Aligning Asynchronous Brain Network Data through Persistent Homology

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[PH-STAT @ github]

October 10, 2024, MICCAI topology workshop

Abstract

Functional brain connectivity at rest does not synchronize across subjects, making direct comparisons nearly impossible. The asynchronous nature of neural activity patterns prevents effective group-level analysis, posing a significant challenge to the clinical relevance of resting-state functional magnetic resonance imaging (rs-fMRI). We leverage persistent homology to align functional human brain networks across time and subjects by matching underlying topology using the Wasserstein distance, a probabilistic version of optimal transport. Our scalable approach enables localized matching of network edges, facilitating precise inference and learning. This method reduces the statistical variability of topological registration inversely proportional to sample sizes, thereby enabling the detection of previously undetectable signals. We demonstrate the application of this method in topological embedding, inference, and learning, highlighting its potential to transform brain network analysis. This talk is partially based on arXiv:2012.00675 (Annals of Applied Statistics) and arXiv:2201.00087 (PLOS Computational Biology).

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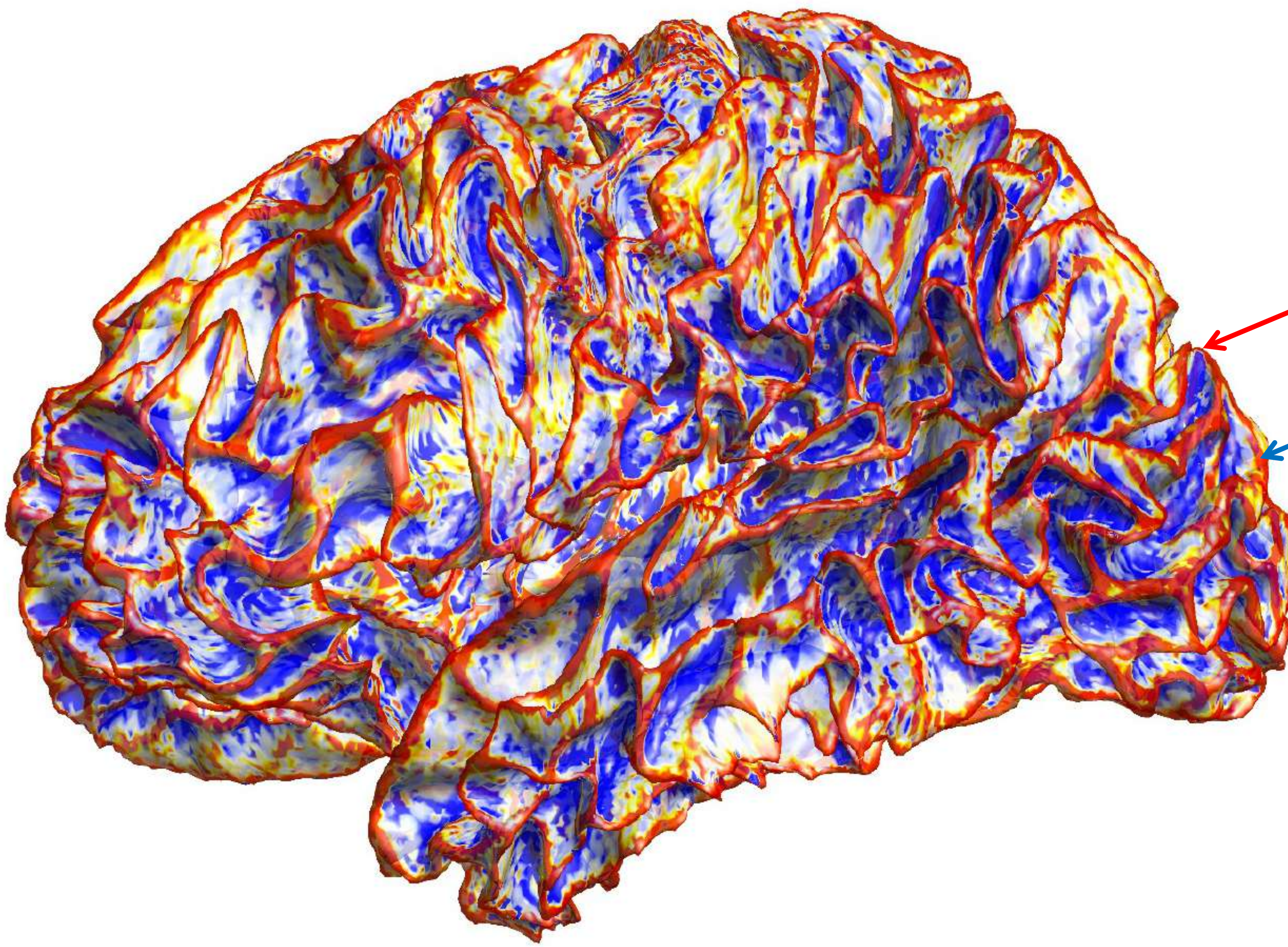
Resting-State Functional-MRI

IEEE TRANSACTIONS ON MEDICAL IMAGING, VOL. 39, NO. 6, JUNE 2020 2201

Fast Polynomial Approximation of Heat Kernel Convolution on Manifolds and Its Application to Brain Sulcal and Gyral Graph Pattern Analysis

Shih-Gu Huang, Ilwoo Lyu, Anqi Qiu, and Moo K. Chung

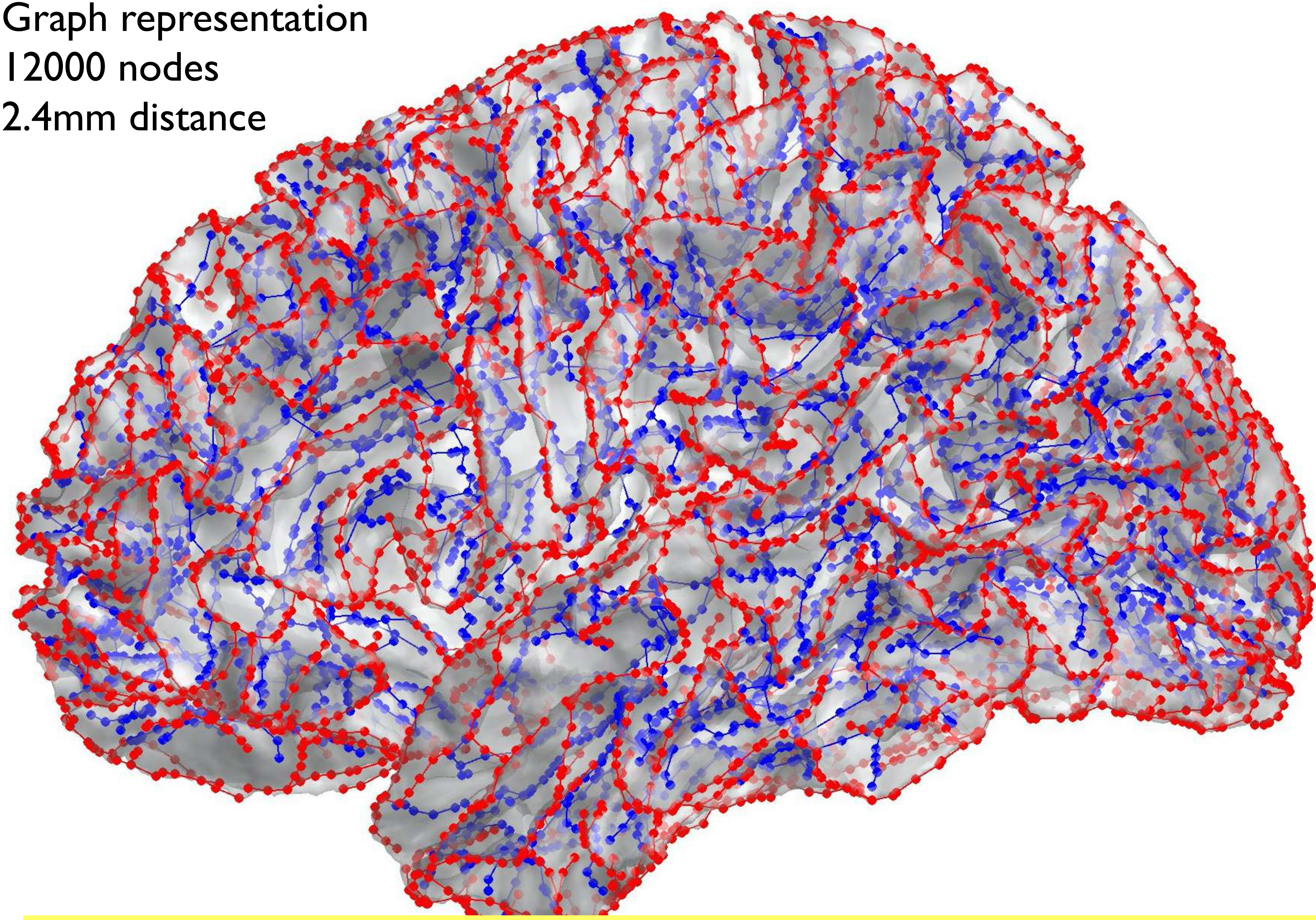


Gyri = red

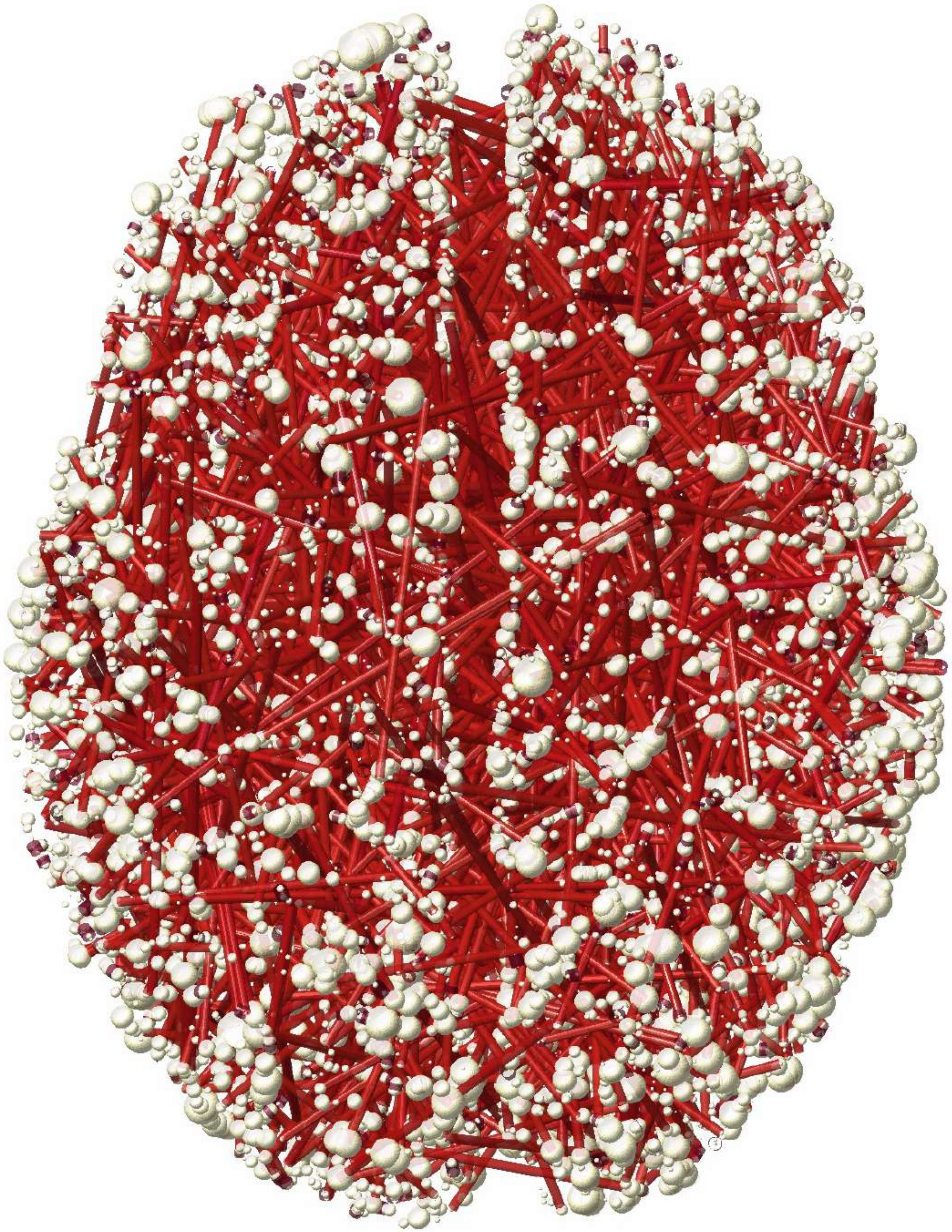
Sulci =blue

Threshold
mean curvatures
+Dijkstra's algorithm

Graph representation
12000 nodes
2.4mm distance



Dynamic brain networks will be built on top of these nodes



Rs-fMRI correlation network (thresholded at 0.7) over 20seconds sliding window at sulcal/gyral regions for 72 seconds

Every 0.72 second is compressed into 0.1 second.

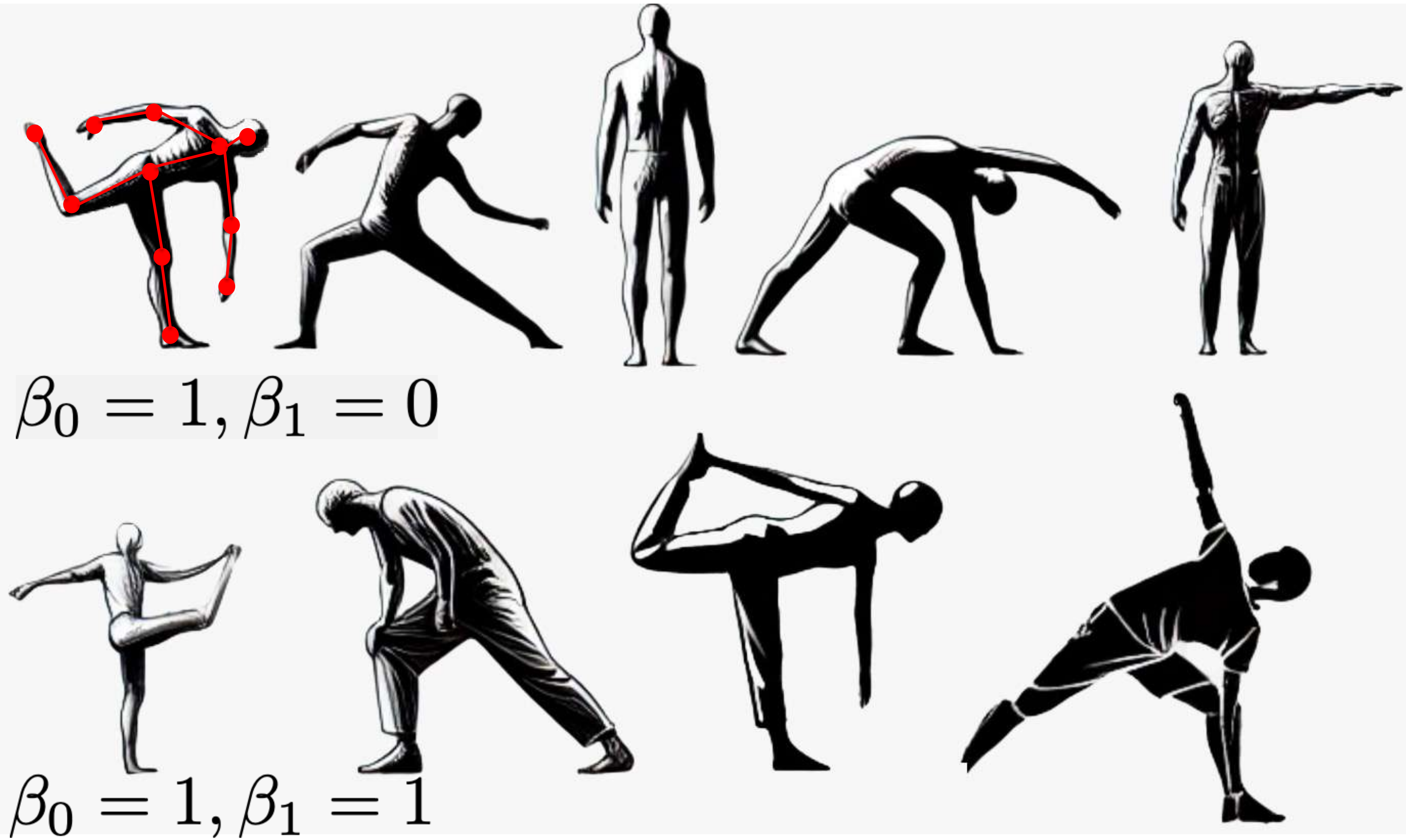
Across time and subjects, they do not align!

