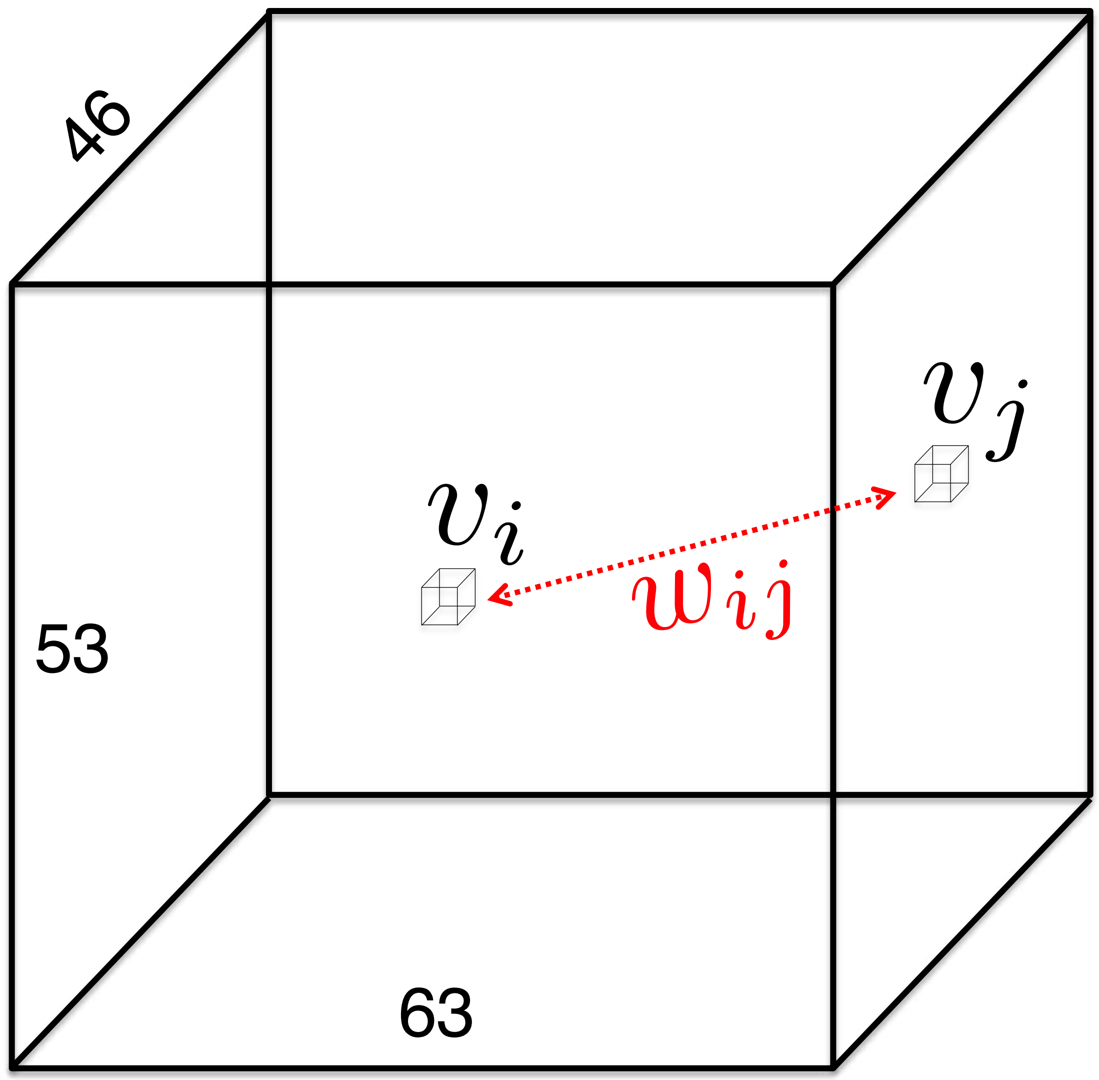
Multiscale brain network

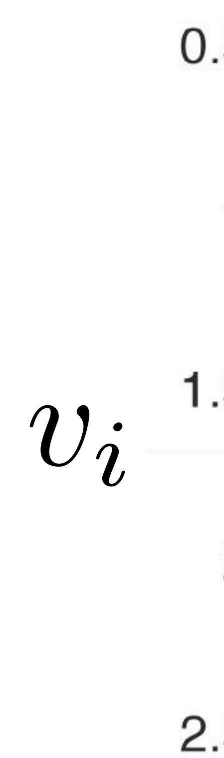
Part III: 3D network graph

Finding: 96% of all nodes are connected to each other to form a <u>tree-like</u> single connected component

<u>Chung et al. 2011 SPIE 7962</u>

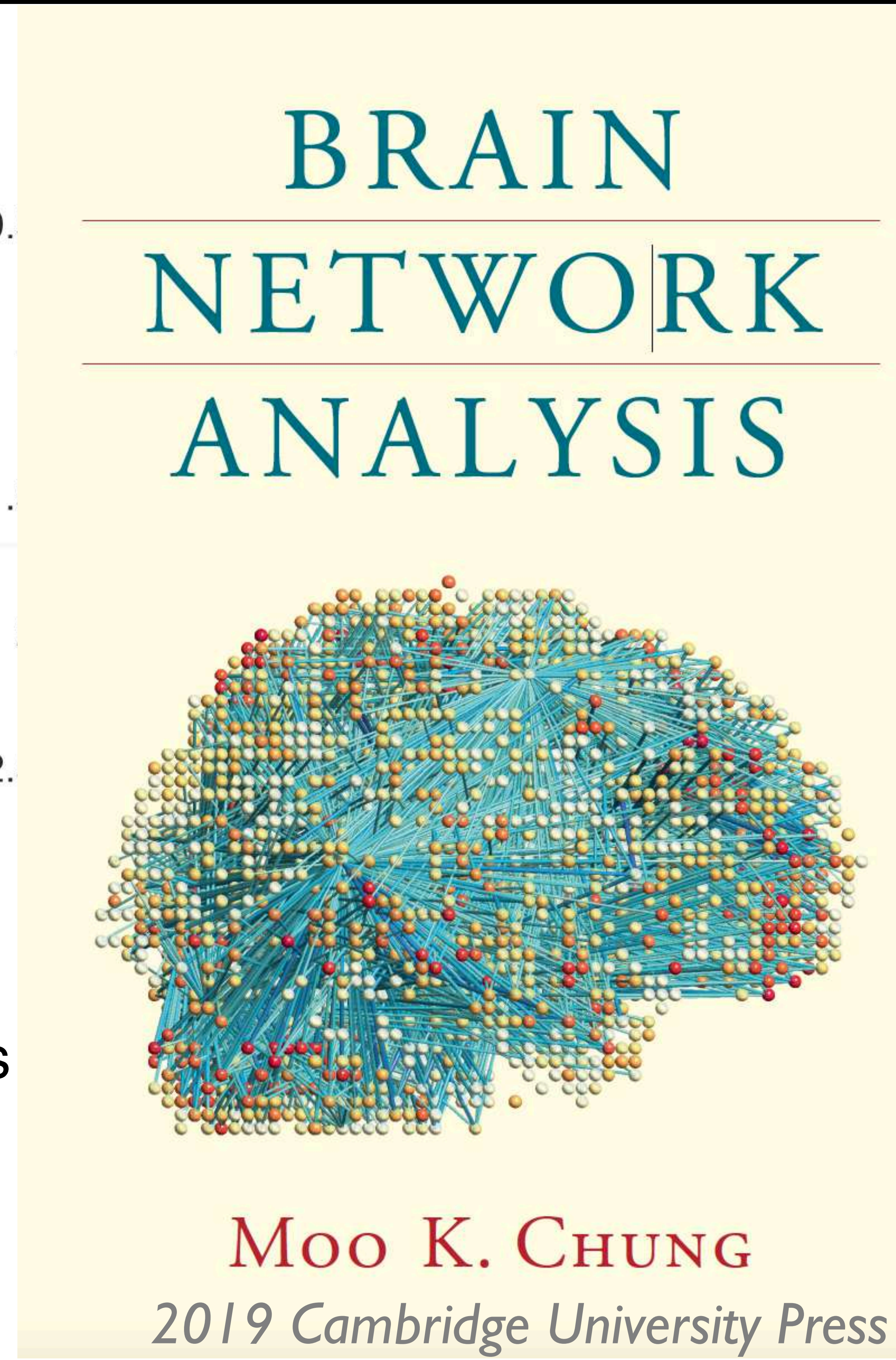
How big is brain network data?



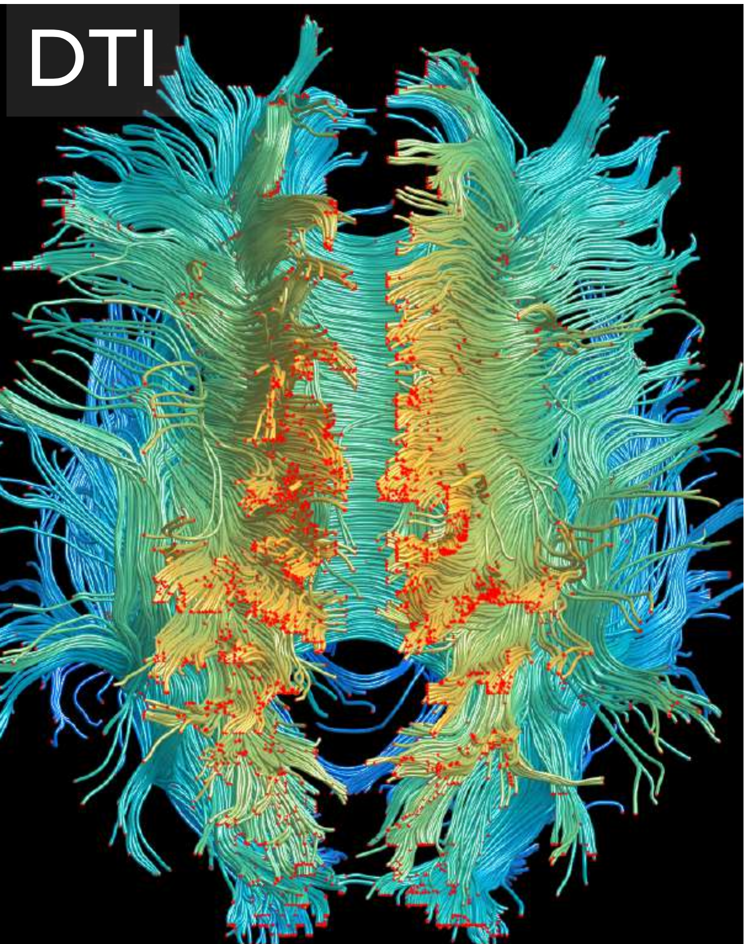


p=25972 voxels (3mm) in the brain
→ 25972 x 25972 = 0.67 billion connections
5.2GB memory

