The Waisman Laboratory
for Brain Imaging and Behavior

University of Wisconsin
SCHOOL OF MEDICINE
AND PUBLIC HEALTH

Persistent homological brain network analysis

Moo K. Chung

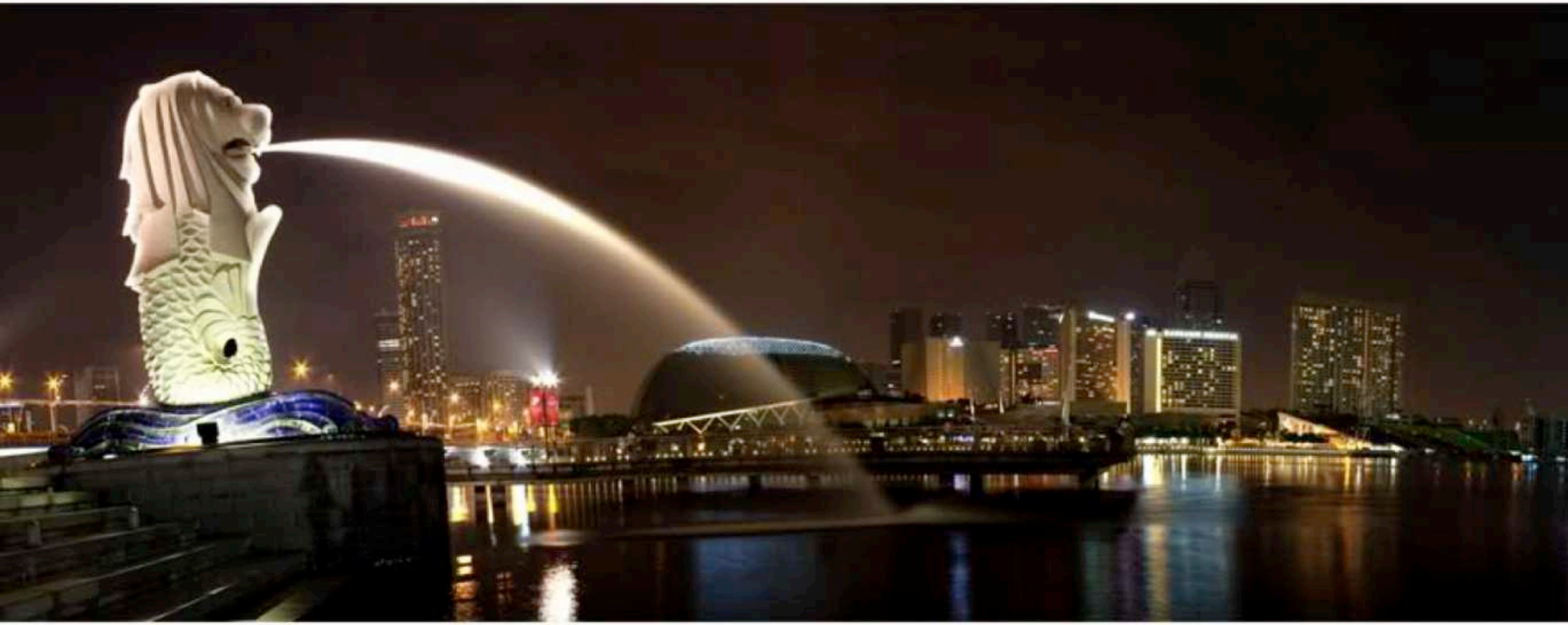
University of Wisconsin-Madison
www.stat.wisc.edu/~mchung

November 24, 2017, Juan-les-Pins, France Winter Workshop

http://nbiasite.wordpress.com

NONSTANDARD BRAIN IMAGE ANALYSIS

ORGANIZERS PROGRAM VENUE REGISTRATION



Satellite Meeting of 2018
OHBM Singapore

June 22-23, 2018

Plenary Talks
Peter Bandettini, Jean-Baptiste Poline

Session on Deep Learning
Dinggang Shen, Daniel Alexander, Jong Chul Ye, Jong-Hwan Lee

Session on Imaging Genetics
Anqi Qiu, Li Shen, Hongtu Zhu, Tomas Nichols

Session on Nonstandard EEG Analysis
Hernando Ombao, Hakmook Kang, Mak Fiecas, Tim Johnson

Session on Nonstandard fMRI Analysis
Martin Lindquist, Alex D. Leow, Bharat Biswal, Christian F. Beckmann

Session on Nonstandard Brain Connectomics
Moo K. Chung, Andrew Zalesky, James C. Gee, Carl-Fredrik Westin

Poster Session

Abstract

Persistent homology, a branch of recently popular computational topology, provides a coherent mathematical framework for quantifying the topological structures of brain networks. Instead of looking at networks at a fixed scale, as usually done in many standard brain network analysis, persistent homology observes the changes of topological features of the network over multiple resolutions and scales. In doing so, it reveals the most persistent topological features that are robust under noise perturbations. This robustness in performance under different scales is needed for obtaining more stable quantification of the network. For the first half of the talk, we will review the basics of persistent homology. The remaining half of the talk will be focused on its applications in EEG and dMRI based brain network analysis. The talk is based on doi.org/10.1109/TMI.2012.2219590.

Acknowledgement

Yuan Wang, Ross Luo, Nagesh Adluru, Andrew Alexander,
Seth Pollack, Richard Davidson, Hill Goldsmith
University of Wisconsin-Madison, USA

Benjamin Lahey *University of Chicago*

Hyekyung Lee, Dong Soo Lee *Seoul National University*

Victorial Villalta-Gil, David Zald Vanderbilt University

Jae Jun Woo, Jong Chul Ye *KAIST, Korea*

Hernando Ombao *KAUST, Saudi Arabia*

Guorong Wu *University of North Carolina – Chapel Hill*

NIH grants: R01 EB022856, R01 MH101504,
P30 HD003352, U54 HD09025

Rips Filtration

Carlsson & de Silva, 2010
Edelsbrunner & Harer, 2009

What is filtration?

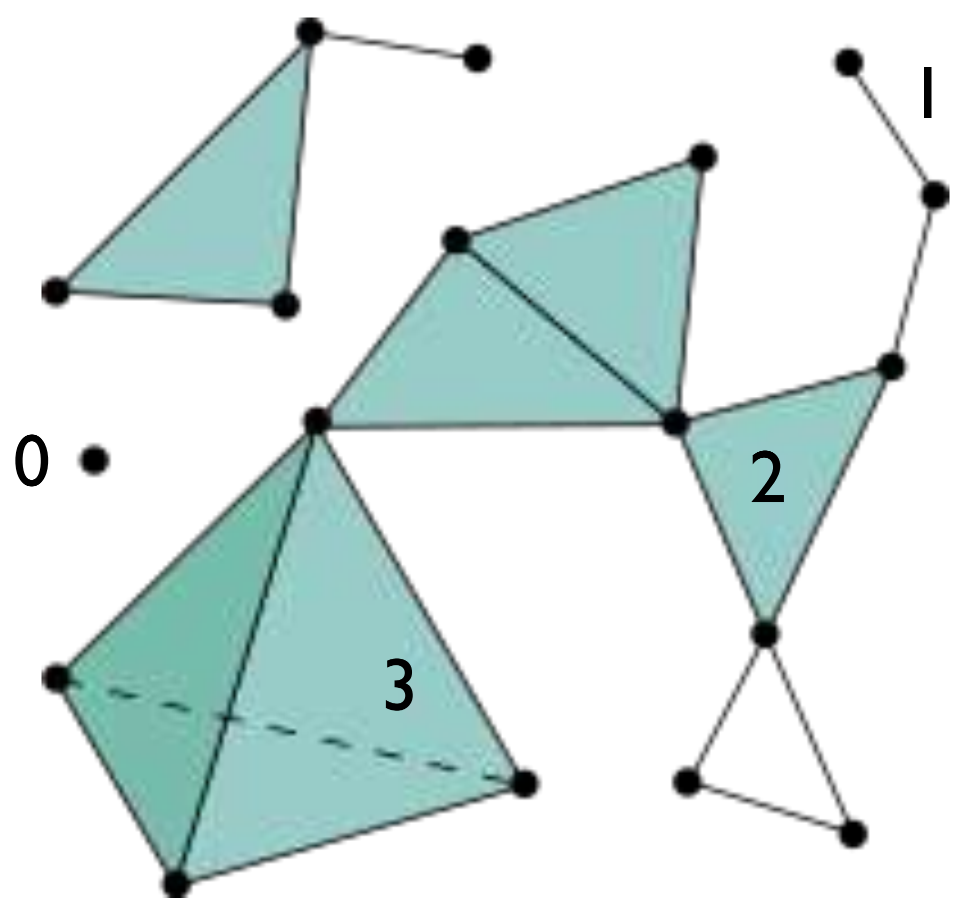
$$\mathcal{G}_1 \subset \mathcal{G}_2 \subset \mathcal{G}_3 \subset \cdots$$

Sequence of nested objects or vector spaces

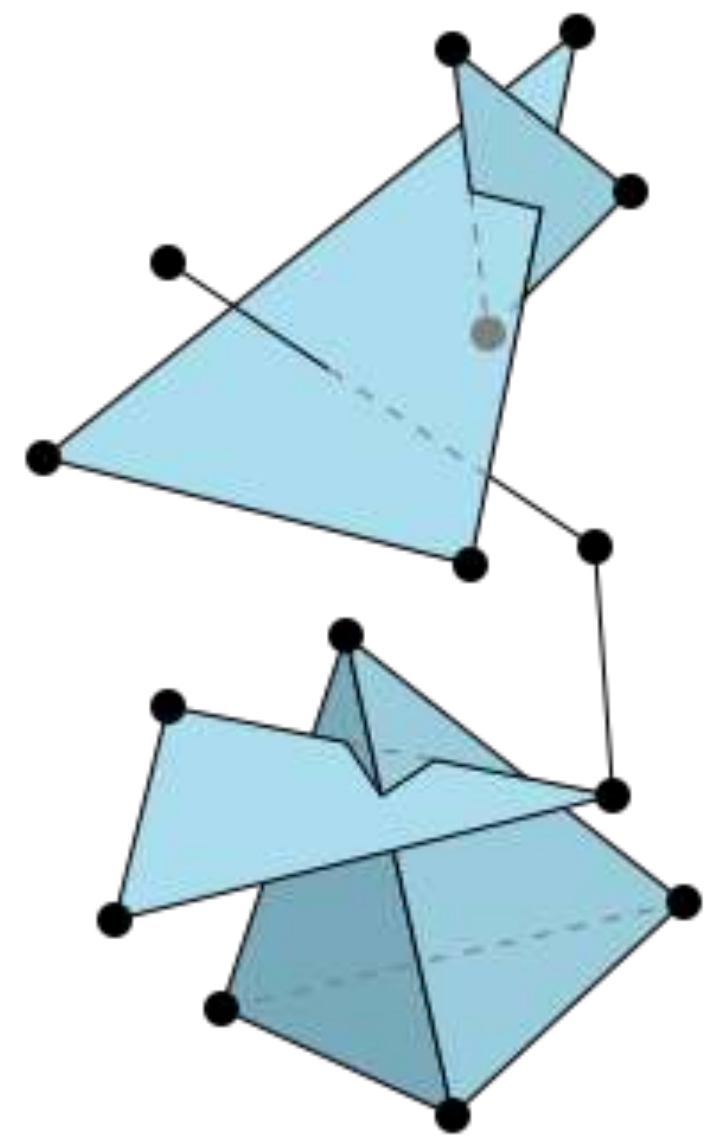
Monotonic feature function

$$\beta_i(\mathcal{G}_1) < \beta_i(\mathcal{G}_2) < \beta_i(\mathcal{G}_3) < \cdots$$

Simplicial complex

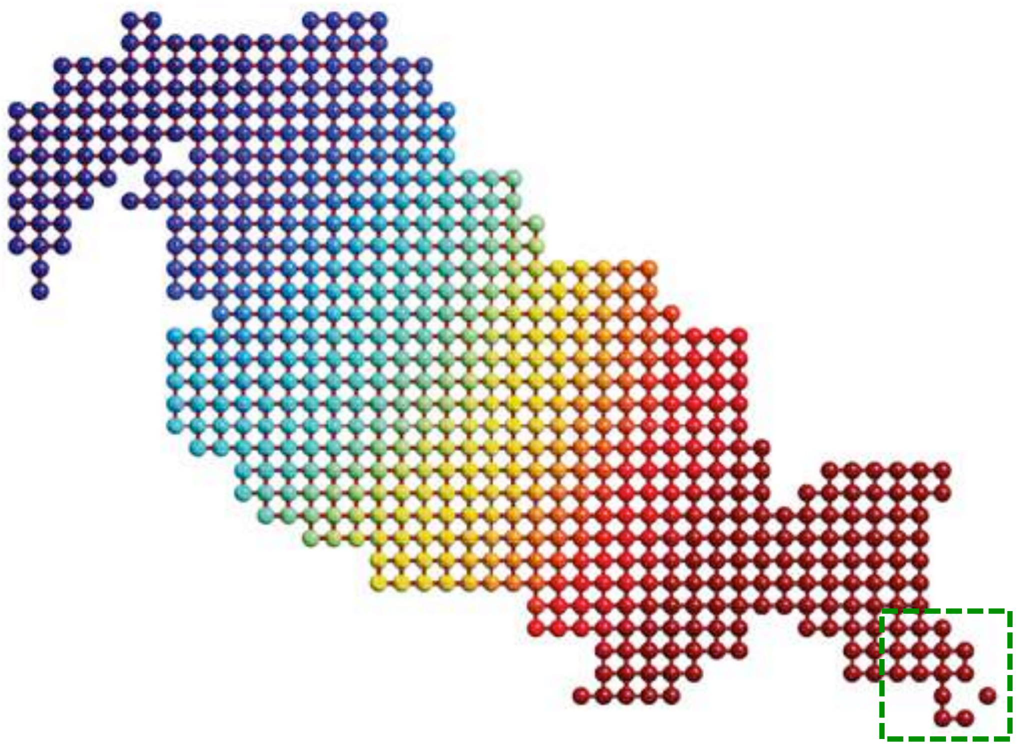


Simplicial complex

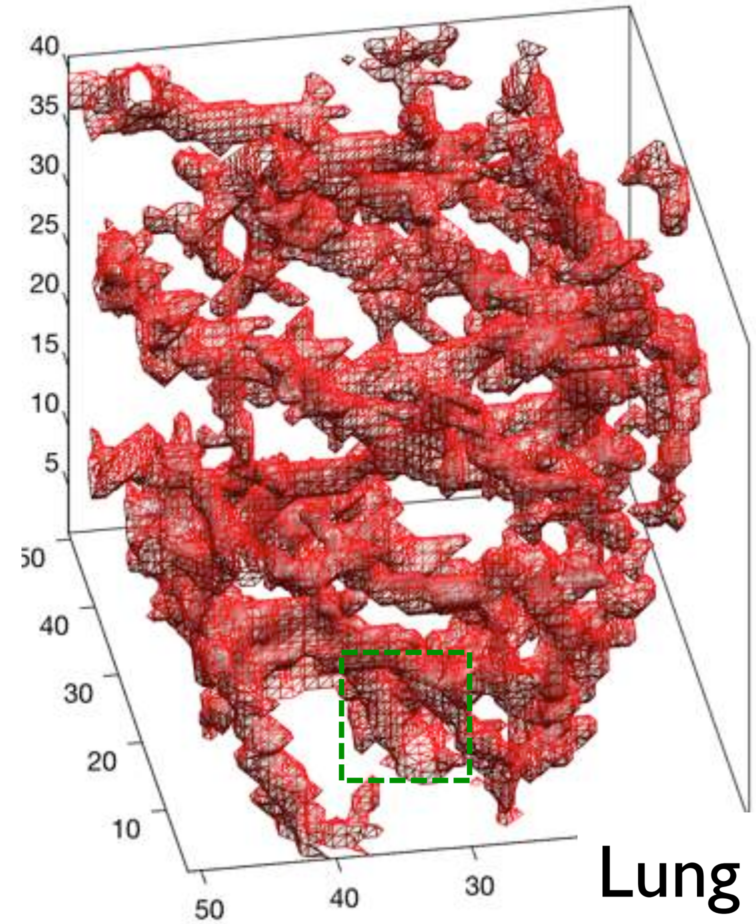


Not a valid simplicial complex

Cubical complex

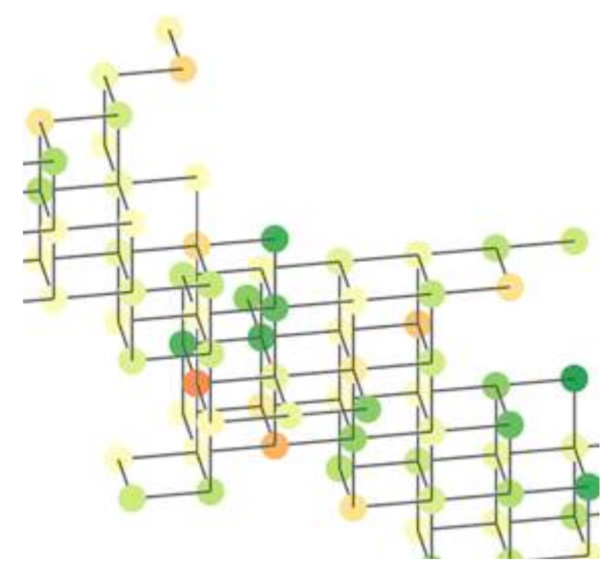


Left central gyrus



Lung blood vessel

4-neighbor connectivity

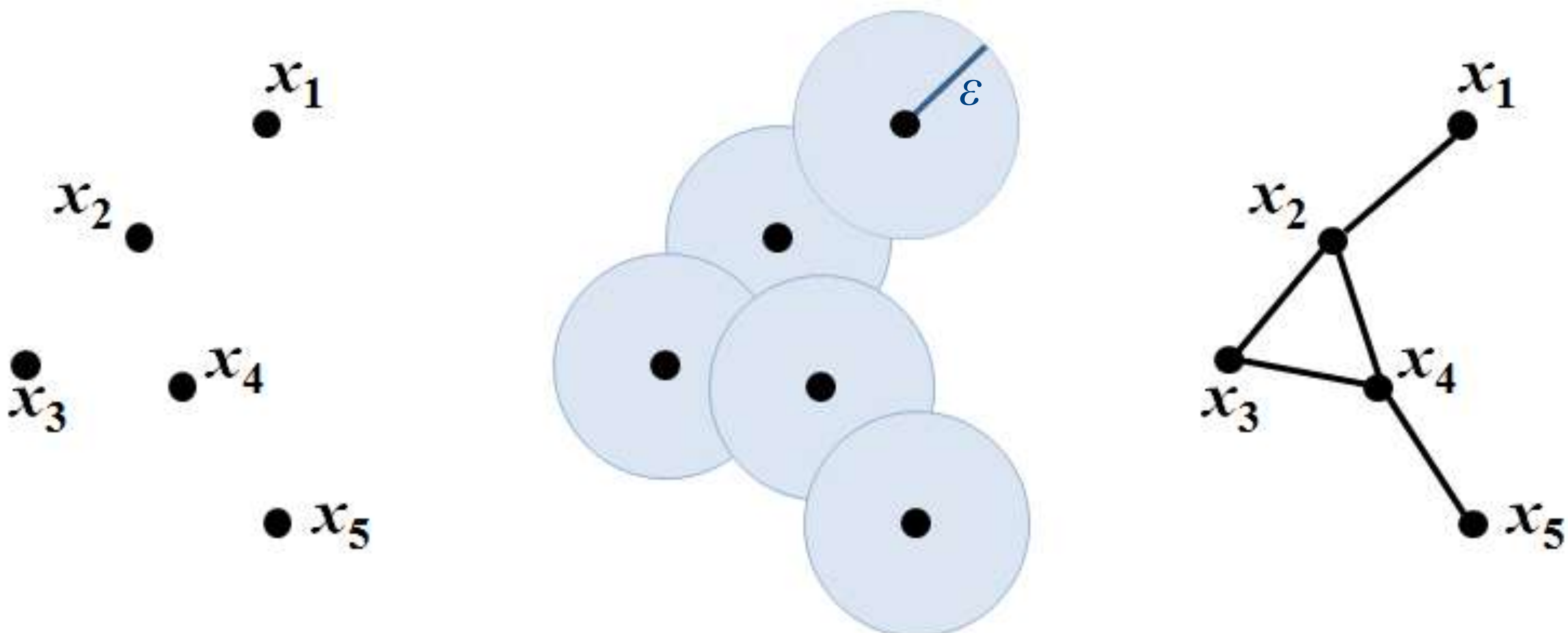


6-neighbor connectivity

[Chung et al. 2018 arXiv:1710.07849](https://arxiv.org/abs/1710.07849)

Rips complex of point cloud data

Rips complex approximates the topology of the point cloud data by connecting two point cloud data, x_i and x_j, if $d(x_i, x_j) < \varepsilon$.

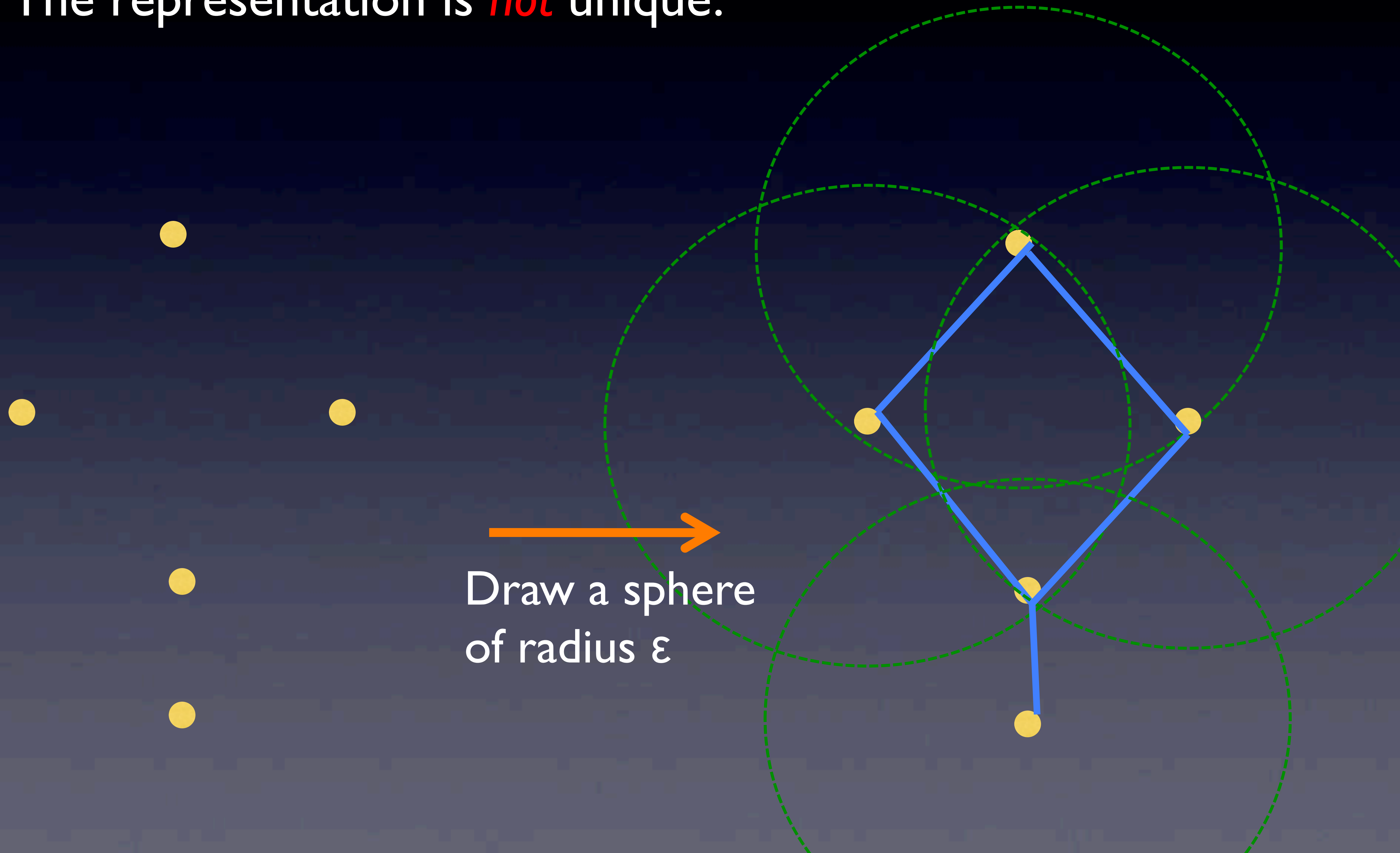


Rips Filtration of cloud point data

Computationally expensive:

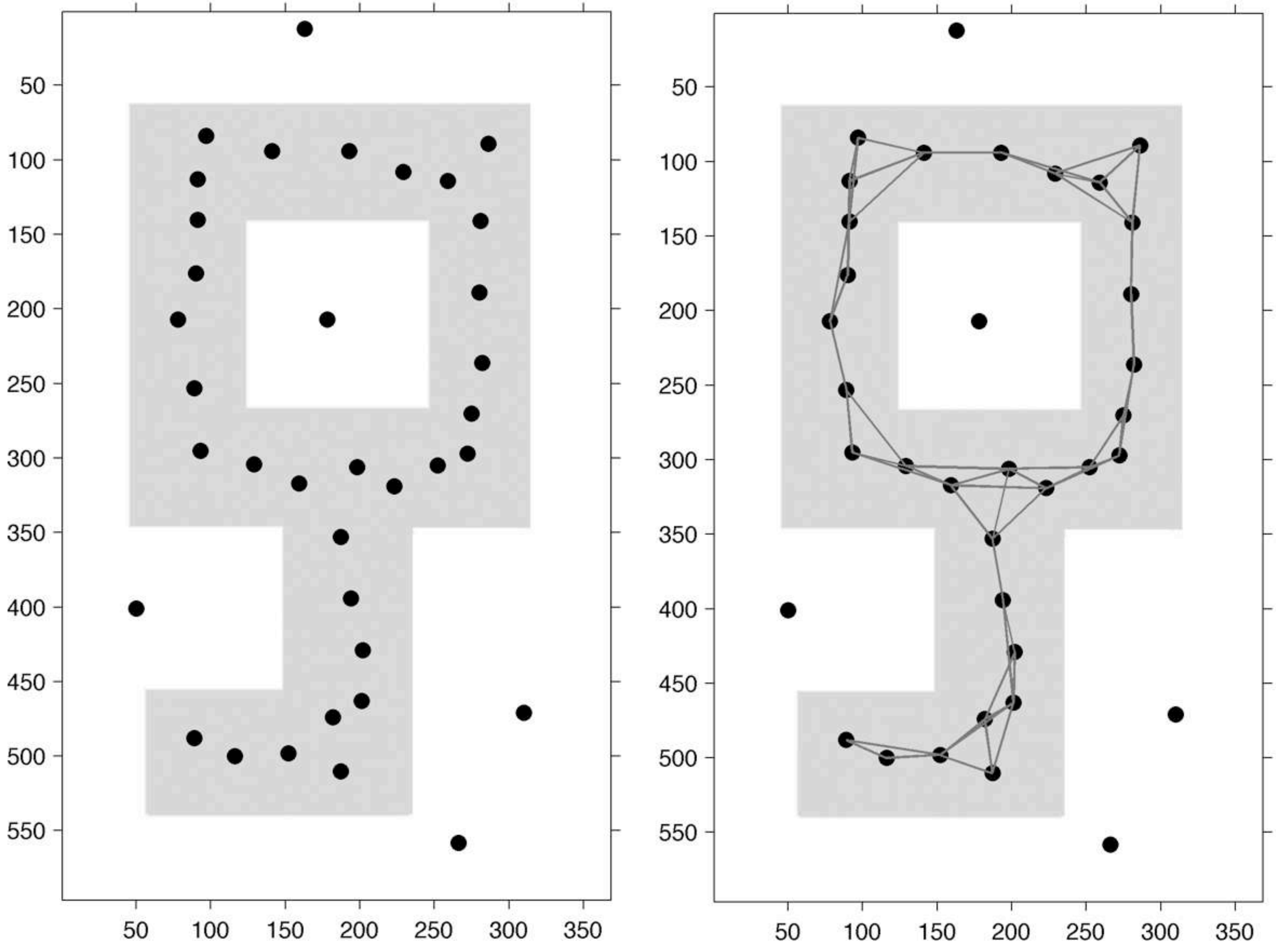
For *n*-nodes, $O(n^{3k+3})$ for the *k*-th Betti number

The representation is *not* unique.