Graph filtration

Reverse filtration
on 1-skeletons

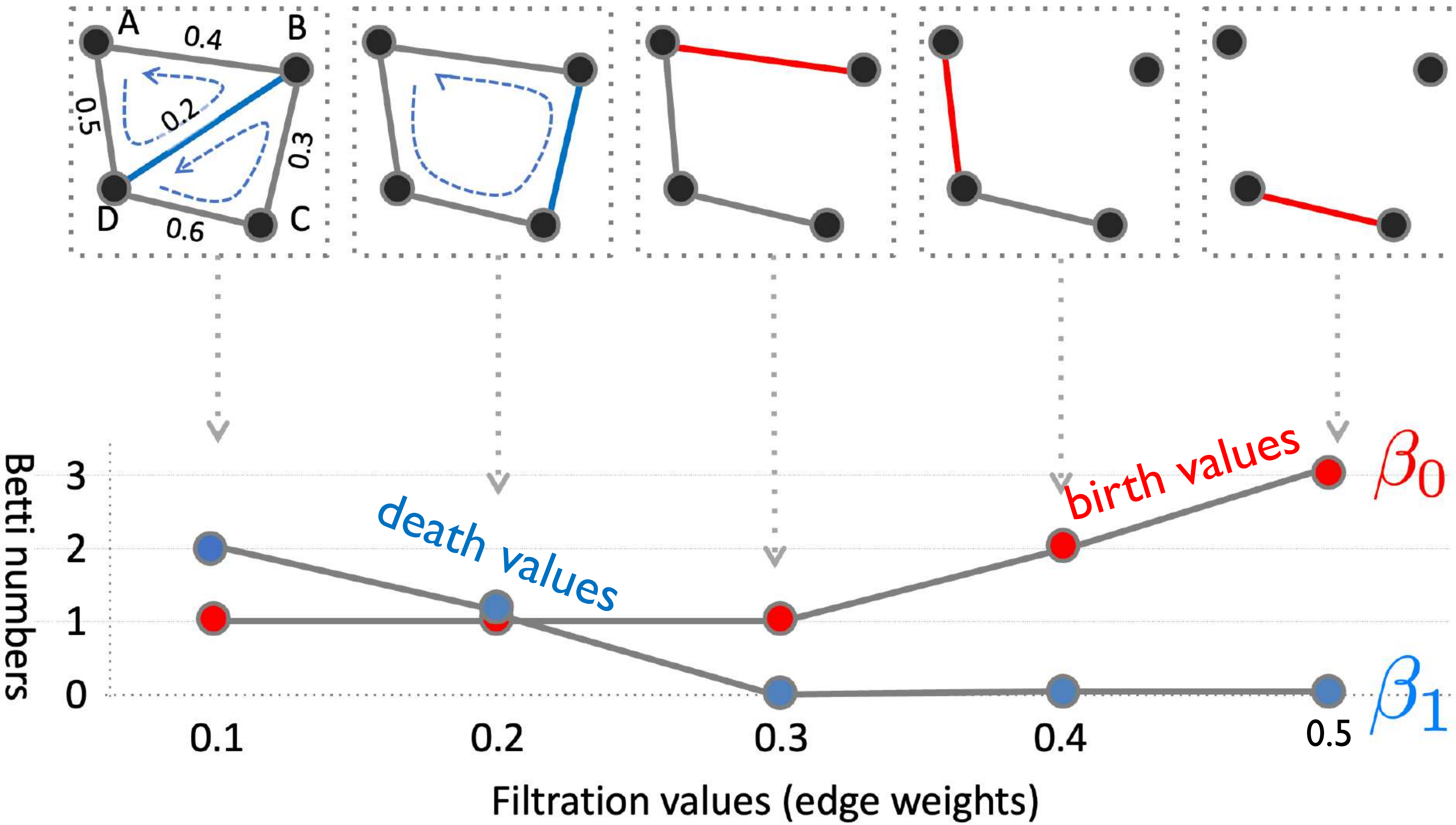
Songdechakraiwut and Chung. 2023, Annals of Appled Statistics

Topological variability is zero.



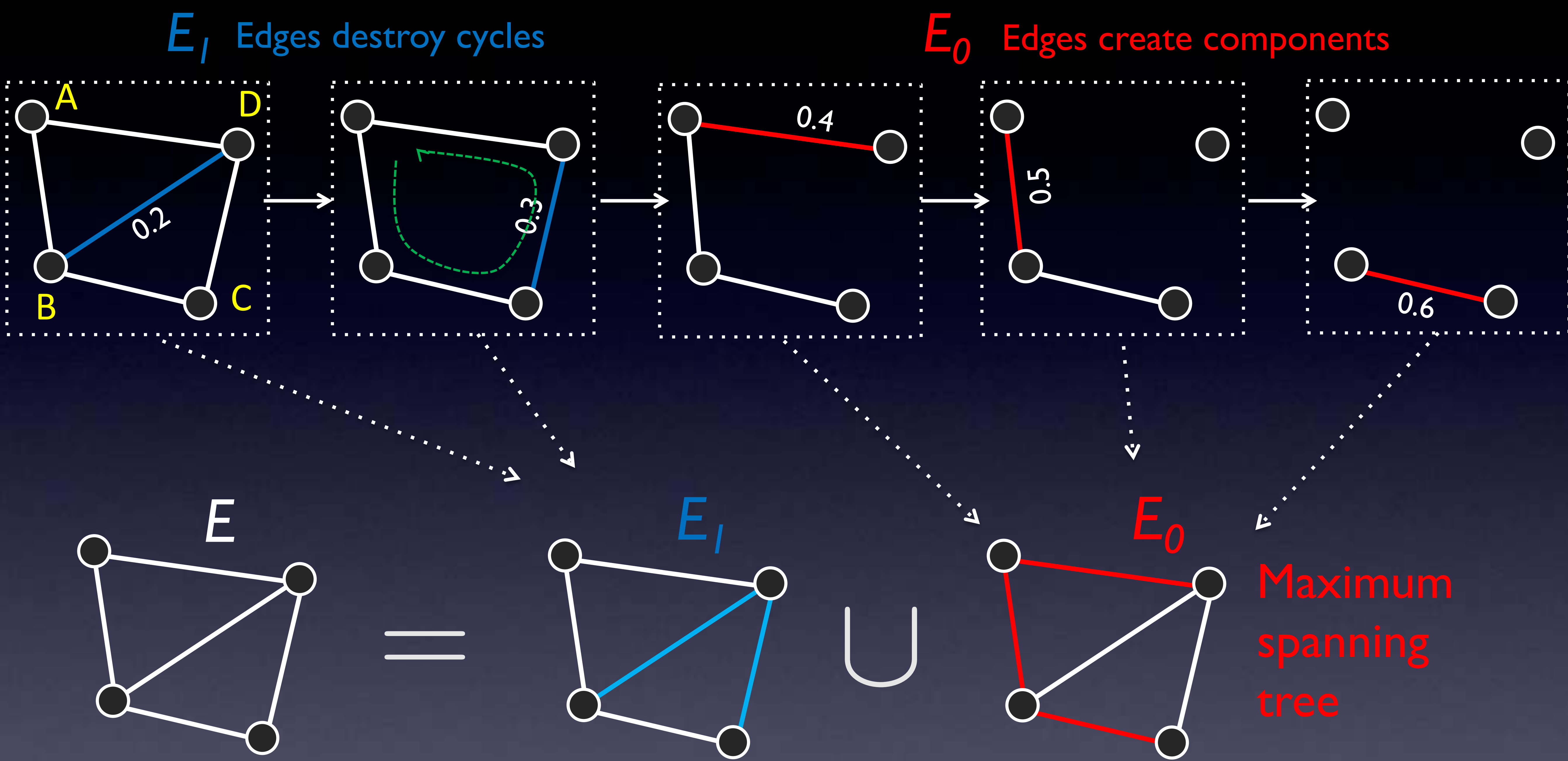
Can you come up with a method that gives 0 variability?

Graph filtration:



Songdechakraiwut and Chung. 2023, Annals of Appled Statistics

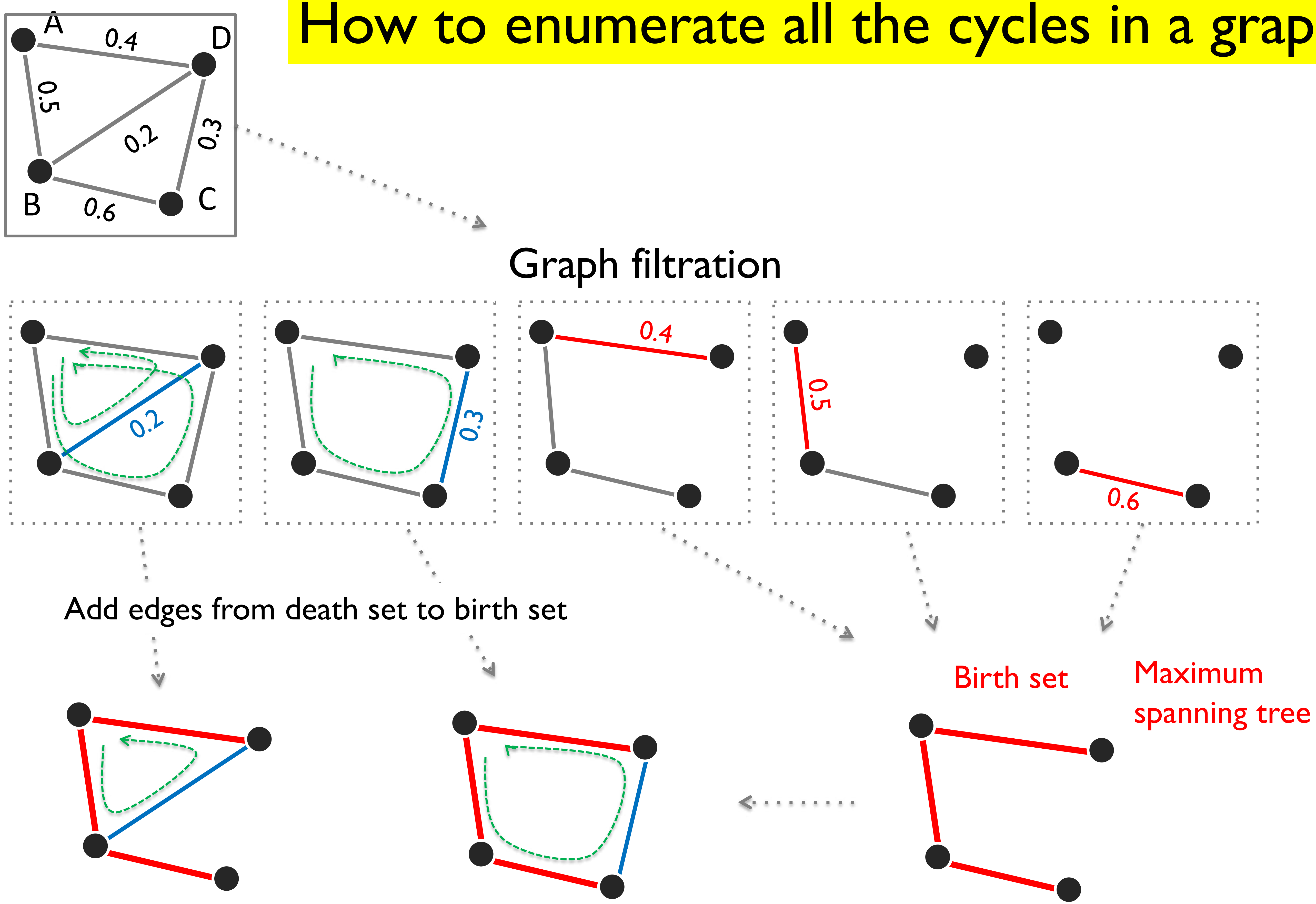
Theorem: Birth & death decomposition



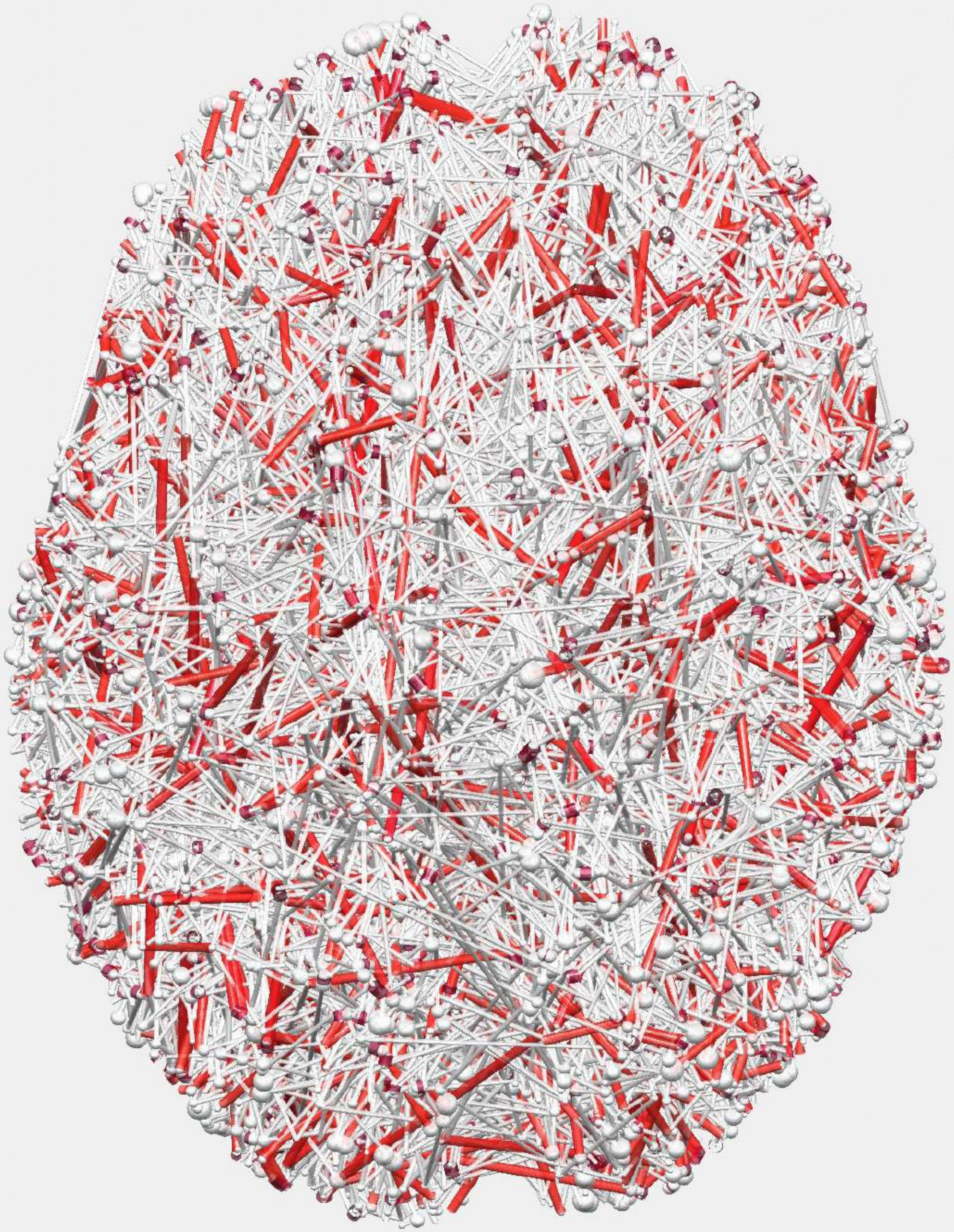
$$\beta_1 = |E_1| = 2$$

Songdechakraiwut and Chung. 2022, Annals of Appled Statistics

How to enumerate all the cycles in a graph?