300000 voxels (1mm)
→ 90 billion connections
→ 700 GB memory



Biological data reduction: Parcellation based network construction



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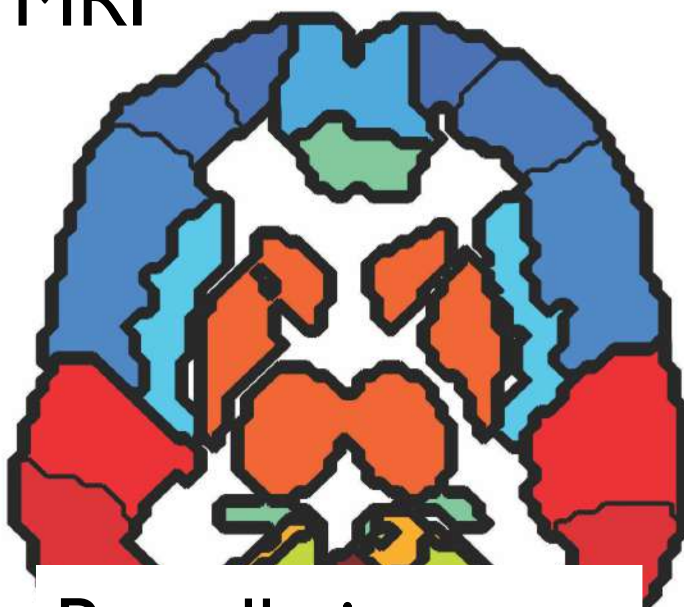
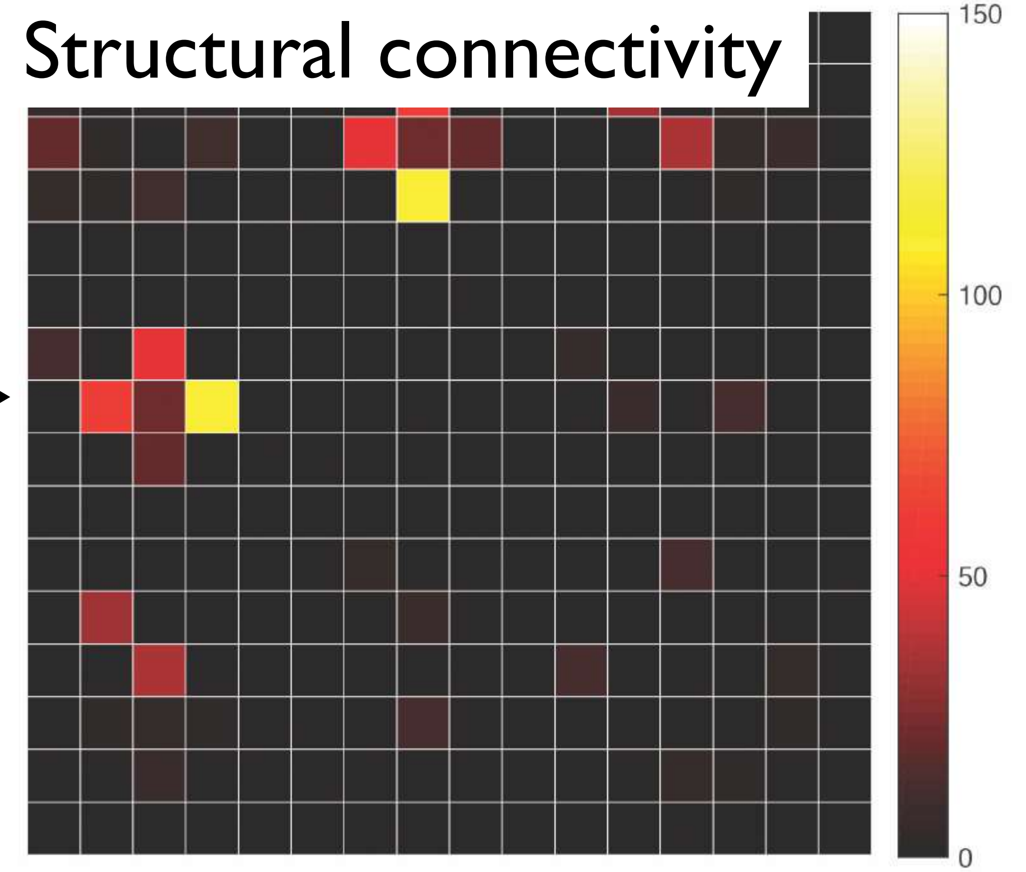
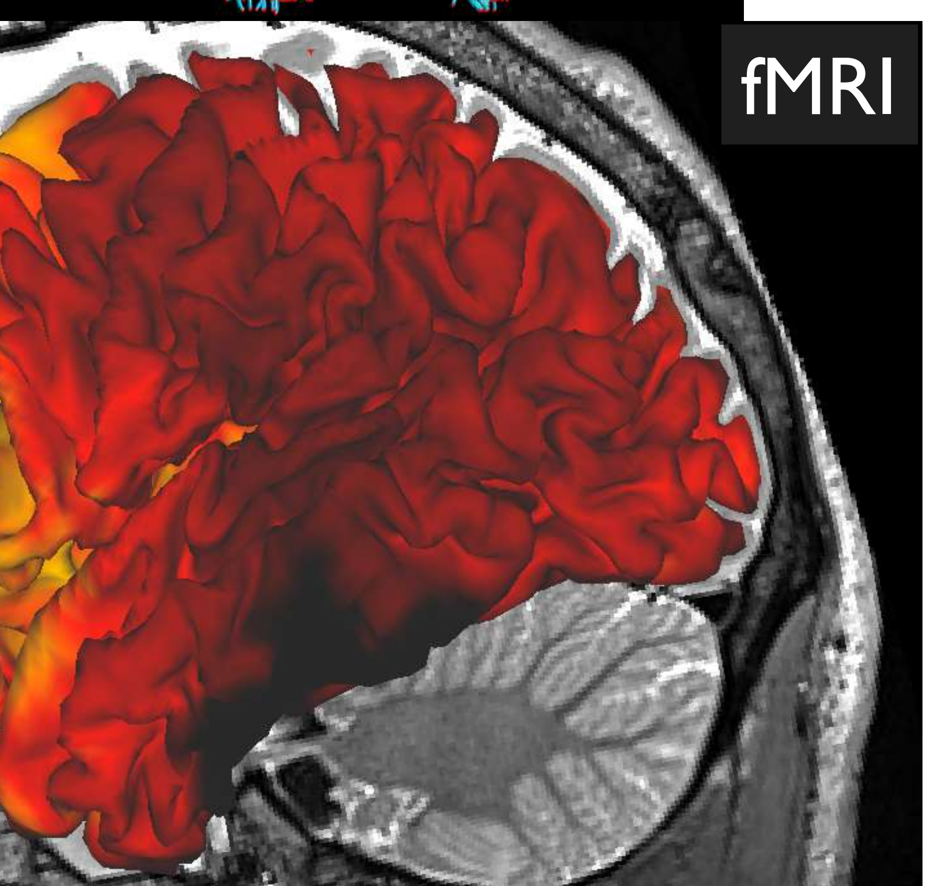


Parcellation partition brain into 116 regions





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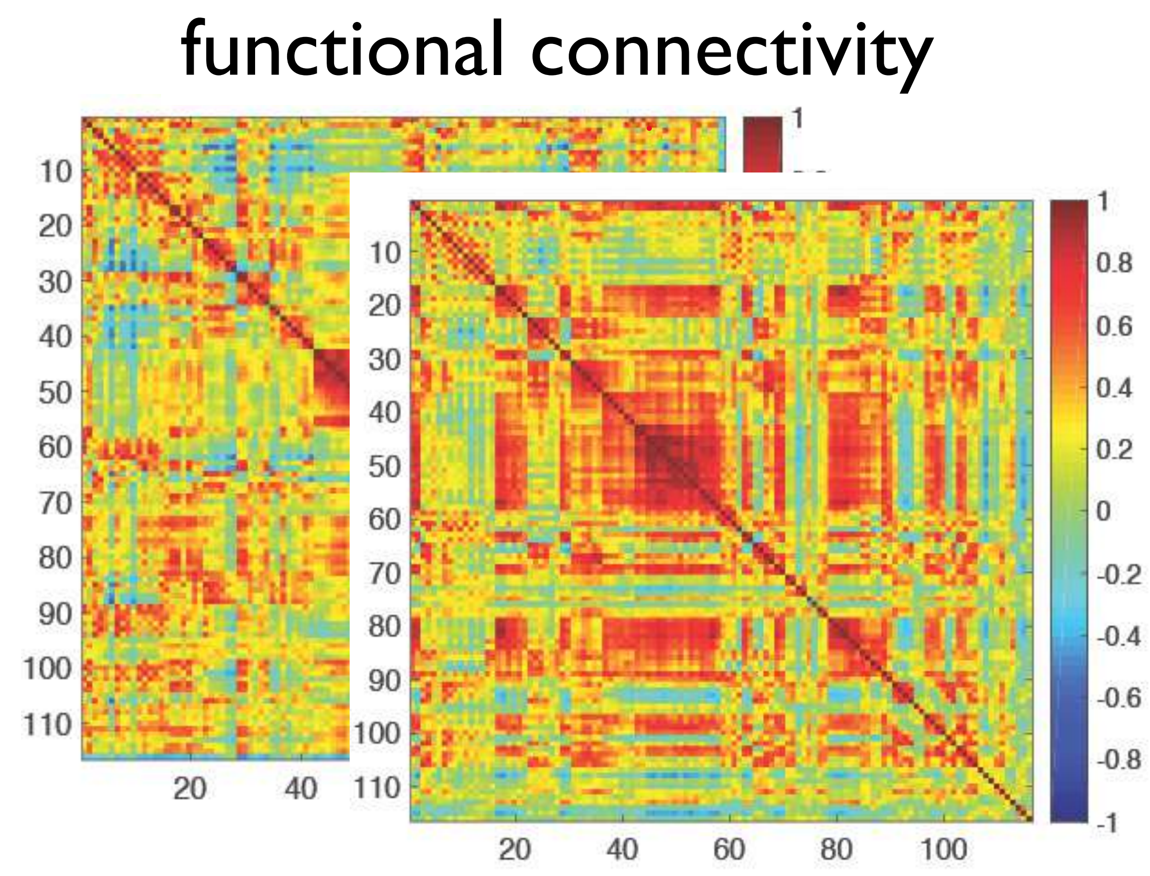
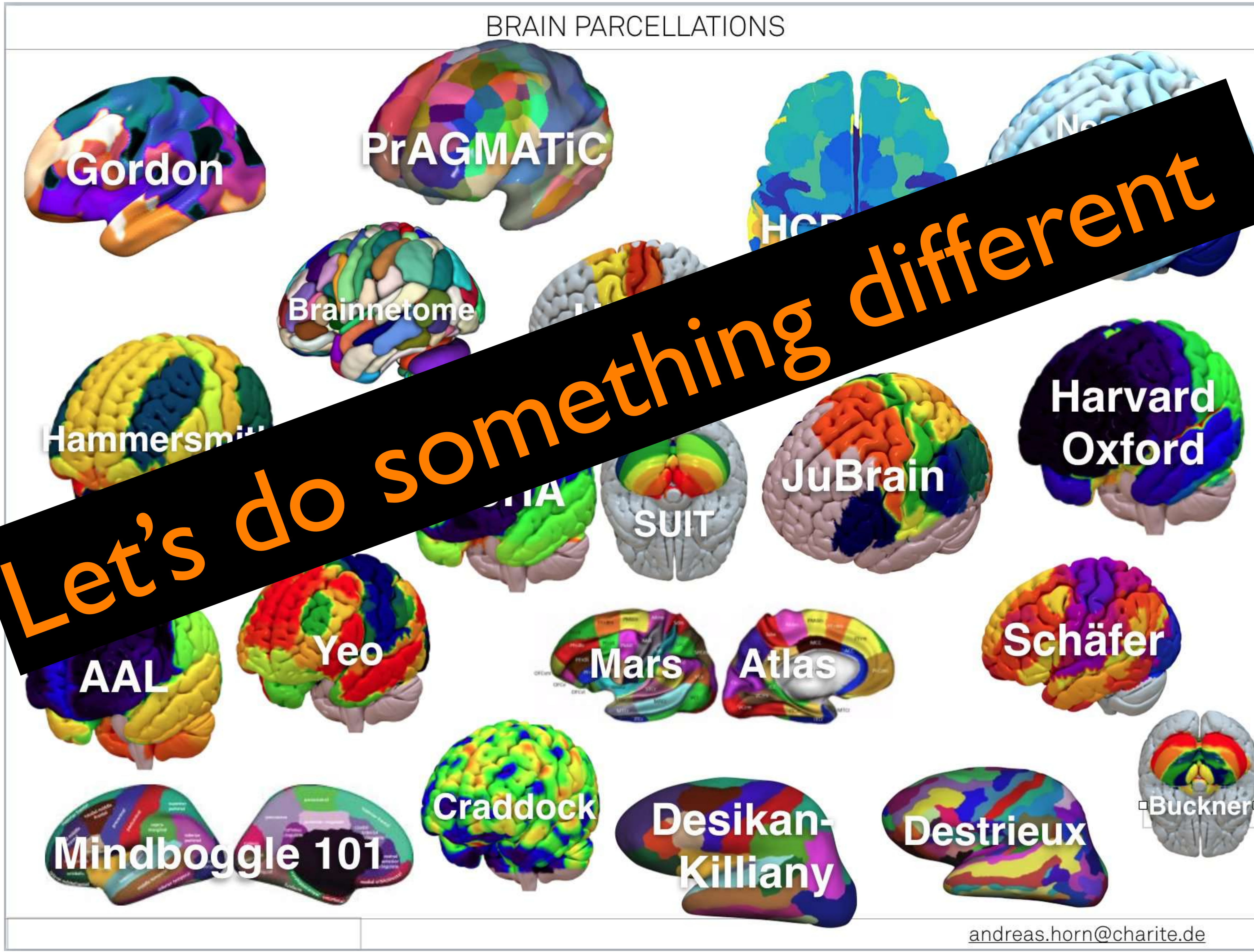
Parcellation boundaries don't overlap across subjects and modality



Gazillions of parcellations. Why?