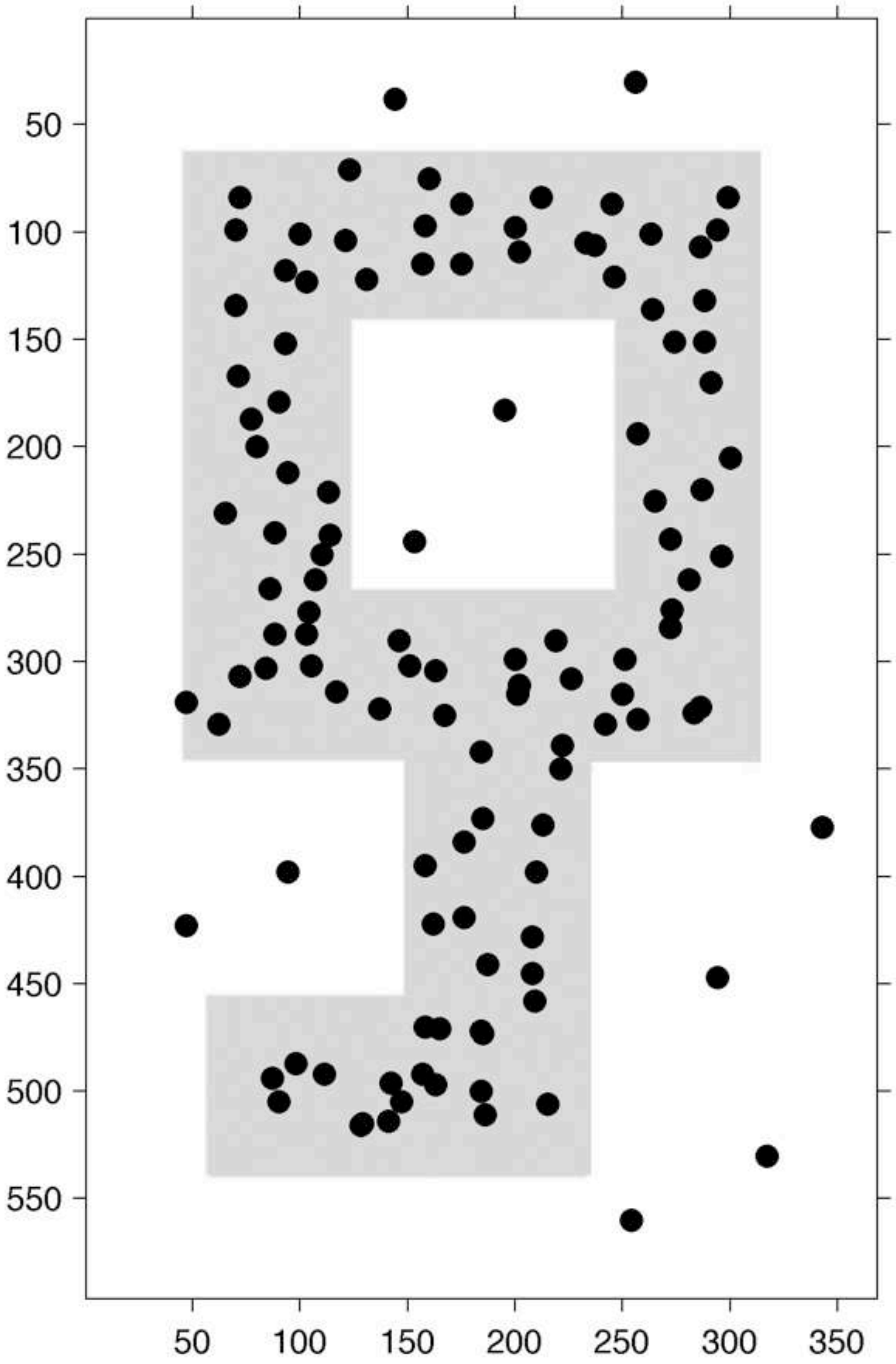
Rips complex of point cloud data

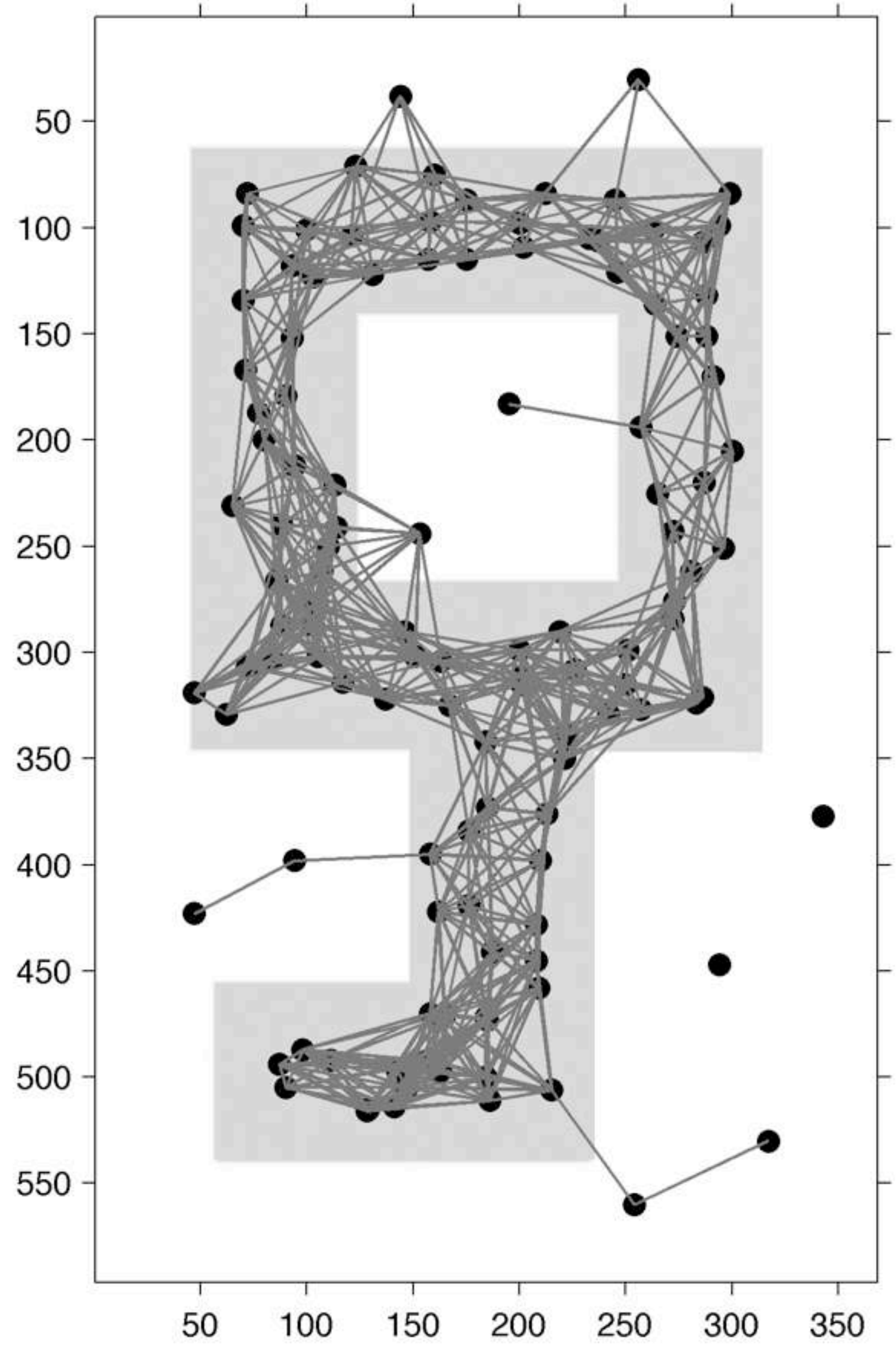
$\varepsilon = 70\text{mm}$



Rips complex of point cloud data

$\varepsilon = 70\text{mm}$

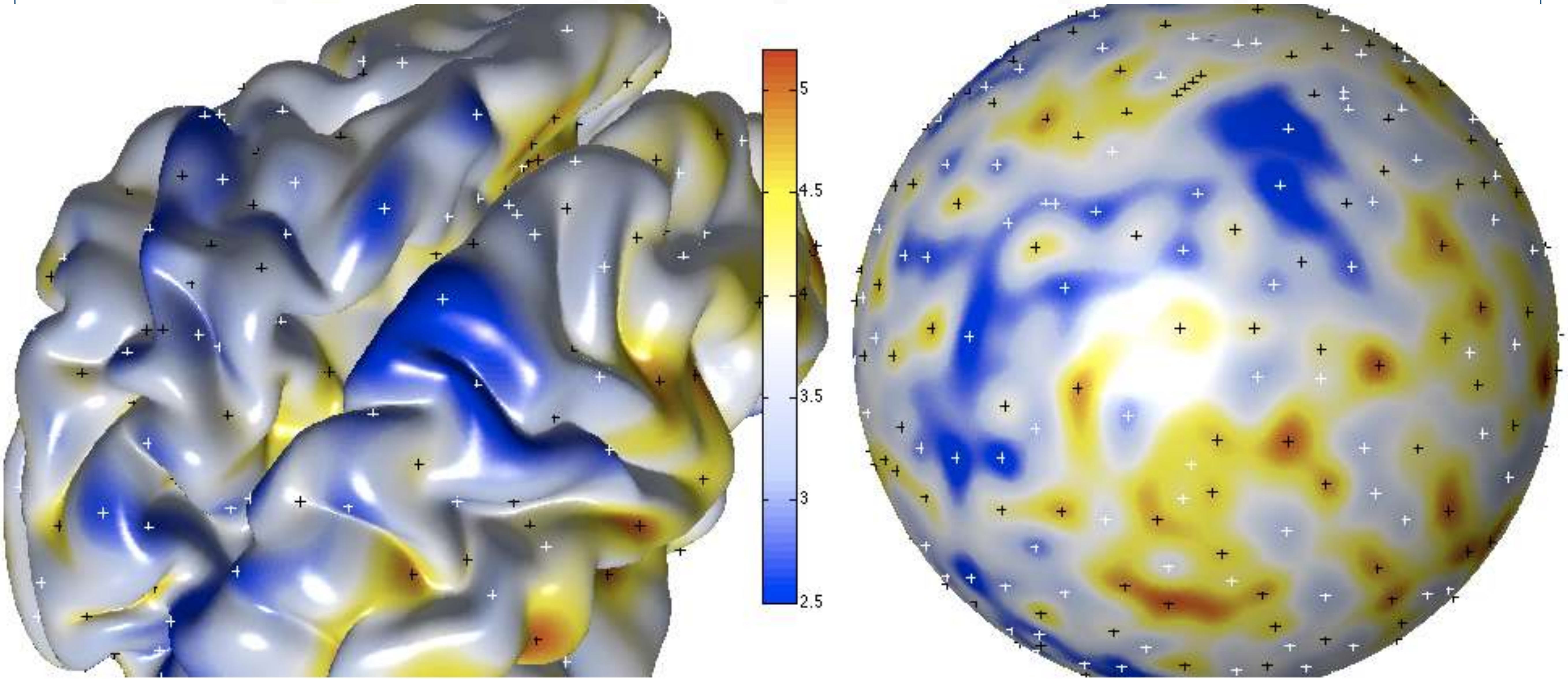




Morse Filtration

Persistence Diagrams of Cortical Surface Data

Moo K. Chung[1,2], Peter Bubenik[3], and Peter T. Kim[4]

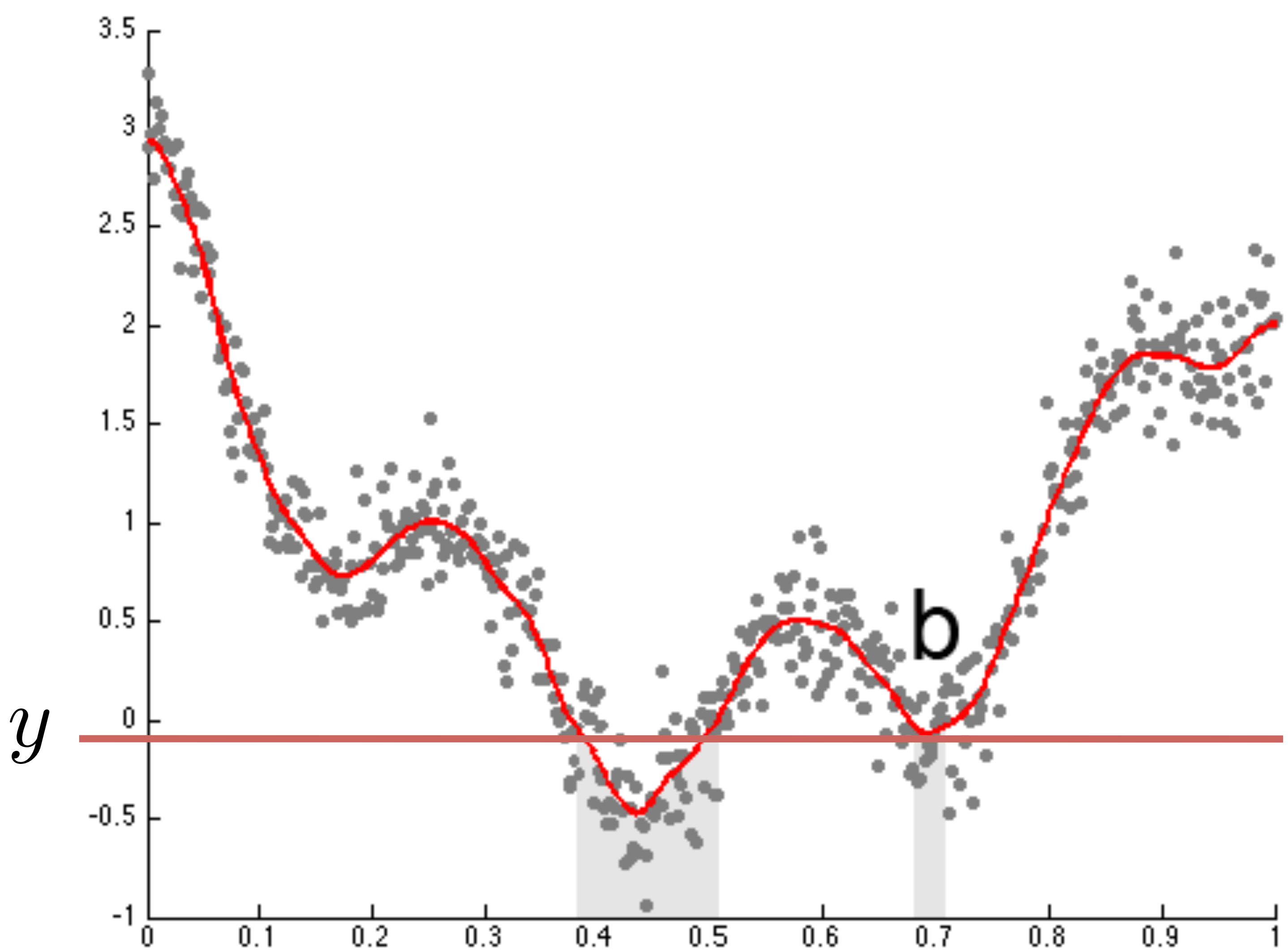


Chung et al., 2009 Information Processing in Medical Imaging (IPMI) 5636:386-397.
Pachauri et al., 2011 IEEE Transactions on Medical Imaging 30:1760-1770

Morse theory in signal processing

$$Y = \mu + \epsilon$$

Unknown signal μ is assumed to be a Morse function: all critical values are unique.



Sublevel set

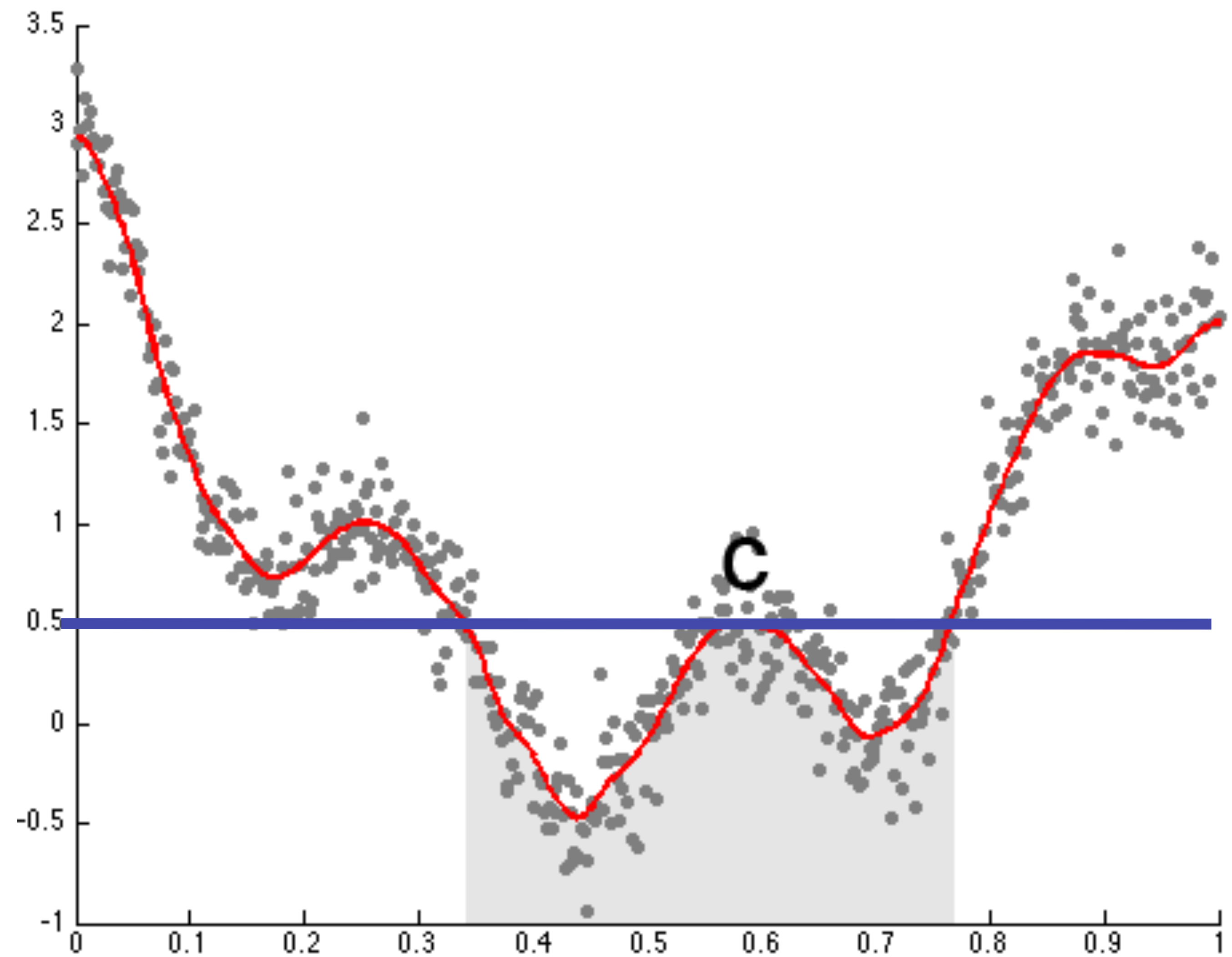
$$R(y) = \mu^{-1}(-\infty, y]$$

Number of connected components $\#R(y)$

Morse filtration

Consider a sublevel set

$$R(y) = \mu^{-1}(-\infty, y]$$



For critical values

$$b < c$$

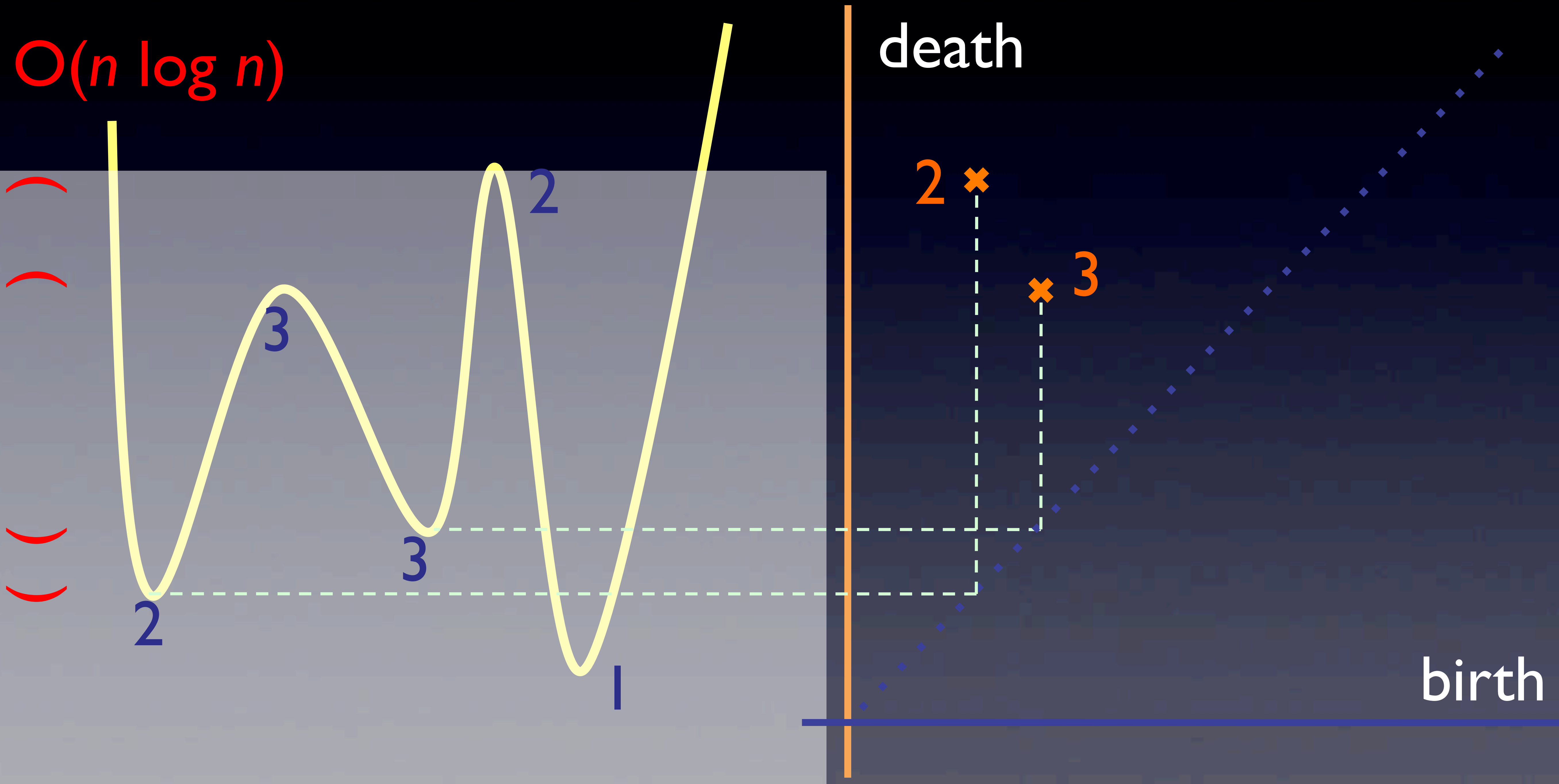
$$R(b) \subset R(c)$$

For all critical values $y_1 < y_2 < \cdots,$

$$R(y_1) \subset R(y_2) \subset \cdots$$

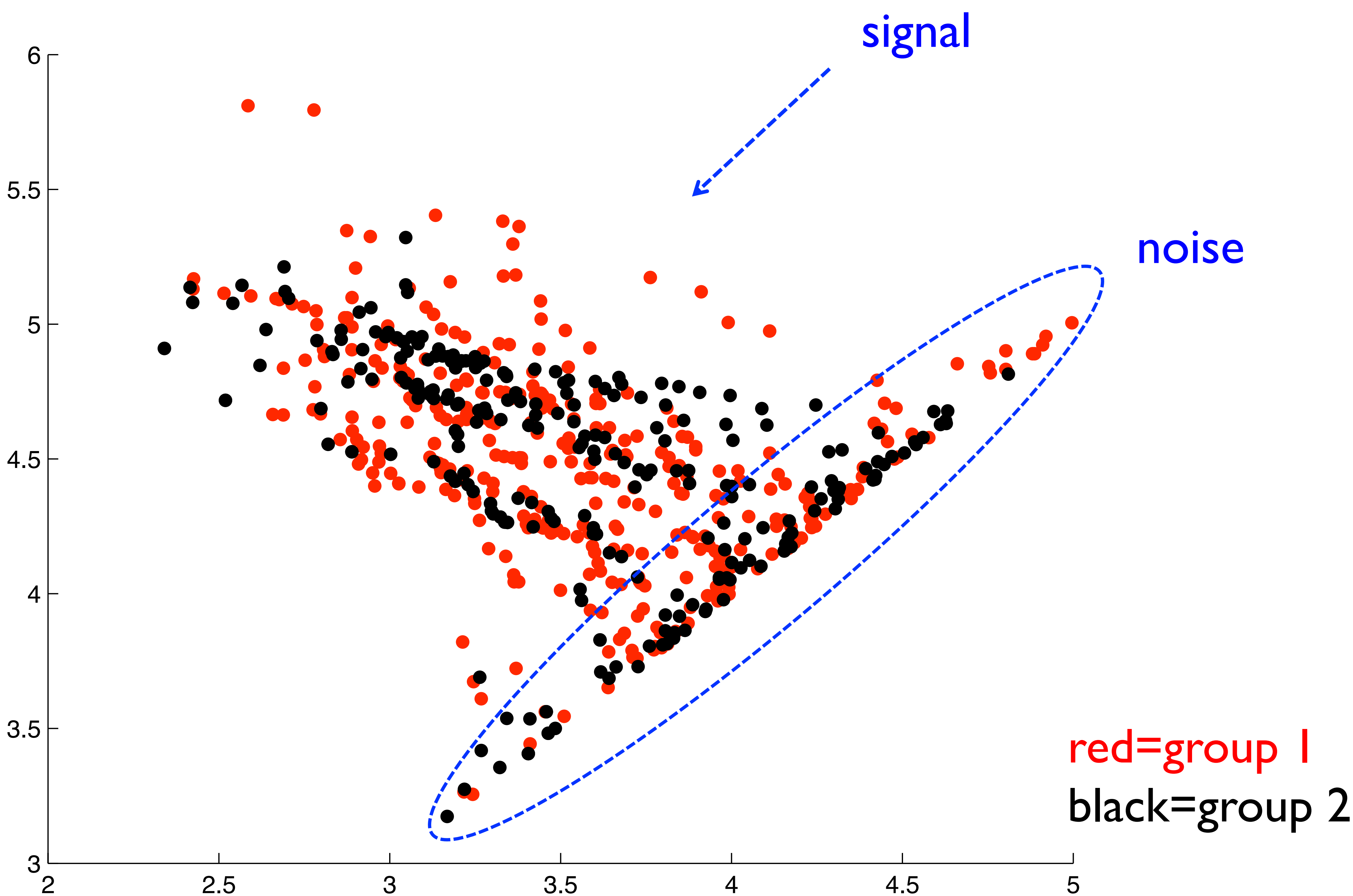
Persistent Diagrams

Persistence Diagram (PD)



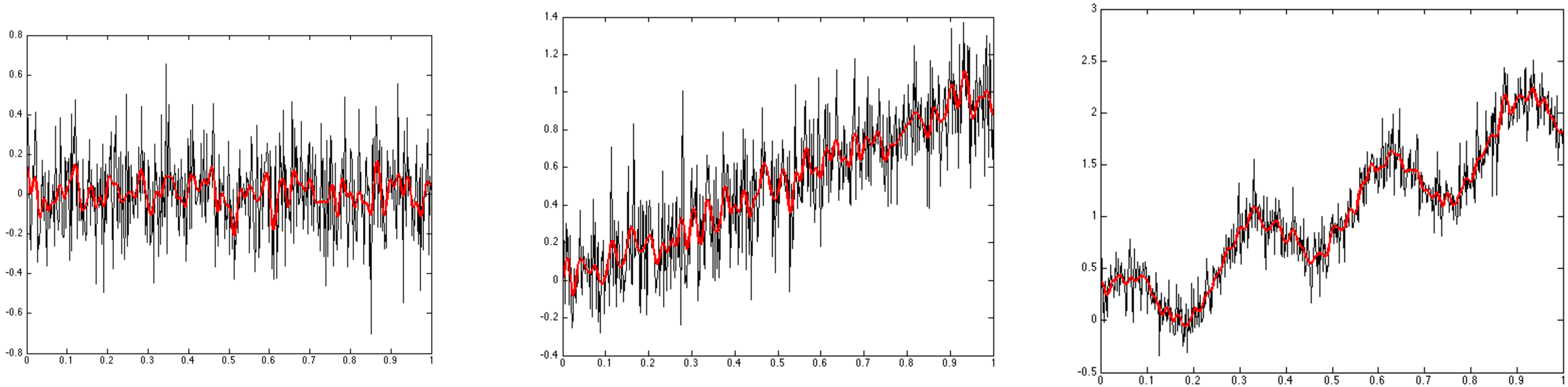
Pair the time of death with the time of the closest earlier birth

Signal in persistent diagrams



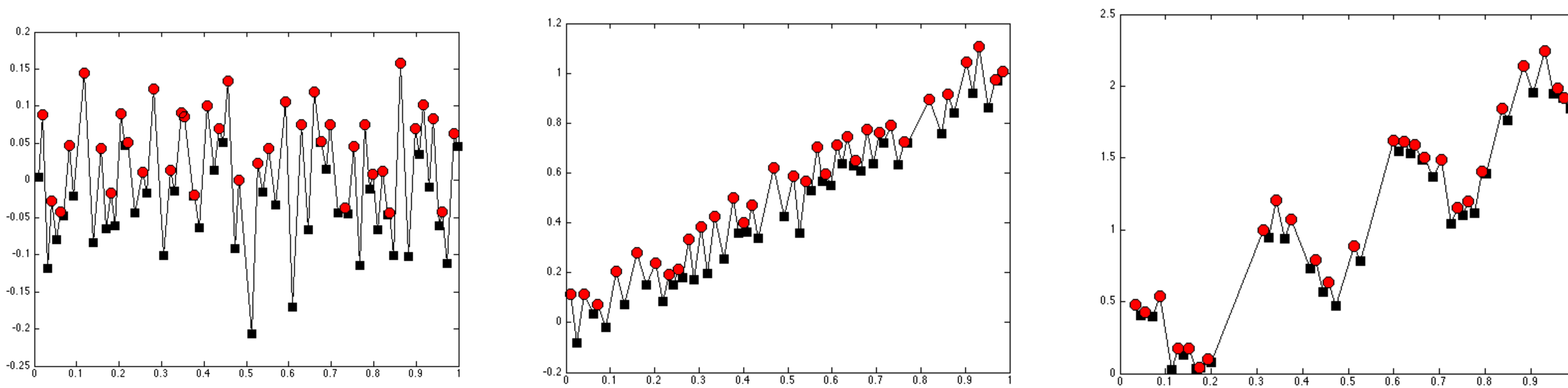
How do we analyze a collection of PDs?

Critical values capture the pattern of signal changes

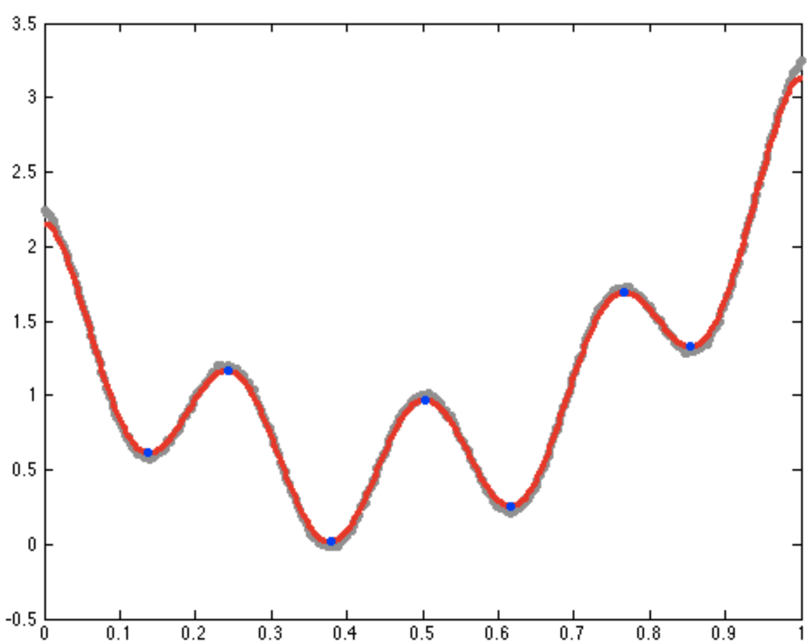


$$f(t) = e(t)$$

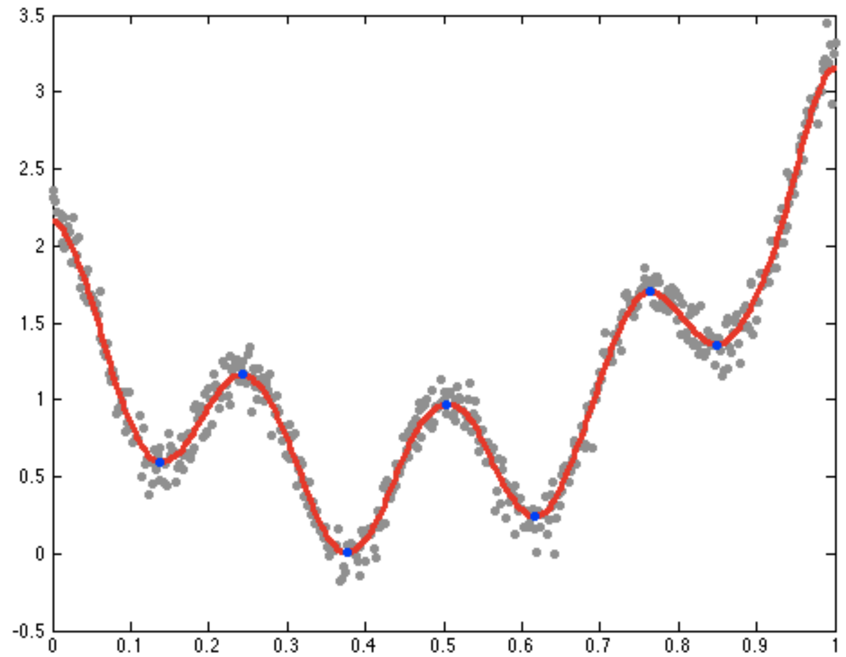
$$f(t) = t + e(t)$$



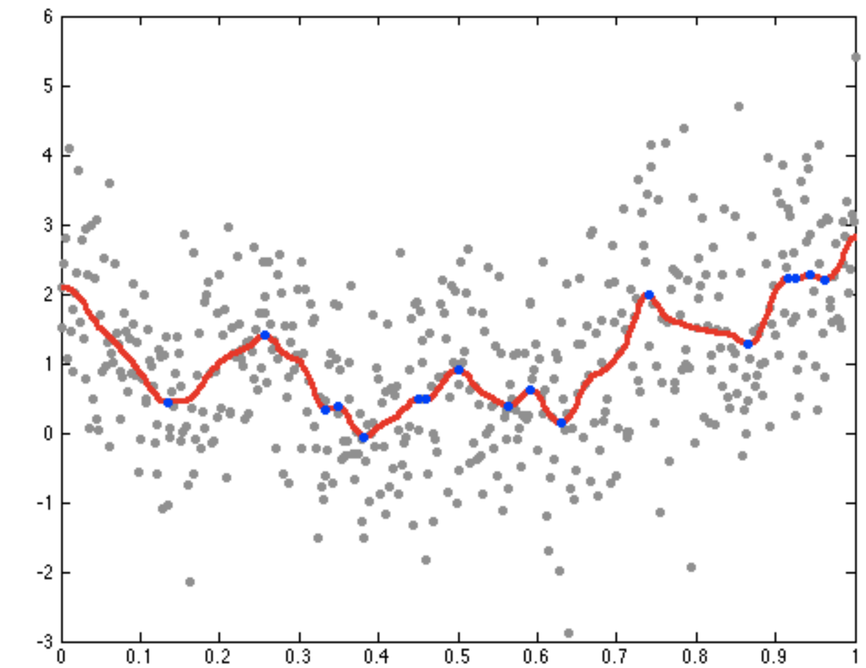
Example: $f(x) = x + 7(x - \frac{1}{2})^2 + \frac{1}{2}\cos(8\pi x) + \epsilon$