Anand & Chung, 2023 IEEE TMI



Dynamics of 12000 nodes rs-fMRI network

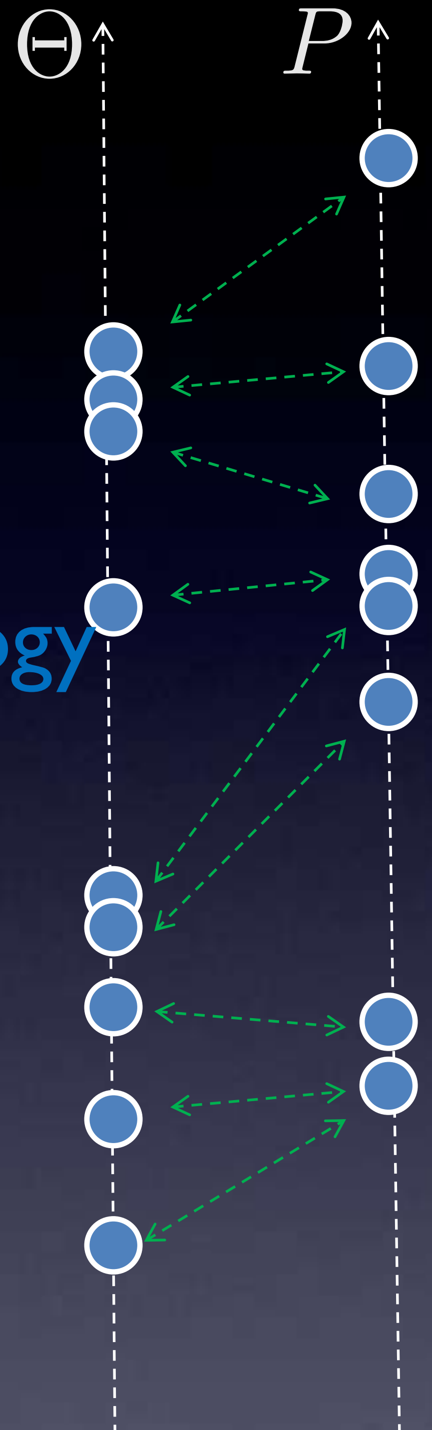
White edges (birth set) = stable backbone 0D topology (maximum spanning tree).

Red edges (death set) = dynamical changes are mostly 1D topology (cycles). thresholded at 0.9

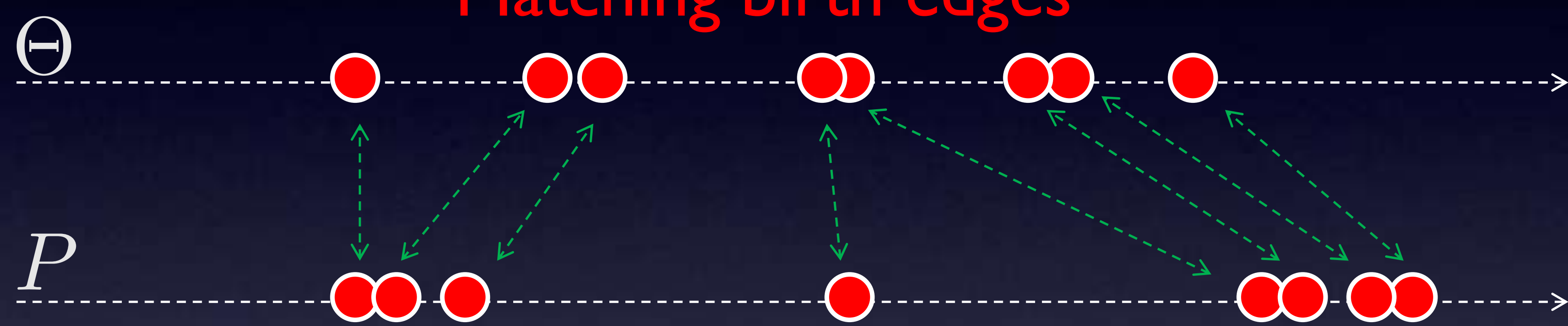
Topological registration via *r*-Wasserstein distance

$$d(X,Y) = \Big(\inf_{f(X,Y)} \mathbb{E}\|X-Y\|^r \Big)^{1/r}$$

1D topology
Matching death edges



0D topology
Matching birth edges



$$d_0(\Theta, P) = \min_{\tau} \sum_{b} |b - \tau(b)|^r$$

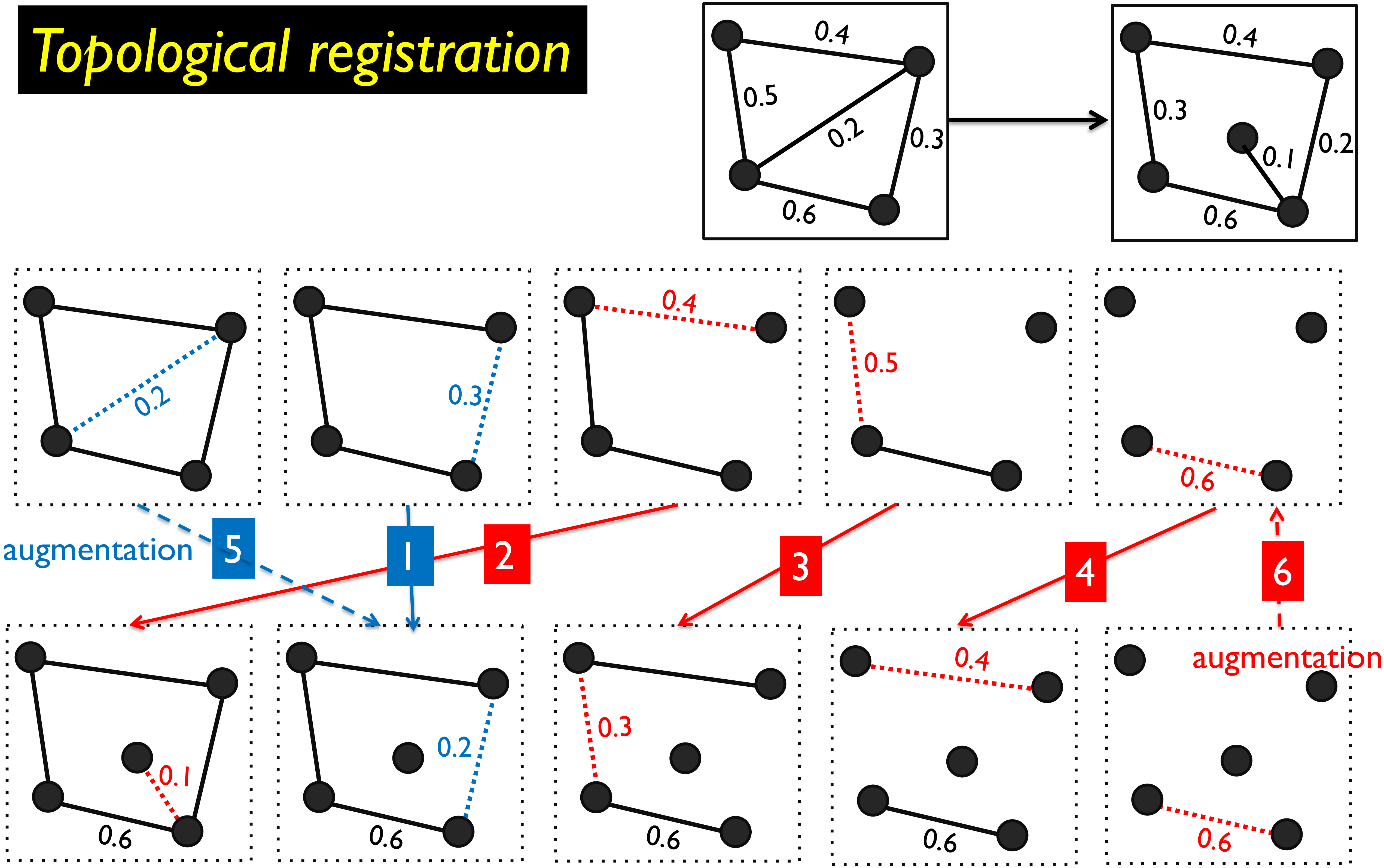
$$d_1(\Theta, P) = \min_{\tau} \sum_{d} |d - \tau(d)|^r$$

$$d_T^2 = d_0^2 + d_1^2$$

Runtime $\mathcal{O}(q \log q)$

Chung et al. 2024, *Foundations of Data Science*

Topological registration



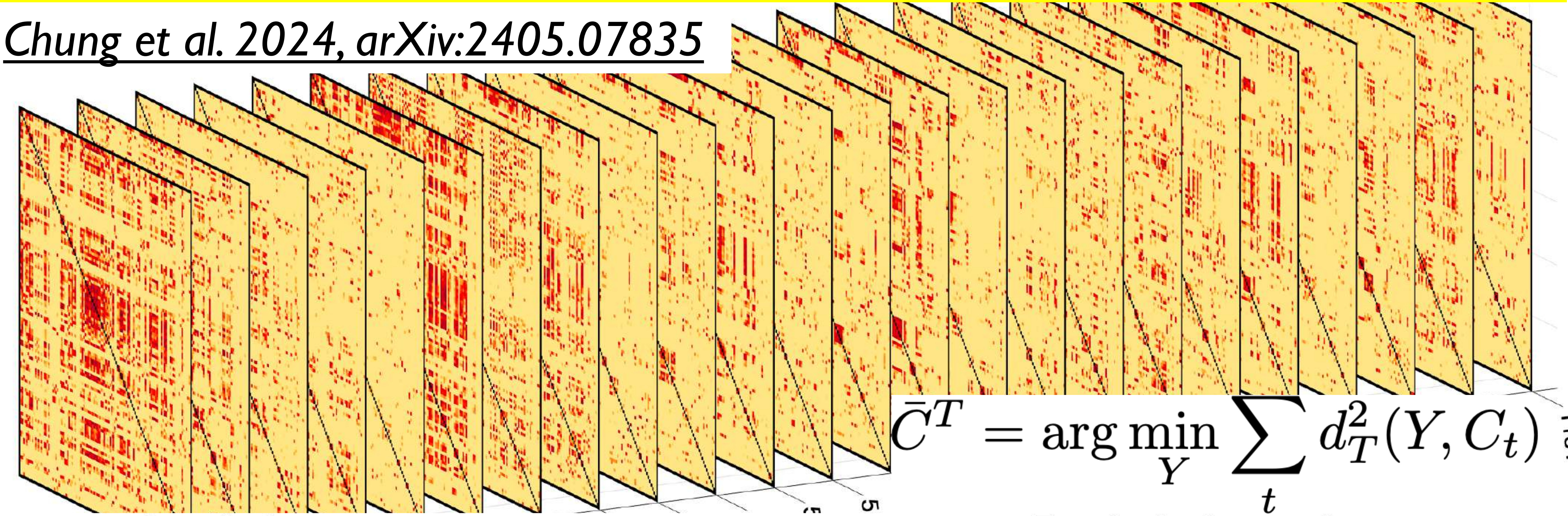
Largest death to largest death

Smallest birth to smallest birth

Songdechakraiwut and Chung. 2023, Annals of Appled Statistics

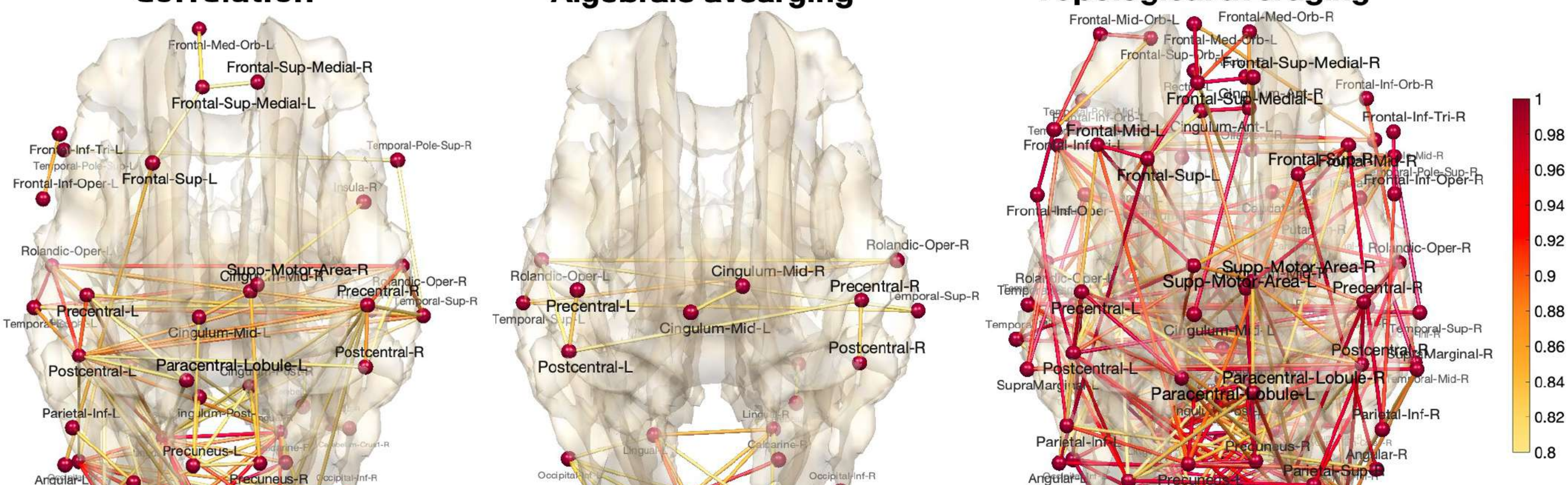
Superiority of topological averaging in rs-fMRI connectivity

Chung et al. 2024, arXiv:2405.07835



$$\bar{C}^T = \arg\min_Y \sum_t d_T^2(Y, C_t)$$

Correlation | **Algebraic avearging** | **Topological averaging**



Sample variance	0.47+-0.02	0.02+-0.01

Why topological methods reduce variability?

Geometric stability: Erdős–Rényi random graphs with connection probability between [0, 1], the maximum spanning tree (MST) is *not stable* under random perturbation of edge weights.