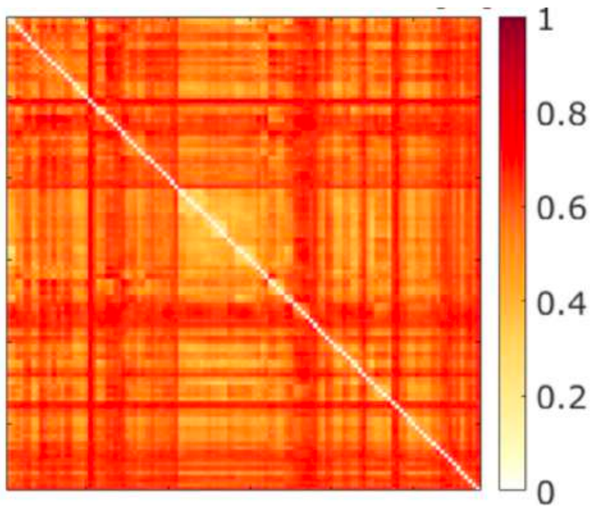


Let's do something different

Proposal: Deformable network

Functional network of subject *k*

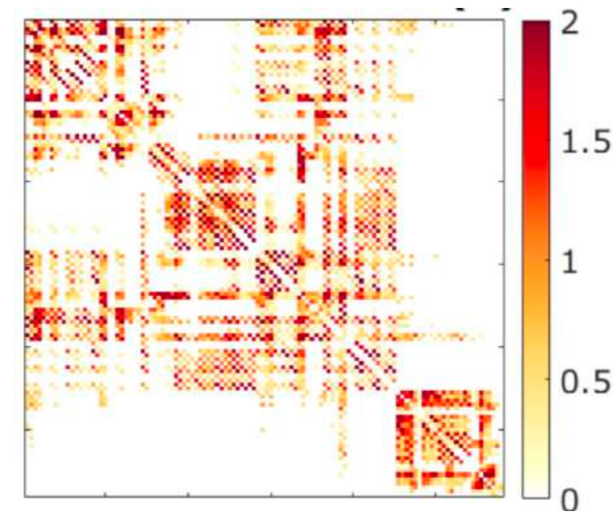
$$G_k = (V, w^k)$$



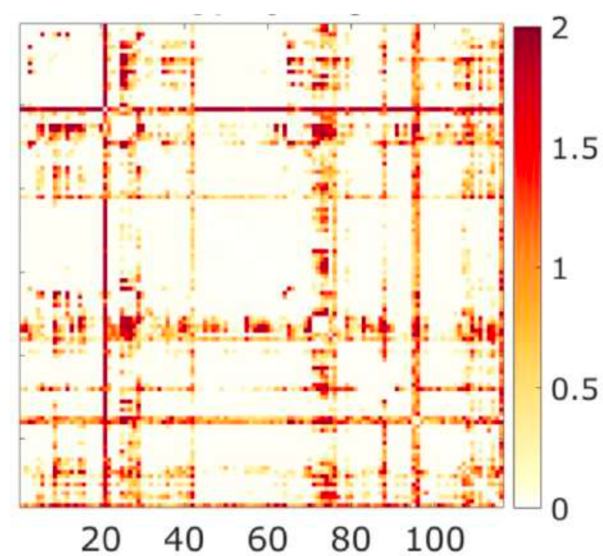
Topological registration

Structural network template

$$P$$



$$\widehat{\Theta}_k$$



$$\widehat{\Theta}_k = arg \min_{\Theta} \mathcal{L}_F(\Theta, G_k) + \lambda \mathcal{L}_{top}(\Theta, P)$$