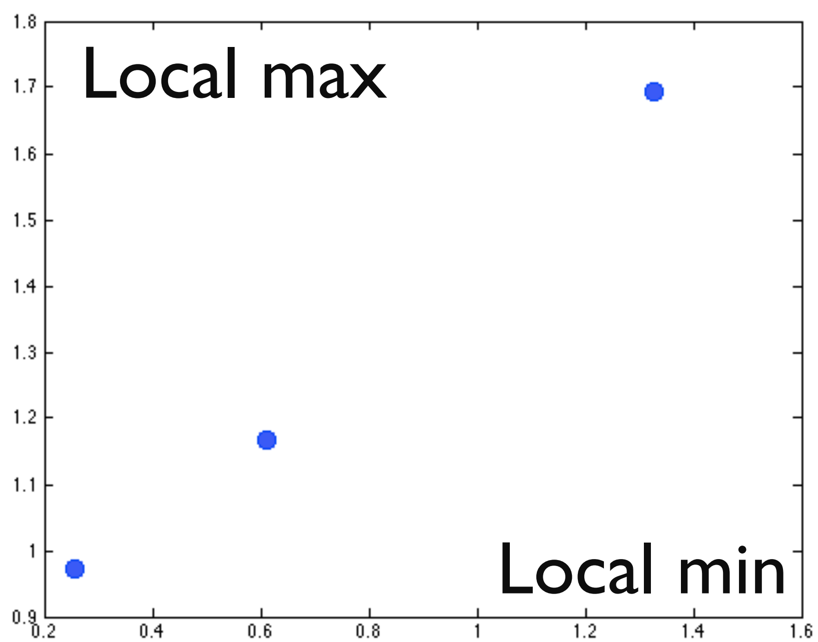
$\epsilon \sim N(0, 0.01^2)$

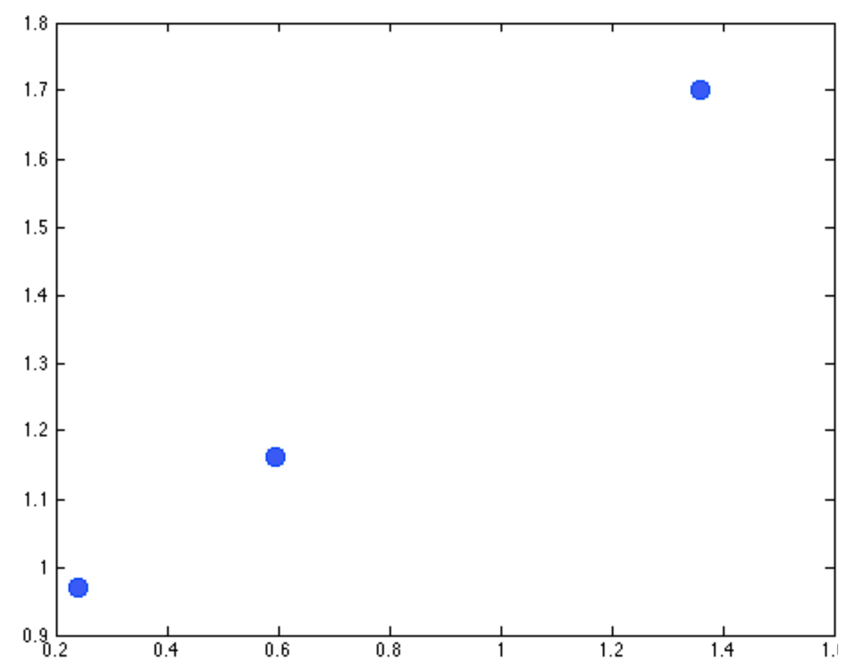


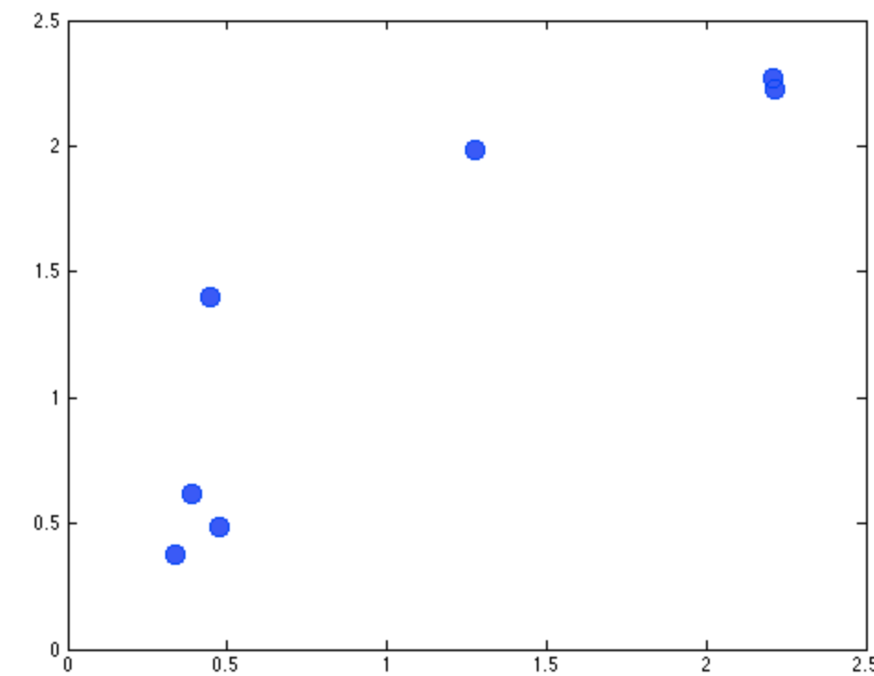
$\epsilon \sim N(0, 0.1^2)$



$\epsilon \sim N(0, 1^2)$

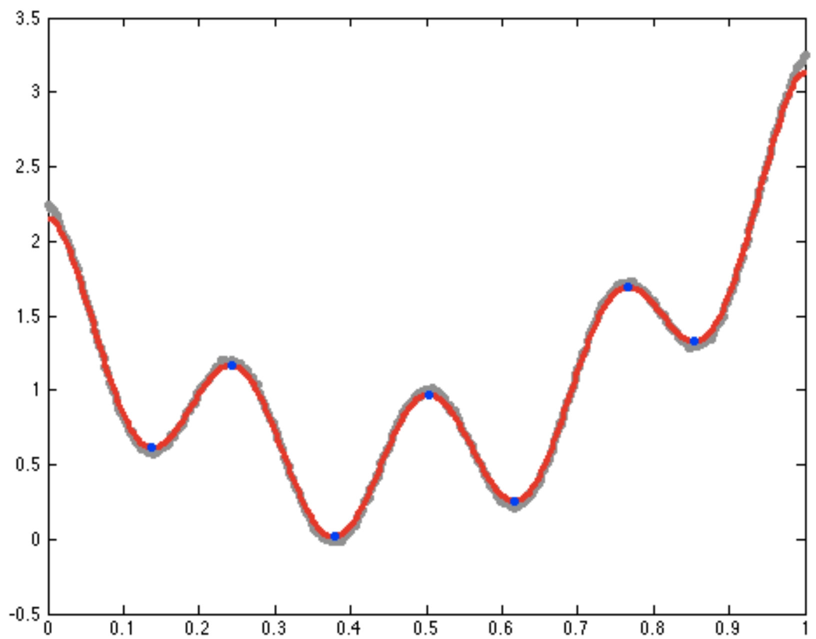


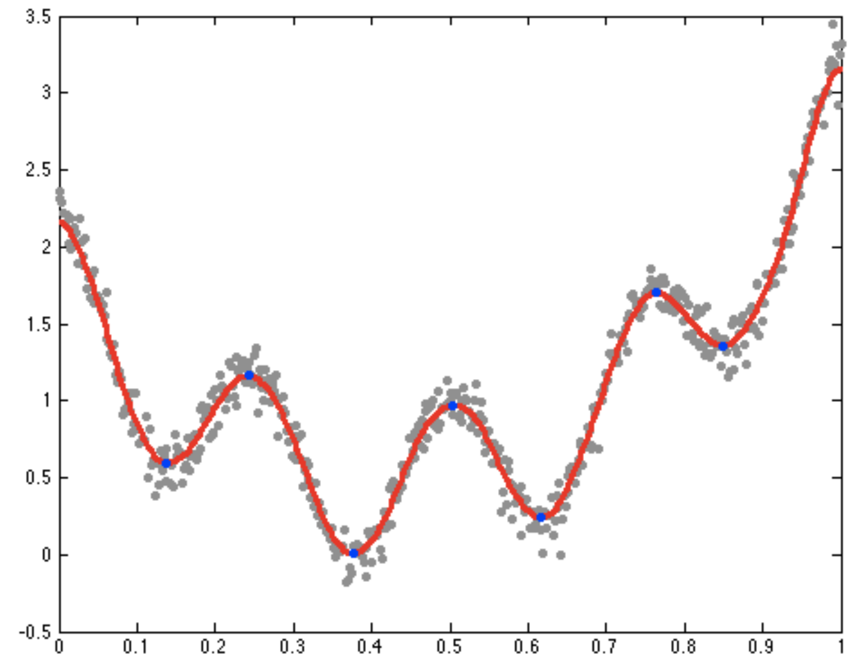




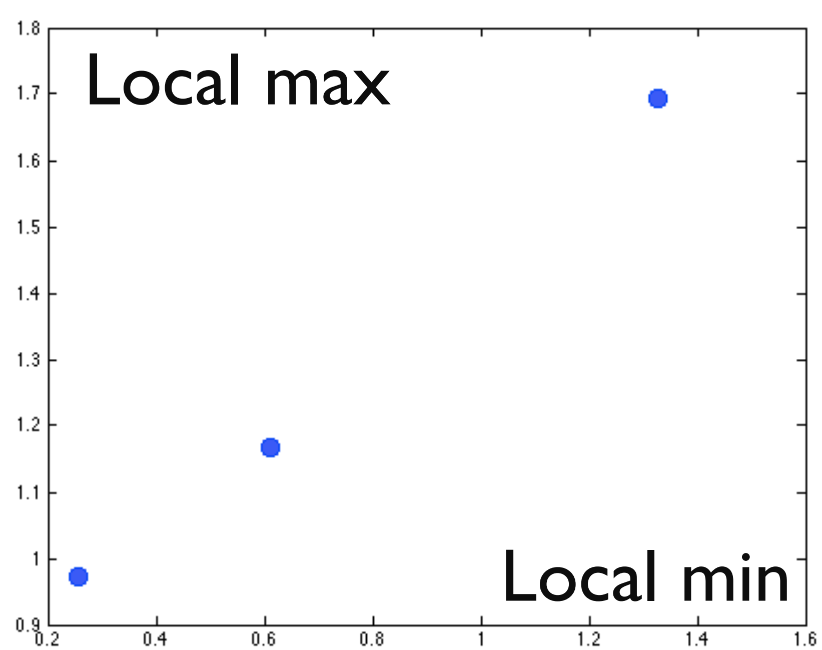
Stability of persistence diagram

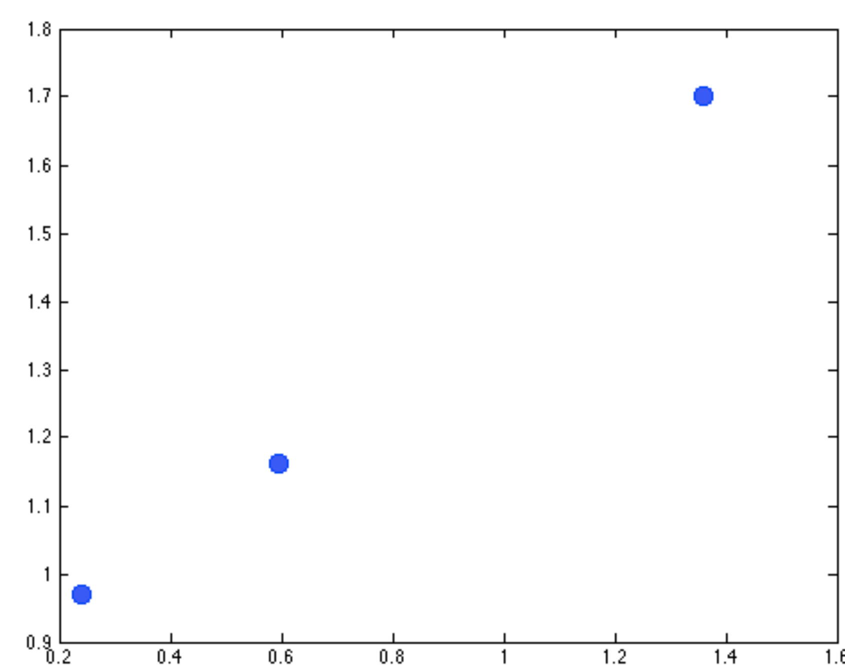
$$d(D(f), D(g)) \leq \|f - g\|_\infty$$



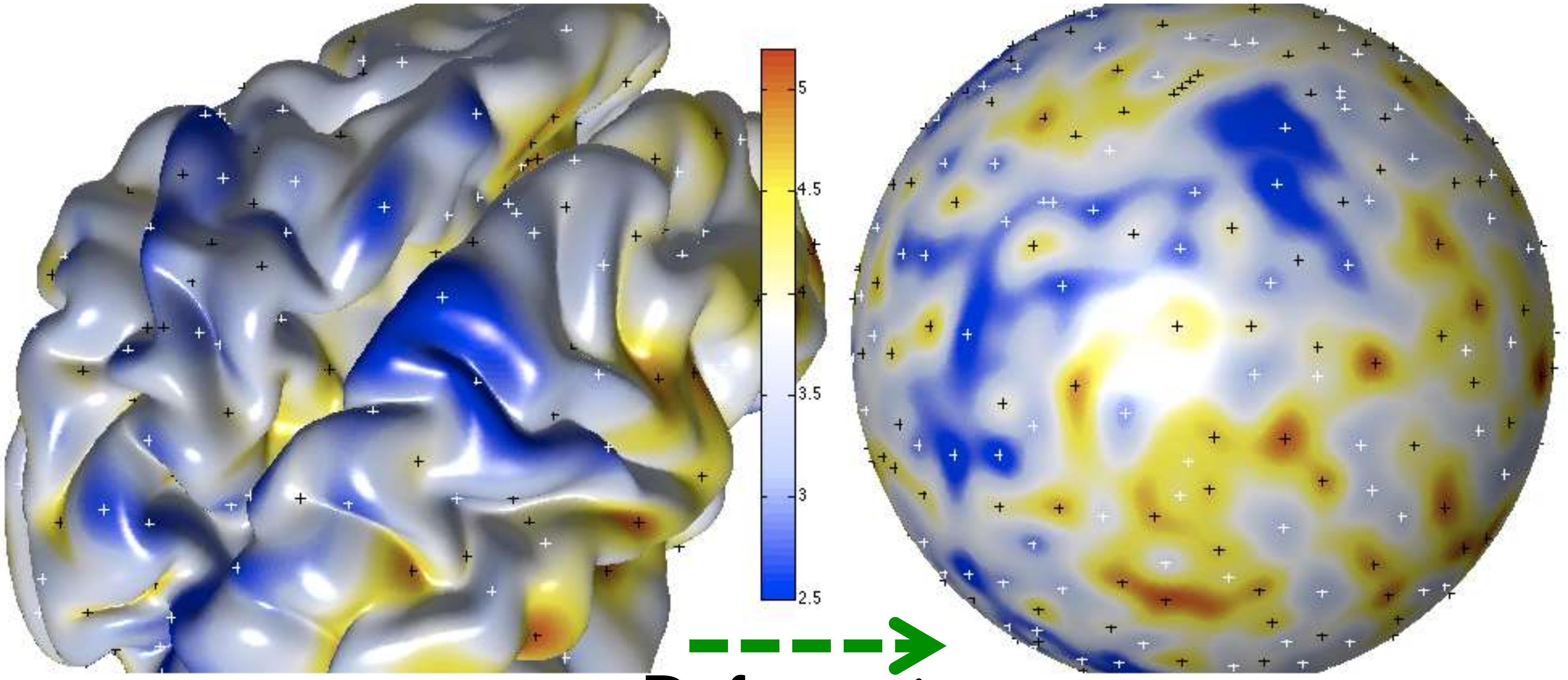


$\epsilon \sim N(0, 0.01^2)$ $\epsilon \sim N(0, 0.1^2)$

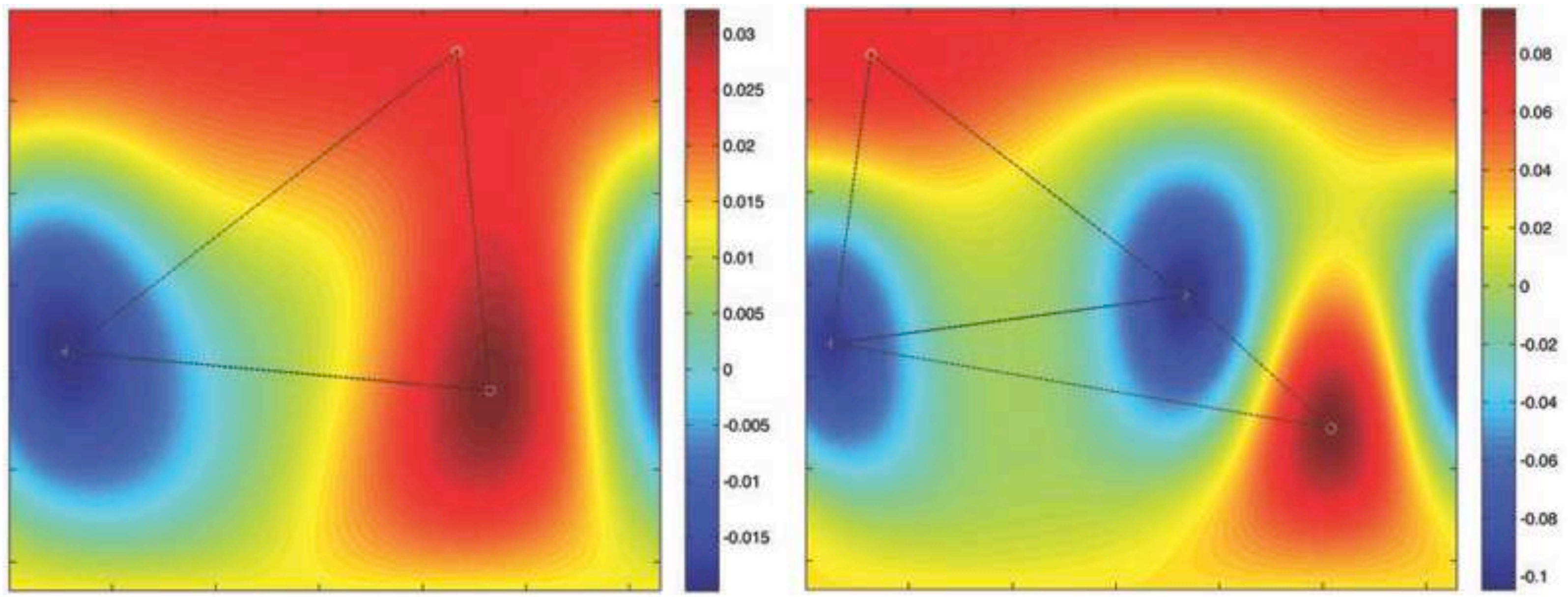




Persistent homology on cortical thickness

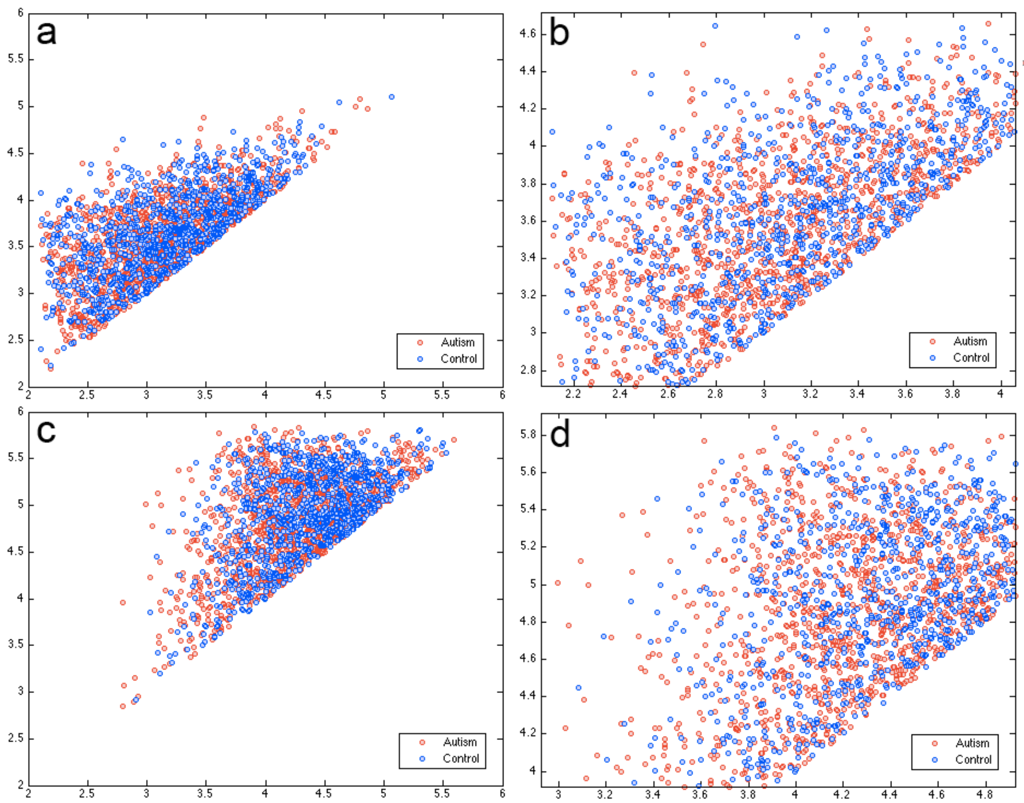


Deformation



Simplex construction

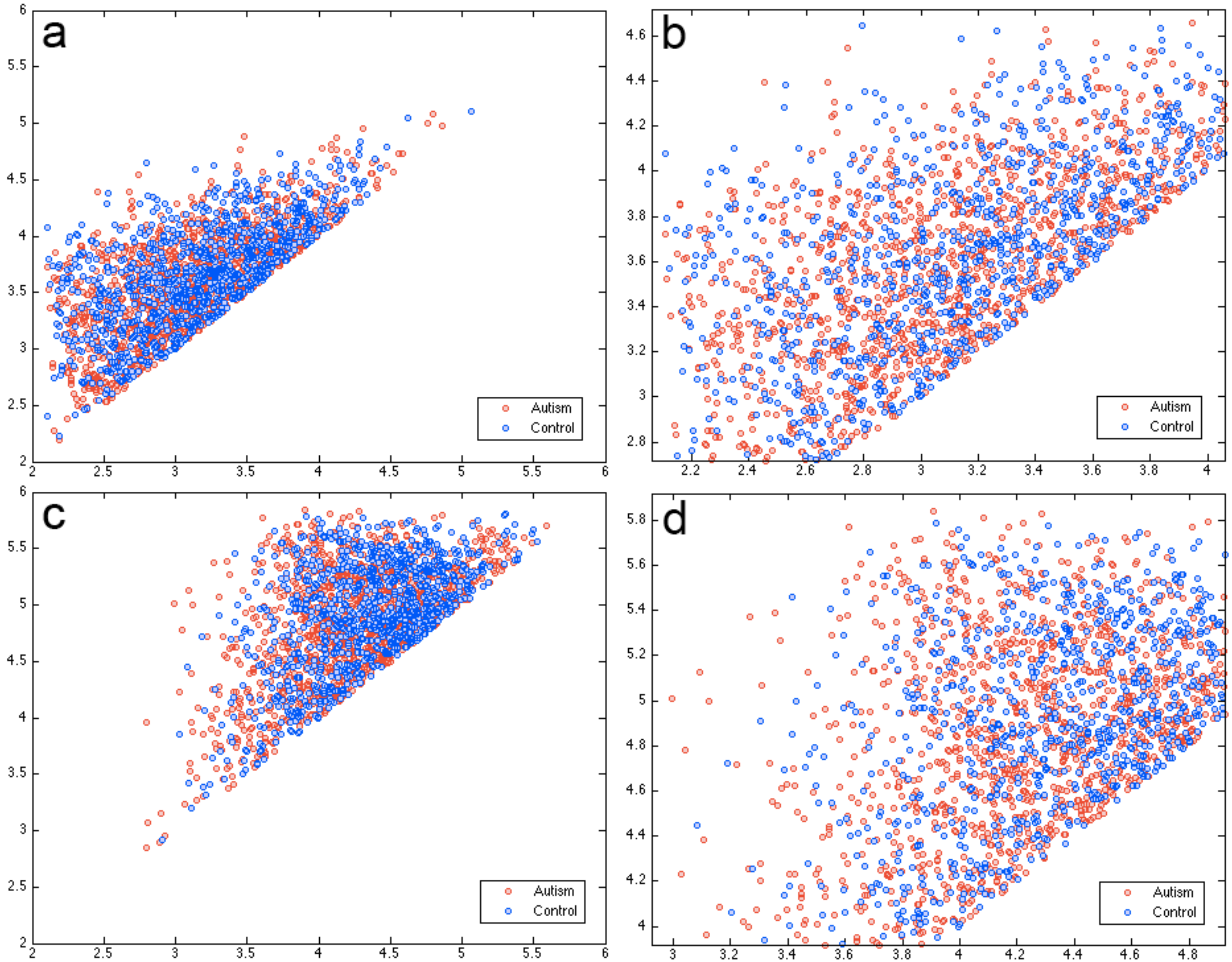
Persistent Diagram



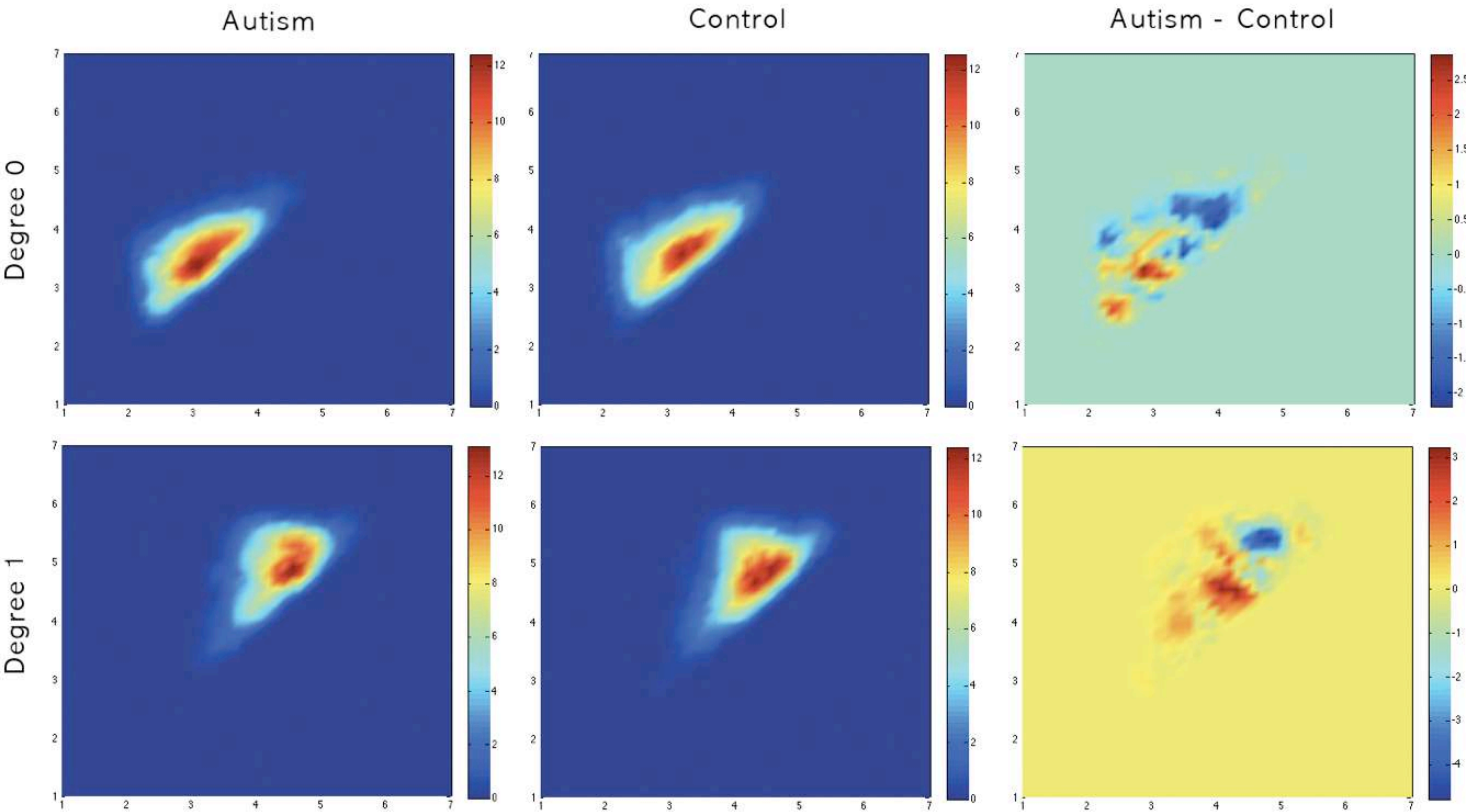
blue= control (n=11) red= autism (n=16)

degree 0
pairing of
saddle points
to minimums

degree 1
pairing of
saddle points
to maximums

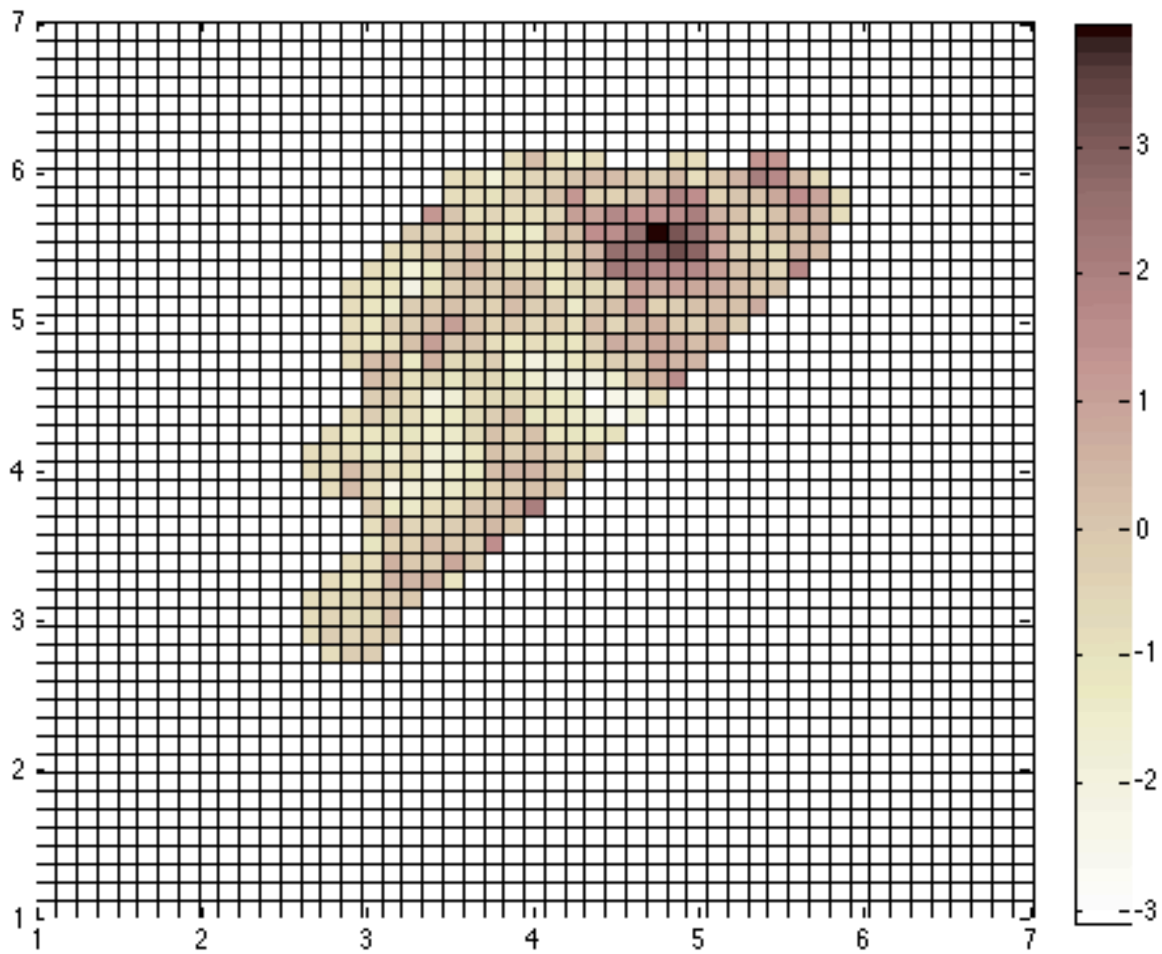


Kernel density (uniform kernel) in persistent diagram



Statistical significance ?