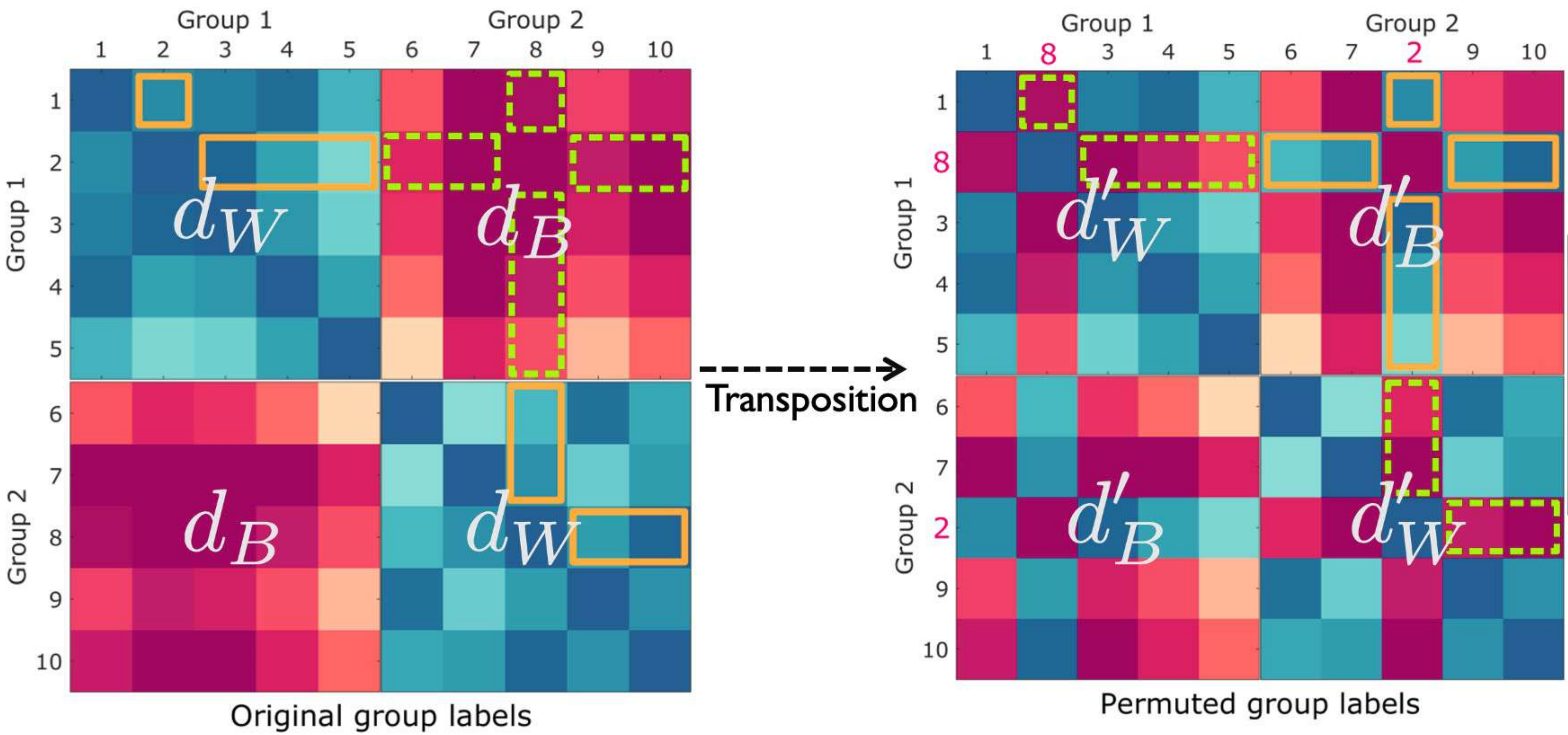
Topological stability for MST:

# of nodes *# of edges*

$$d_T(M_t, M_s) \leq \frac{(p-1)q}{(q+1)(q+2)} = \mathcal{O}\left(\frac{1}{p}\right)$$

Topological inference: online permutation test

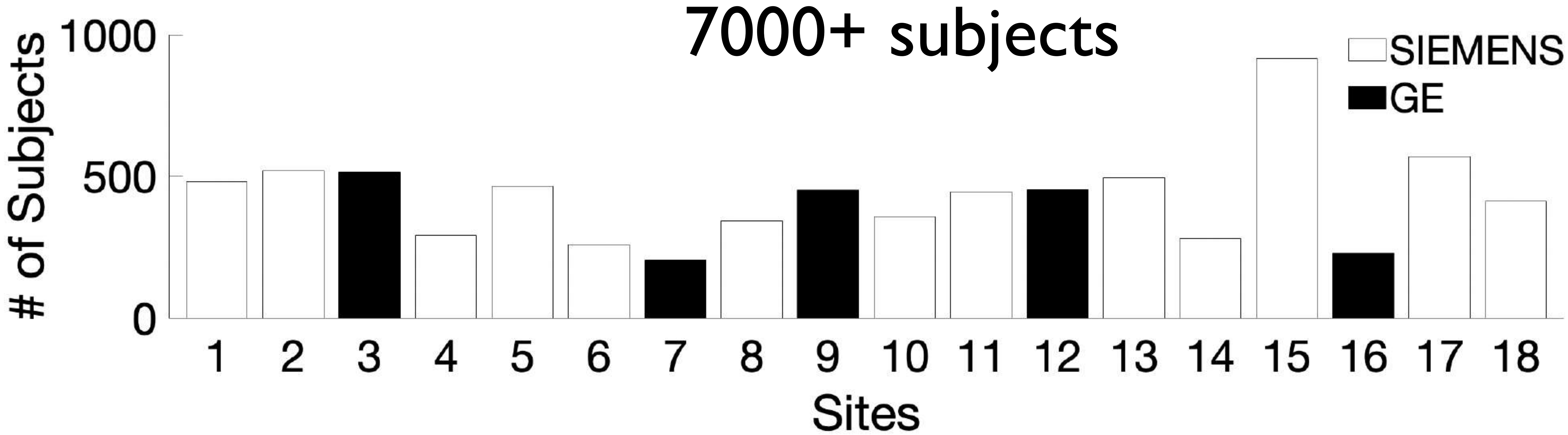
$$H_0 : Group_1 = Group_2 \rightarrow H_0 : d_B = 0$$

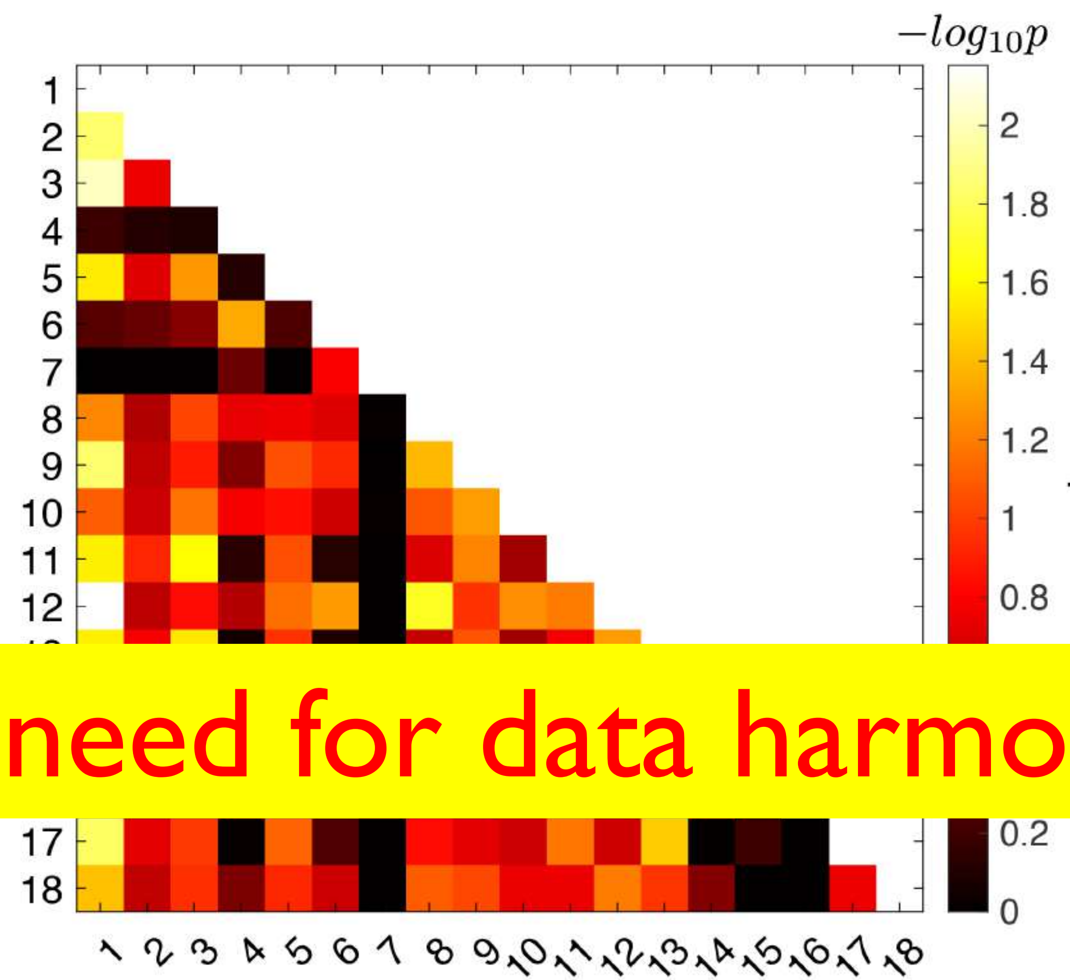


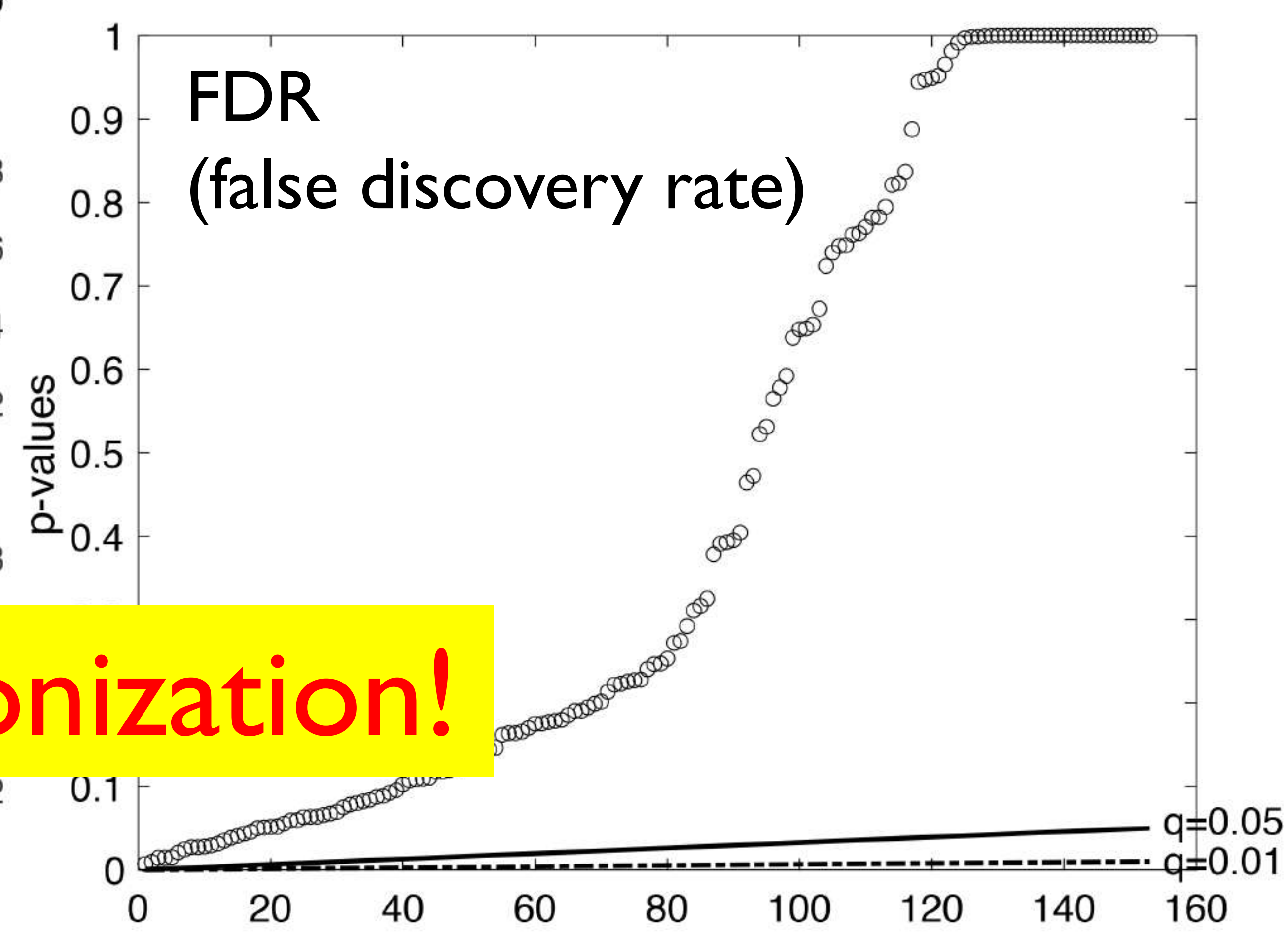
$$d'_B = d_B + \Delta(transposition)$$

100 million transpositions < 2 mins

Topological distance will not detect site effects – ABCD data



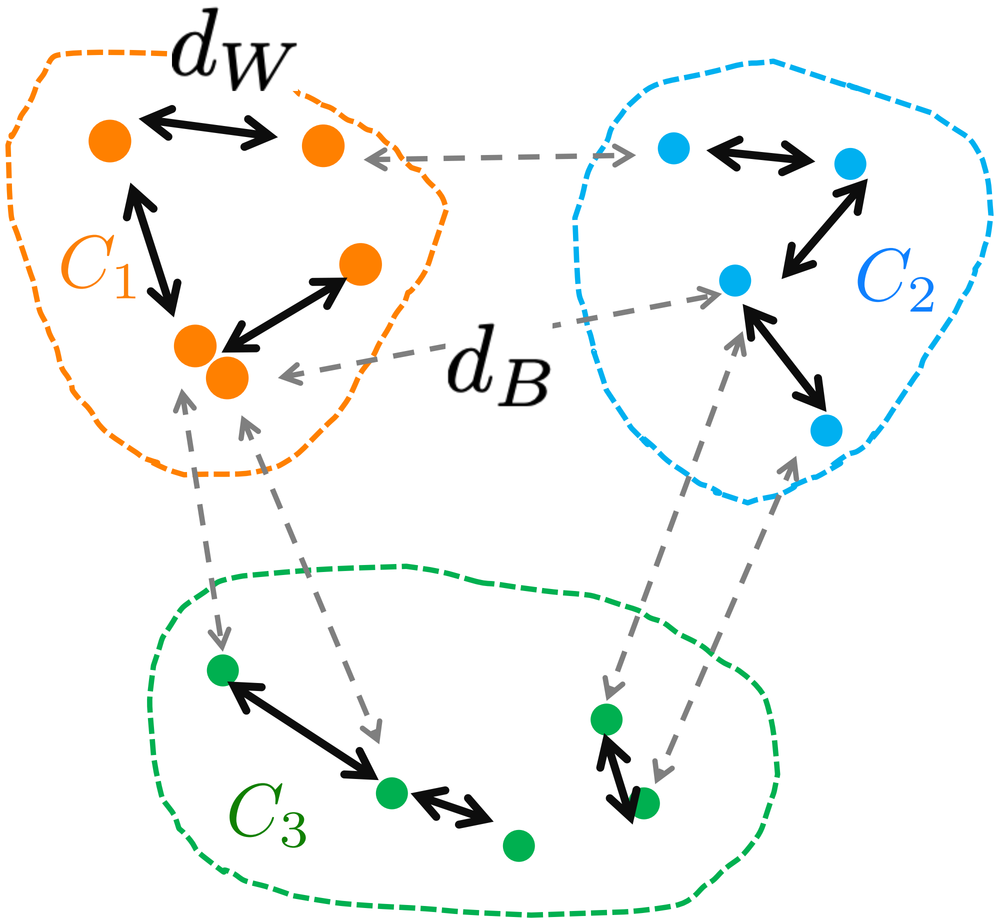




No need for data harmonization!