Goodness-of-fit Frobenius norm

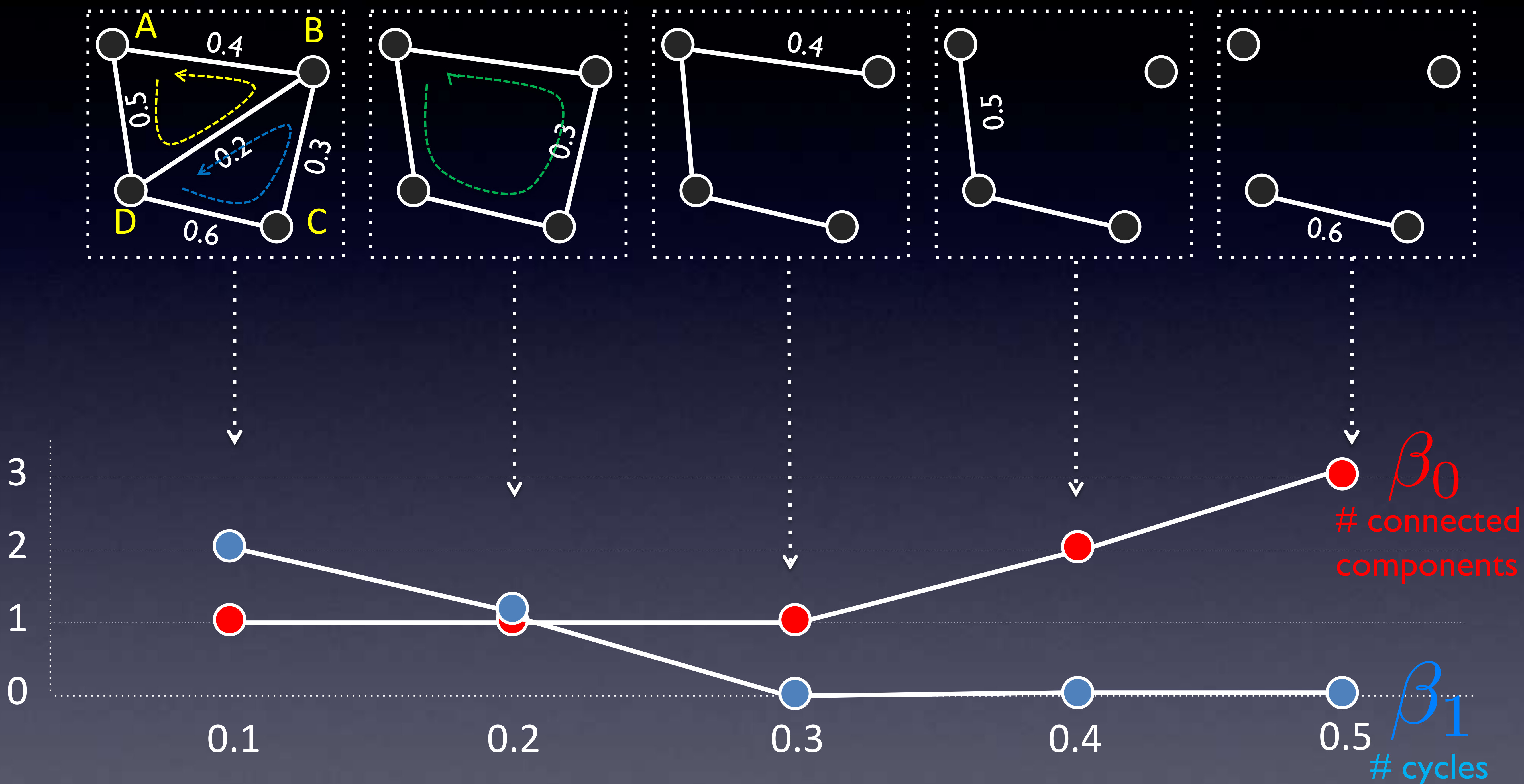
Control amount of topology

Topological loss

Graph filtration

Lee et al. 2012 IEEE Transactions on Medical Imaging

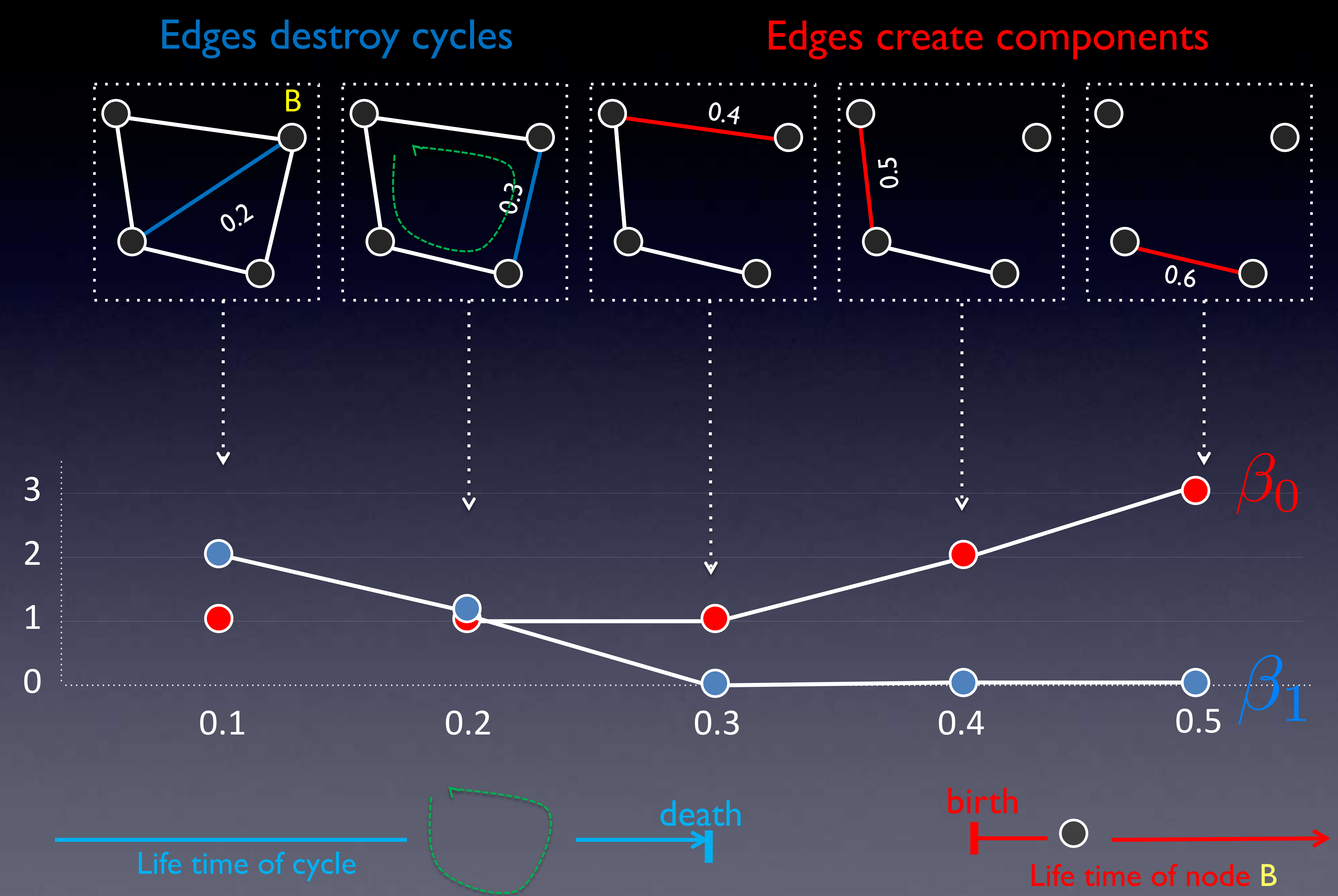
ADCD = ADB + DCB → vector space



Monotonicity of Betti curves

Chung et al. 2019 Network Neuroscience

Persistence = Life time (death – birth) of a feature



Theorem 1 Barcodes partition the edge set

$$E = E_0 \cup E_1$$

E_1 Edges destroy cycles

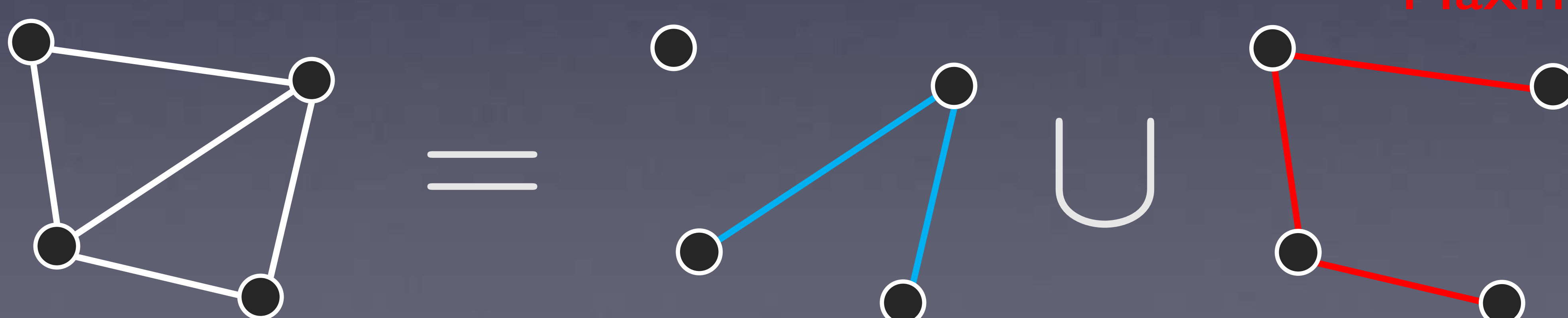
E_0 Edges create components

$$\#(E_1) = 1 + \frac{|V|(|V|-3)}{2}$$

$$\#(E_0) = |V| - 1$$

$$\#(E) = \frac{|V|(|V|-1)}{2}$$

Maximum spanning tree

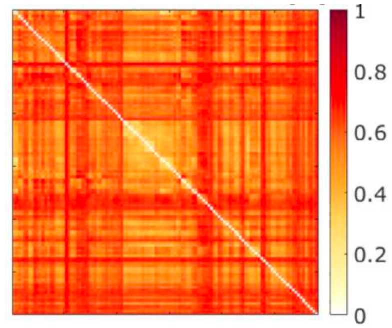


$$O(|E| \log |V|)$$

Topological loss

$\Theta = (V^{\Theta}, w^{\Theta})$

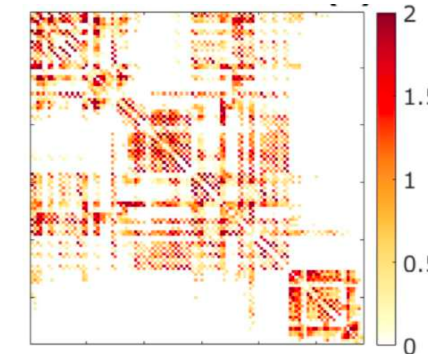
Functional network



$\xrightarrow[\tau]{\text{bijection}}$

$P = (V^{P}, w^{P})$

Structural network



$$\mathcal{L}_{top}(\Theta, P) = \mathcal{L}_{0D}(\Theta, P) + \mathcal{L}_{1D}(\Theta, P)$$

$$\mathcal{L}_{0D}(\Theta, P) = \min_{\tau} \sum_{b \in E_0} \big[b - \tau(b)\big]^2$$

$$\mathcal{L}_{1D}(\Theta, P) = \min_{\tau} \sum_{d \in E_1} \big[d - \tau(d)\big]^2$$

Theorem 2 Optimal topological matching

$$\mathcal{L}_{0D}(\Theta, P) = \min_{\tau} \sum_{b \in E_0} \left[b - \tau(b) \right]^2$$

$$= \sum_{b \in E_0} \left[b - \tau_0^*(b) \right]^2$$

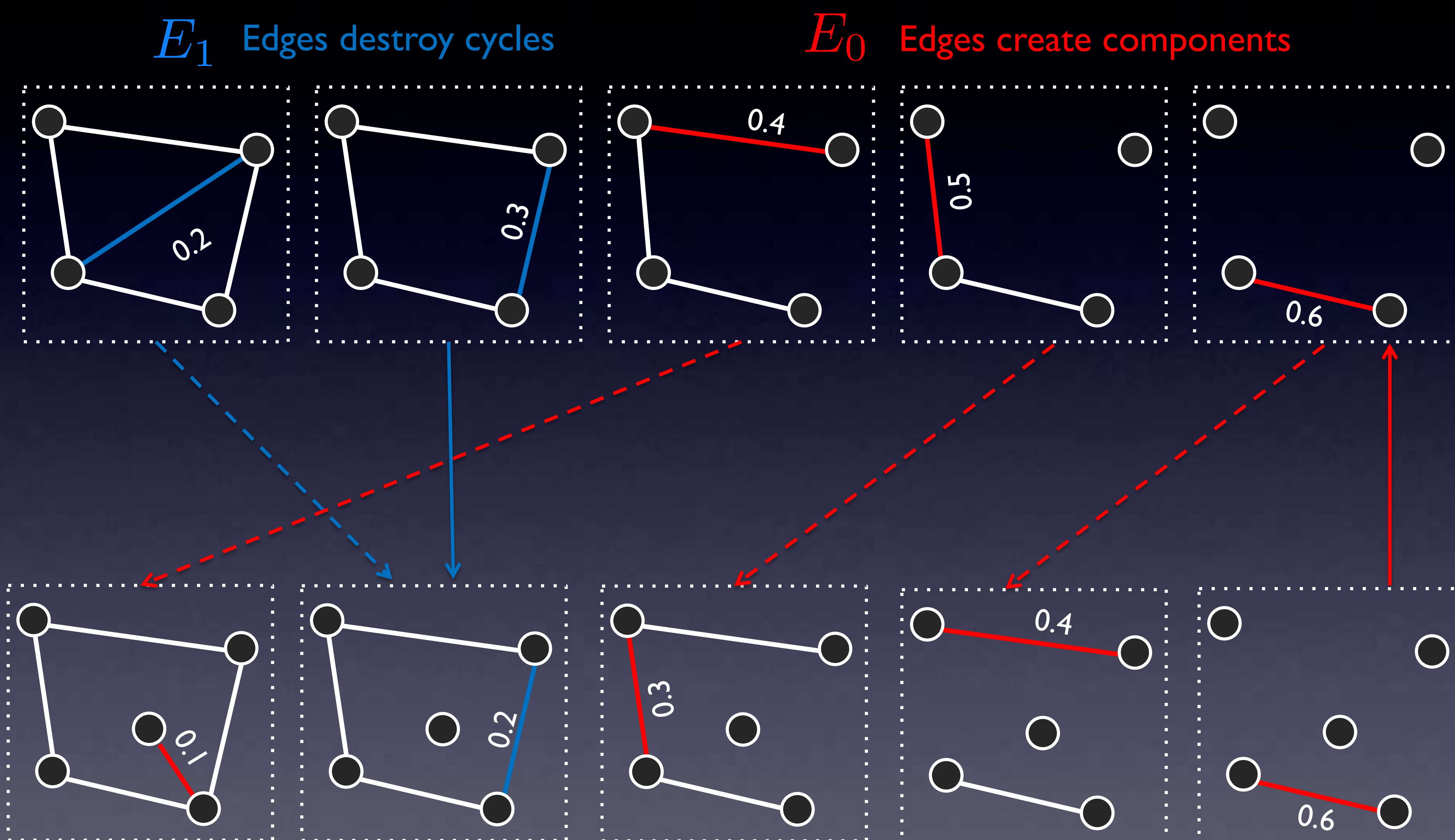
τ_0^* *The i-th smallest birth value to the i-th smallest birth value*

$$\mathcal{L}_{1D}(\Theta, P) = \min_{\tau} \sum_{d \in E_1} \left[d - \tau(d) \right]^2$$

$$= \sum_{d \in E_1} \left[d - \tau_1^*(d) \right]^2$$

The i-th smallest death value to the i-th smallest death value

Topological matching via sorting with data augmentation

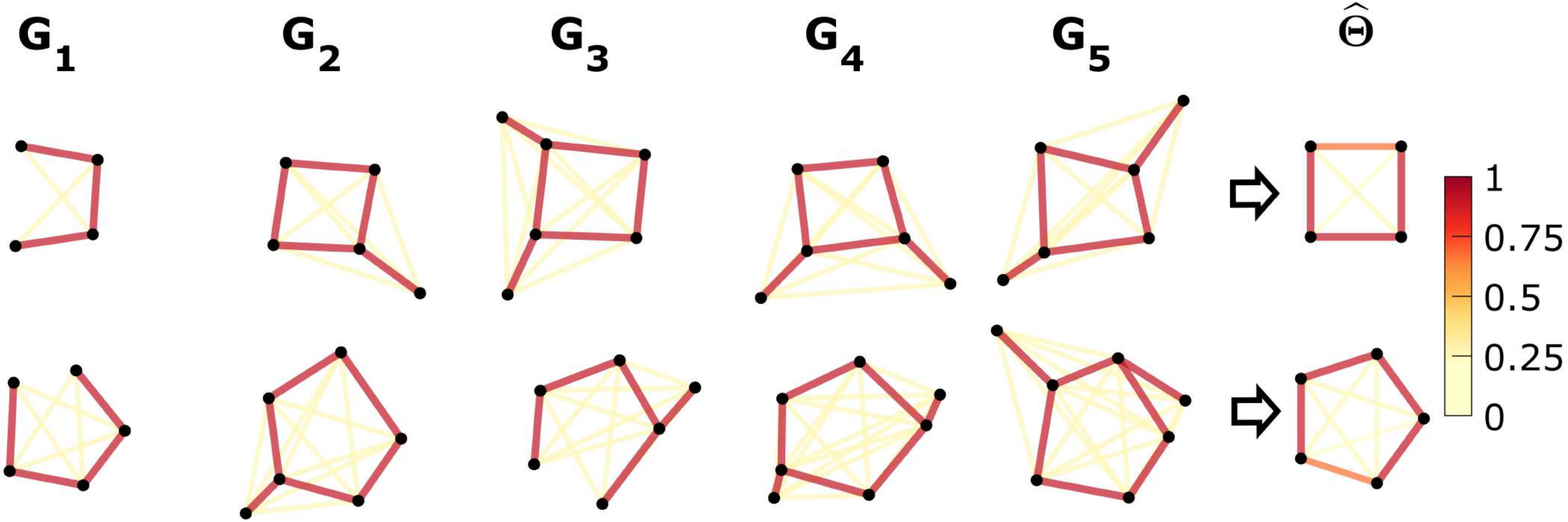


Topological mean

$$\widehat{\Theta} = \arg\min_{\Theta} \sum_{k=1}^{n} \mathcal{L}_{top}(\Theta, G_k)$$

Death values of Θ are given by averaging the sorted death values of all the networks G_k .