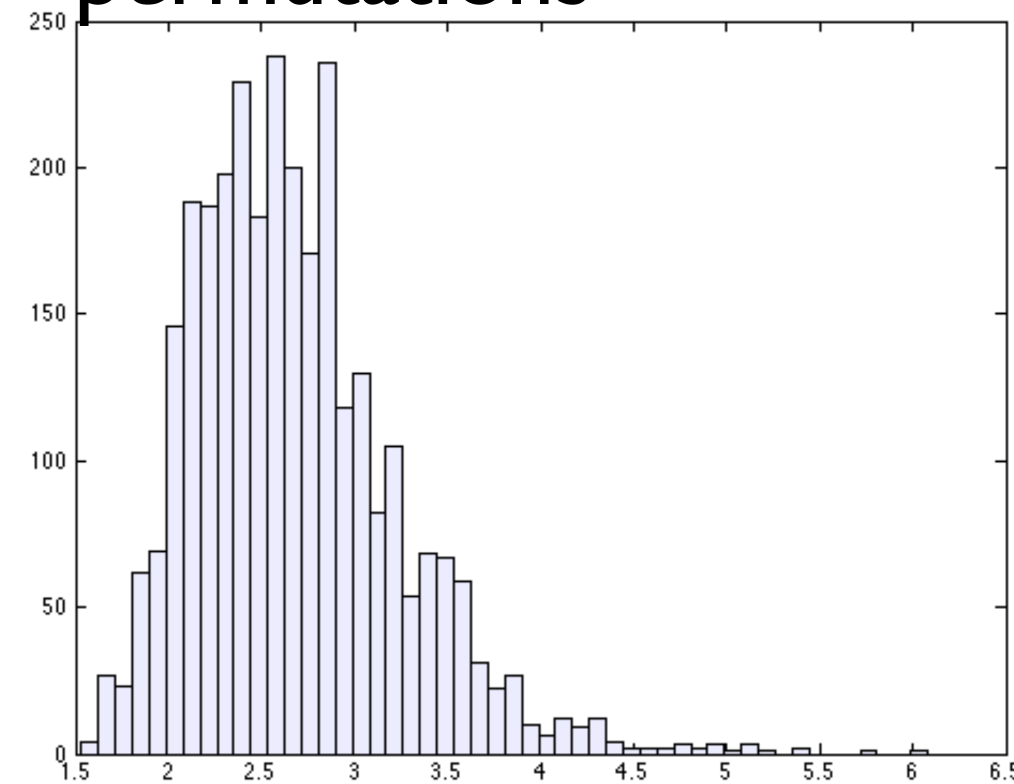
Degree-1 distribution



Max t = 3.9507

Min t = -3.0961

Permutation test based on 5000 random permutations



95 percentile = 3.6432

5 percentile = -4.0237

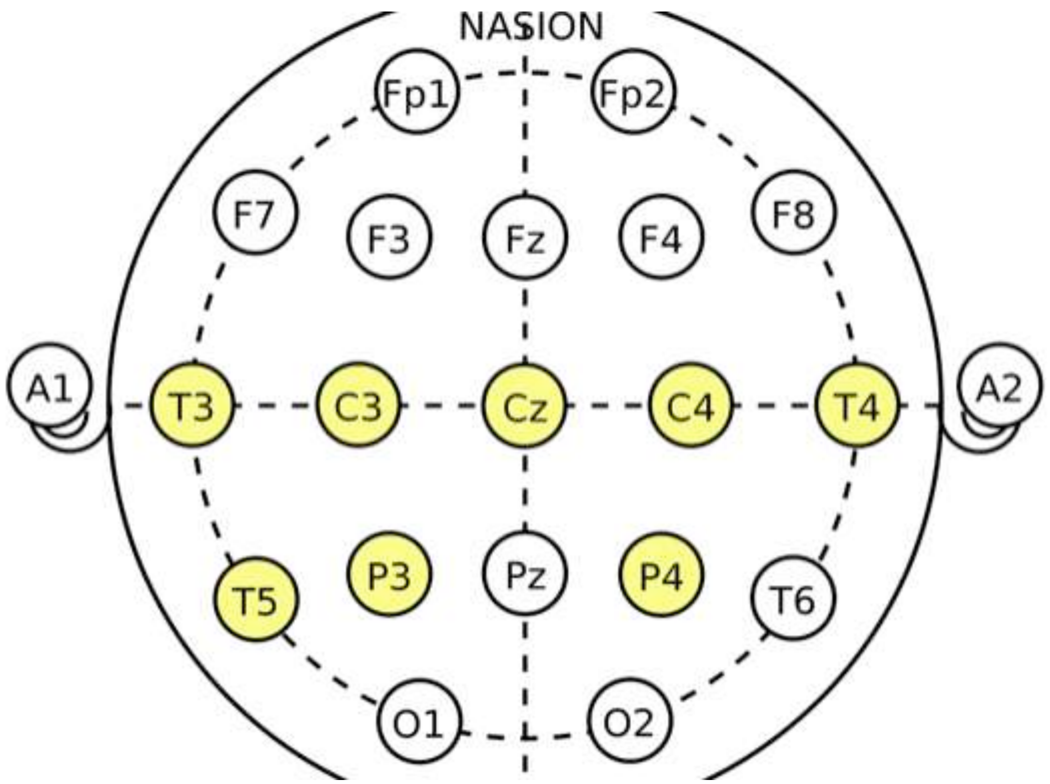
More pairings for the control subjects

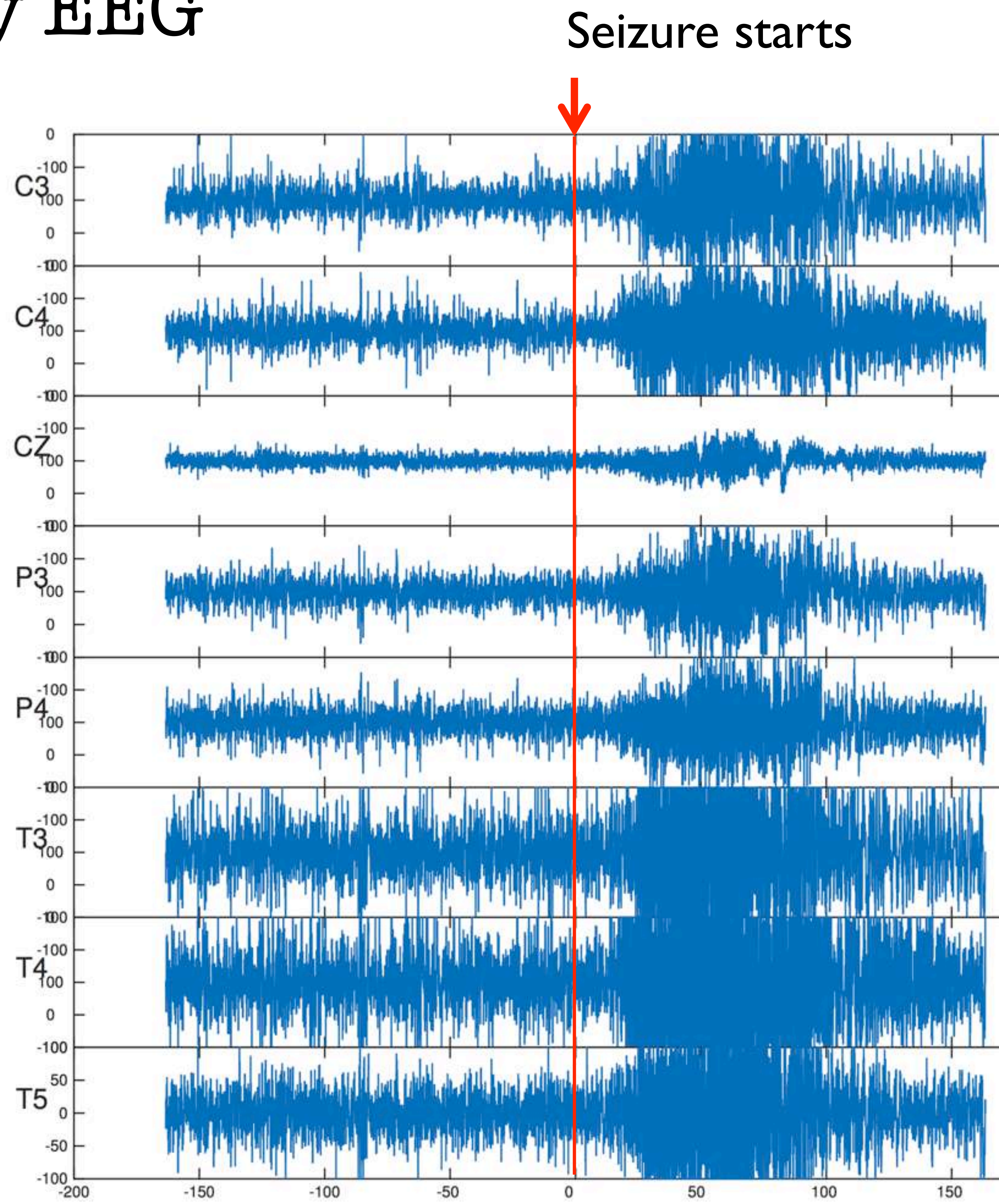
= More cortical folding

Persistent Landscape

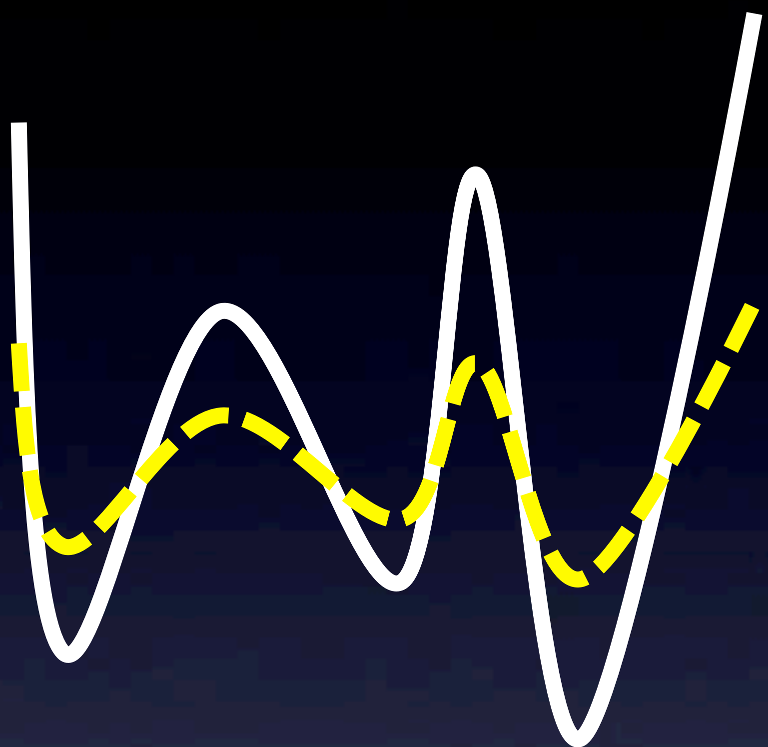
Bubenik, 2015 Journal of Machine Learning Research
Wang et al. 2014 Distinguished Paper Award in ENAR
Wang et al. 2018 Annals of Applied Statistics, in press

Temporal epilepsy EEG

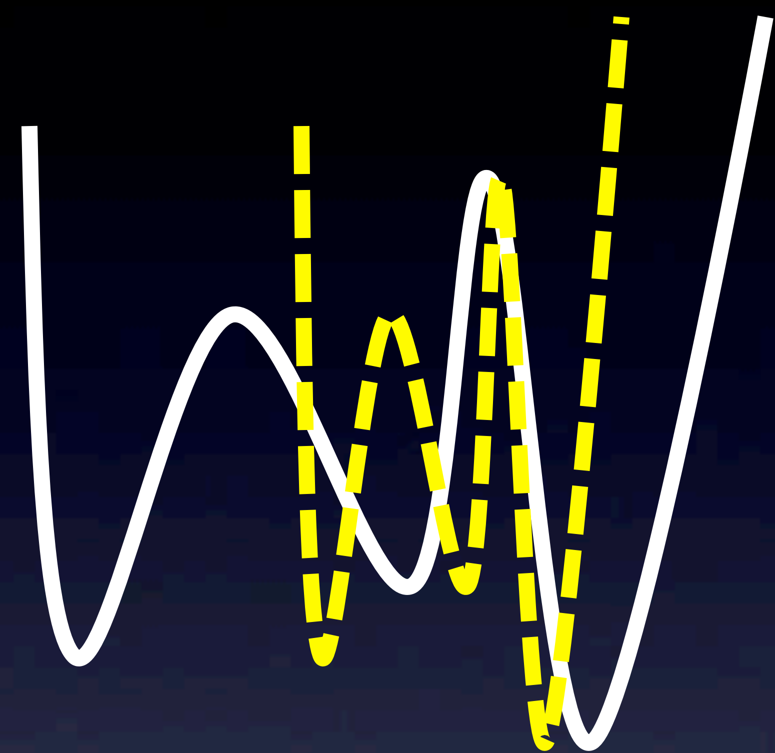




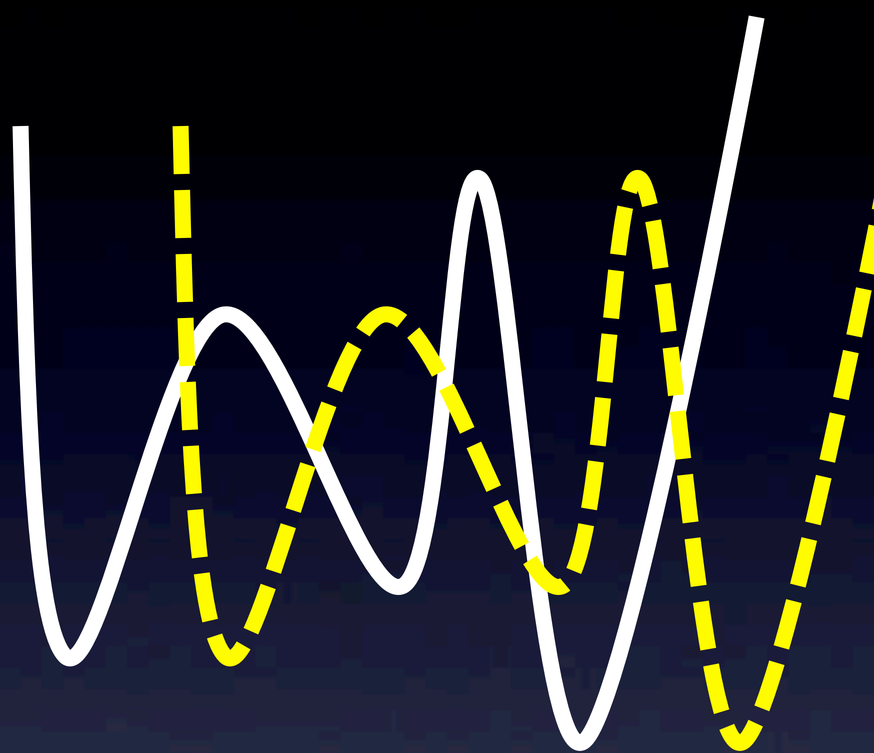
Existing methods are too sensitive



Scaling



Frequency change



Translation

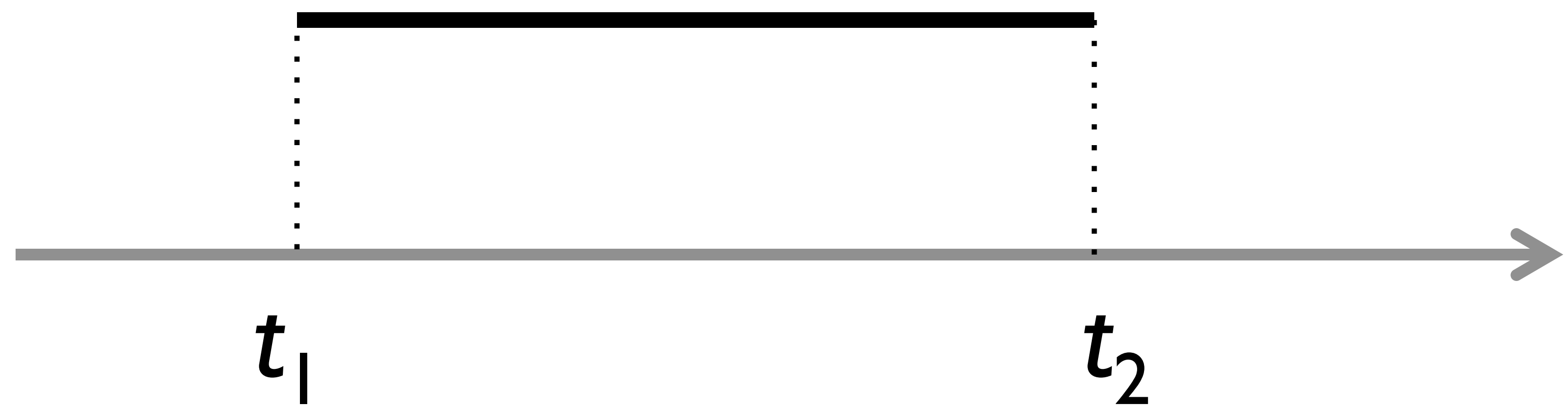
What method will *not* detect the deforation of signal

Barcodes & persistent landscapes

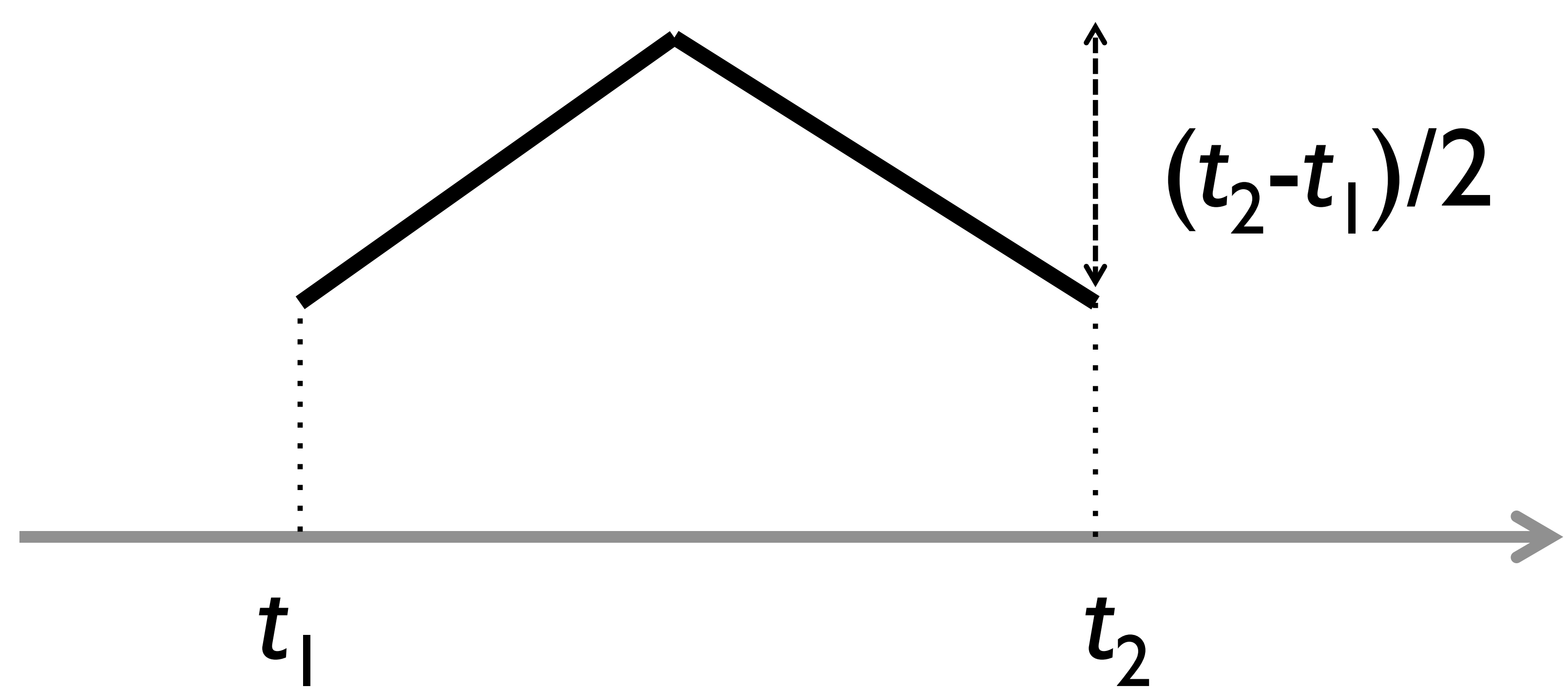
Birth of a component

Death of a component

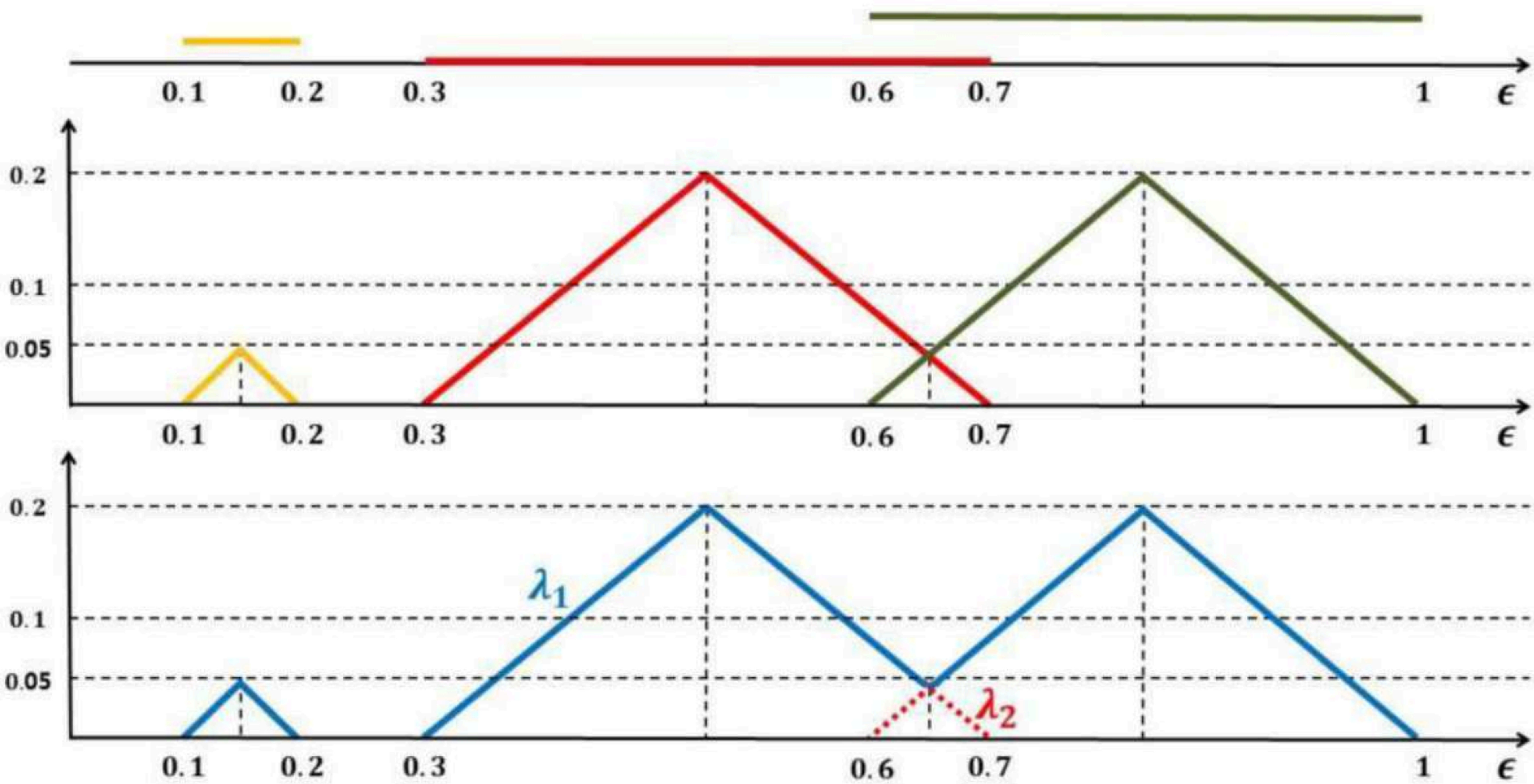
Barcode



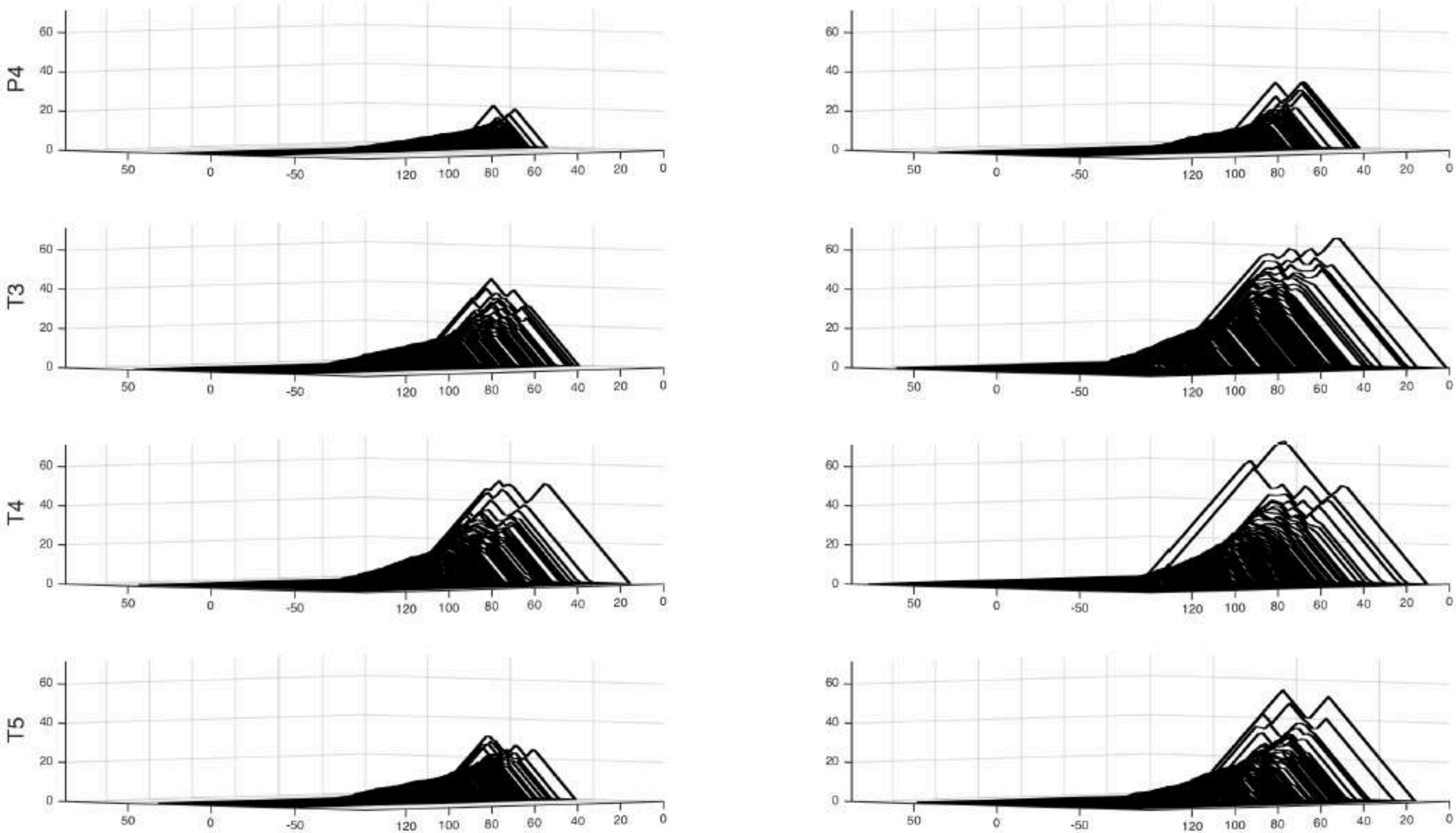
Persistent landscape



Barcodes & persistent landscapes

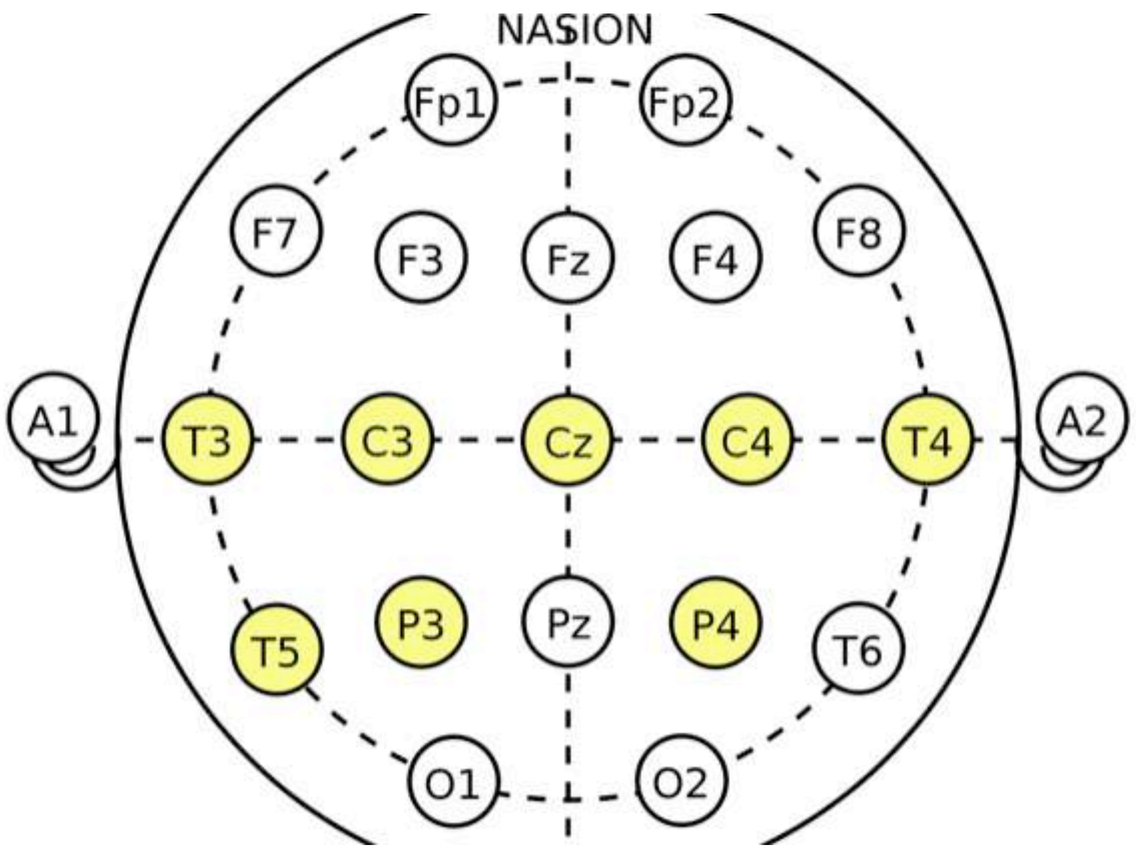


Persistent landscapes



before seizure

during seizure



Corrected *p*-value

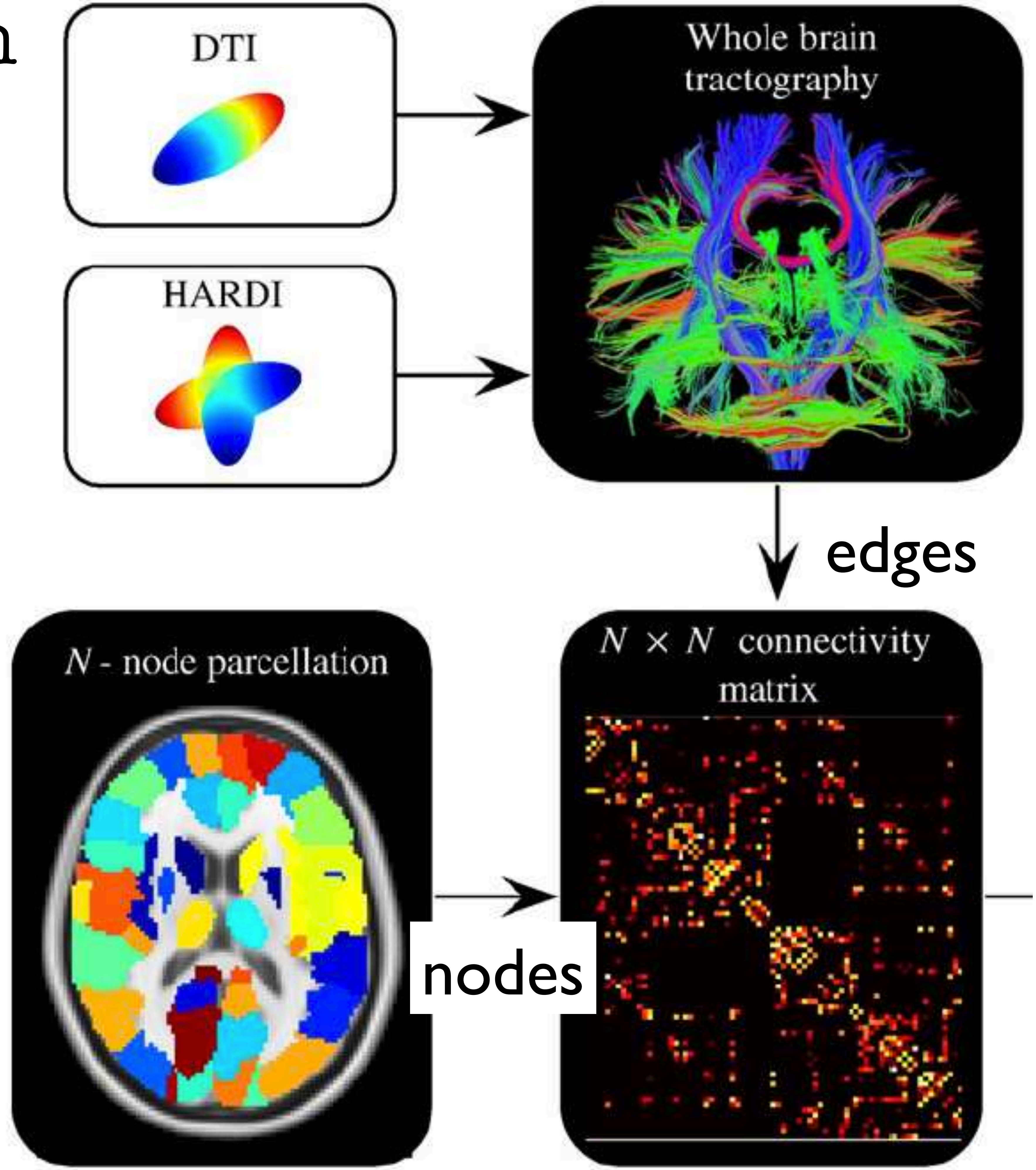
	Our method	Local variance ($\times 10^{-45}$)
C3	0.0057	0.0001
C4	0.0054	0.0001
Cz	0.0001	0.0001
P3	0.0029	0.0001
P4	0.0001	0.0001
T3	0.0661	0.6721
T4	0.0162	0.0001
T5	0.1044	0.0001

No signal is signal!