Topological clustering = topological inference

Within-group distance $d_W \propto \sum_k \sum_{i,j \in C_k} d_0(\mathcal{X}_i, \mathcal{X}_j) + d_1(\mathcal{X}_i, \mathcal{X}_j)$



Clustering accuracy

$$\frac{dA}{dp} = \frac{dA}{d(d_W)} \frac{d(d_W)}{dp} \leq 0$$

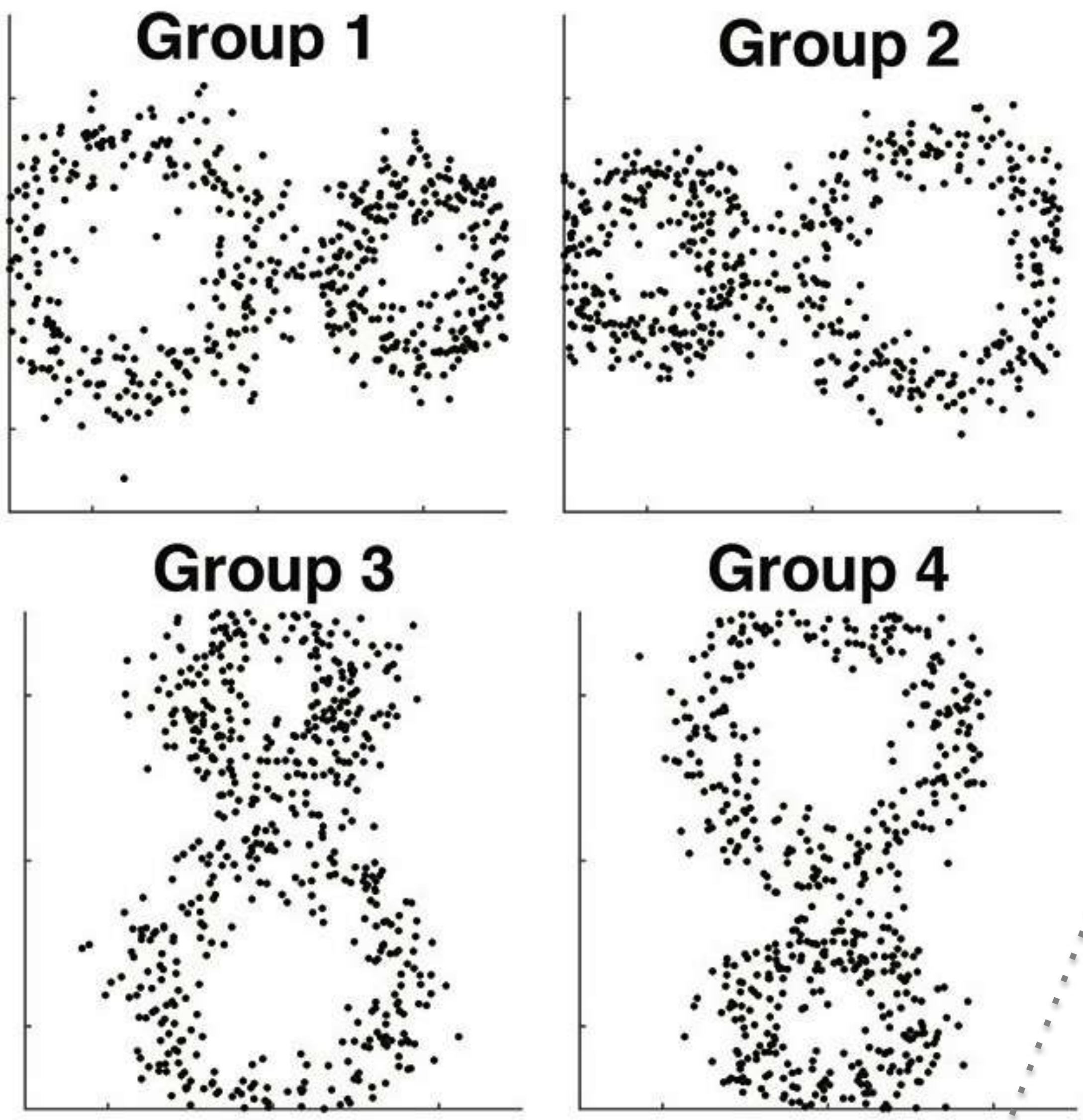
p-value

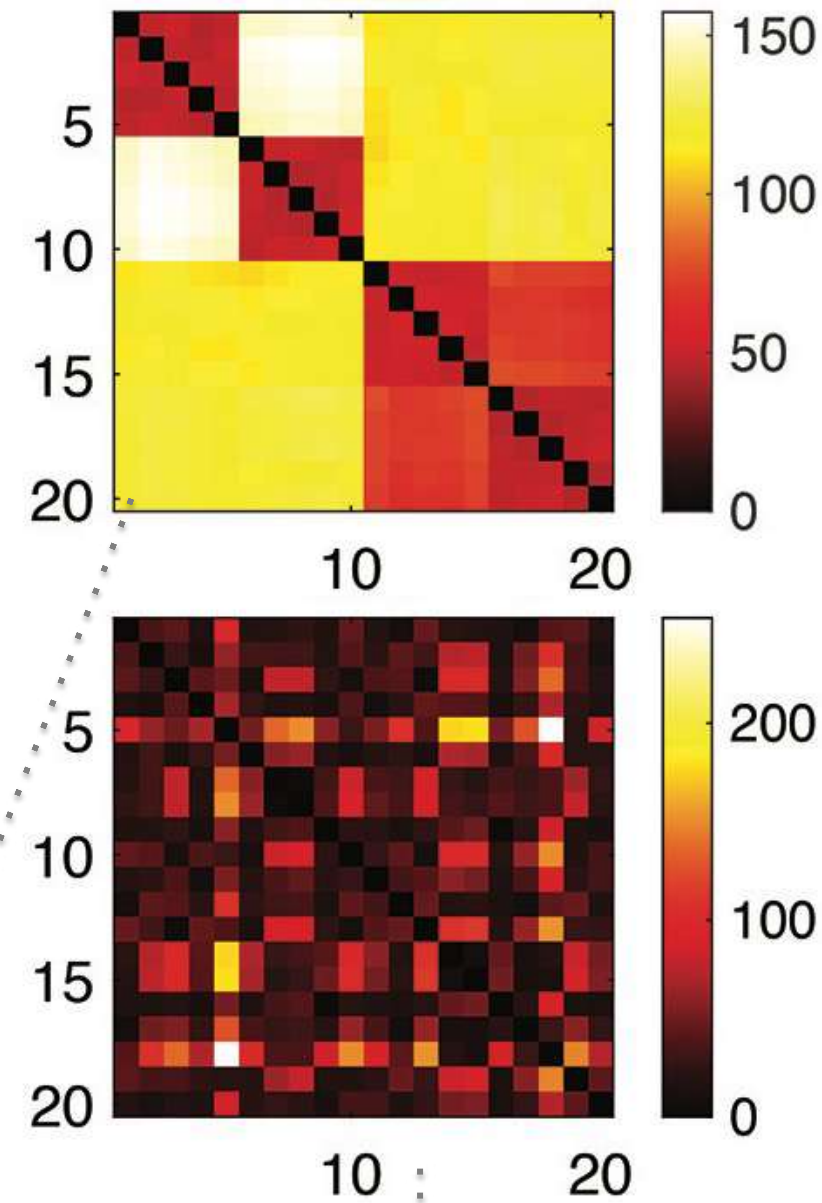
There exists a monotone decreasing function *f* satisfying *p* = *f*(*A*)