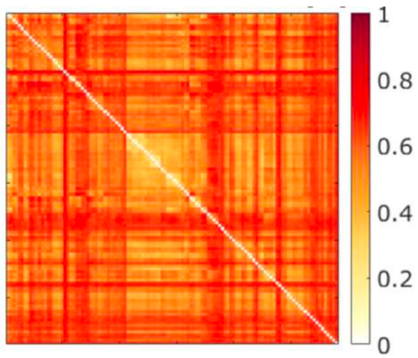
1. Sort birth/death values.
2. Match them
3. Average



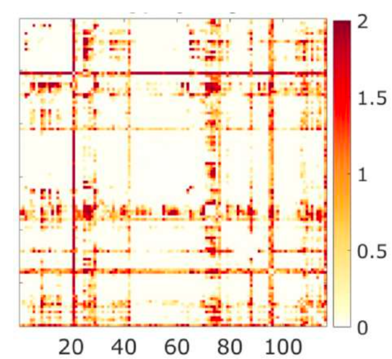
Template-based brain network analysis

Functional network

$G_k = (V, w^k)$

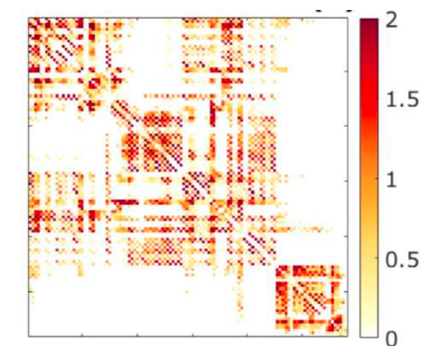


$\widehat{\Theta}_k$



Structural network

P



Align <u>individual</u> functional network to structural template

$$\widehat{\Theta}_k = arg\min_{\Theta} \mathcal{L}_F(\Theta, G_k) + \lambda \mathcal{L}_{top}(\Theta, P)$$

Frobenius norm

Control amount of topology

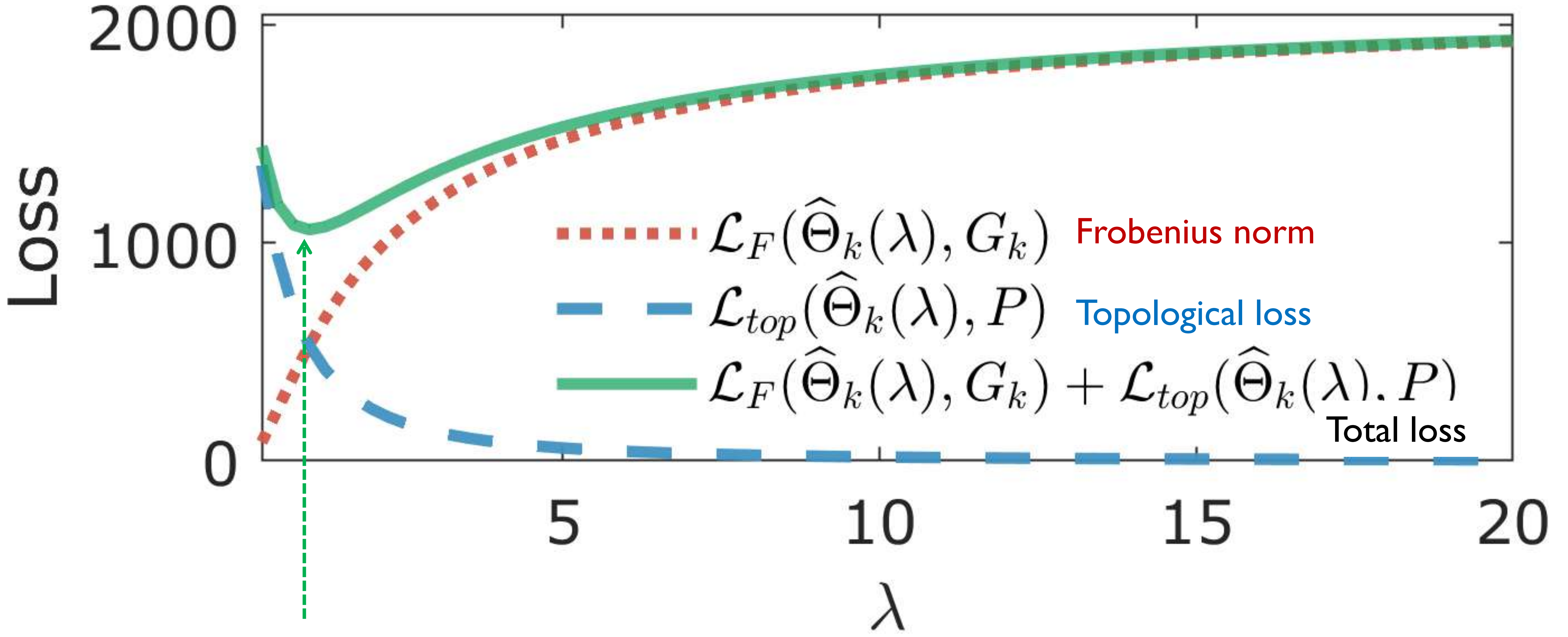
Topological loss

Topological gradient descent

$$\frac{\partial \mathcal{L}_{top}(\Theta, P)}{\partial w_{ij}^{\Theta}} = \begin{cases} 2\left[w_{ij}^{\Theta} - \tau_{0*}(w_{ij}^{\Theta})\right] & \text{if } w_{ij}^{\Theta} \in E_0; \\ 2\left[w_{ij}^{\Theta} - \tau_{1*}(w_{ij}^{\Theta})\right] & \text{if } w_{ij}^{\Theta} \in E_1 \end{cases}$$

Run time $O(|E| \log |V|)$

Optimal amount of topology?



1.0000 ± 0.0002
over 412 subjects

Topological stability

Topological learning at group level

Functional networks $G_1 = (V, w^1), \cdots, G_n = (V, w^n)$

Structural network P

Register every functional network to structural template

$$\widehat{\Theta}_k = arg \min_{\Theta} \frac{1}{n} \sum_{k=1}^{n} \mathcal{L}_F(\Theta, G_k) + \lambda \mathcal{L}_{top}(\Theta, P)$$