Topological invariance → seizure origin

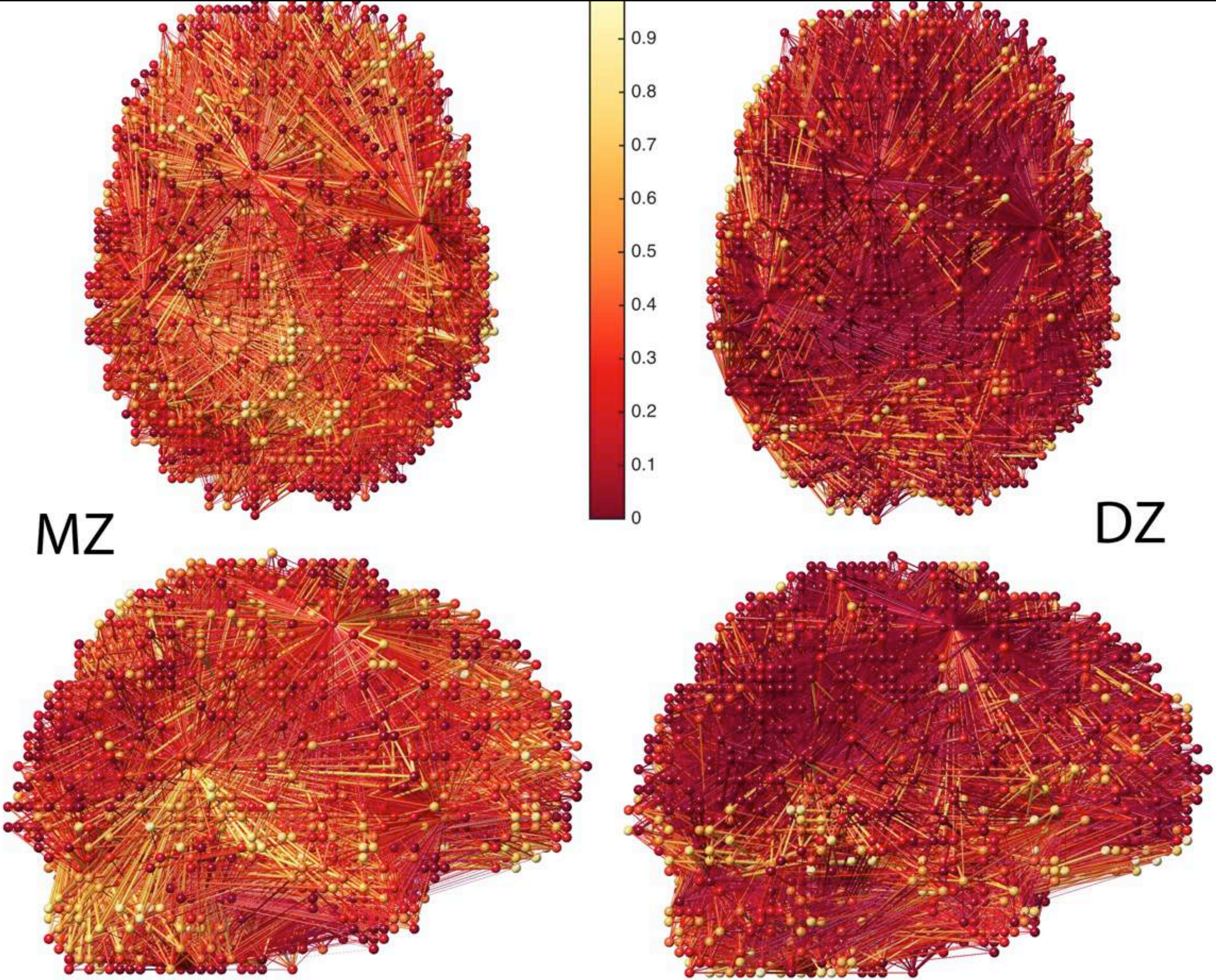
Standard brain network analysis

Standard brain connectivity analysis framework

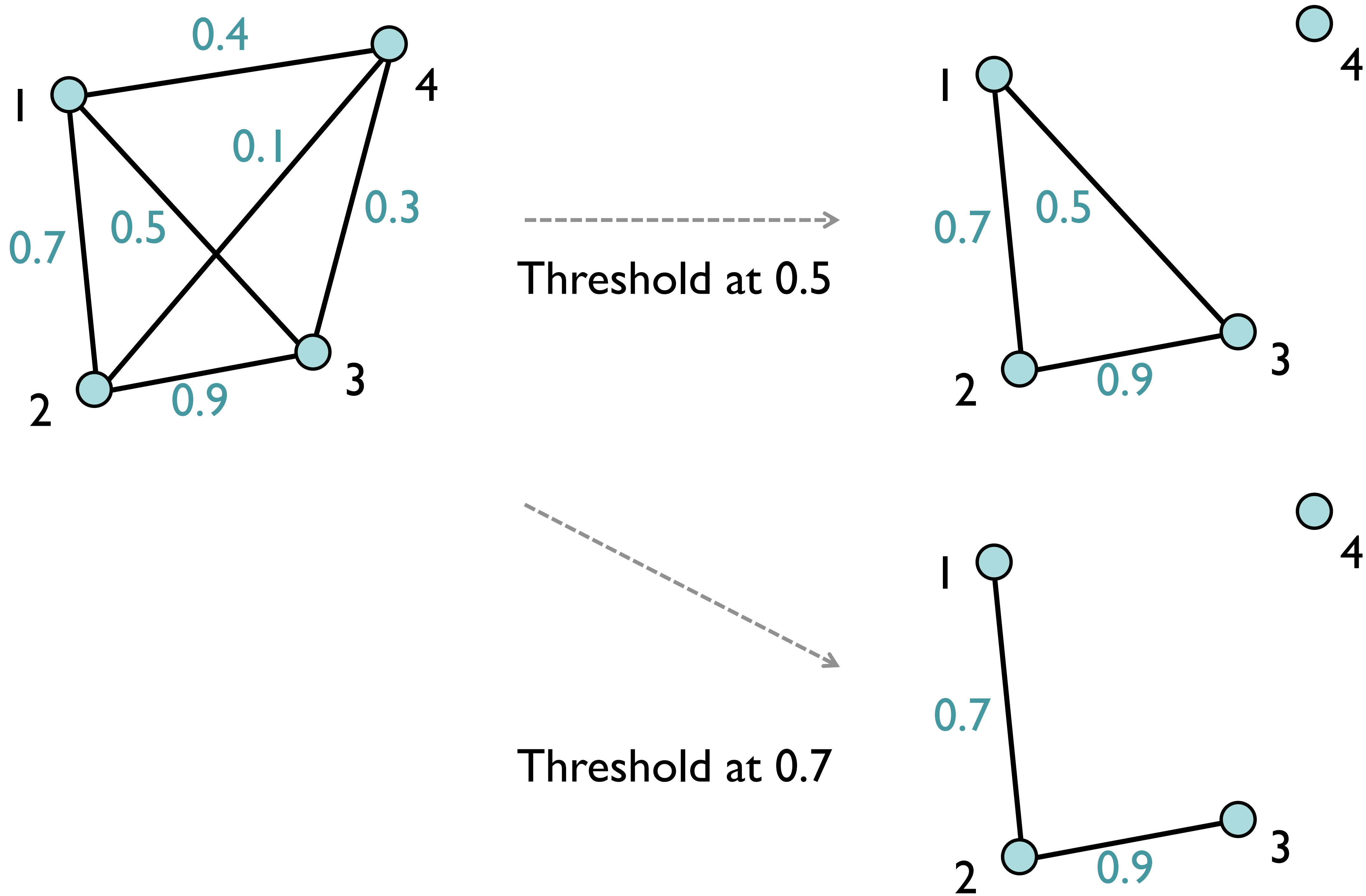


Zalesky et al. 2010 NeuroImage

Dense fMRI cross-correlation networks

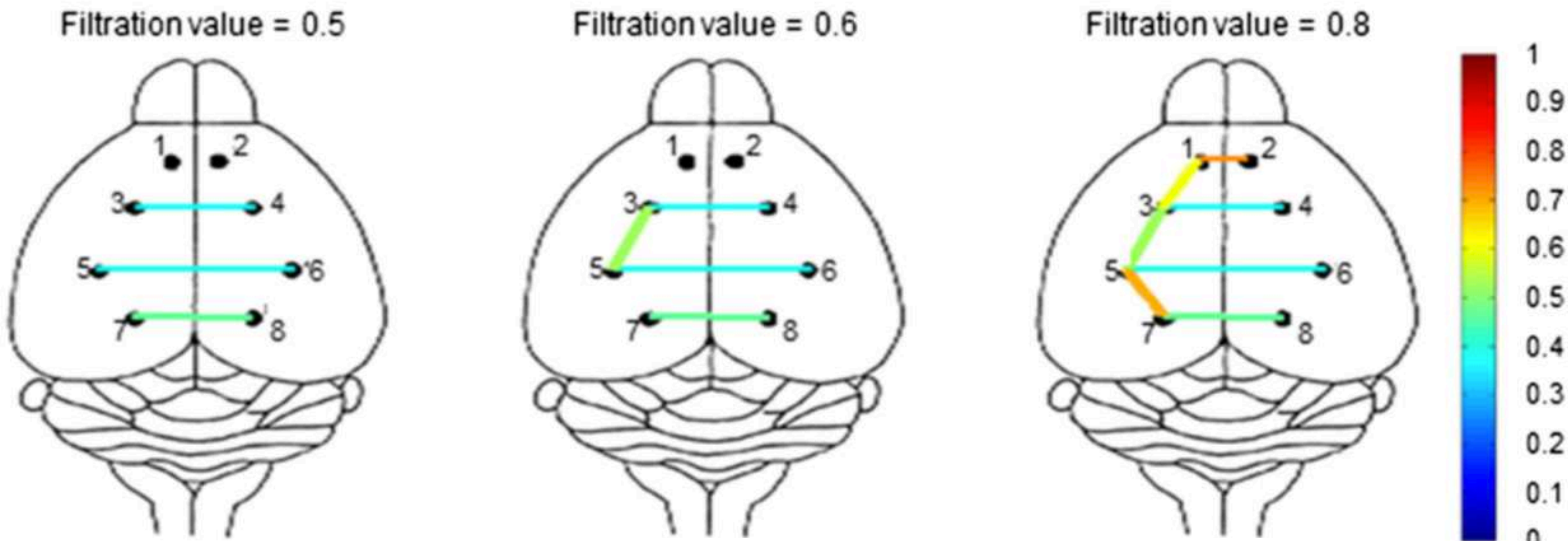


Topology changes depend on thresholds

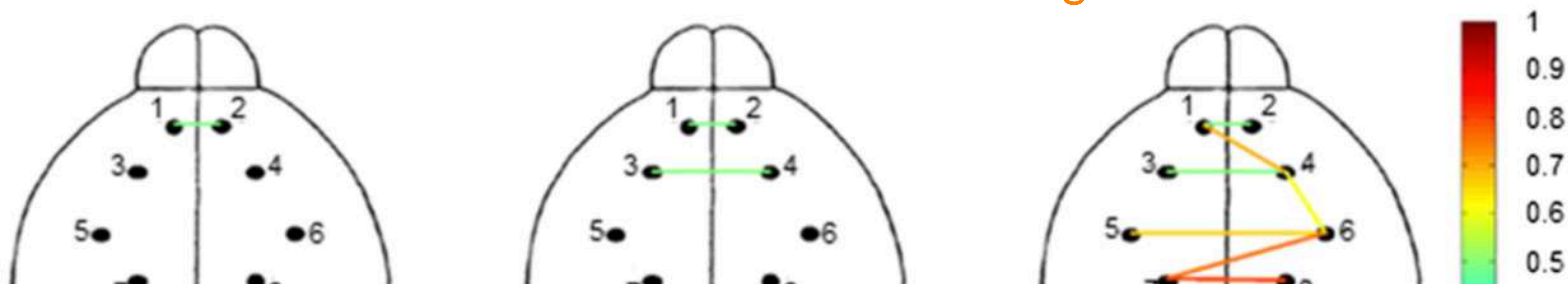


Tracing the evolution of multi-scale functional networks in a mouse model of depression using persistent brain network homology

Arshi Khalid [a], Byung Sun Kim [a], Moo K. Chung [b,d], Jong Chul Ye [c,*], Daejong Jeon [a,**]



Khalid et al. 2014 NeuoImage 101:351-363



Connectivity in fMRI: A Review and a Preview

Victor Solo, *Life-Fellow, IEEE,* Jean-Baptiste Poline, Martin A. Lindquist, Sean L. Simpson, F. DuBois Bowman, Moo K. Chung, Ben Cassidy, *Member, IEEE.*

Solo et al. 2018 IEEE Transactions on Medical Imaging

Graph theory

Feature based
Too many features
No models

Graphical models

Comp. Bottleneck
Often Bayesian

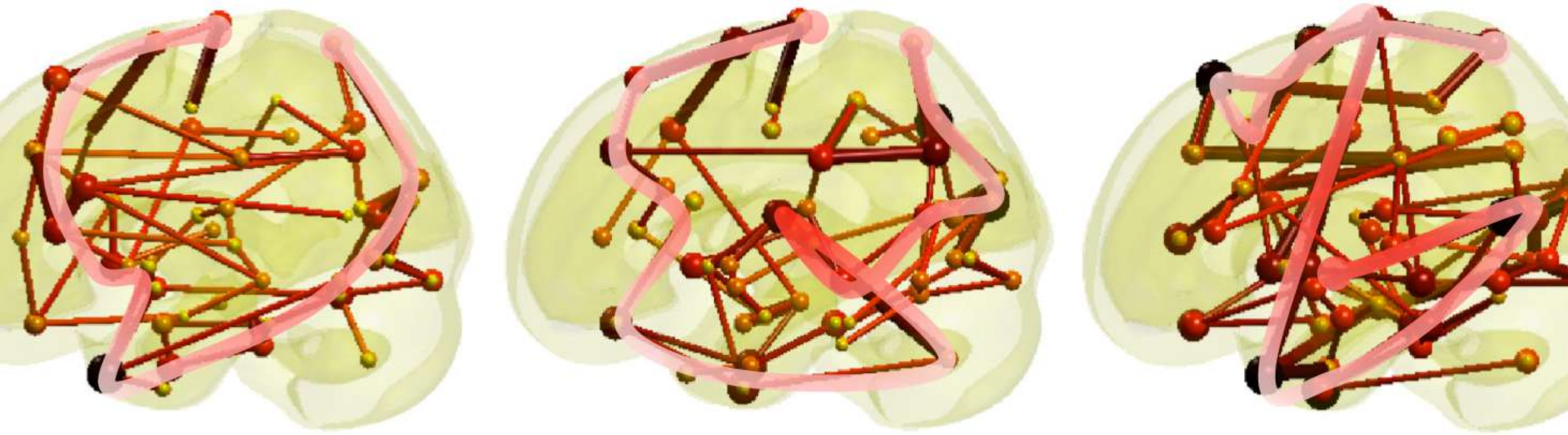
Persistent homology

Topological invariants
Model on topology
Very robust

Graph Filtration

Computing the Shape of Brain Networks Using Graph Filtration and Gromov-Hausdorff Metric

Hyekyoung Lee[1,2,3], Moo K. Chung[2,6,7], Hyejin Kang[1,3], Boong-Nyun Kim[5], and Dong Soo Lee[1,3,4]



ADHD ASD PedCon

Lee et al. 2011 MICCAI 302-309

Lee et al. 2012 IEEE Transactions on Medical Image 31:2267-2277

Network as a metric space

Nodes: $V = \{1, 2, \cdots, p\}$

Edge weights: $w = (w_{ij})$

$$w_{i,j} \geq 0,\ w_{ii} = 0,\ w_{ij} = w_{ji}$$

$$w_{ij} \leq w_{ik} + w_{kj}$$

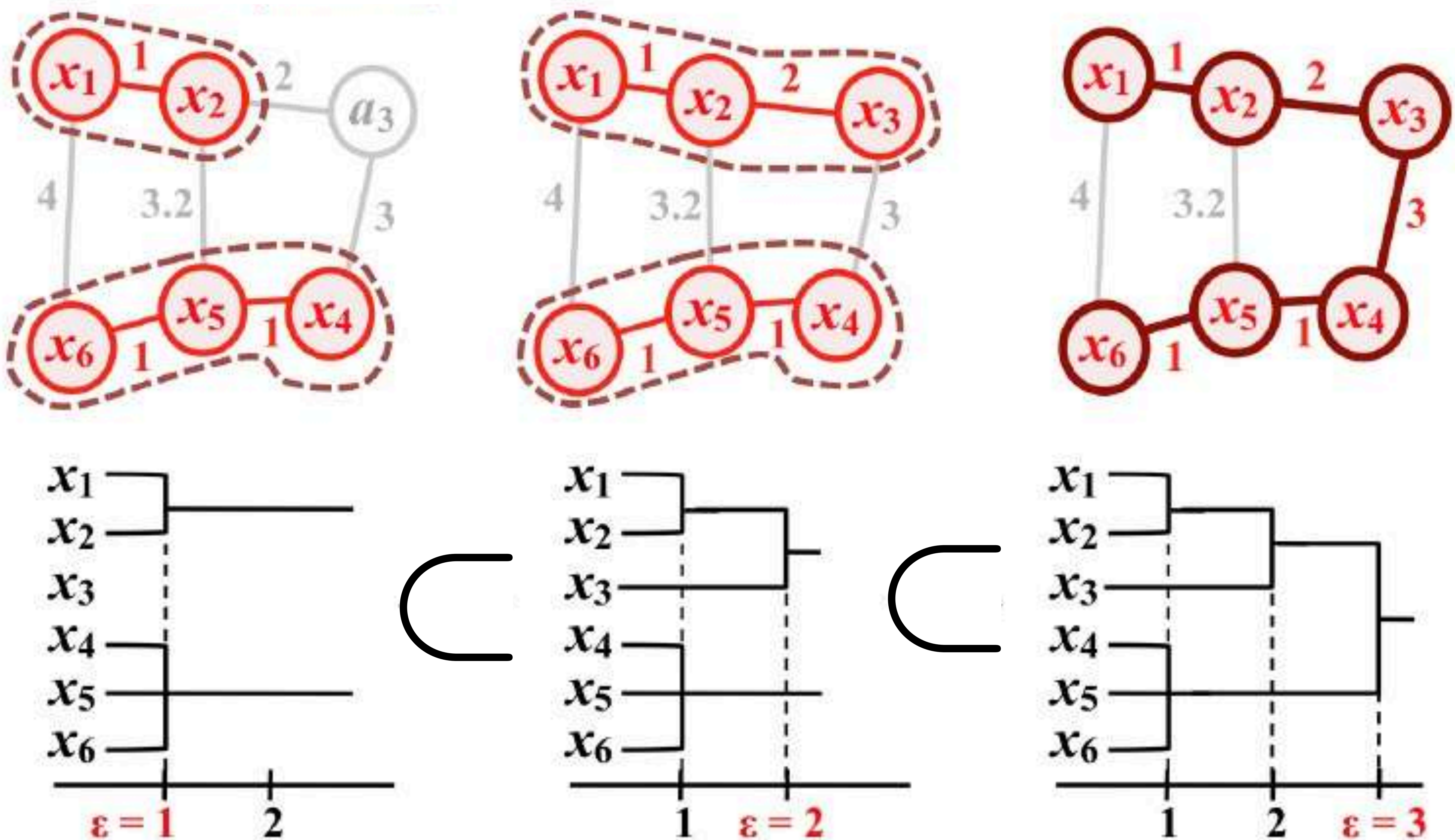
$\mathcal{X} = (V, w)$ is a metric space

Correlation metric

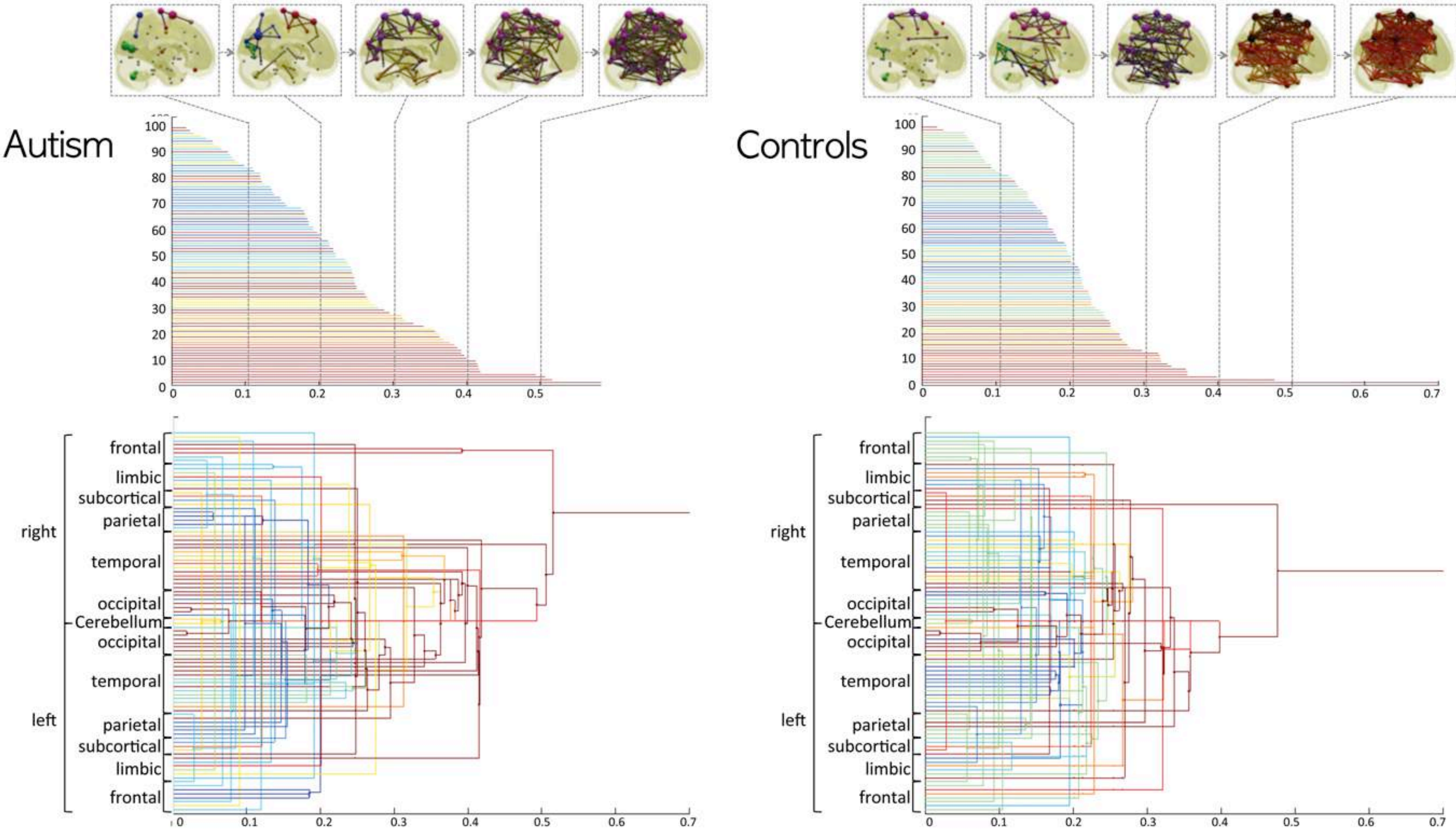
$$1 - \mathrm{corr}(\mathbf{x}_i, \mathbf{x}_j)$$ is not a metric

$$\sqrt{1 - \mathrm{corr}(\mathbf{x}_i, \mathbf{x}_j)}$$ is a metric

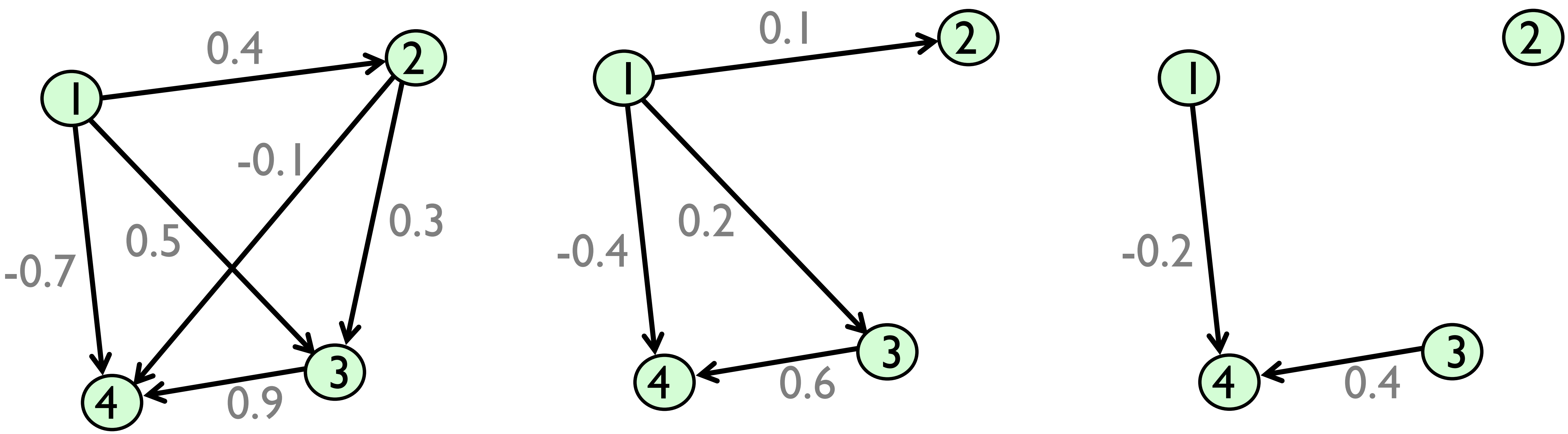
Graph filtration=single linkage dendrogram



Brain network as dendrogram

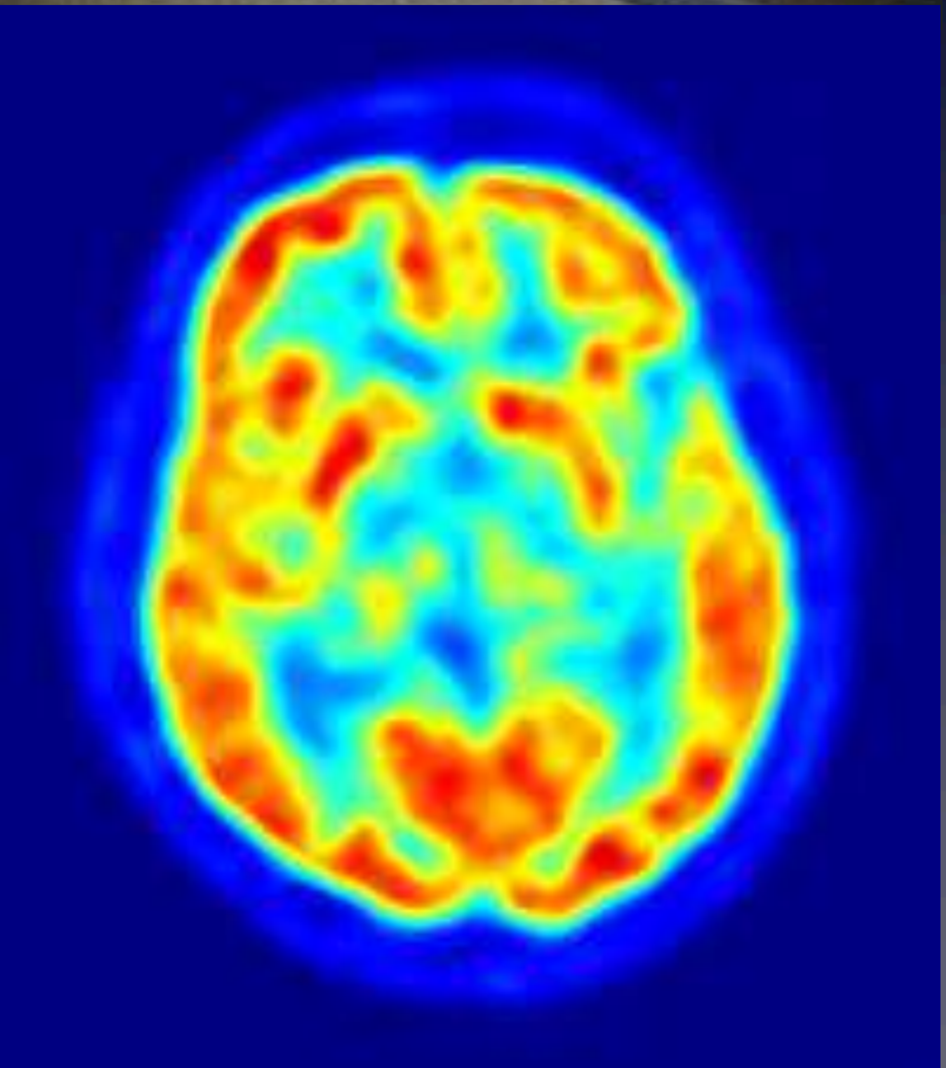


Graph filtration on directed graphs



$$G(0) \supset G(0.3) \supset G(0.5)$$

PET metabolic connectivity

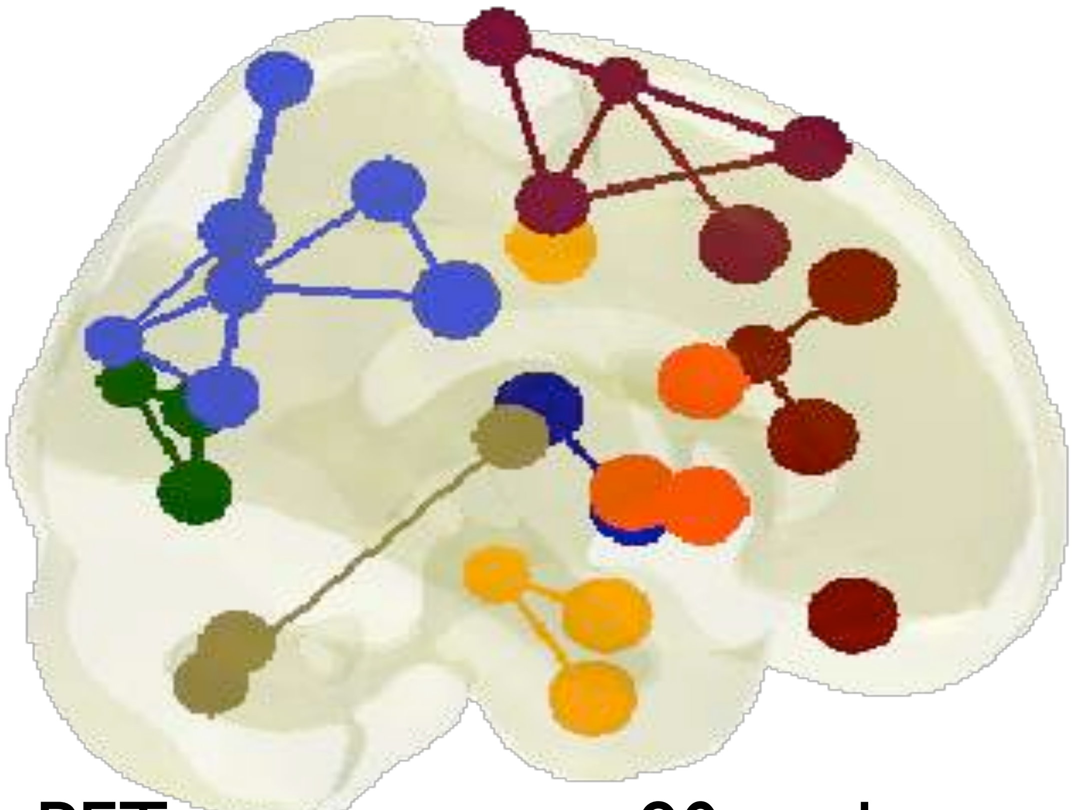


24 attention deficit hyperactivity disorder (ADHD) children

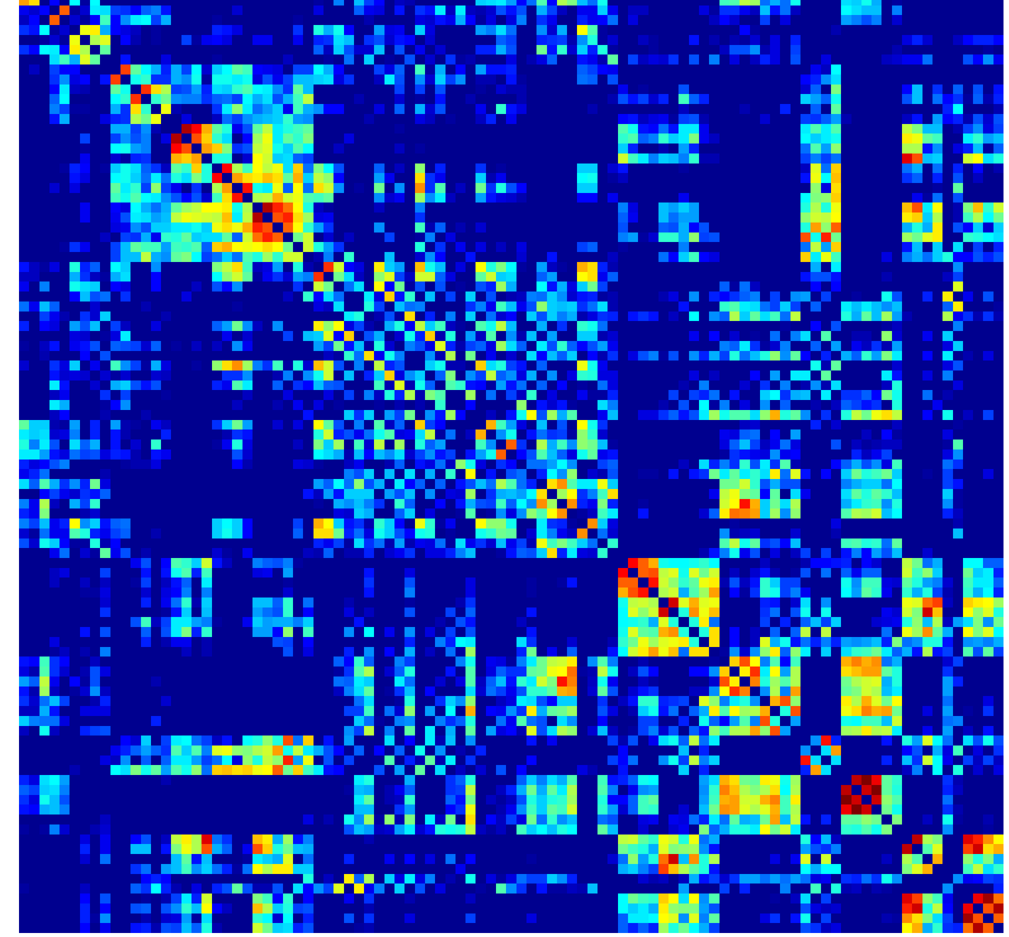
26 autism spectrum disorder (ASD) children

11 pediatric control subjects

Pet metabolic connectivity

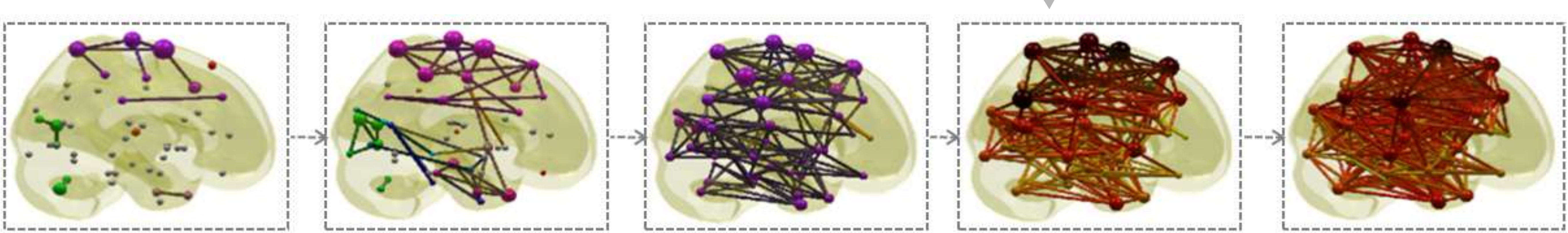


PET measures on 90 nodes

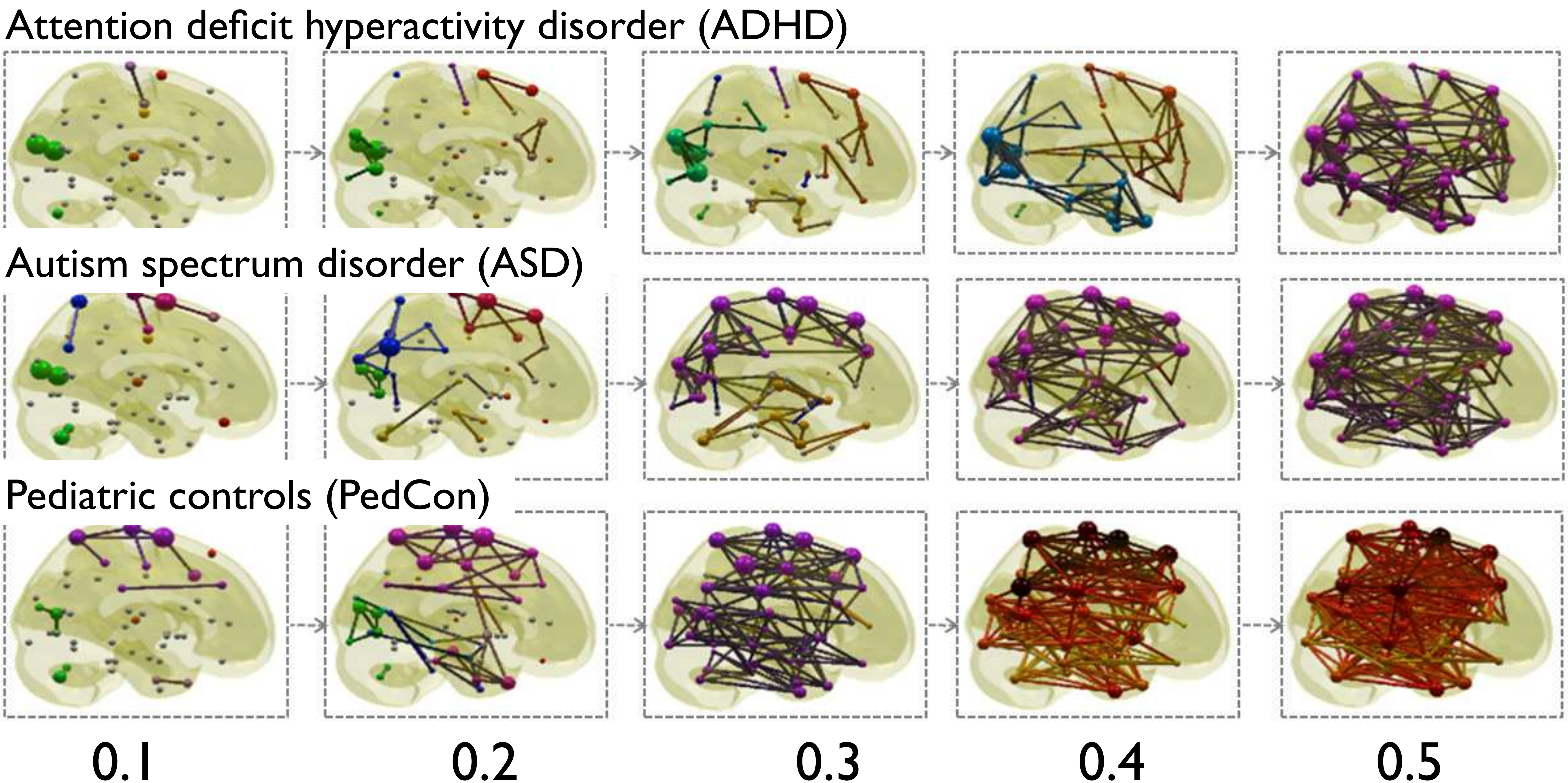


90 x 90 correlation map

Rips filtration on 1- correlation



Graph filtrations



1-correlation

Maltreated multimodal study

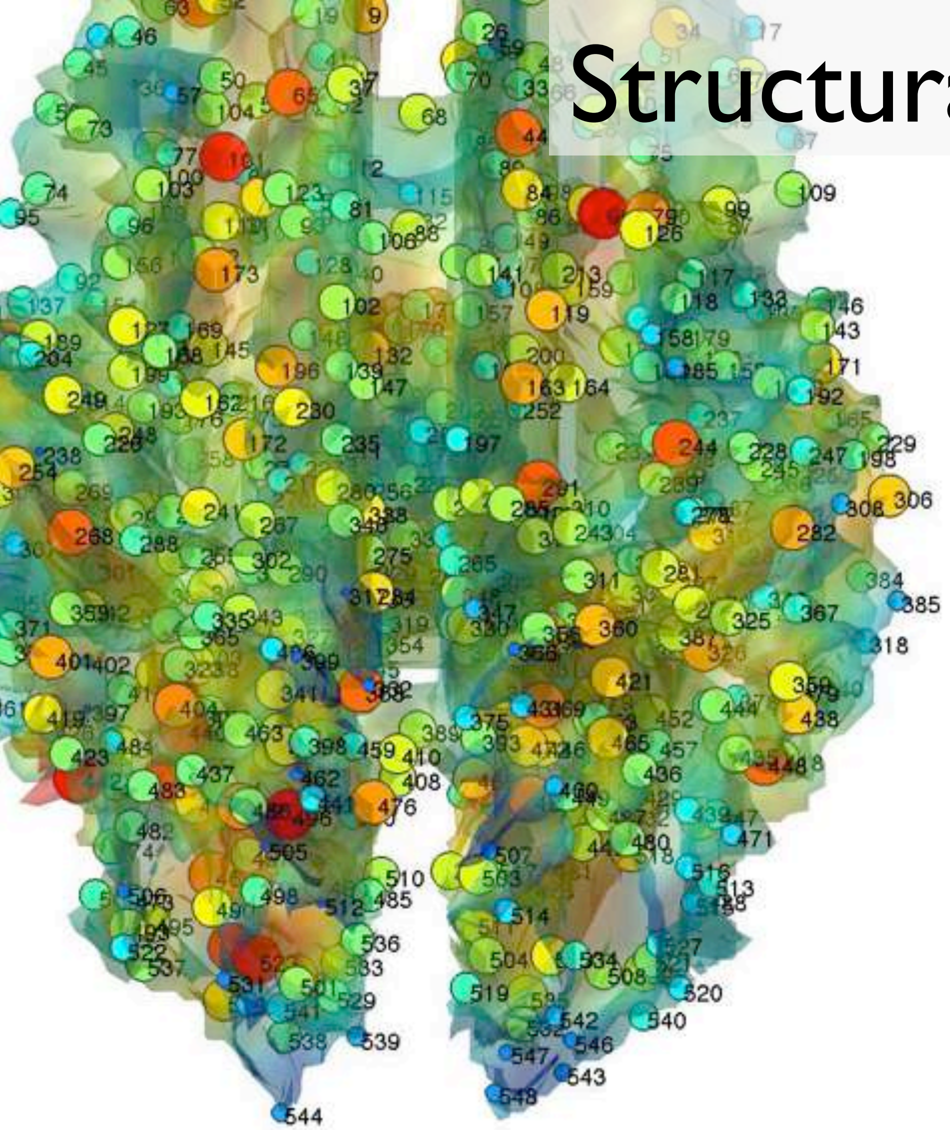
31 normal controls (12 ± 2 yrs.)