Proof in

Chung et al. 2023 NeuroImage

Topological distance robust against false positives





Euclidean

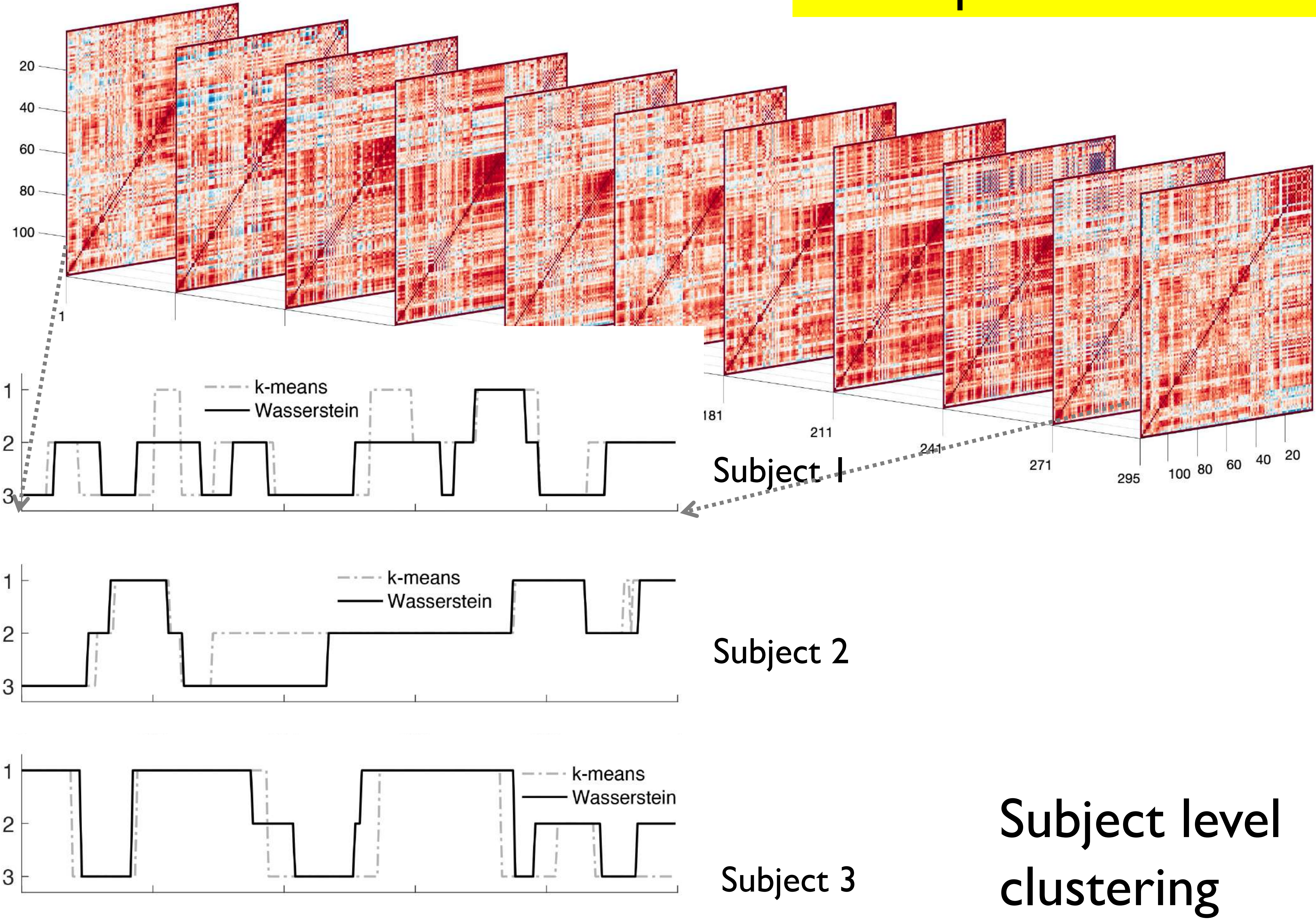
Topological

All false positives

K-means clustering
0.98 +- 0.01
Hierarchical clustering
1.00 +- 0.00

Topological clustering
0.63 +- 0.04

State space estimation



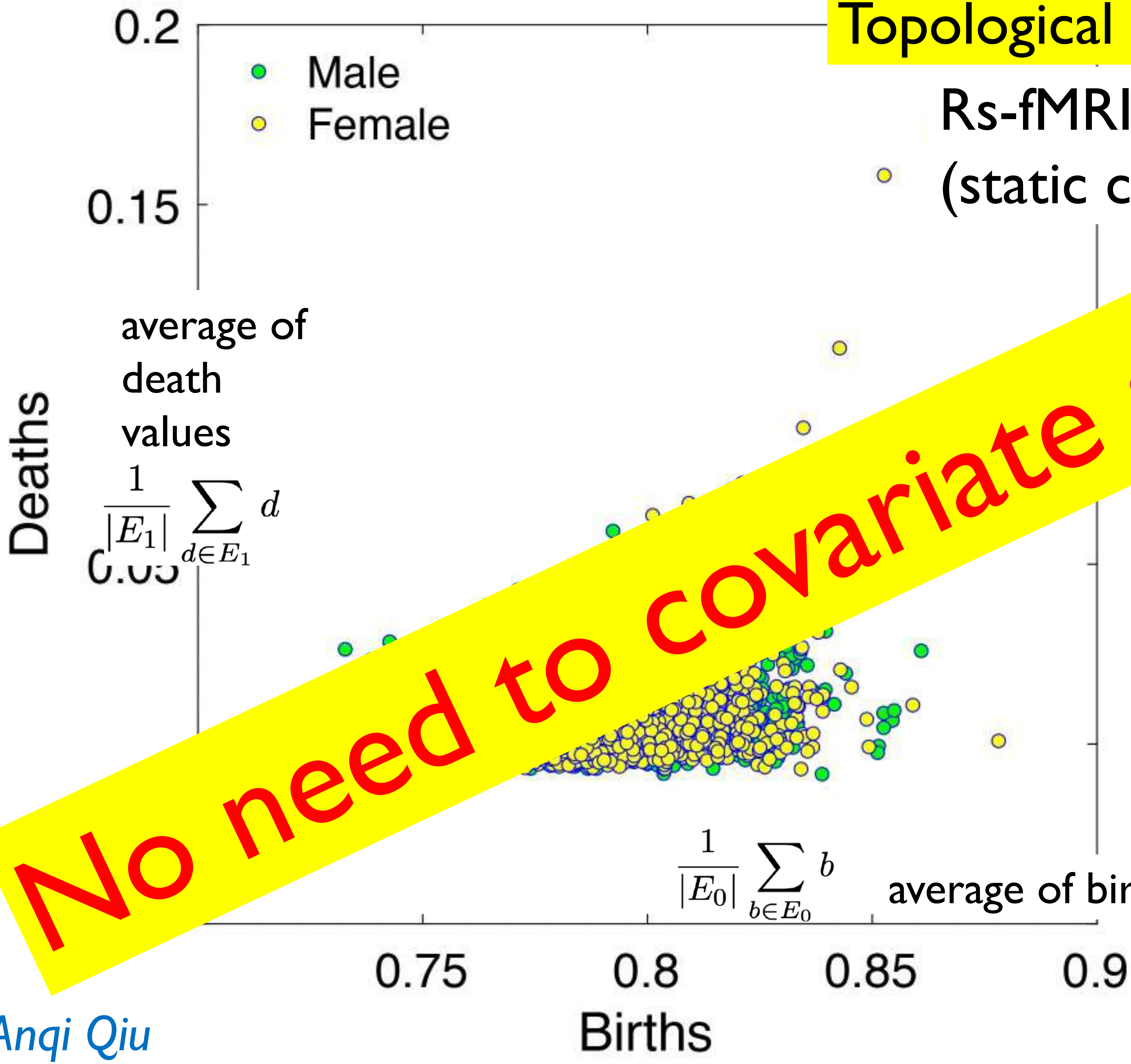
Subject level clustering

Topological Embedding

Chung et al. 2024 arXiv:2405.07835

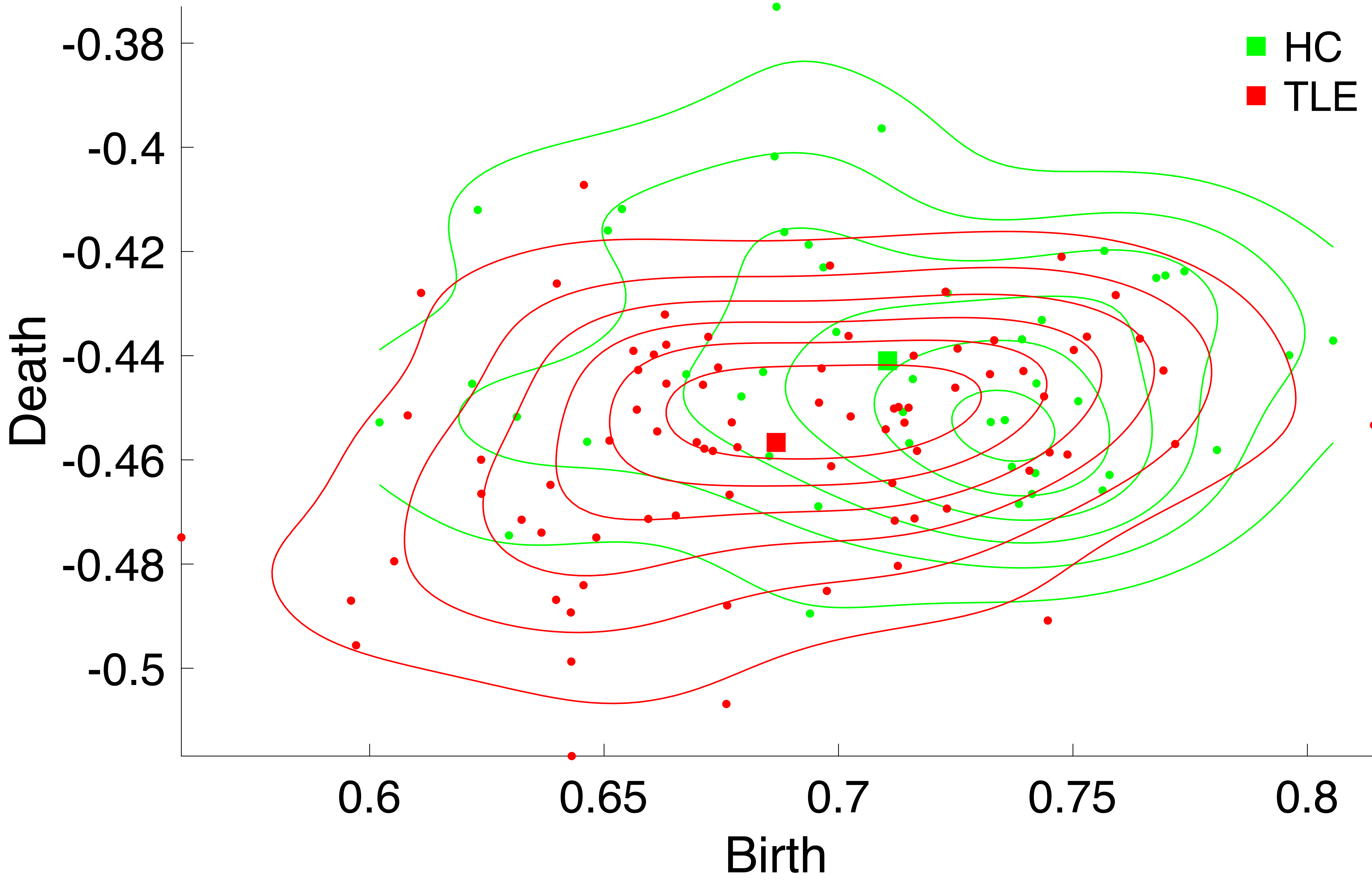
Topological Embedding

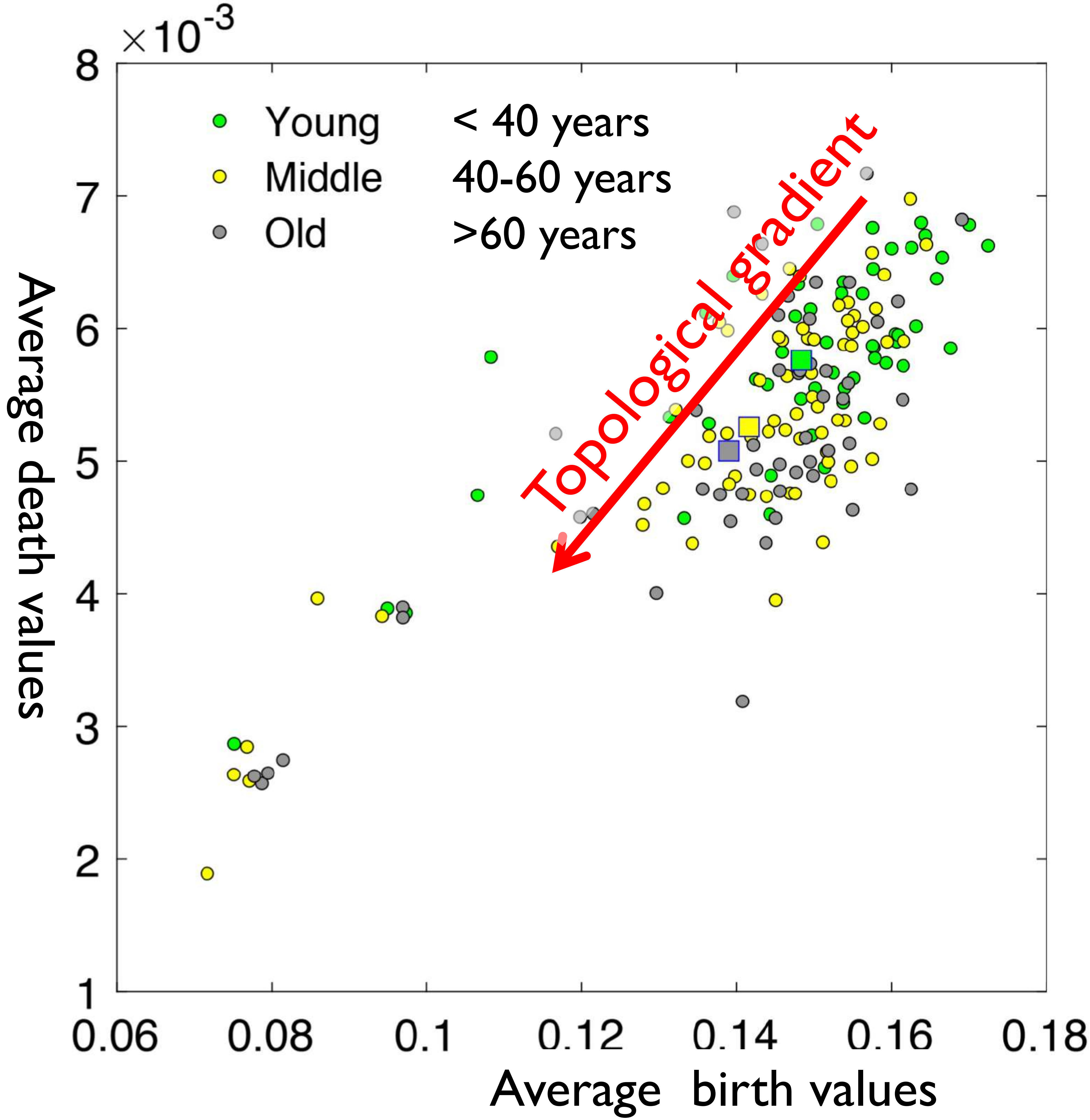
Rs-fMRI Network
(static correlation)



Anqi Qiu

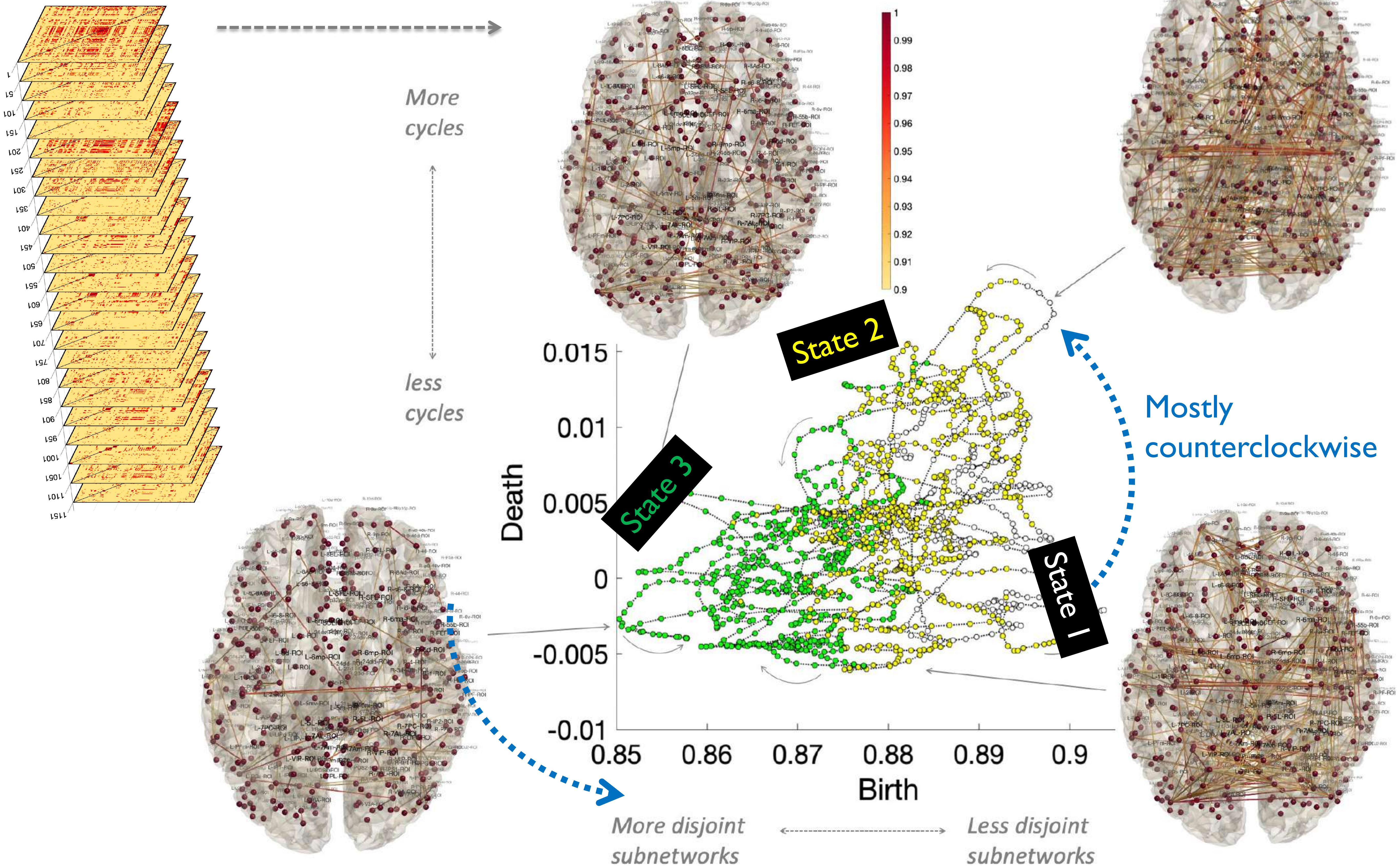
Structural connectivity from Diffusion-MRI (HCP-epilepsy)