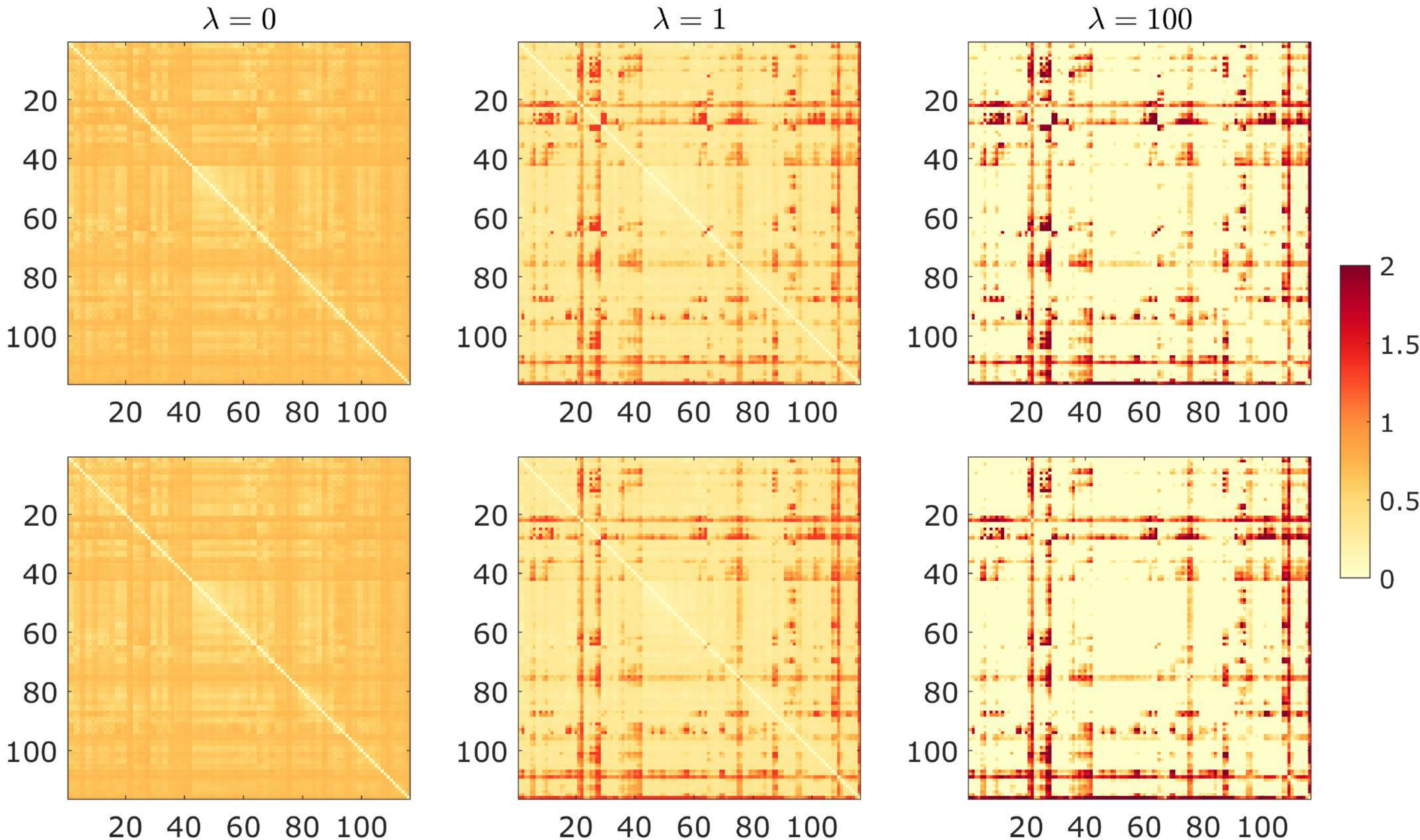
Frobenius norm

Topological loss

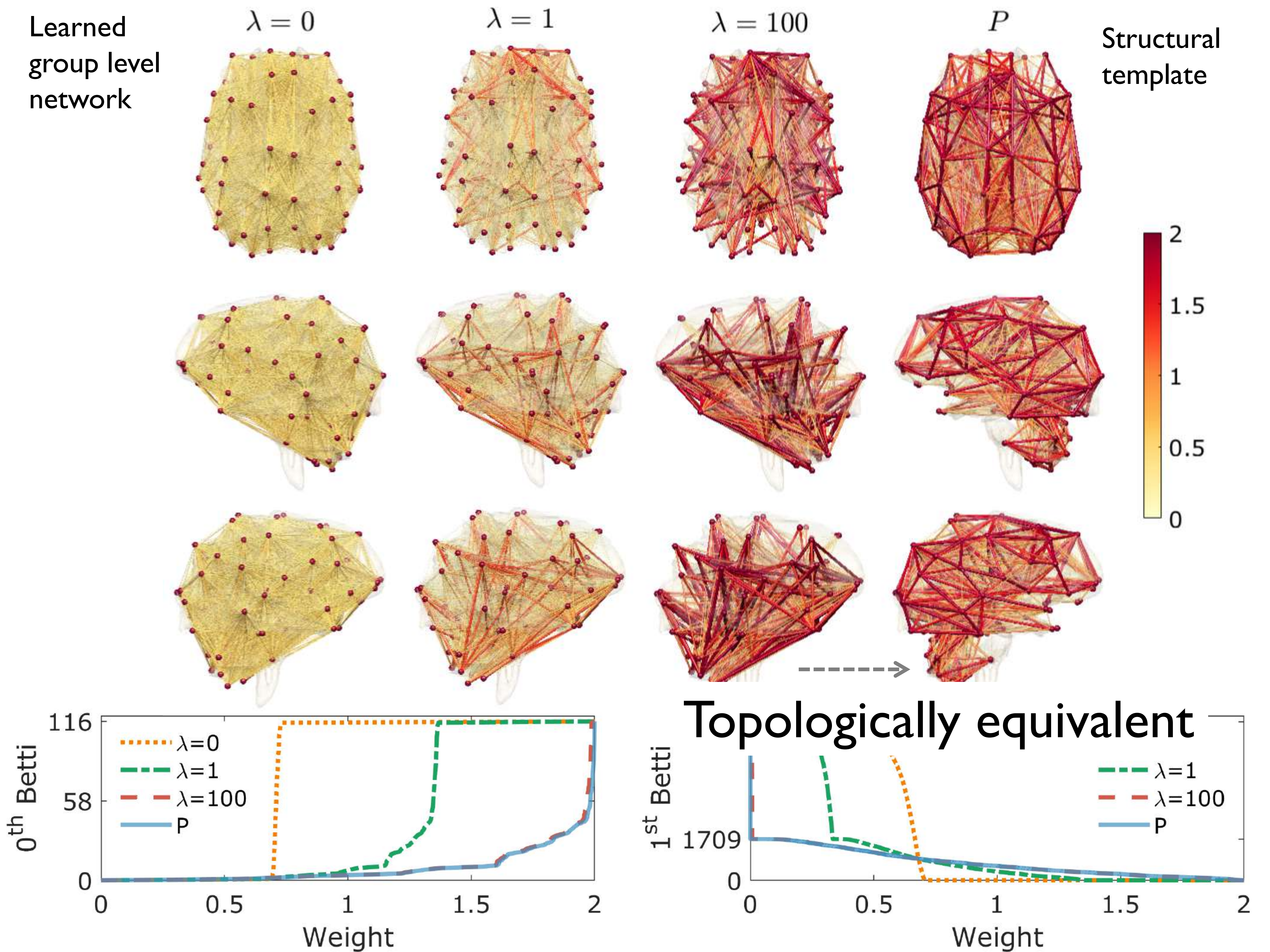
Control amount
of topological learning

Topological learning at group level

232 females



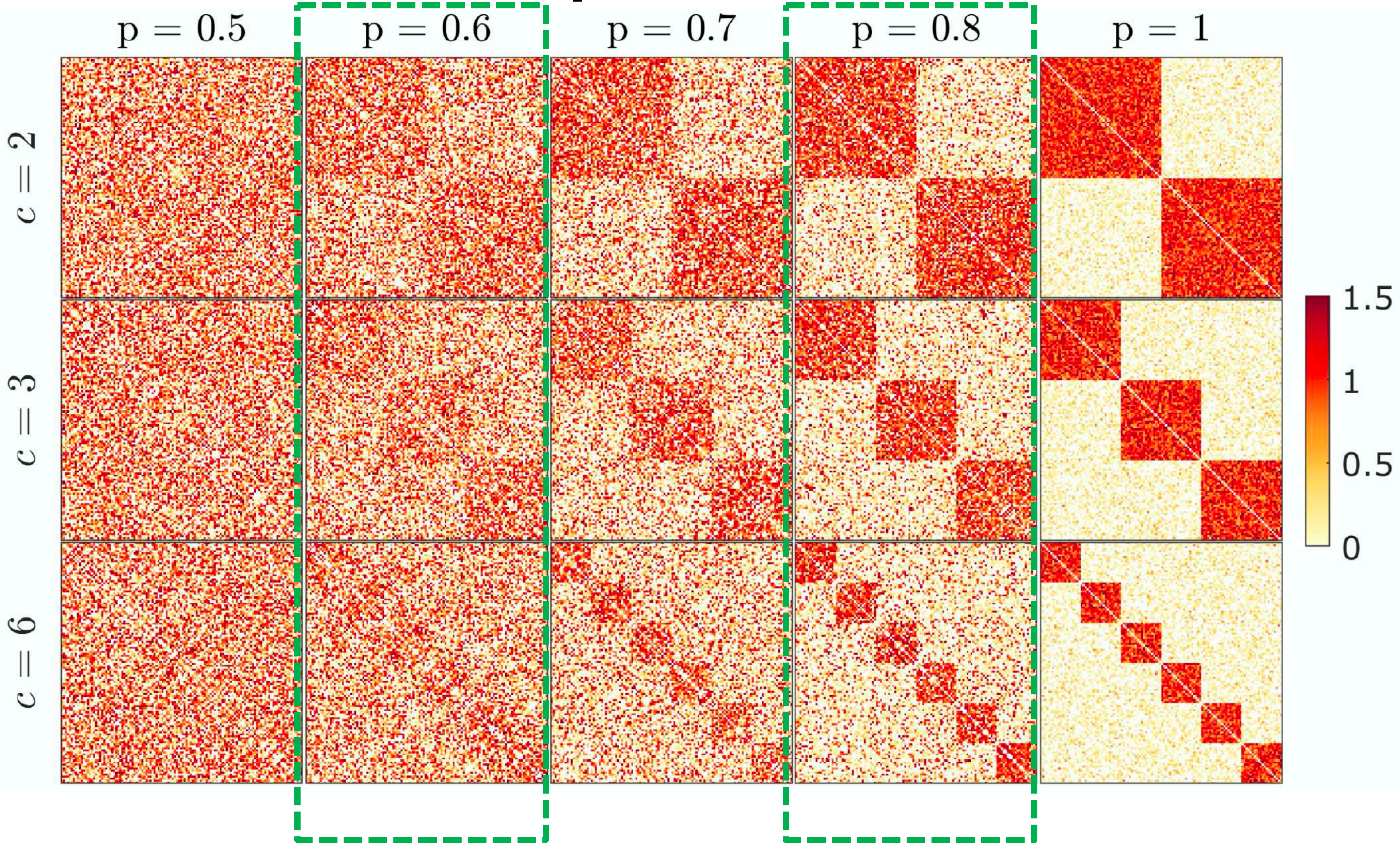
168 males



Learned group level network
$\lambda = 0$
$\lambda = 1$
$\lambda = 100$
P
Structural template
2
1.5
1
0.5
0
Topologically equivalent
0^{th} Betti
116
58
0
λ=0
λ=1
λ=100
P
Weight
0
0.5
1
1.5
2
1^{st} Betti
1709
0
λ=1
λ=100
P
Weight
0
0.5
1
1.5
2

Simulation study

Within module connection probability p
Between module connection probability $1-p$



generate10 networks vs. 10 networks

Permutation test for topological loss

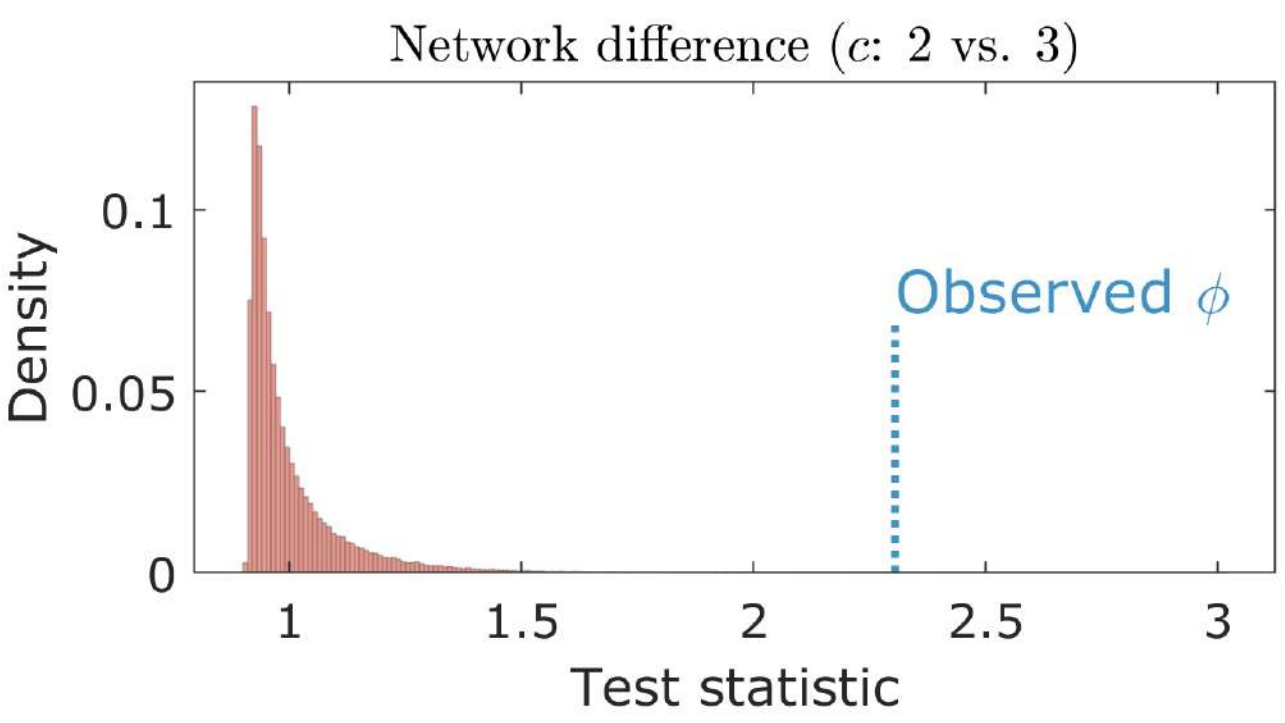
Between-class loss

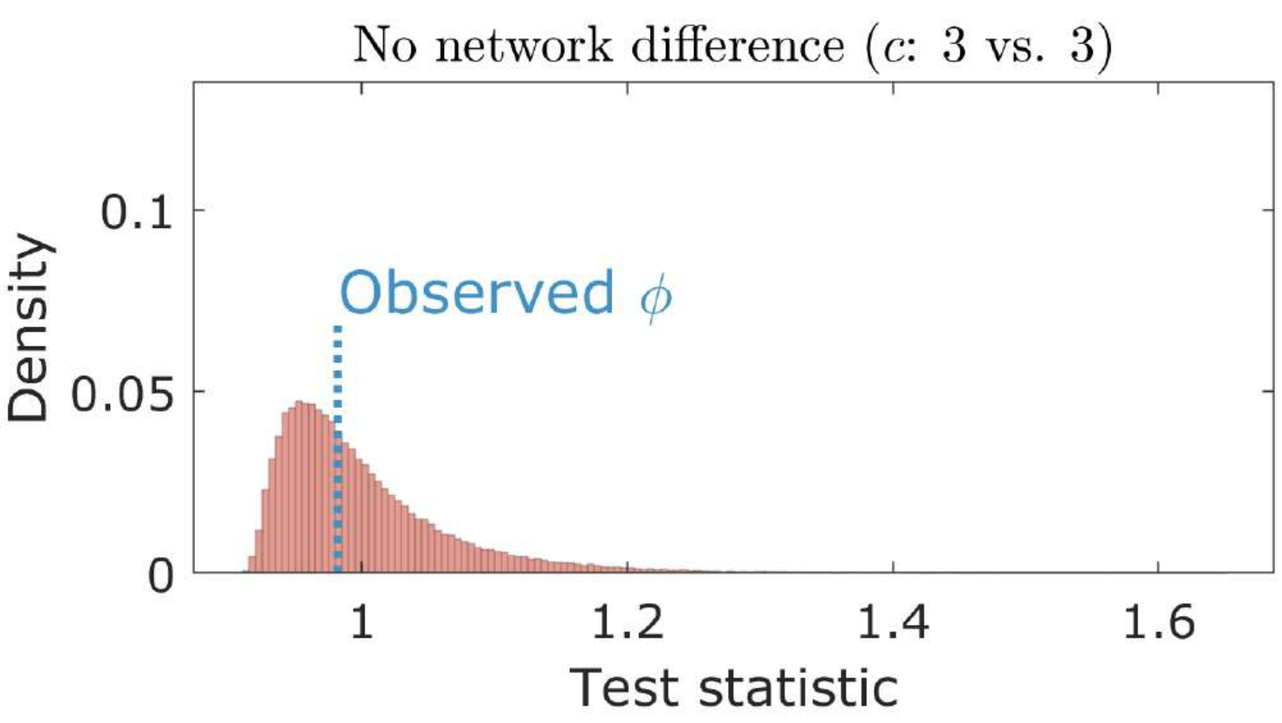
$$\overline{\mathcal{L}}_B \propto \sum_{i \in C_1, j \in C_2} \mathcal{L}(G_i, G_j)$$