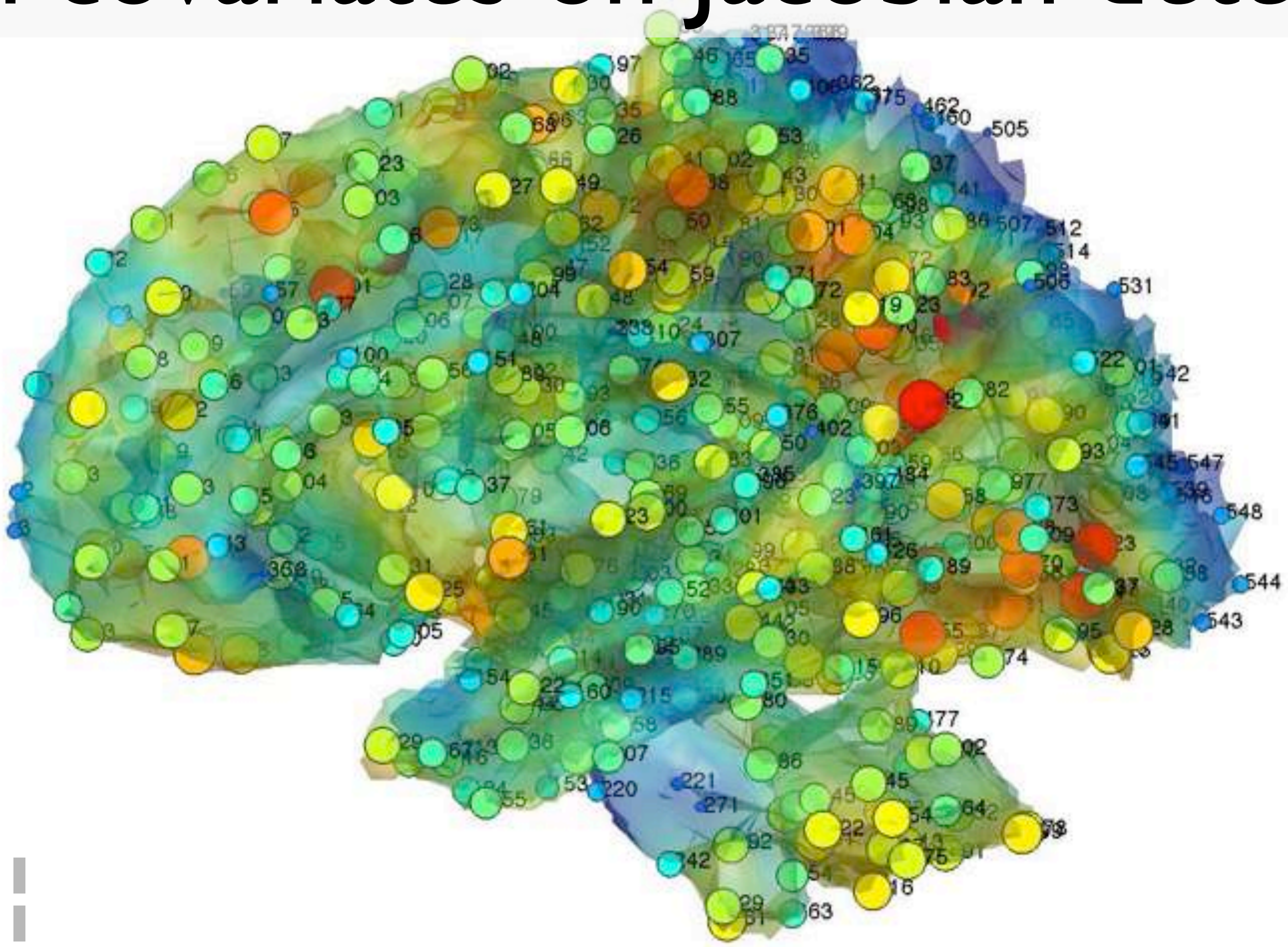
23 maltreated while living in post-institutional settings (2.5±1.4 yrs.) before adopted (11 ± 2 yrs.)

MRI → Jacobian determinant

DTI → FA-values

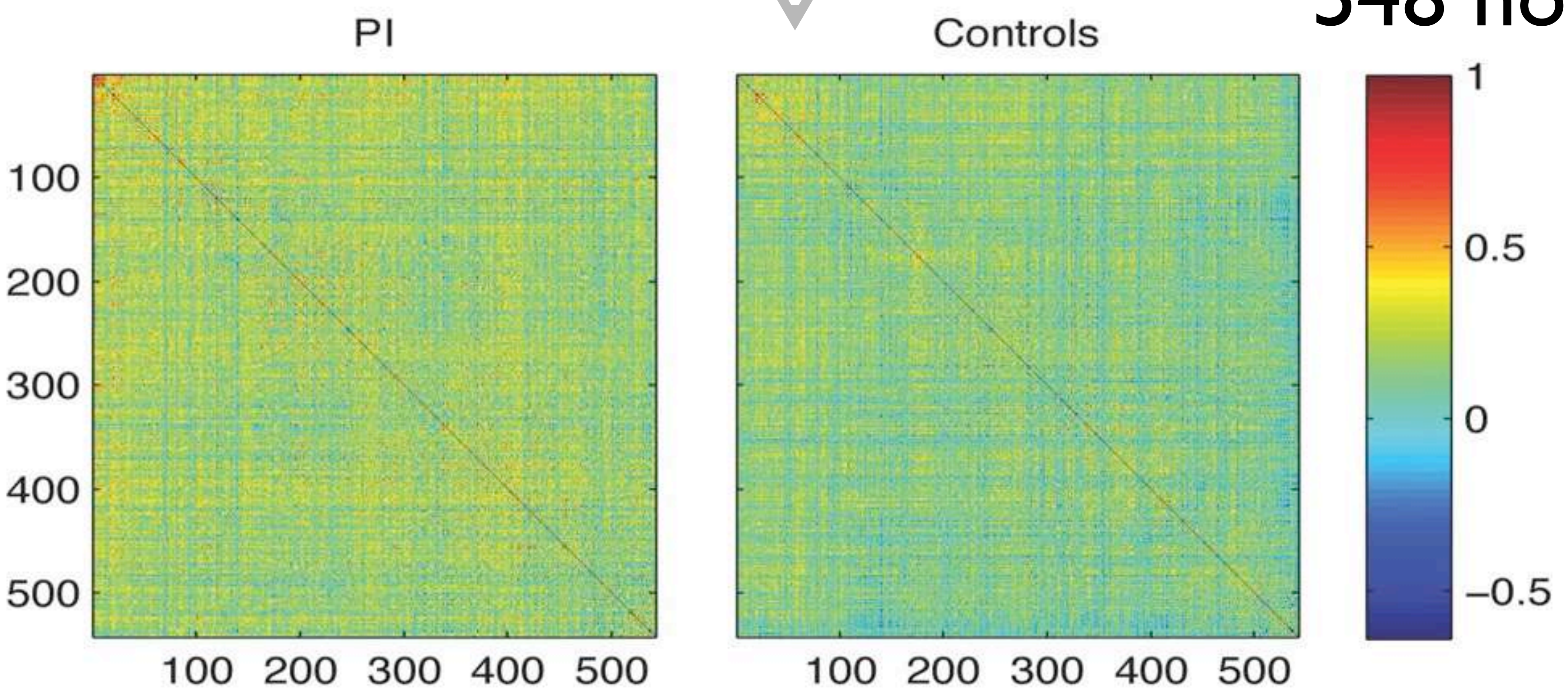
Structural covariates on Jacobian determinants



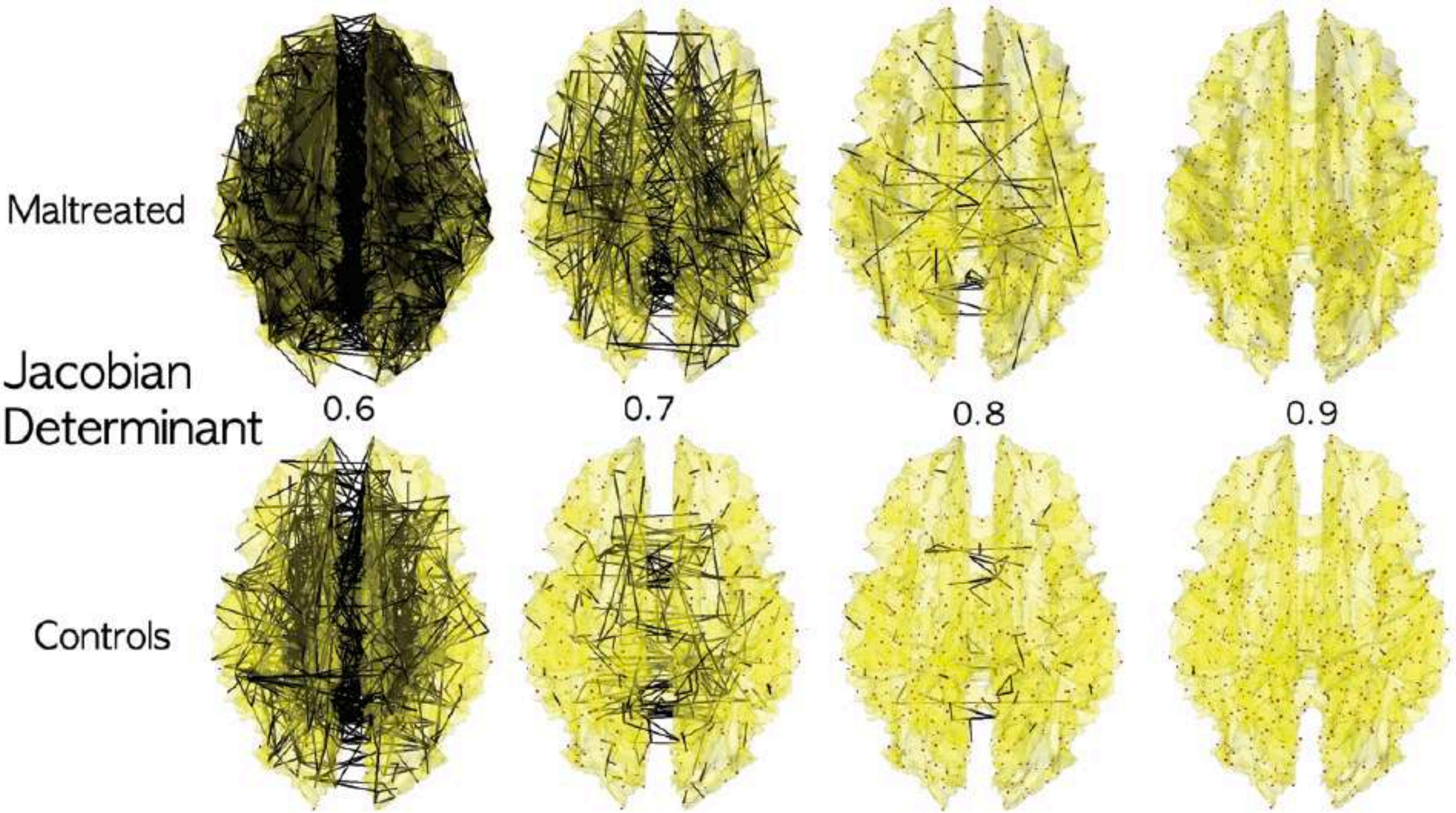


15.7mm
internodal
distance

548 nodes correlation

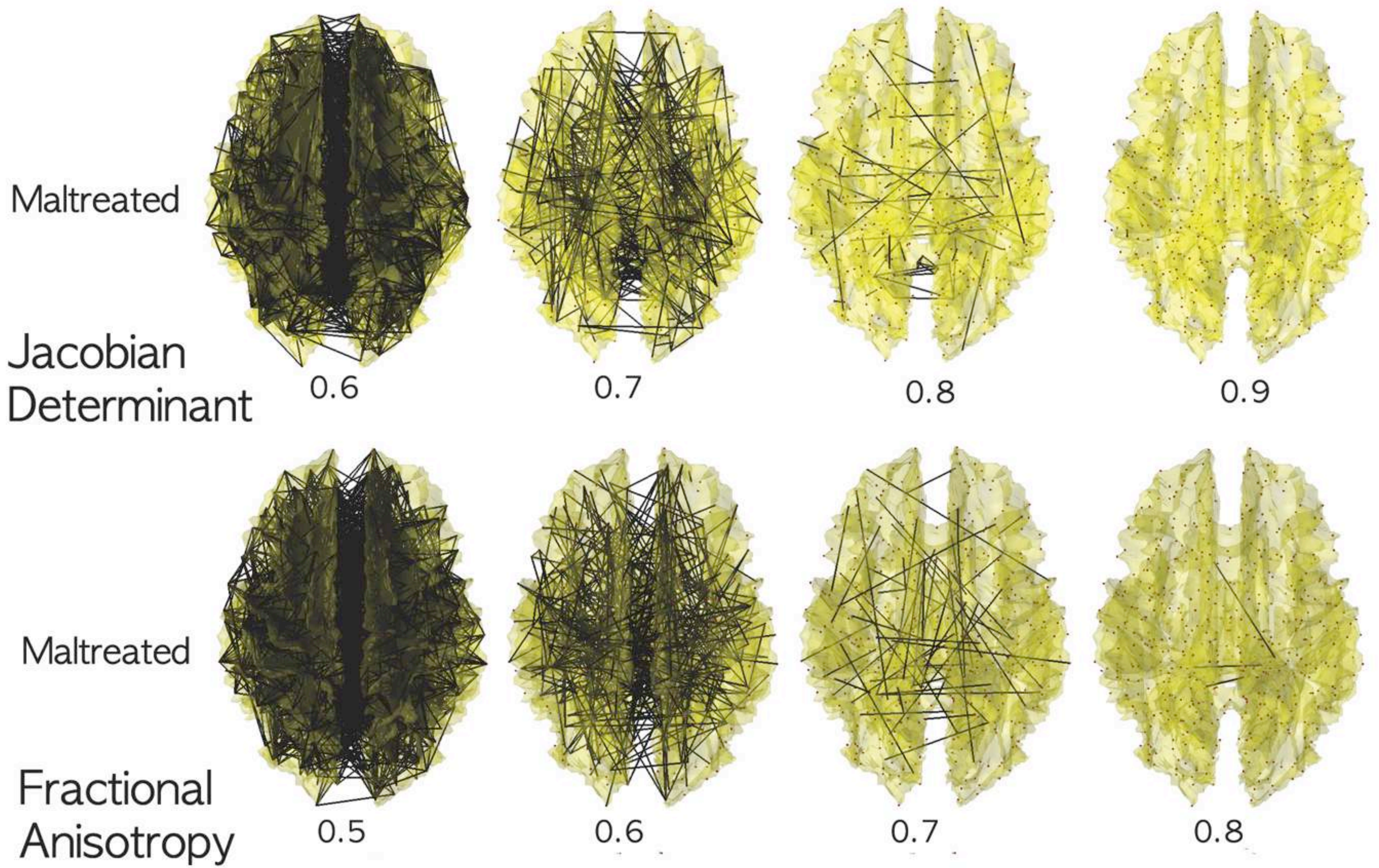


Graph filtrations on Jacobian determinant



Maltreated children are anatomically more homogenous

Graph filtrations on FA-values

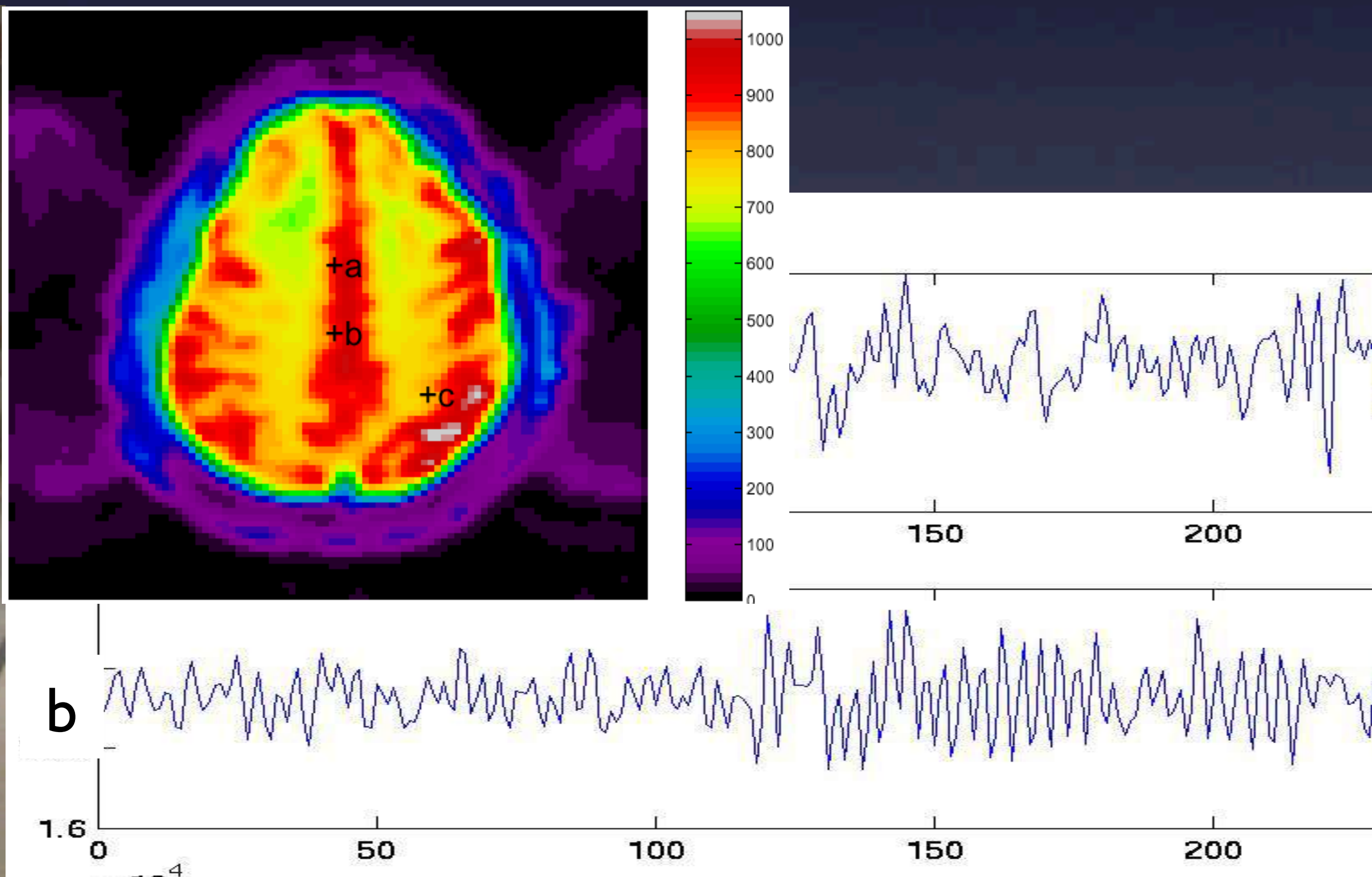


Tennessee twin fMRI study

11 monozygotic (MZ) twins

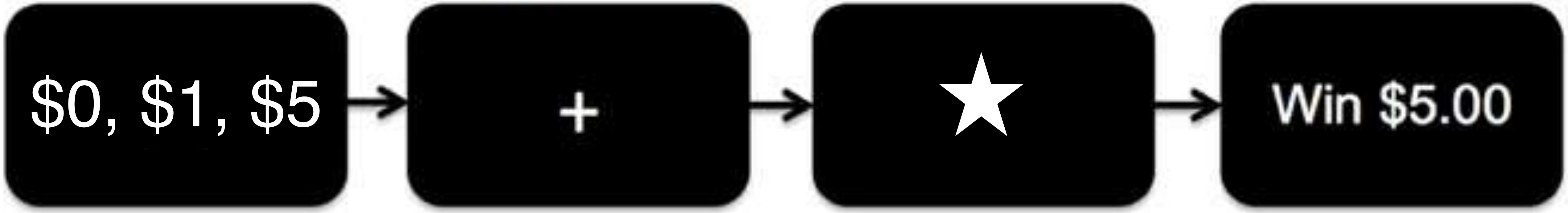
14 dizygotic (DZ) twins

- 9 same-sex DZ pairs (5 male, 4 female)
- 5 different-sex DZ pairs



Paired statistical contrast images

Monetary incentive delay task



3 runs of 40 trials

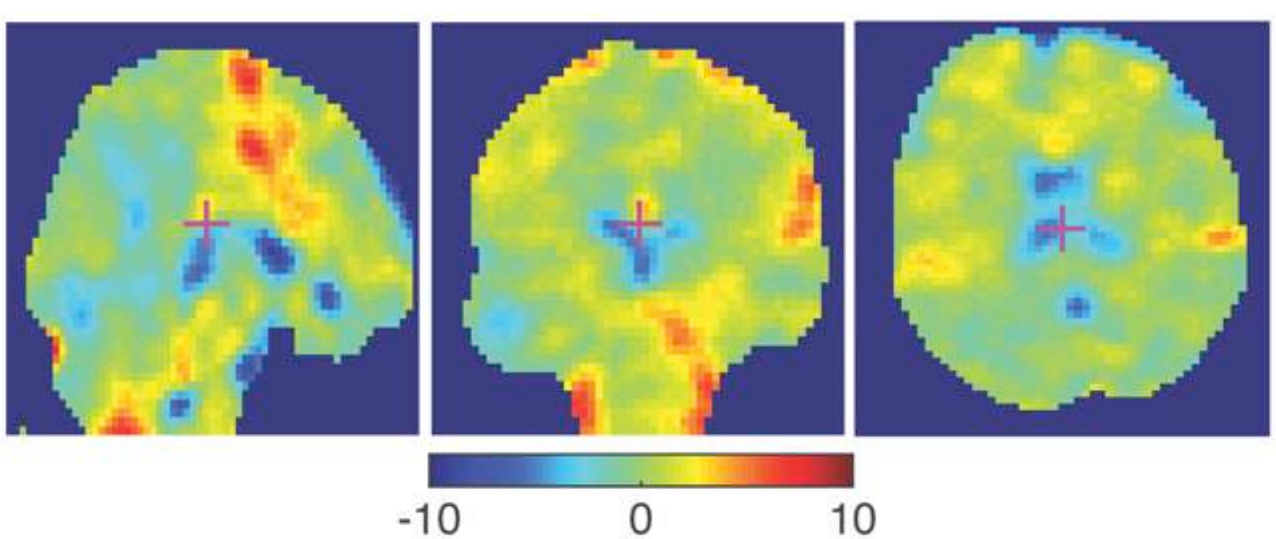
delay for $0 trials
delay for $1 trials
delay for $5 trials