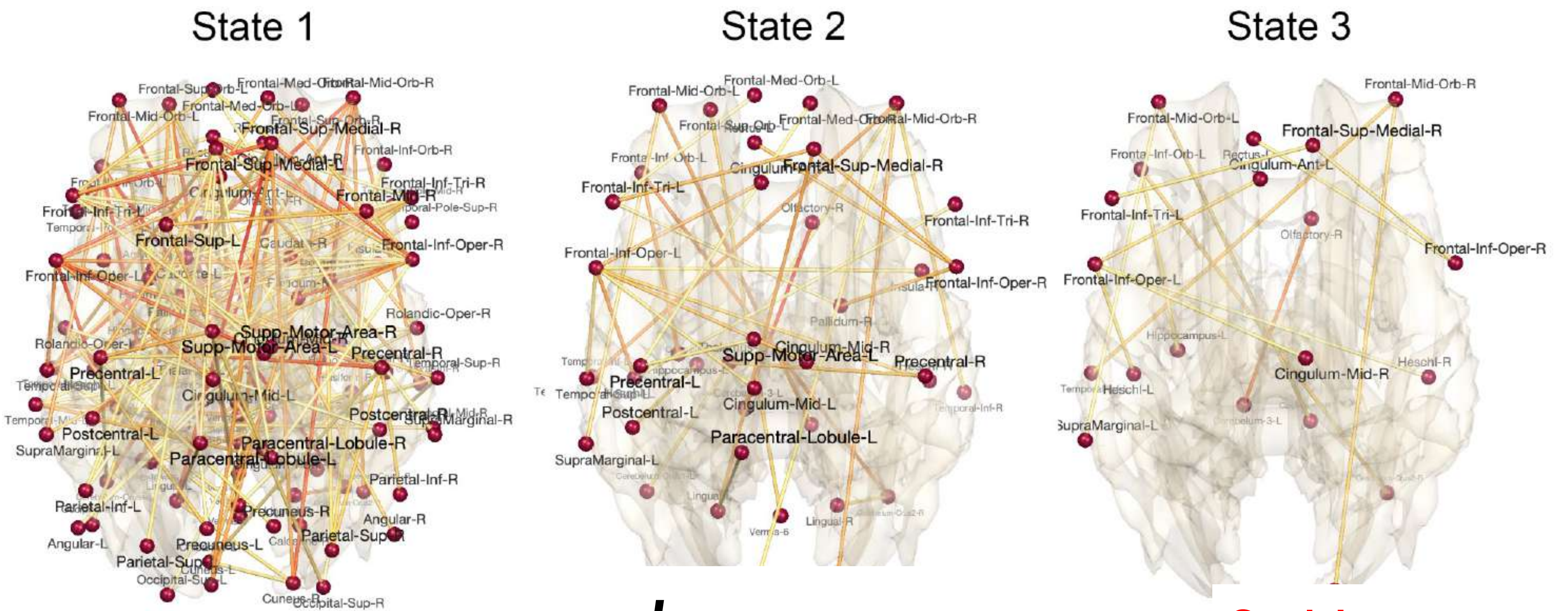
173 subjects
structural
connectivity

Topological Embedding



Embedding takes 2 hours per subjects for 12000 nodes

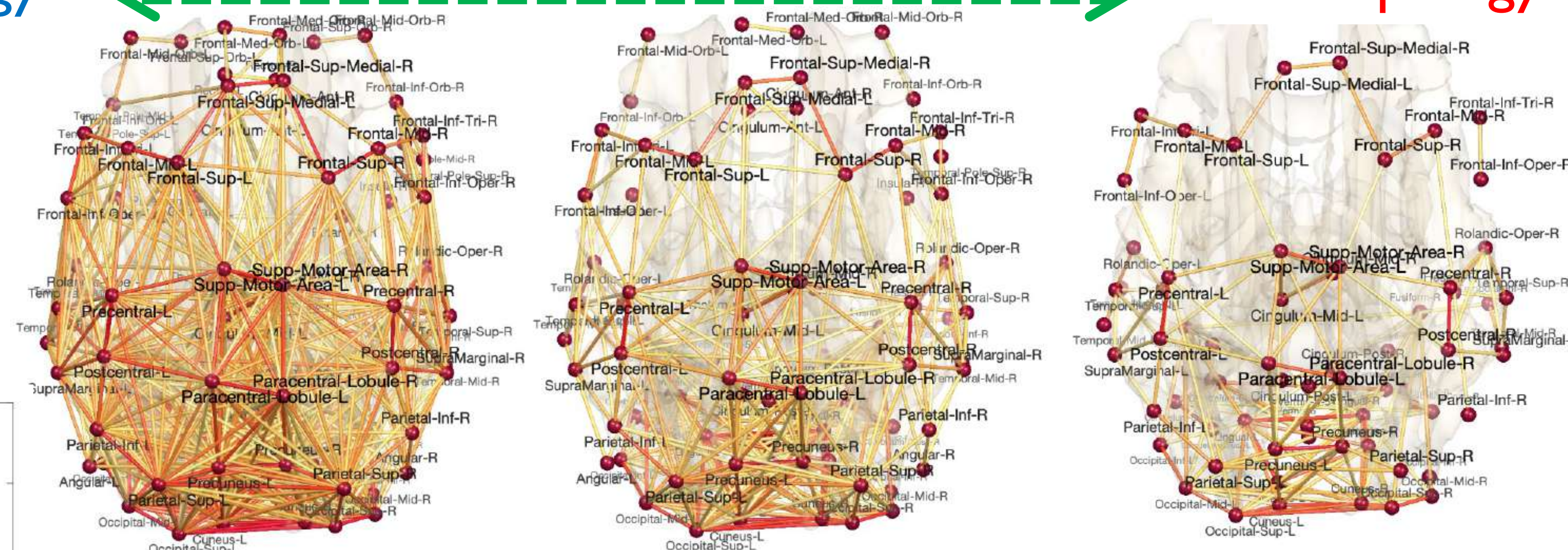
479 subjects
UW-Madison
twin study



Fluctuating
1D topology

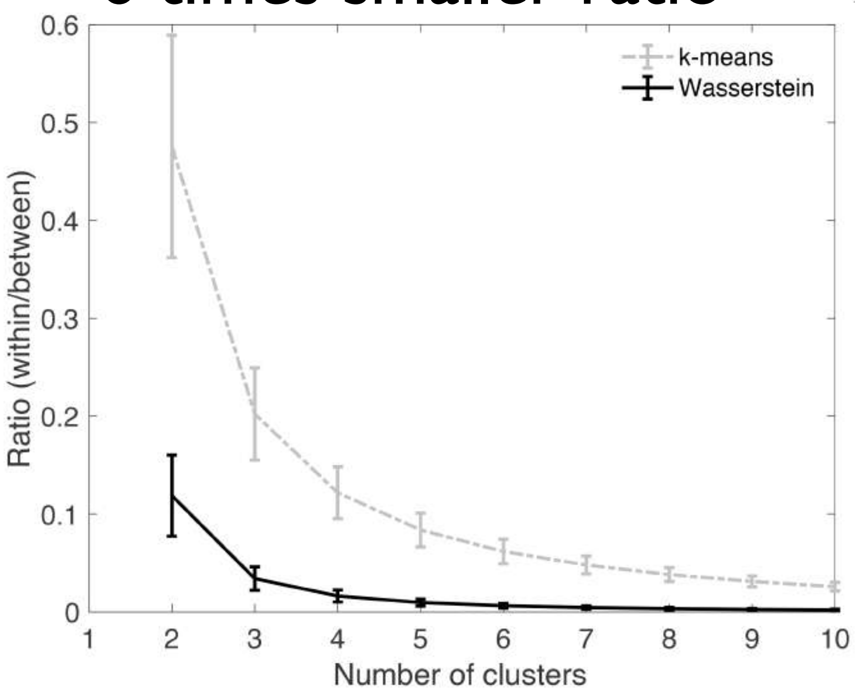
k-means

Stable
0D topology



Topological clustering

6 times smaller ratio



<u>*Chung at al. 2024 PLOS Computational BIology*</u>

Cerebral Cortex, December 2017;27: 5626–5634

doi: 10.1
Advance
Original

OXFORD

ORIGINAL ARTICLE

Heritability of the Effective Conn Resting-State Default Mode Net

Junhai Xu[1,2,3], Xuntao Yin[2], Haitao Ge[2], Yan
Baolin Liu[1], Shuwei Liu[2] and Karl Friston[3]

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Neuroimaging, Institute of Neurology, University College Londo
Affiliated Hospital of Medical College, Qingdao University, Qing
Epidemiology, Qingdao Municipal Central for Disease Control ar

Tables 3 Additive genetics/common environment/unique environment (A/C/E ive connecti

Difference is heritability index

DMN effective connectivity	r_{MZ}	r_{DZ}	V_A	V_C	V_E	P values
PCC-> mPFC	0.79	0.58	0.44	0.32	0.24	0.37
PCC->LPC	0.76	0.63	0.40	0.33	0.28	<0.001*
PCC->RPC	0.94	0.53	0.56	0.36	0.08	<0.001*
PCC->PCC	0.78	0.55	0.18	0.49	0.33	0.025*
mPFC->PCC	0.86	0.55	0.76	0.09	0.15	0.068
mPFC->LPC	0.62	0.49	0.15	0.44	0.42	0.92
mPFC->RPC	0.34	0.72	0.00	0.54	0.46	0.28
mPFC->mPFC	0.56	0.14	0.51	0.00	0.49	0.43
>PCC	0.89	0.6	0.44	0.42	0.14	<0.001*
>mPFC	0.82	0.61	0.39	0.40	0.21	0.33
>RPC	0.75	0.51	0.38	0.30	0.32	0.077
>LPC	0.84	0.71	0.24	0.58	0.18	0.43
>PCC	0.68	0.72	0.36	0.44	0.20	<0.001*
>mPFC	0.61	0.63	0.33	0.39	0.28	0.24
RPC->LPC	0.47	0.39	0.38	0.15	0.47	0.83
RPC->RPC	0.75	0.55	0.37	0.35	0.28	0.65