Within-class loss

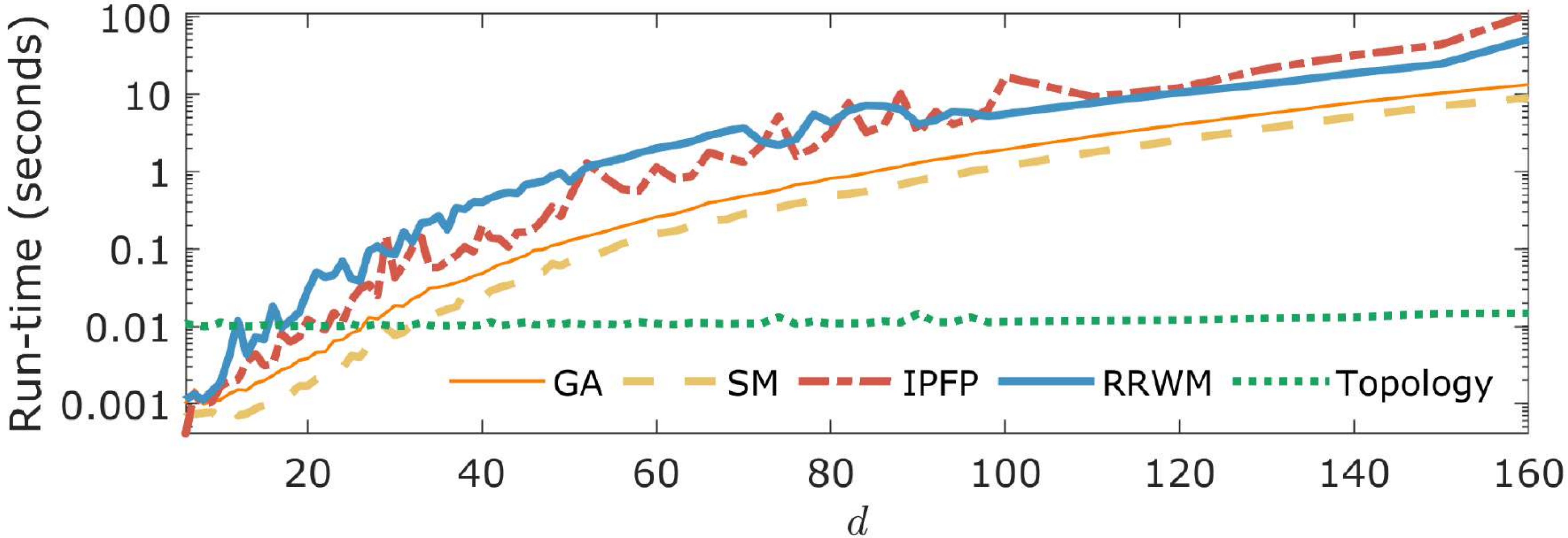
$$\overline{\mathcal{L}}_W \propto \sum_k \sum_{i,j \in C_k} \mathcal{L}(G_i, G_j)$$

Statistic $\phi = \dfrac{\overline{\mathcal{L}}_B}{\overline{\mathcal{L}}_W}$





Permutation test *is* not *easy to* apply to existing graph matching algorithms!



100 second per permutation

→ permutation test with 100000 permutations

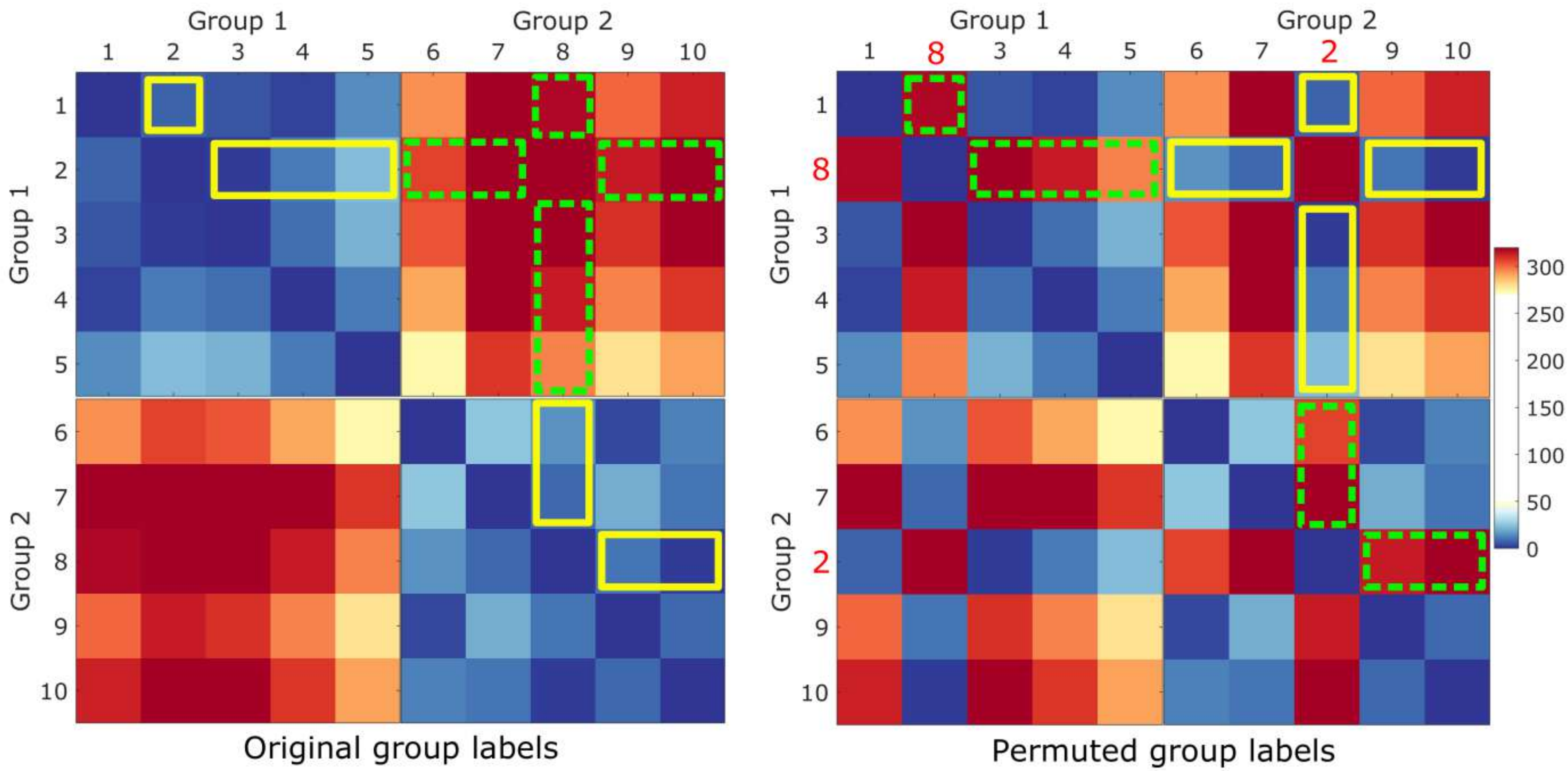
= 2778 hours = 115 days

→ Permutation test via random transpositions

Chung et al. 2019 Connectomics in NeuroImaging

Transposition test on loss functions

Subject 2 in group 1 swapping with subject 8 in group 2



Compute the incremental change of loss functions over transposition

$$\overline{\mathcal{L}}_W \to \overline{\mathcal{L}}_W + \Delta(tranposition)$$

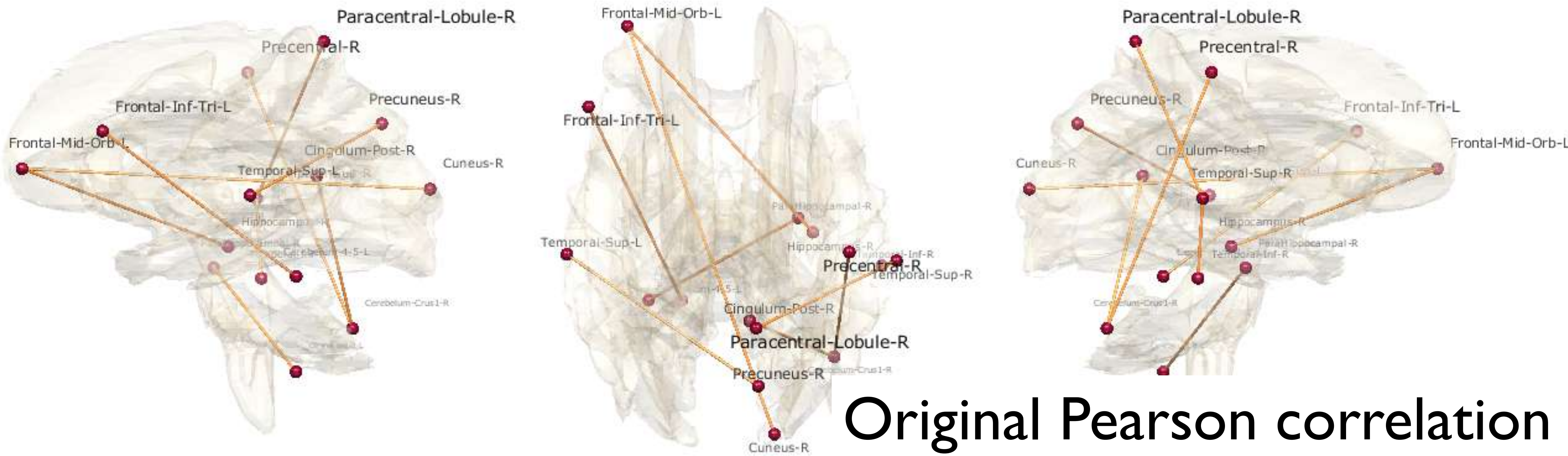
$$\overline{\mathcal{L}}_B \to \overline{\mathcal{L}}_B + \Delta(tranposition)$$