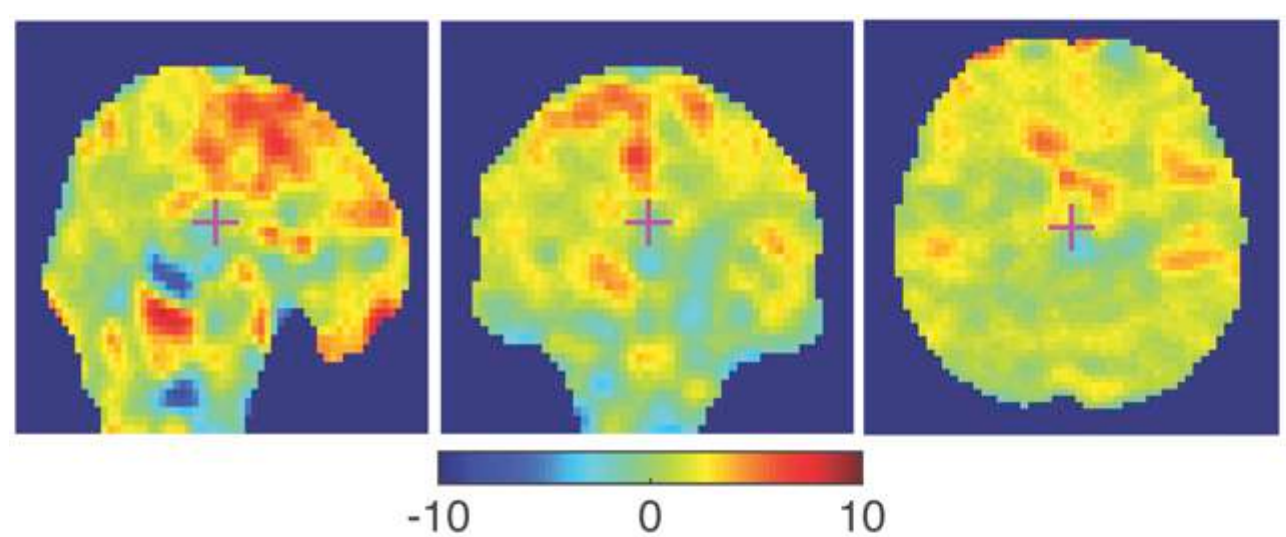
c

General Linear Model

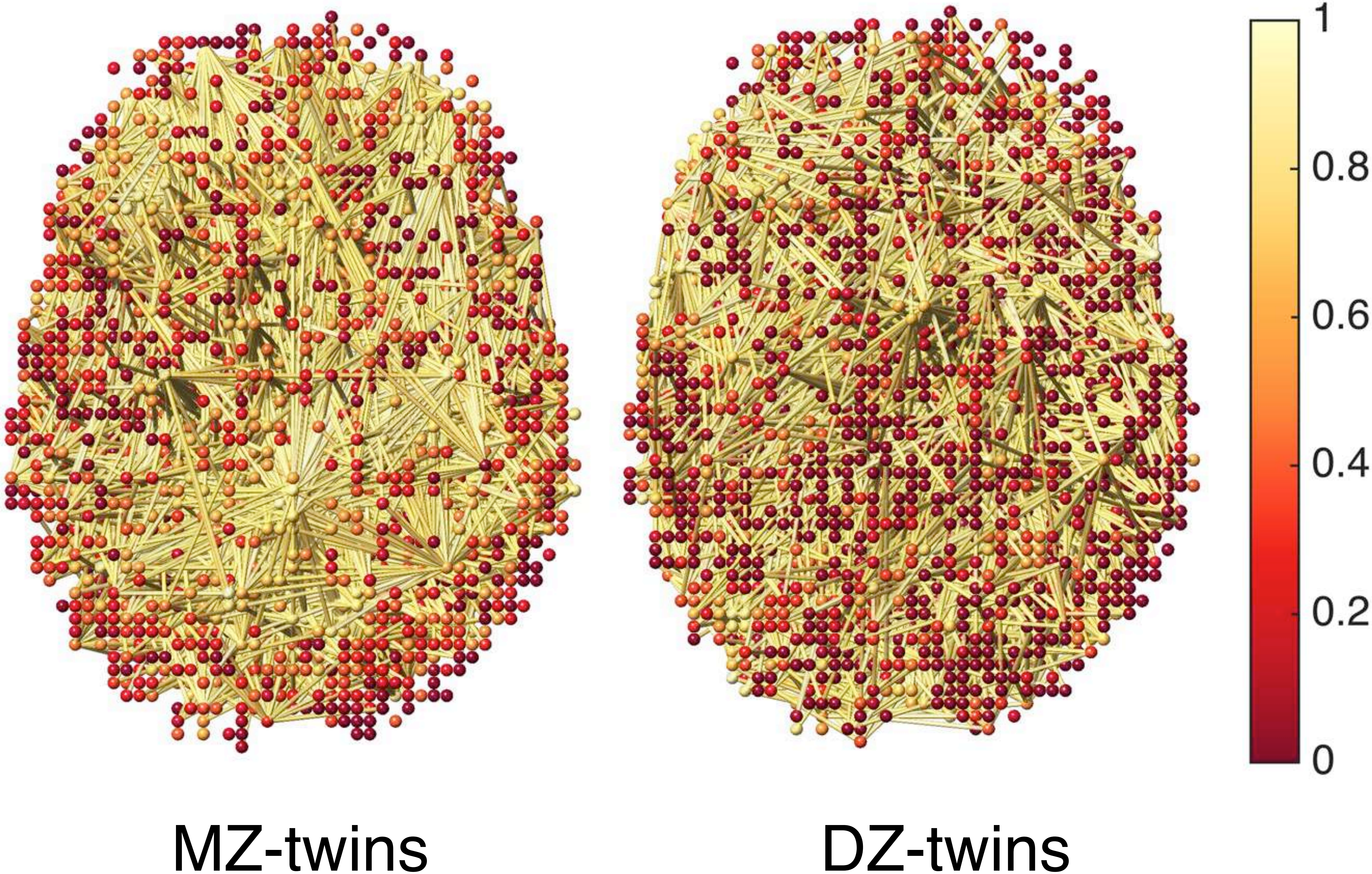
$$W(v_i) = Zb(v_i) + \varepsilon(v_i)$$

$c^T b(v_i)$ Contrast map

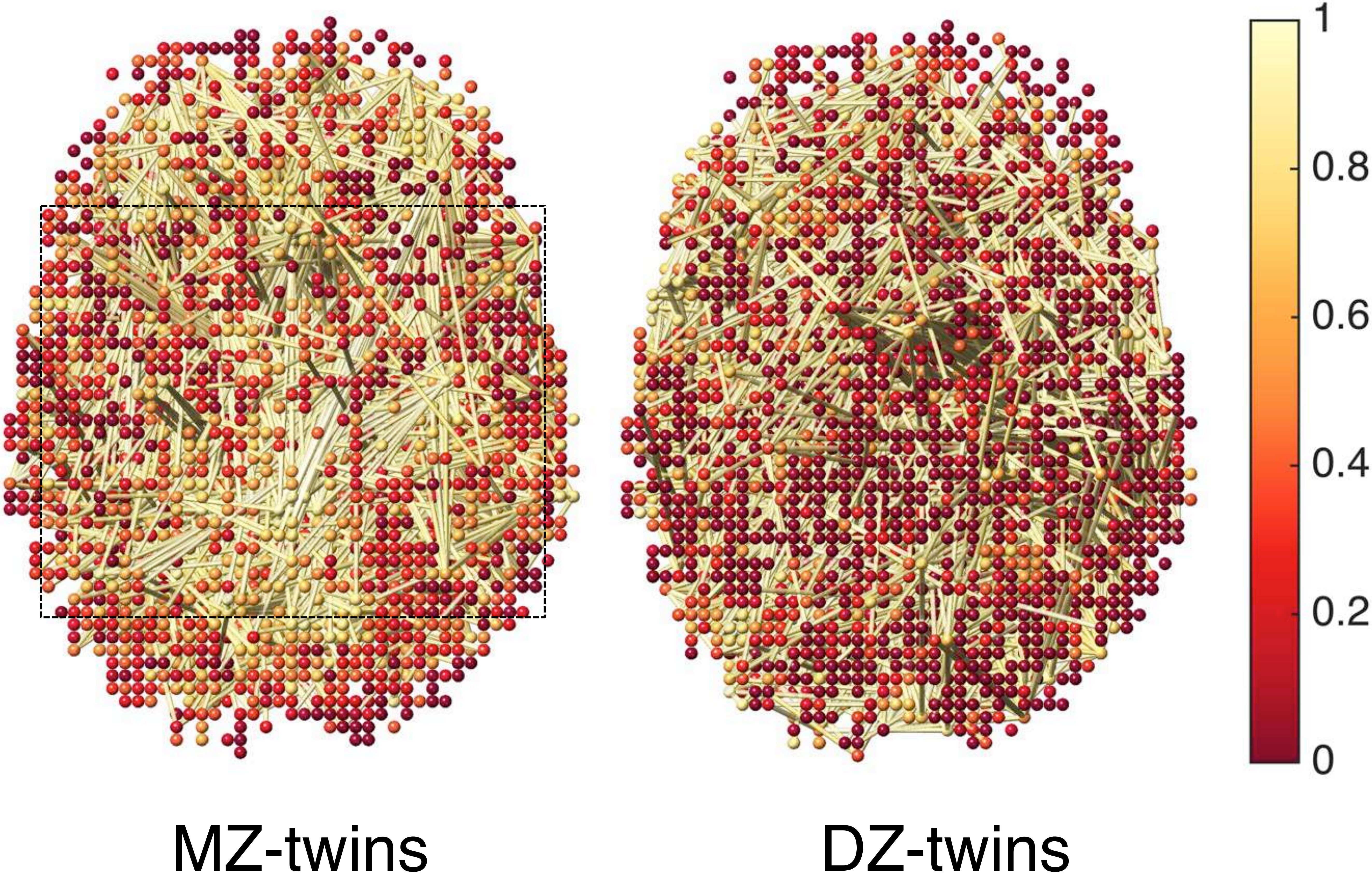




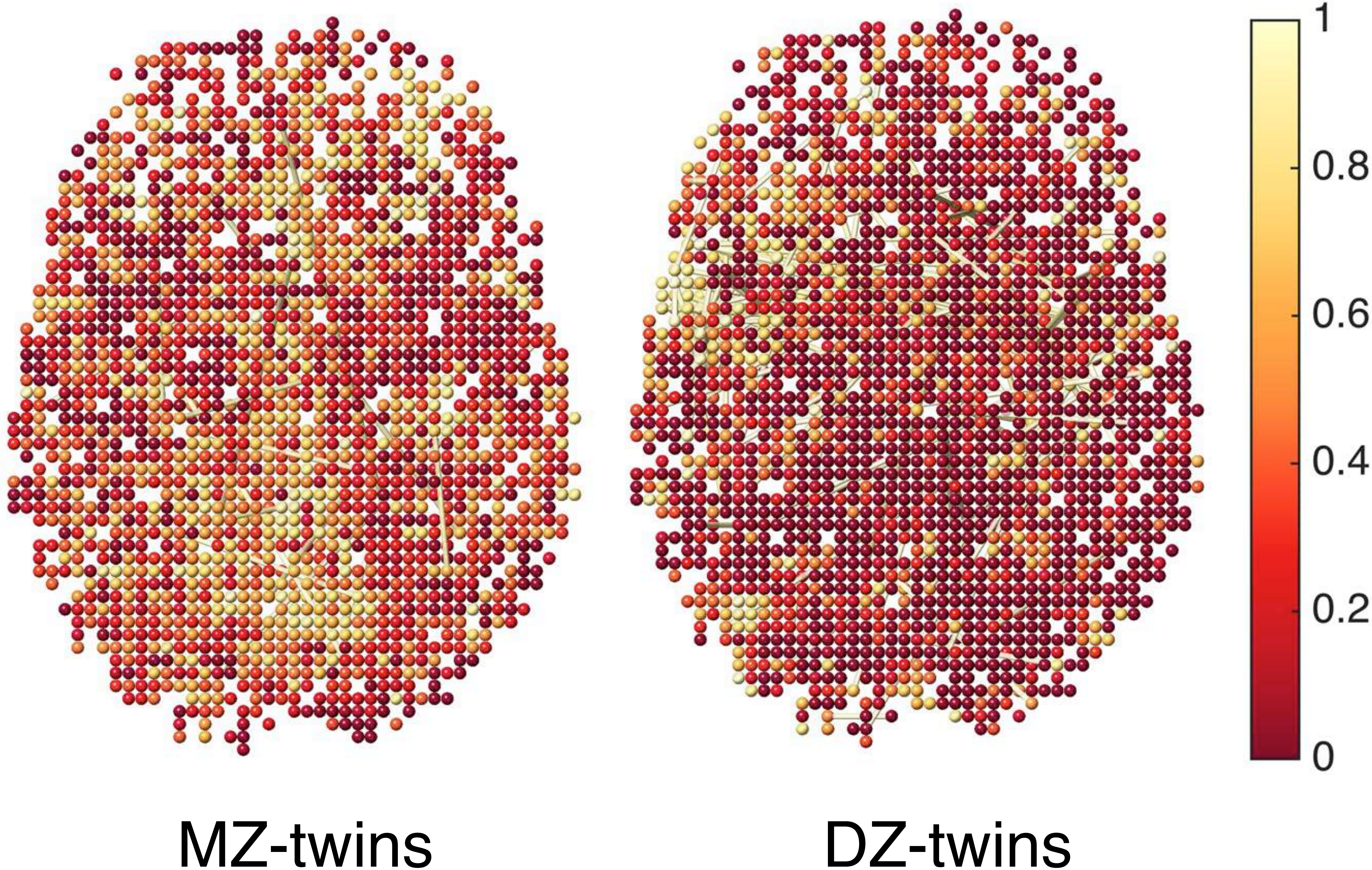
Networks at filtration value 0.7



Networks at filtration value 0.8

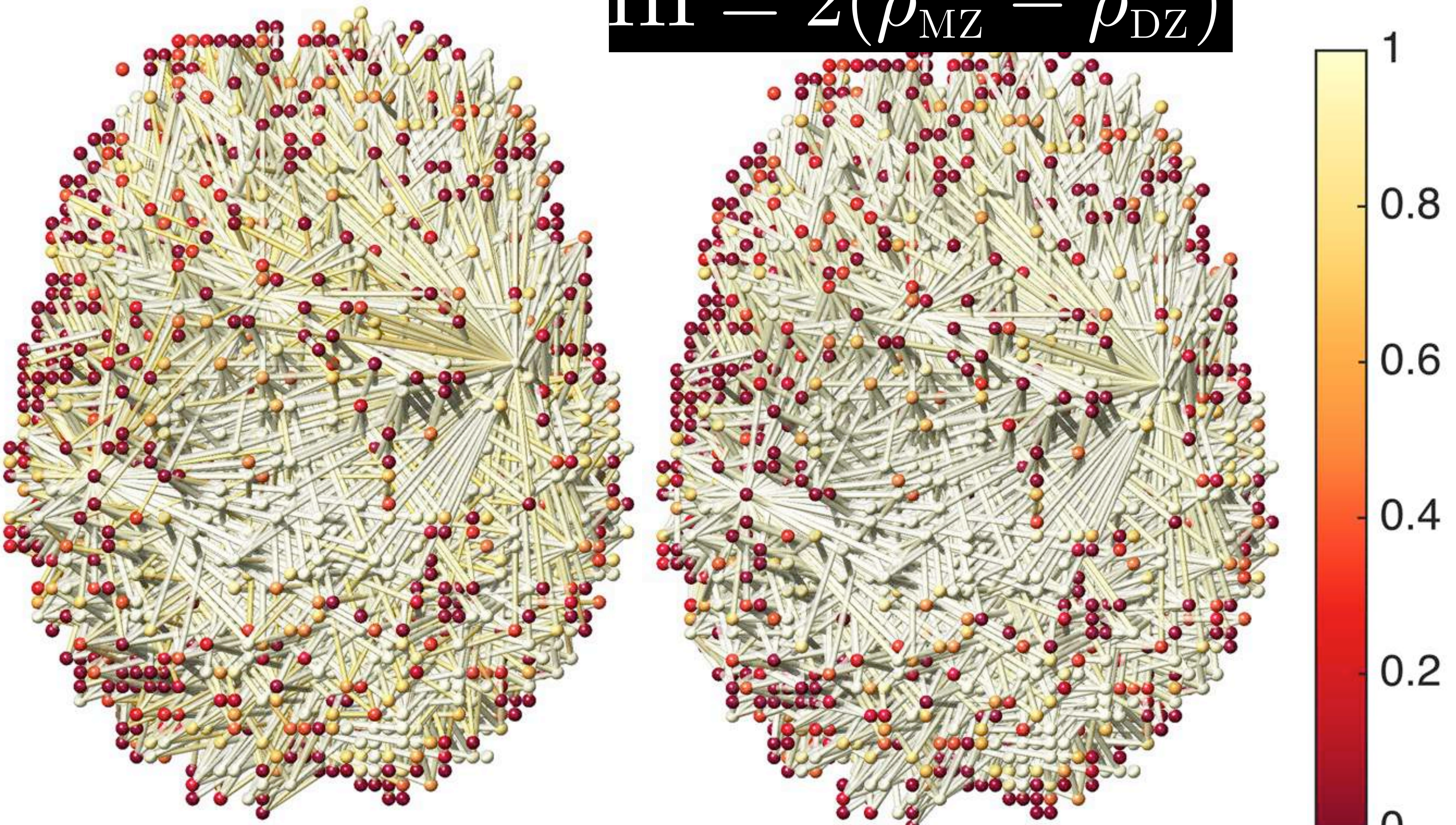


Networks at filtration value 0.9



Heritability Index (at both nodes and edges)

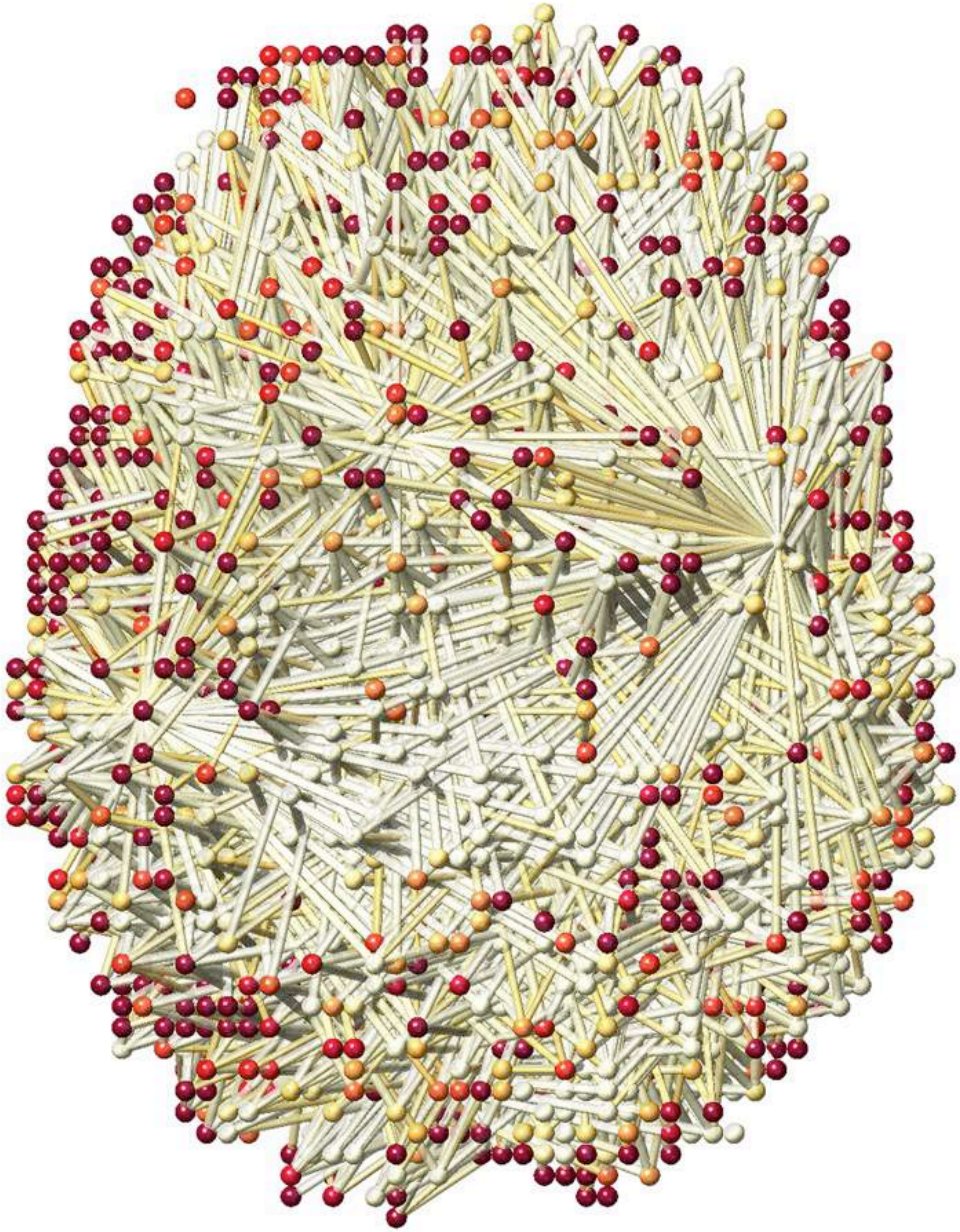
$$\mathrm{HI} = 2(\rho_{\mathrm{MZ}} - \rho_{\mathrm{DZ}})$$



Filtration value 0.7 Filtration value 0.9

p-value < 0.0002

Heritability index map



+25000 nodes

+0.6 billion connections

Voxel-level functional network

Chung et al. 2017 IPMI

Betti Numbers

Betti numbers β_i

of i-dimensional holes/loops

β_0 = # of connected components = 3

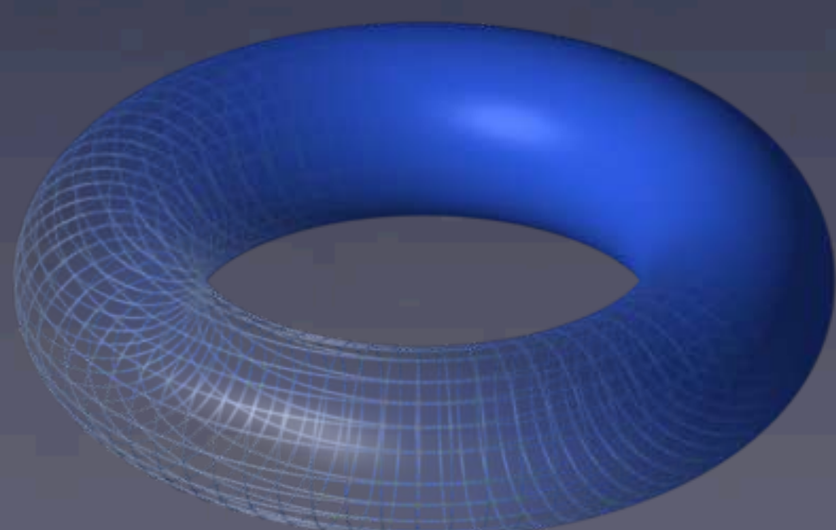
β_1 = # of 1D holes = 1

β_2 = # of 2D cavities =0

Representation: (3,1,0,0,...)

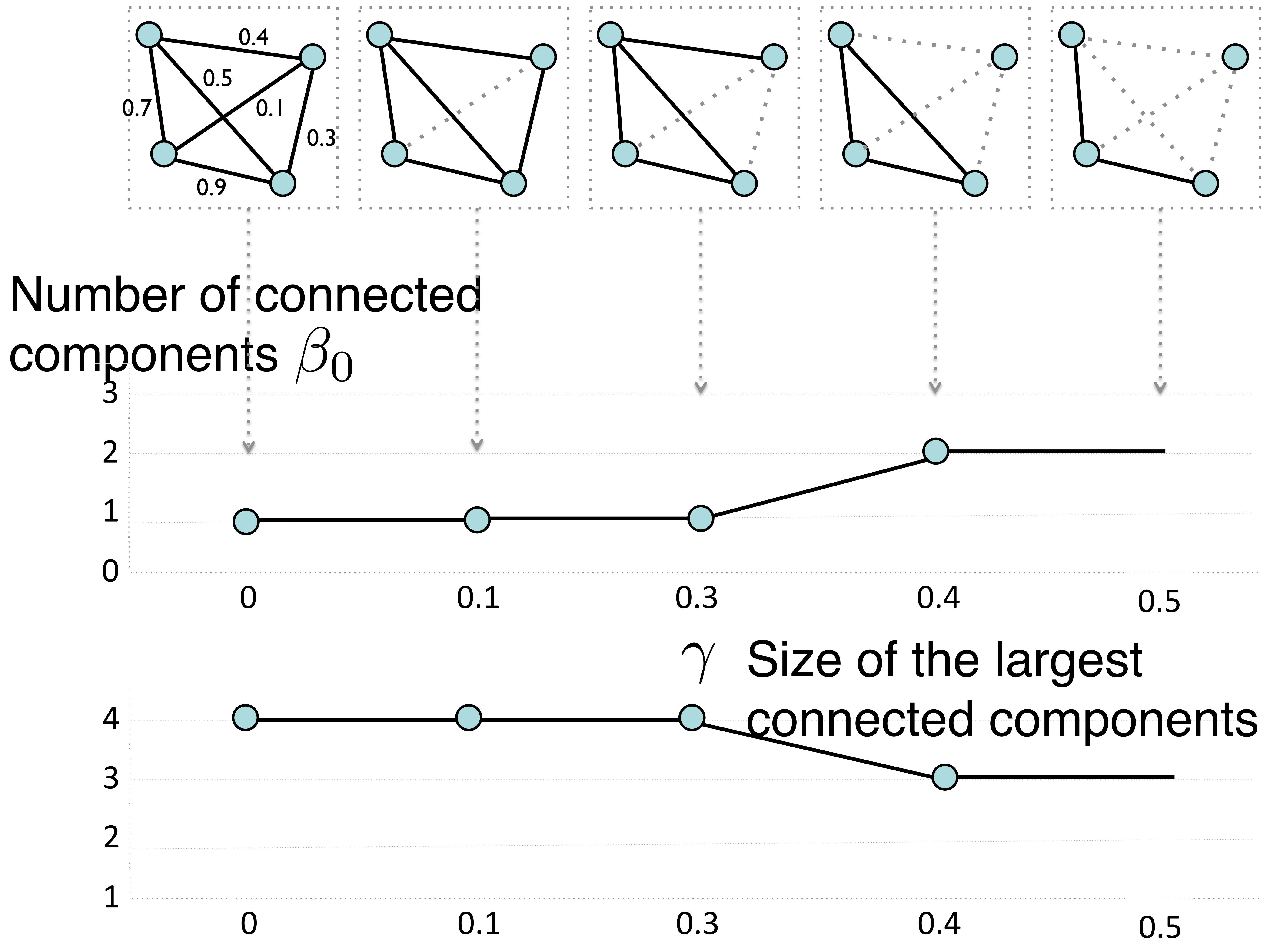
Euler characteristic:

$$\chi = \beta_0 - \beta_1 = 2$$



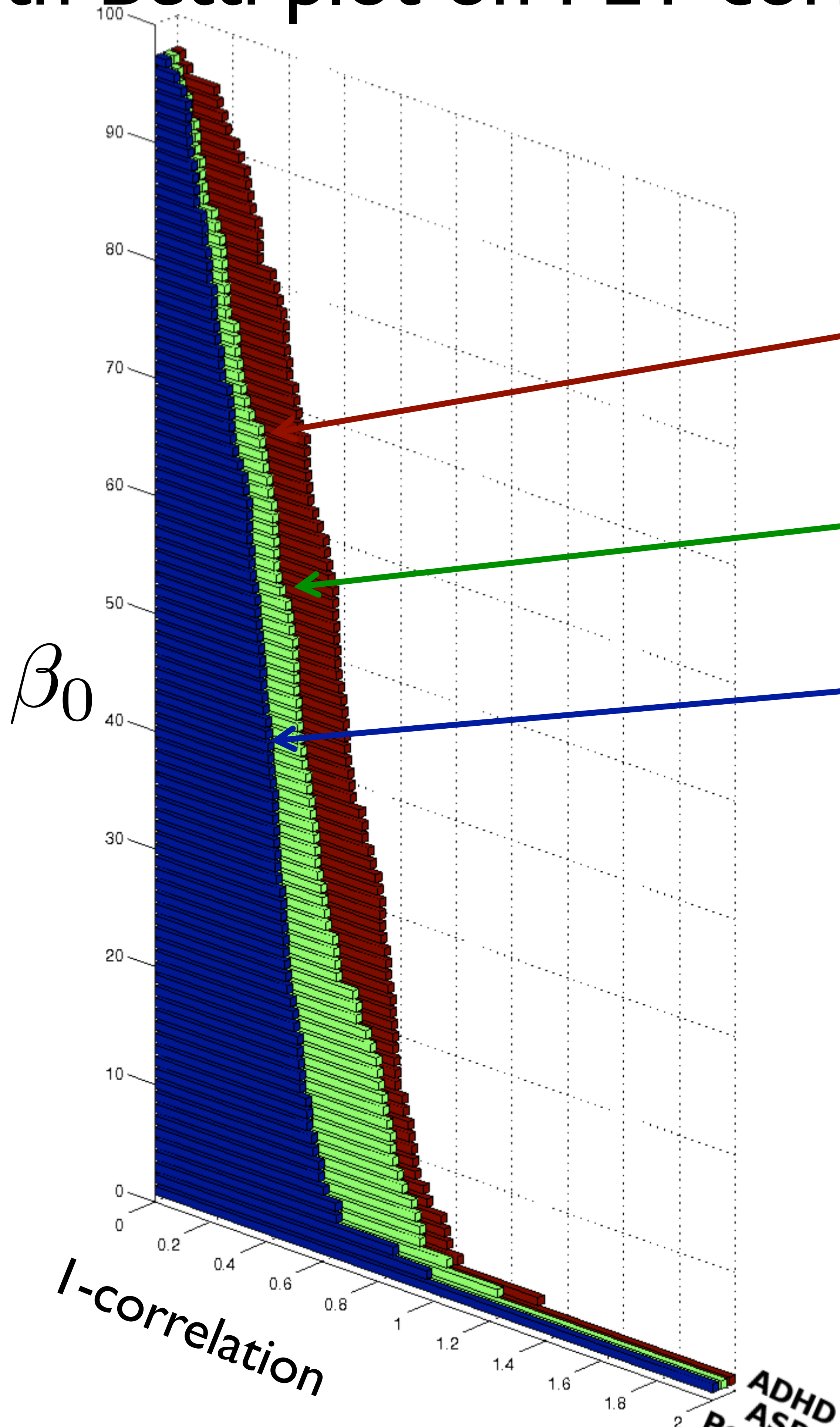
$$\beta_0 = 1, \beta_1 = 2, \beta_2 = 1$$

Representation: (1,2,1,0,0,...)



0.4
0.5
0.7
0.1
0.3
0.9
Number of connected components β_0
3
2
1
0
0
0.1
0.3
0.4
0.5
γ Size of the largest connected components
4
3
2
1
0
0.1
0.3
0.4
0.5

0-th Betti plot on PET correlation network



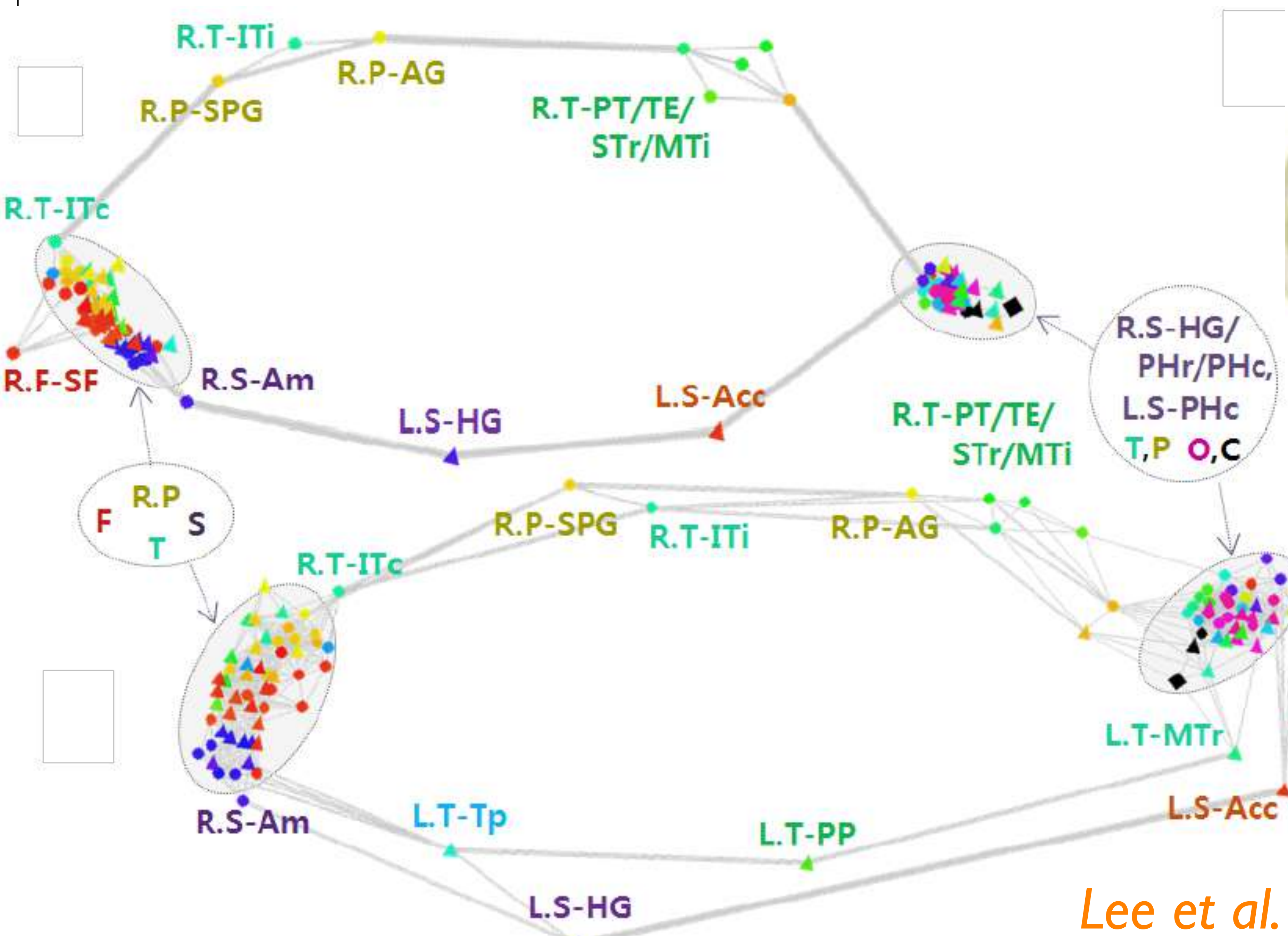
24 attention deficit hyperactivity disorder (ADHD) children

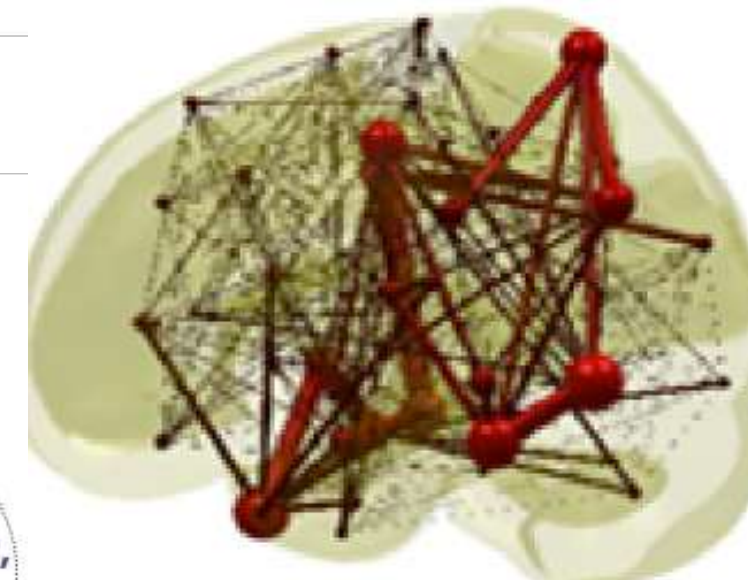
26 autism spectrum disorder (ASD) children

11 pediatric control subjects

Hole Detection in Metabolic Connectivity of Alzheimer's Disease Using k−Laplacian

Hyekyoung Lee[1], Moo K. Chung[2], Hyejin Kang[1], and Dong Soo Lee[1]





Lee et al. 2014 MICCAI 297-304

Persistent homology on hierarchical connectivity

Chung et al. 2017 BioRxiv 209635

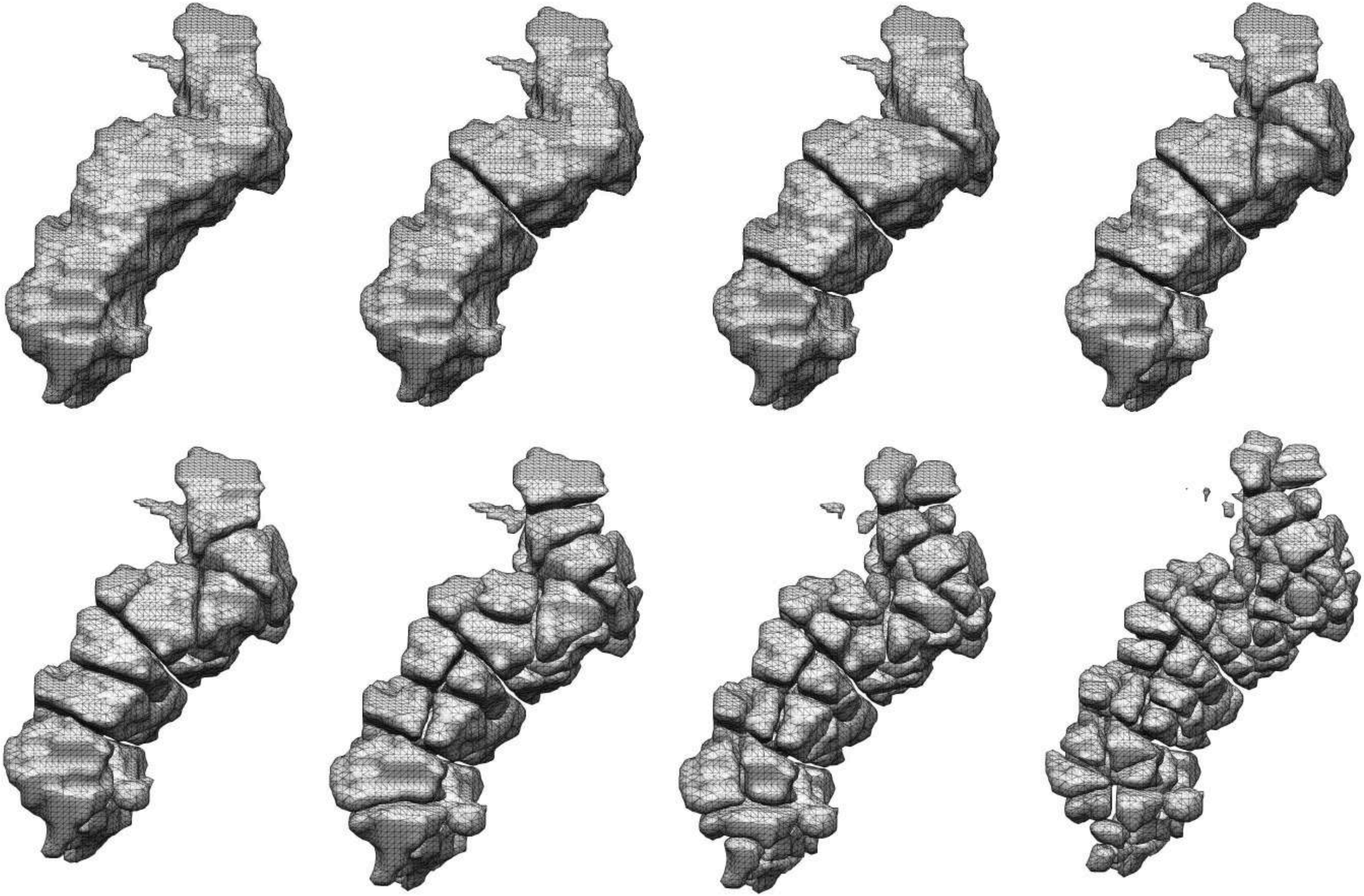
Winsconsin Twin Project

58 Monozygontic (MZ) twin pairs
53 same-sex dizygotic (DZ) twin pairs

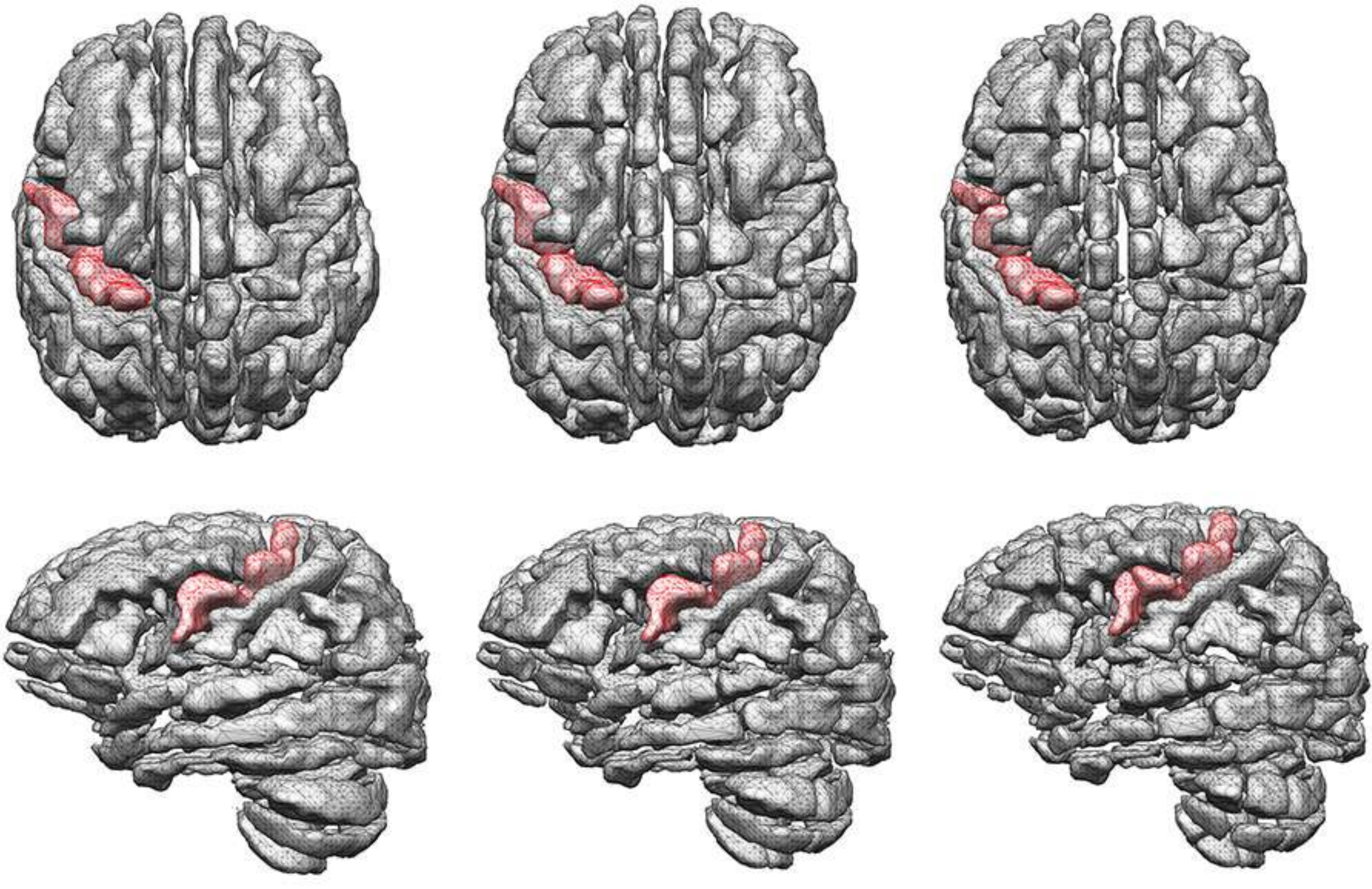
111 pairs = 222 subjects

6 non-DWI: b=0
63 DWI: b=500 (9 dir.), 800 (18 dir.) , 2000 (36 dir.)
Isotropic 2mm resolution