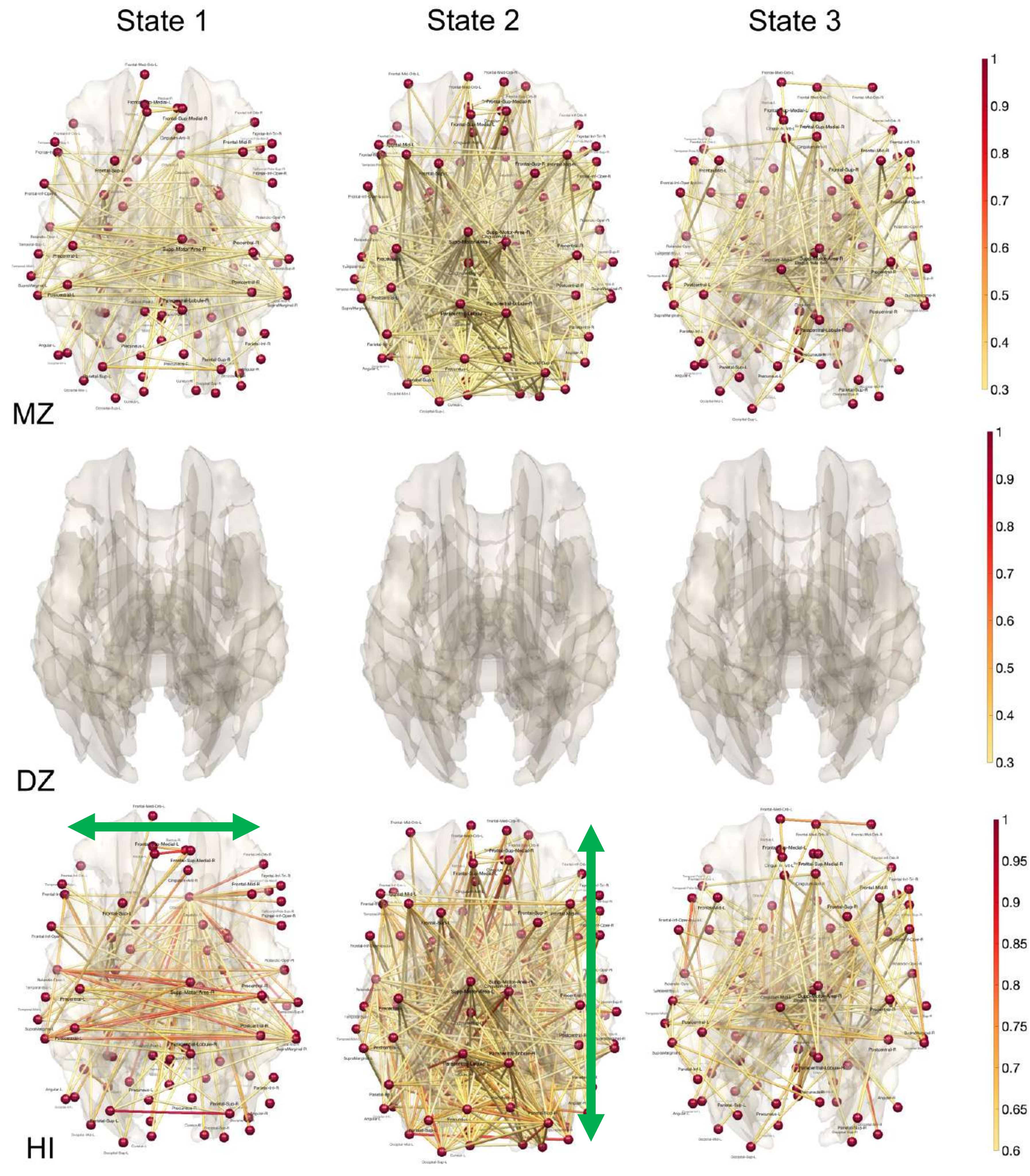
*P < 0.05. V ment
nce esti

These will not even pass multiple comparisons corrections

Structural equation models

low heritability index up to 0.4

Overfitting likely caused too many false positives



479 subjects
UW-Madison
twin study

Rs-fMRI network far more heritable than literature reports

Our heritability index

Chung et al. 2024
arXiv:2201.00087
PLOS Computational Biology

Topological Causal Model

Yaagoubi et al. 2024 arXiv:2407.13514, MICCAI TDA workshop

Hodge decomposition

Edge flow

Gradient

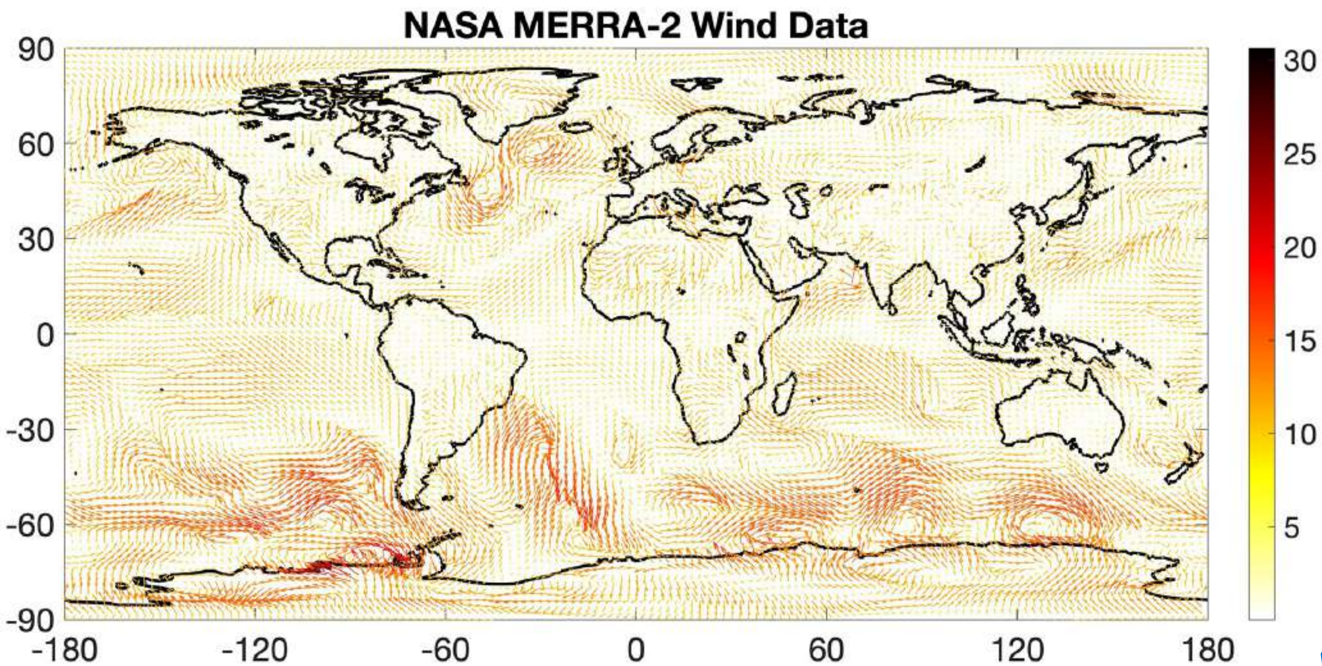
Curl

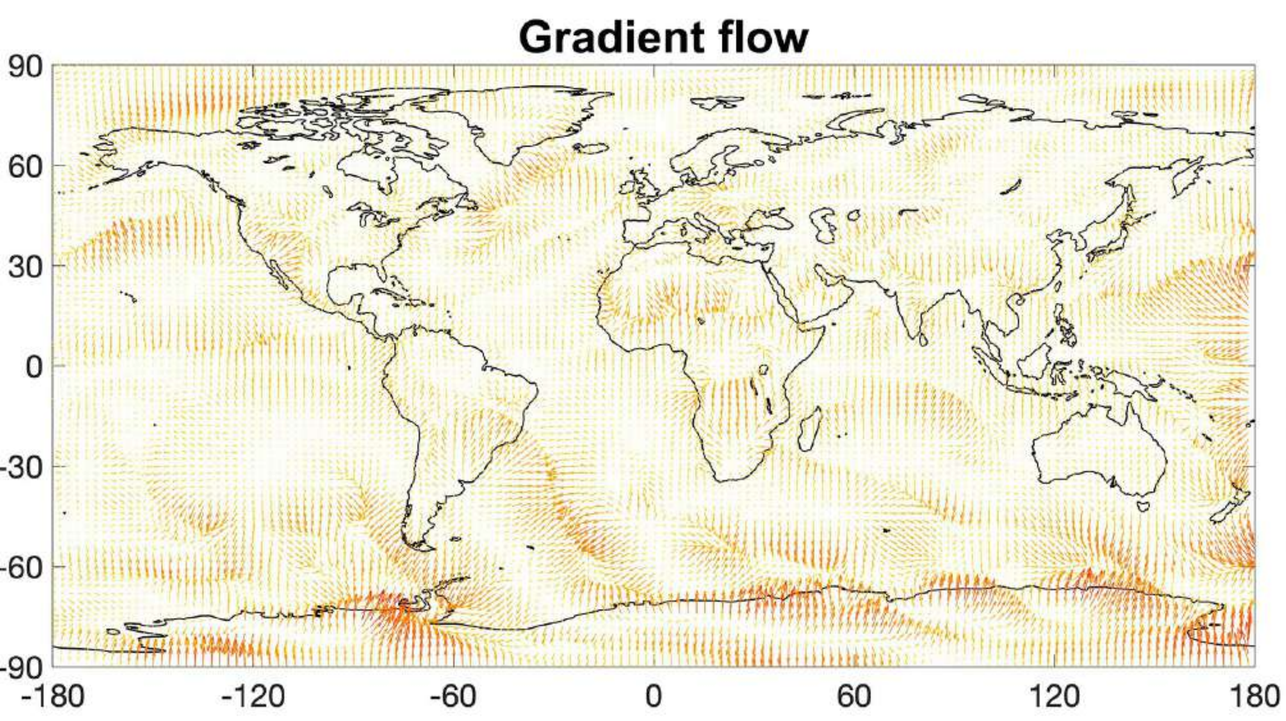
Harmonic

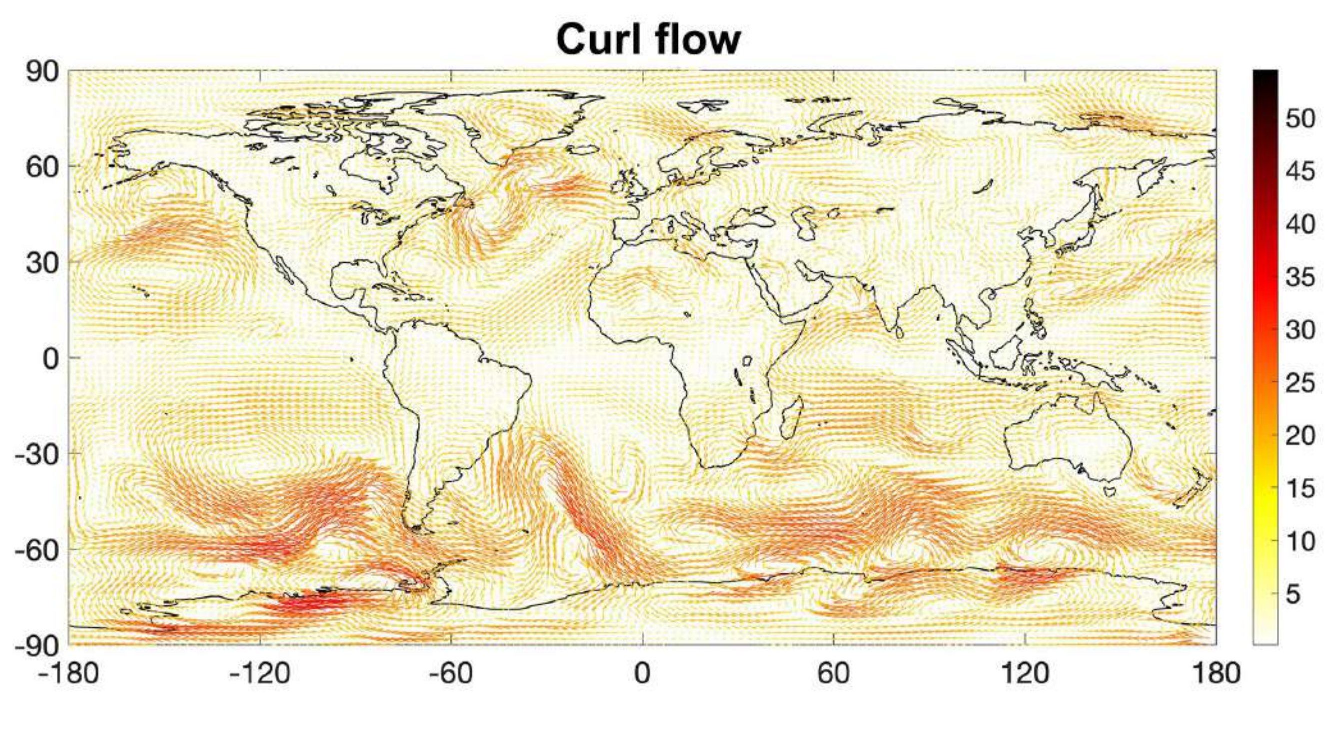
$$X = X_G + X_C + X_H = \boxed{\partial_1^\top s} + \boxed{\partial_2 \phi} + X_H$$

Function over edge?

Function over triangle







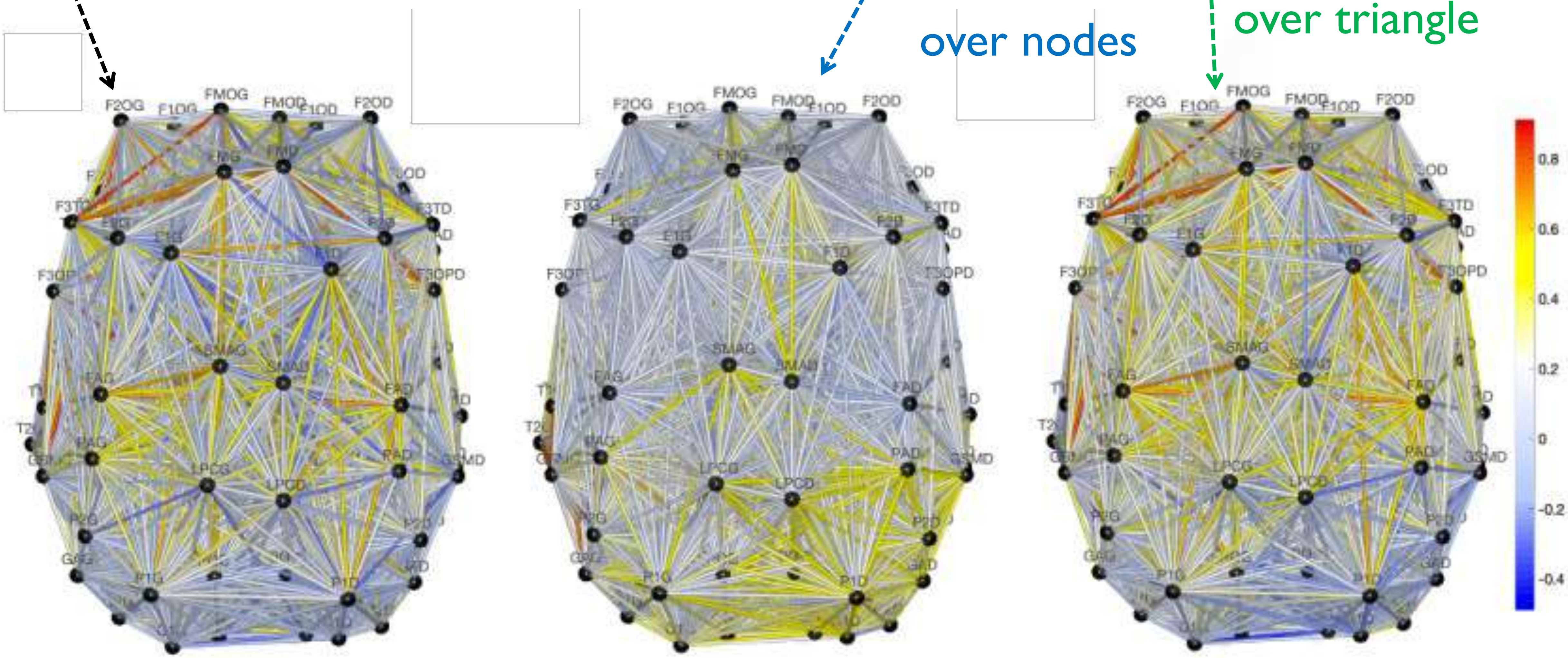
Hodge decomposition

Directed edge flow | Gradient | Curl | Harmonic

$$X = X_G + X_C + X_H = \boxed{\partial_1^\top s} + \boxed{\partial_2 \phi} + X_H$$

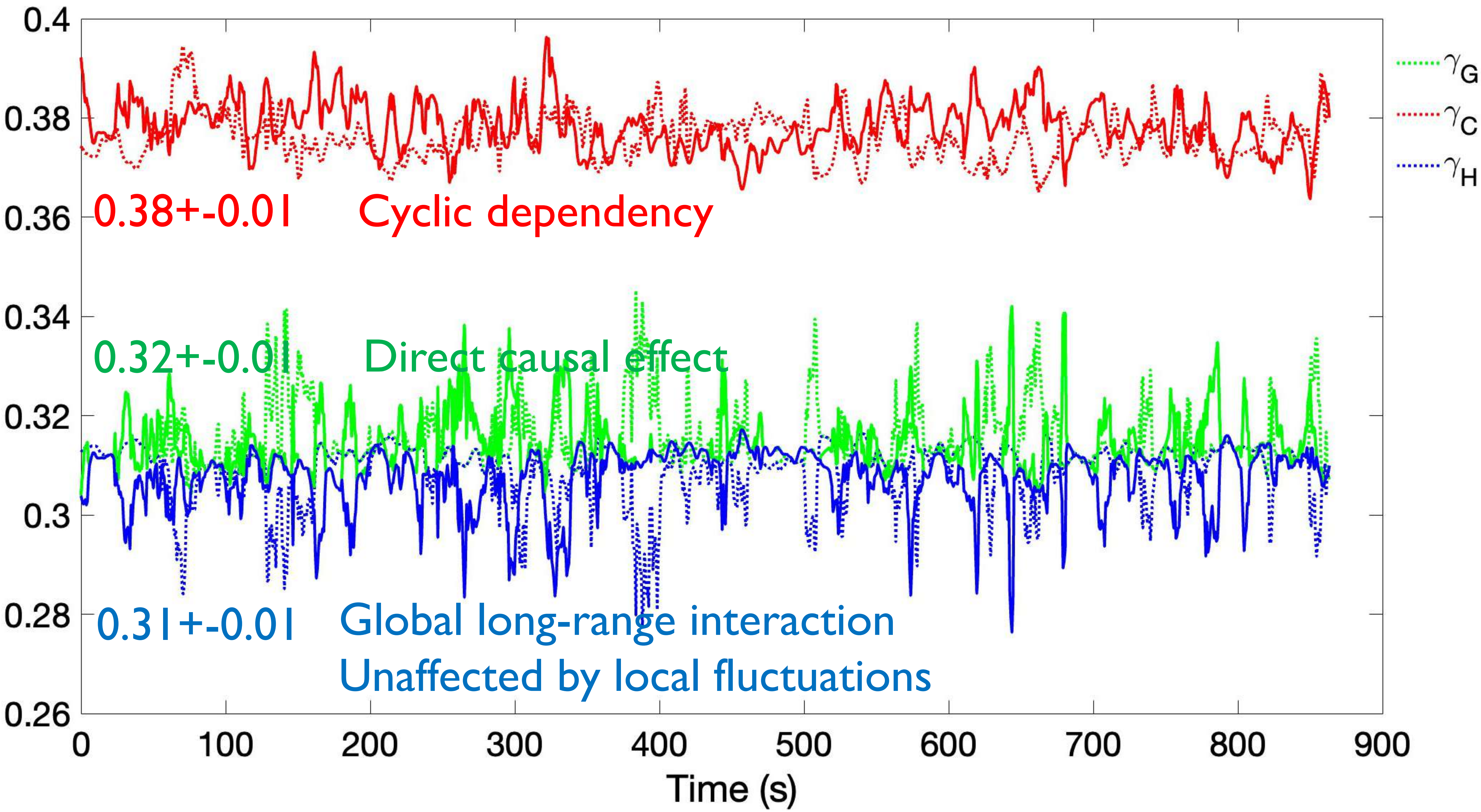
Function over nodes

Function over triangle



Anand & Chung, 2024 ISBI (arXiv: 2211.10542)

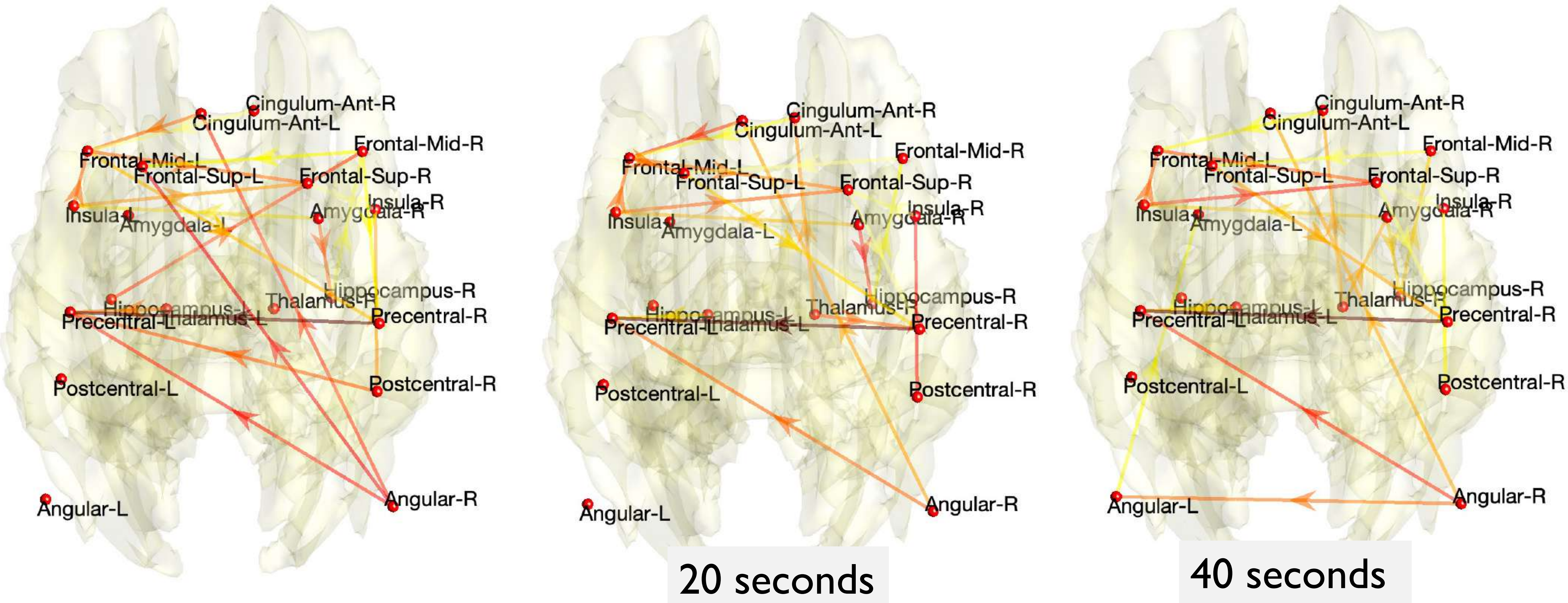
Dynamics of Hodge decomposition over time



$$\gamma_G = \frac{\|\boldsymbol{\partial}_1^\top s\|_2}{\|vec\ X\|_2}, \gamma_C = \frac{\|\boldsymbol{\partial}_2 \phi\|_2}{\|vec\ X\|_2}, \gamma_H = 1 - \gamma_G - \gamma_C$$

Stability of direct causal effects over 40 seconds

20 largest gradients components



Right precentral gyrus to the left precentral gyrus has the highest causal ranking (largest magnitude of gradient)

Thank you.