Average p-value in 50 independent simulations

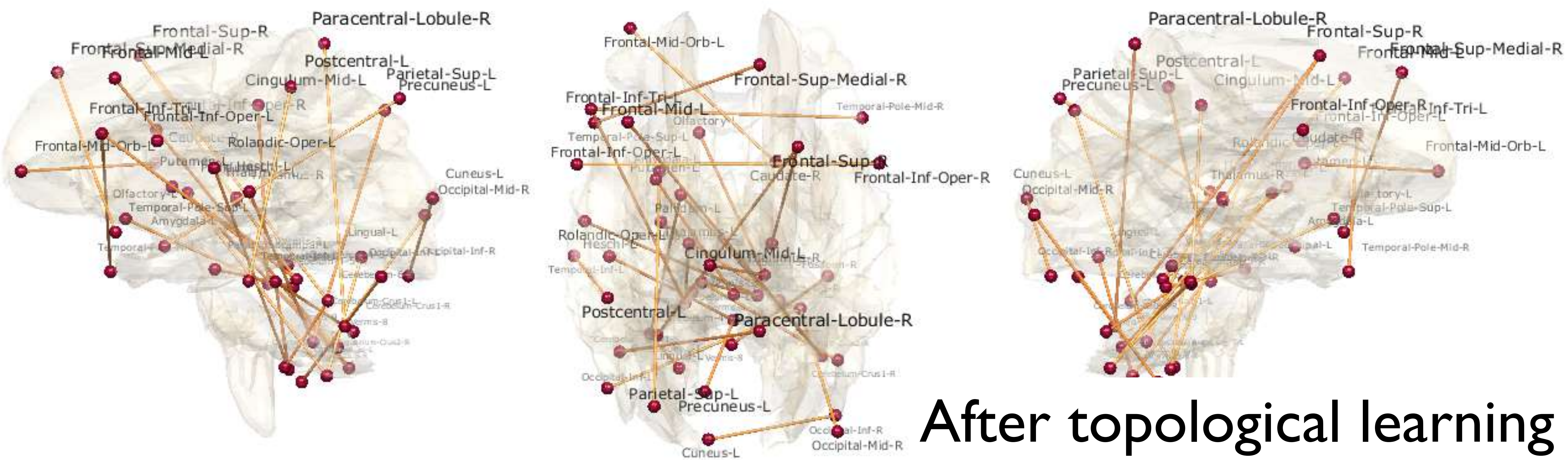
nodes	modules	p	GA (Graduated assignment)	SM (Spectral matching)	RRWM (Reweighted random walk matching)	IPFP (Integer projected fixed point)	$\mathcal{L}_{top}$
12 vs. 12	2 vs. 3	0.6	0.45 ± 0.27	0.48 ± 0.30	0.28 ± 0.31	0.34 ± 0.28	0.08 ± 0.16
		0.8	0.26 ± 0.24	0.30 ± 0.28	0.06 ± 0.12	0.28 ± 0.28	0.01 ± 0.03
	2 vs. 6	0.6	0.06 ± 0.10	0.17 ± 0.20	0.04 ± 0.13	0.23 ± 0.28	0.00 ± 0.00
		0.8	0.00 ± 0.01	0.01 ± 0.03	0.00 ± 0.00	0.02 ± 0.04	0.00 ± 0.00
	3 vs. 6	0.6	0.40 ± 0.29	0.35 ± 0.28	0.24 ± 0.26	0.35 ± 0.28	0.06 ± 0.13
		0.8	0.21 ± 0.23	0.28 ± 0.27	0.08 ± 0.14	0.26 ± 0.25	0.00 ± 0.01
18 vs. 18	2 vs. 3	0.6	0.25 ± 0.23	0.41 ± 0.26	0.26 ± 0.24	0.42 ± 0.28	0.01 ± 0.02
		0.8	0.12 ± 0.17	0.19 ± 0.22	0.00 ± 0.00	0.04 ± 0.05	0.00 ± 0.00
	2 vs. 6	0.6	0.02 ± 0.05	0.07 ± 0.17	0.00 ± 0.00	0.14 ± 0.20	0.00 ± 0.00
		0.8	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
	3 vs. 6	0.6	0.28 ± 0.24	0.37 ± 0.31	0.21 ± 0.24	0.37 ± 0.30	0.01 ± 0.01
		0.8	0.15 ± 0.22	0.13 ± 0.14	0.00 ± 0.01	0.16 ± 0.18	0.00 ± 0.00
24 vs. 24	2 vs. 3	0.6	0.23 ± 0.25	0.30 ± 0.26	0.14 ± 0.20	0.31 ± 0.28	0.00 ± 0.01
		0.8	0.06 ± 0.11	0.12 ± 0.19	0.00 ± 0.00	0.01 ± 0.05	0.00 ± 0.00
	2 vs. 6	0.6	0.00 ± 0.01	0.03 ± 0.06	0.00 ± 0.00	0.09 ± 0.13	0.00 ± 0.00
		0.8	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00
	3 vs. 6	0.6	0.24 ± 0.26	0.29 ± 0.28	0.10 ± 0.13	0.37 ± 0.26	0.00 ± 0.00
		0.8	0.07 ± 0.12	0.13 ± 0.19	0.00 ± 0.01	0.12 ± 0.19	0.00 ± 0.00

Heritability index = 2 (corr(MZ) – corr (DZ))

HI above 1.00

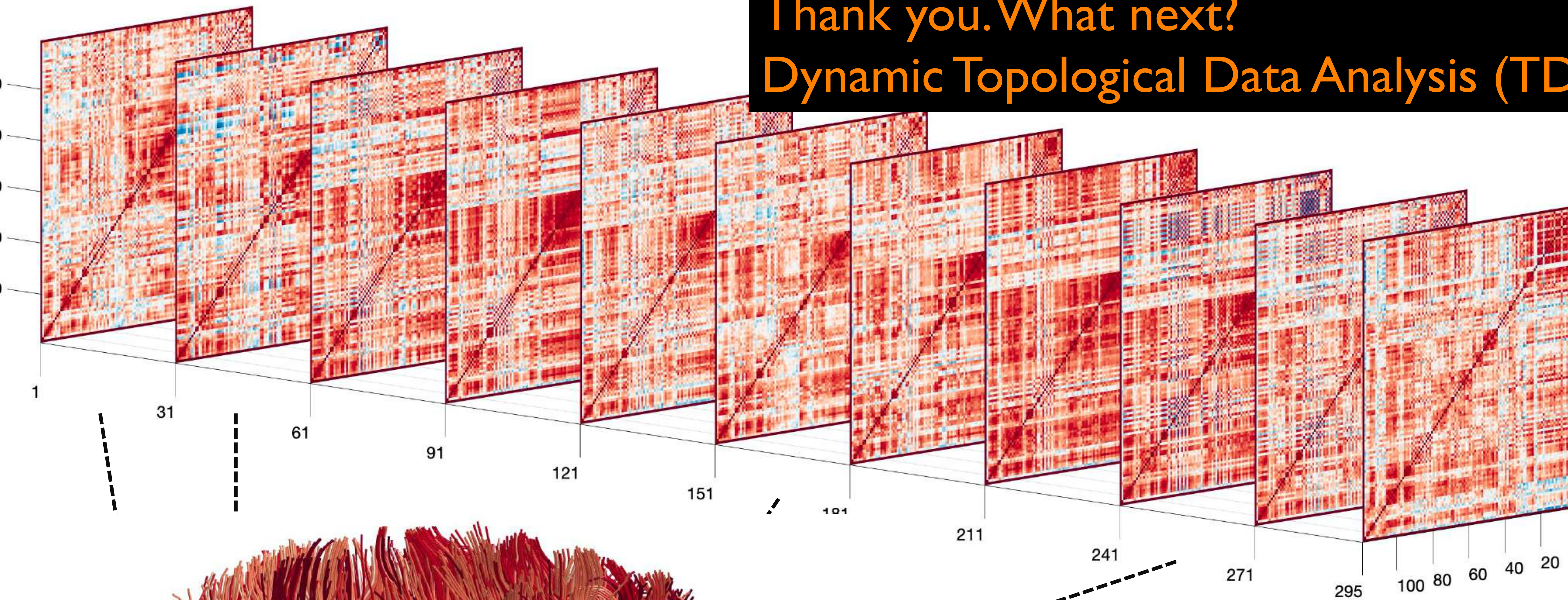


Original Pearson correlation

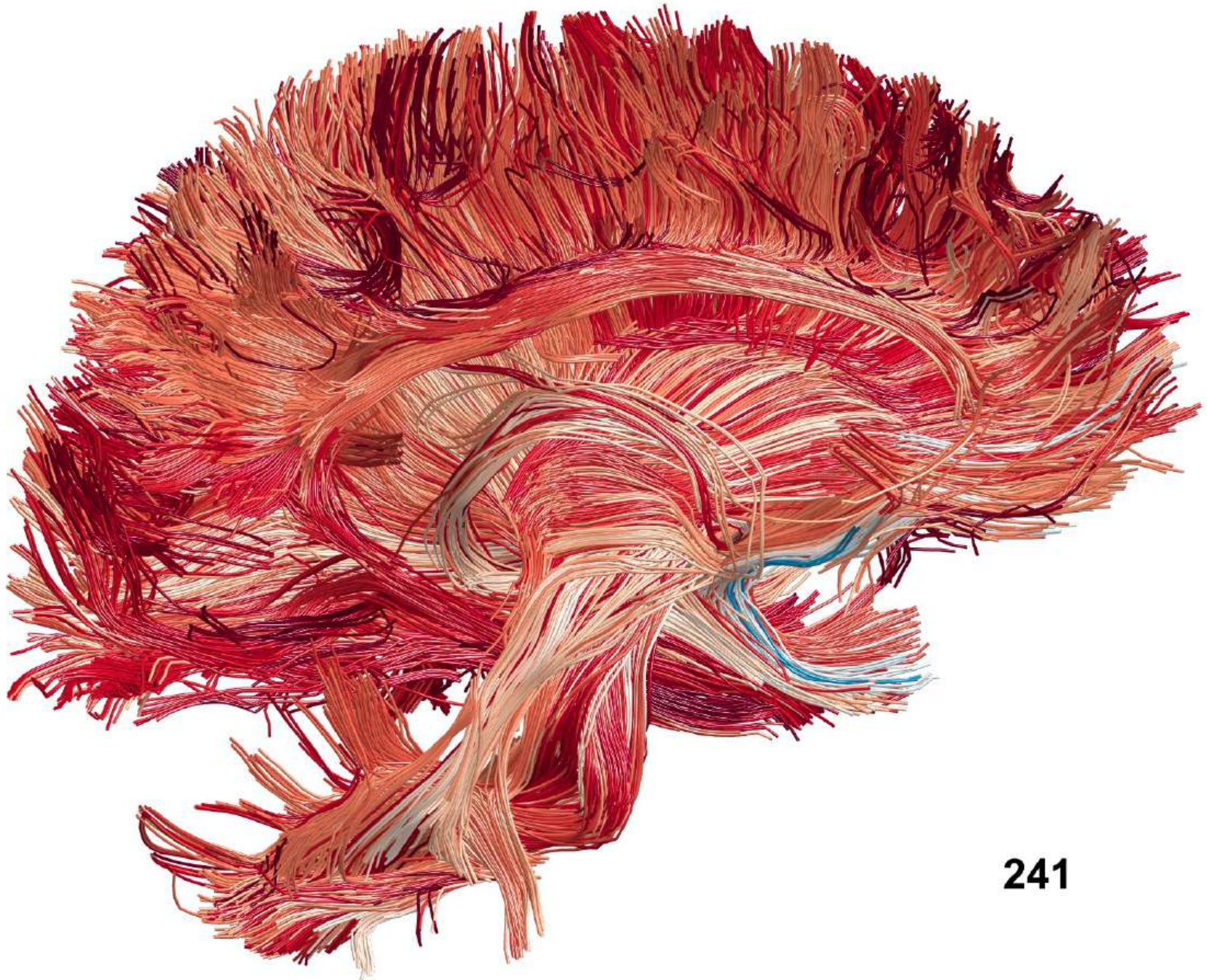


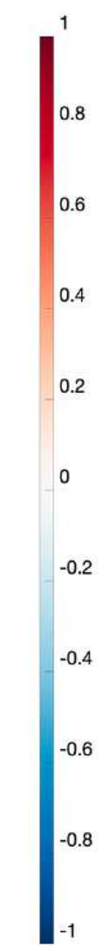
After topological learning

Thank you. What next?
Dynamic Topological Data Analysis (TDA)



Pearson correlation over sliding window





116 nodes functional network on top of white matter fiber tracts