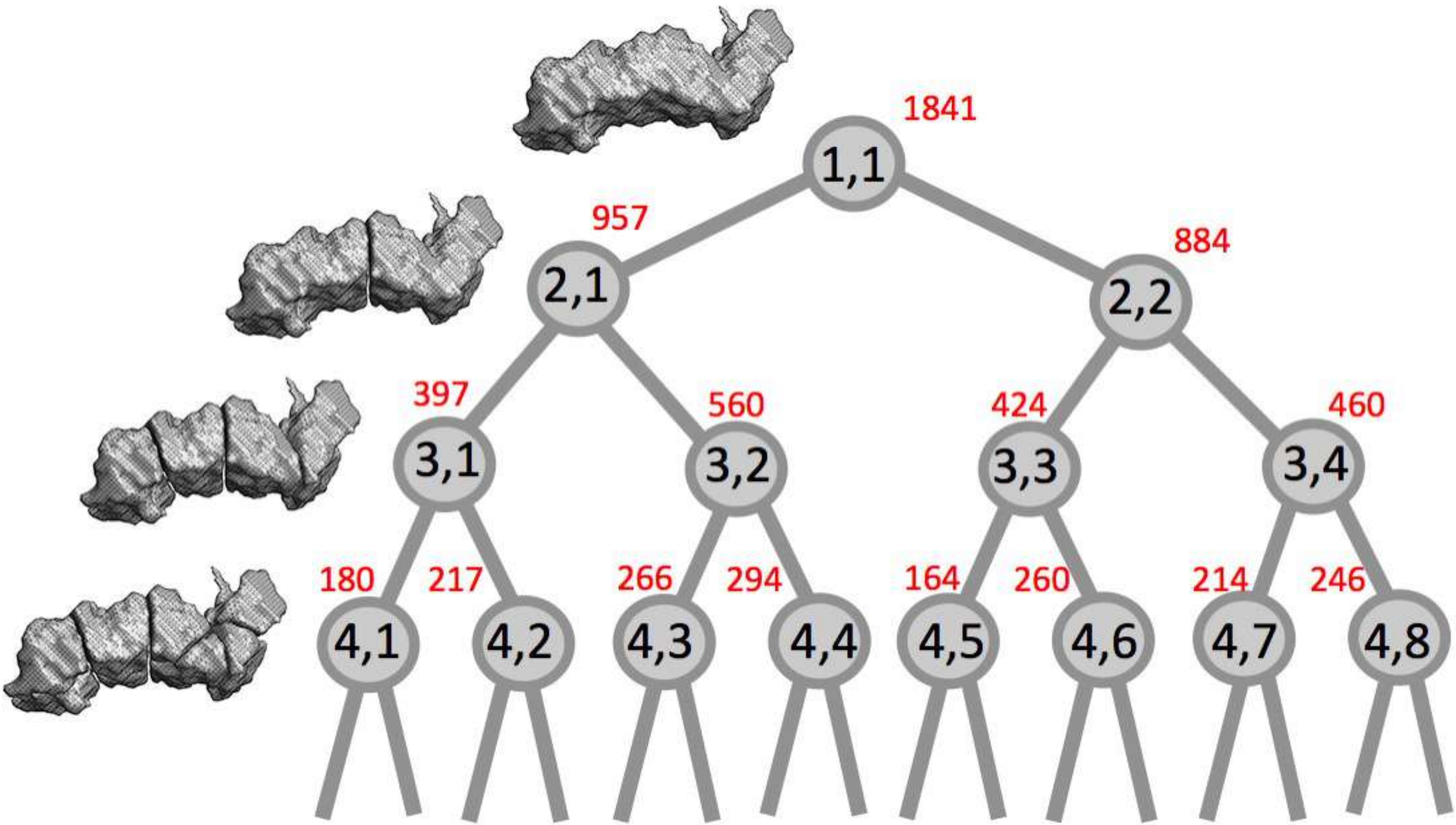
20-layer hierarchical parcellation



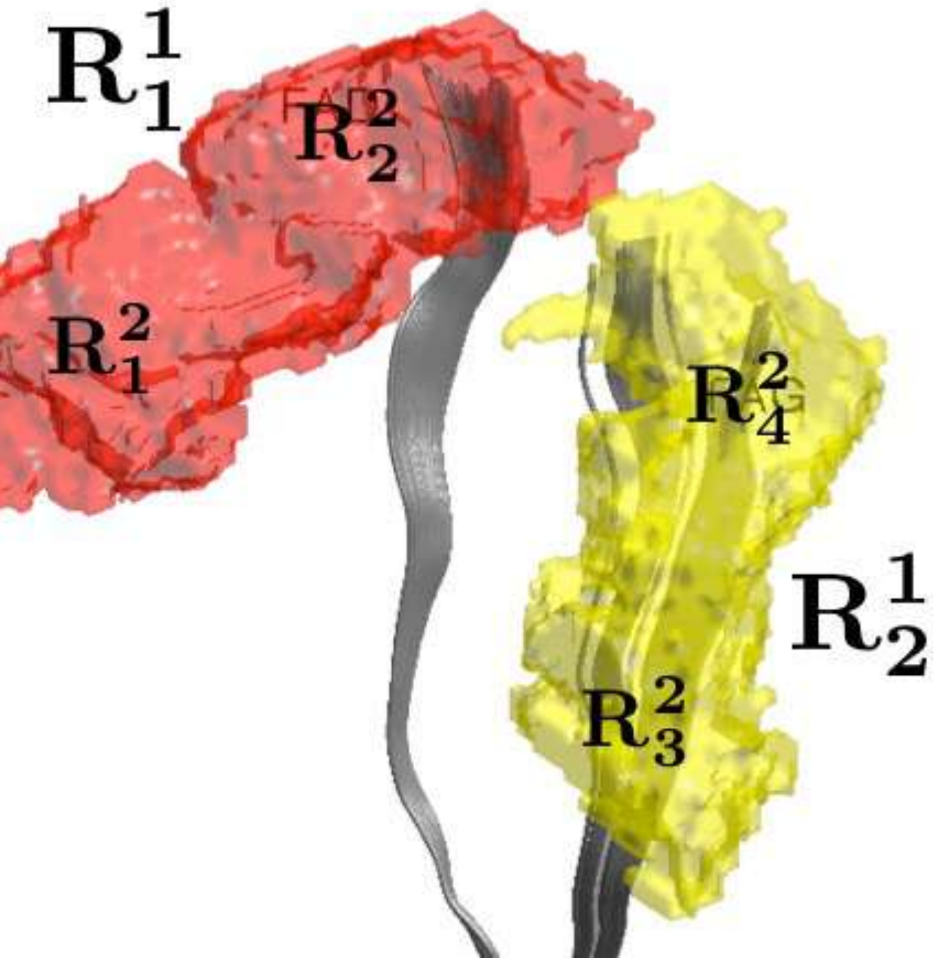
20-layer hierarchical parcellation

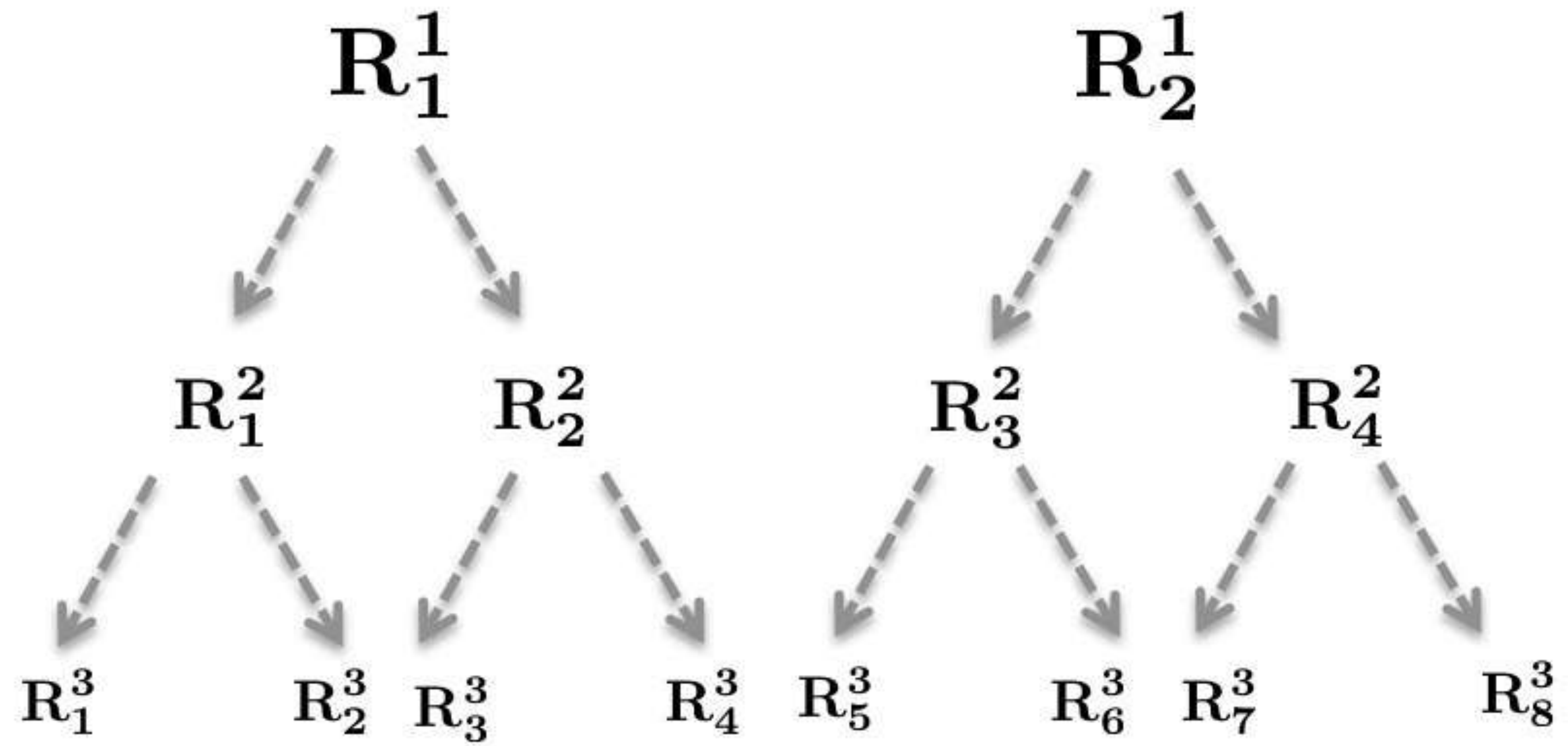


Number of voxels in each layer



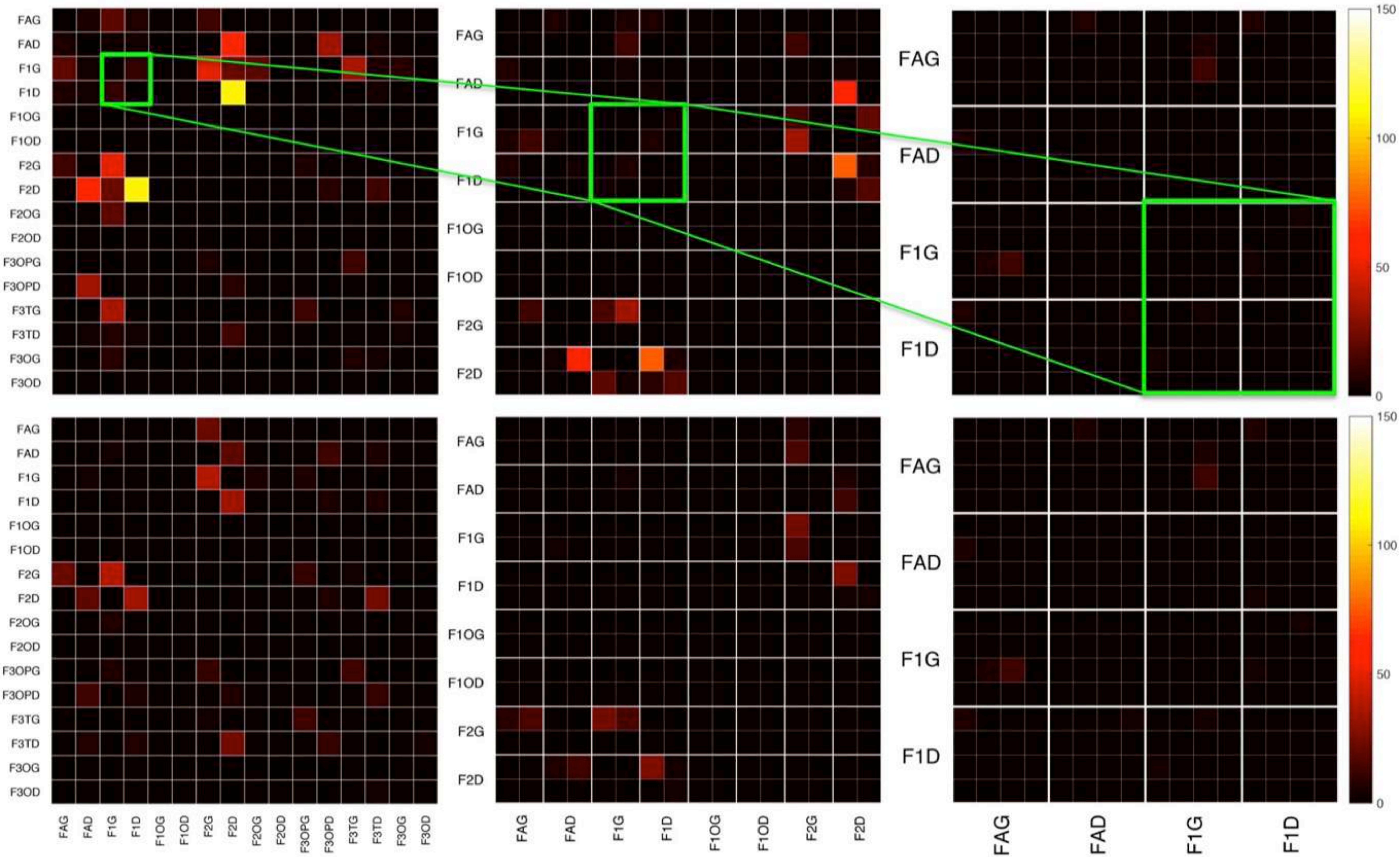
Hierarchical connectivity S^i_{jk}



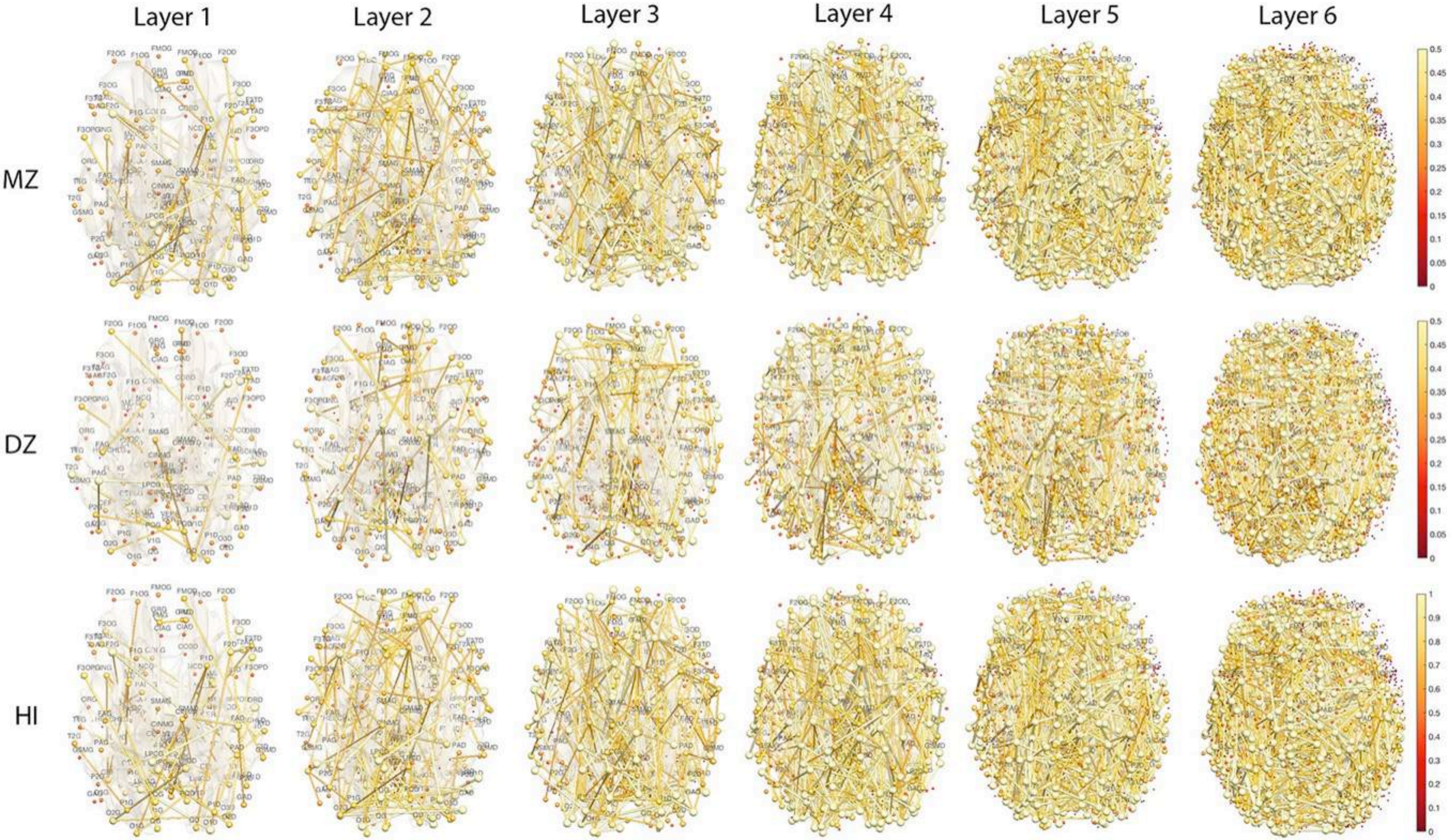


$$S^i_{jk} = \sum_{\mathbf{R}^{i+1}_l \subset \mathbf{R}^i_j} \sum_{\mathbf{R}^{i+1}_m \subset \mathbf{R}^i_k} S^{i+1}_{lm}$$

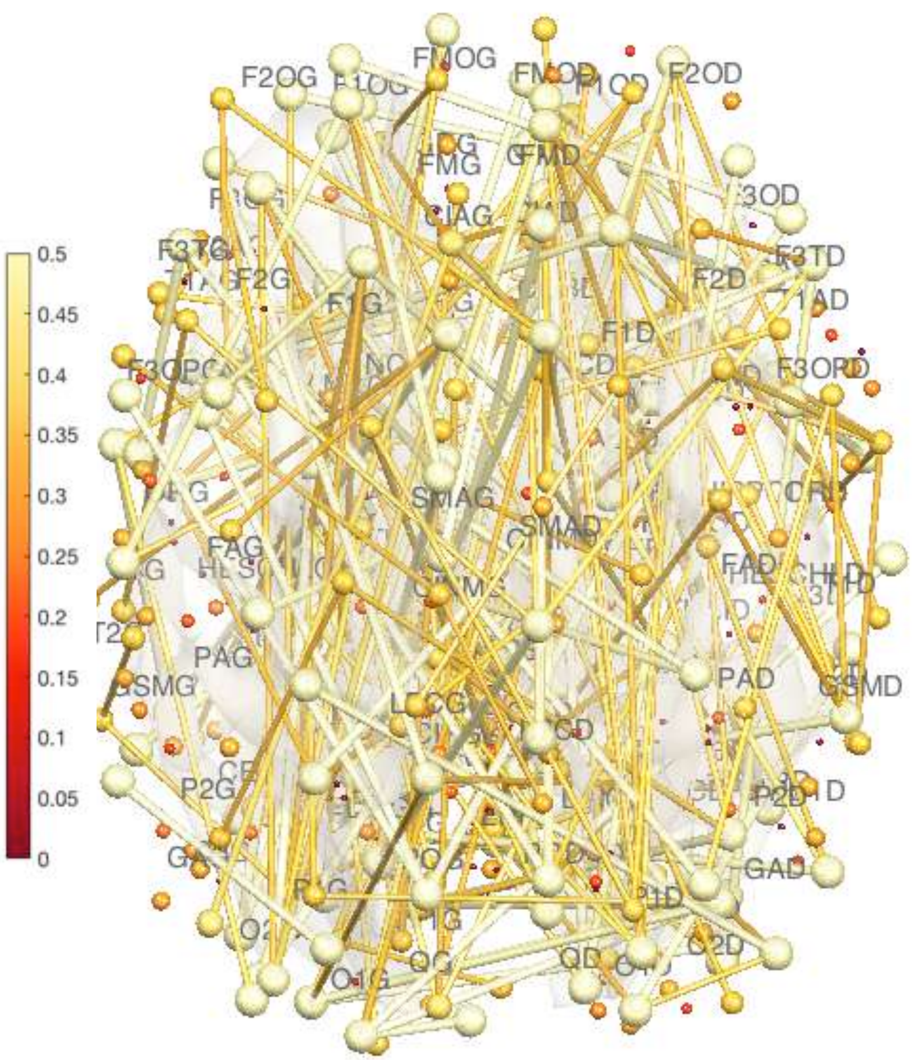
Hierarchical connectivity matrix



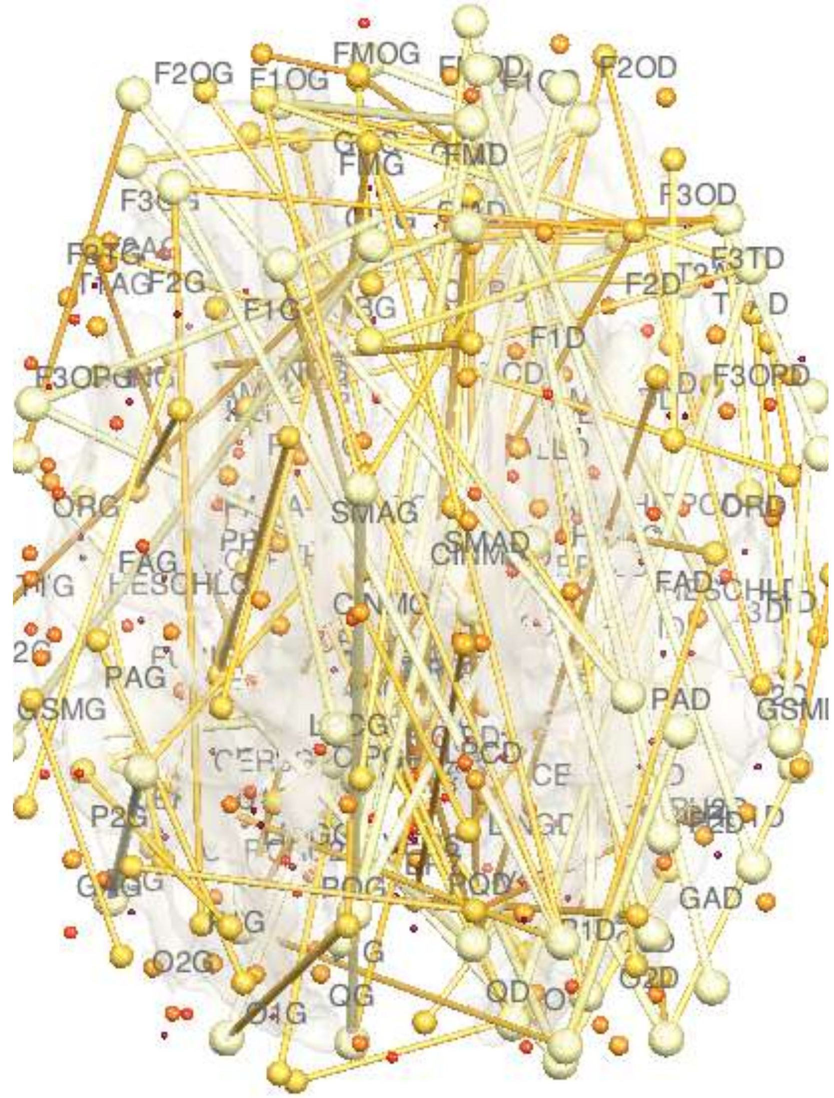
Twin correlations & heritability index



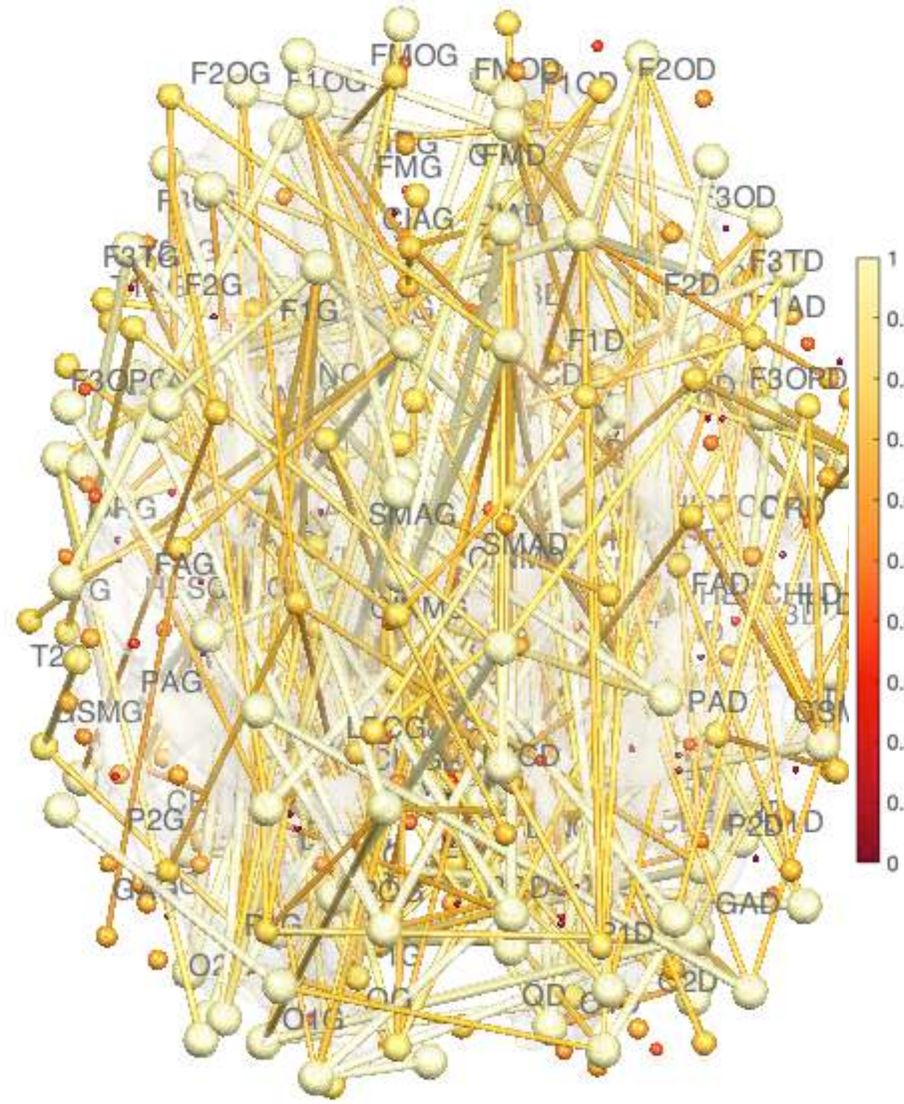
Twin correlations & heritability index (layer 3)



MZ

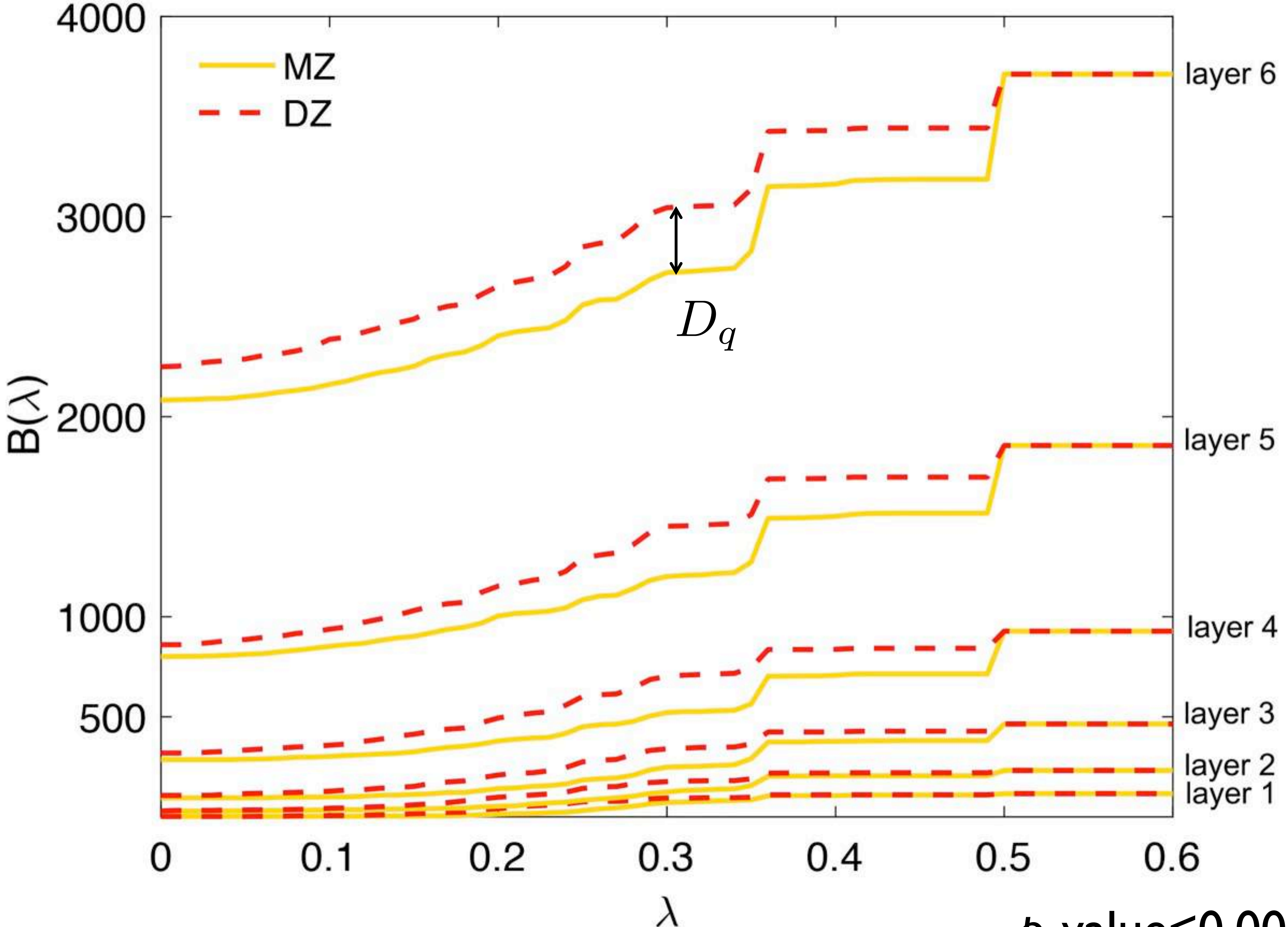


DZ



HI

Betti-0 plot (# of connected components)



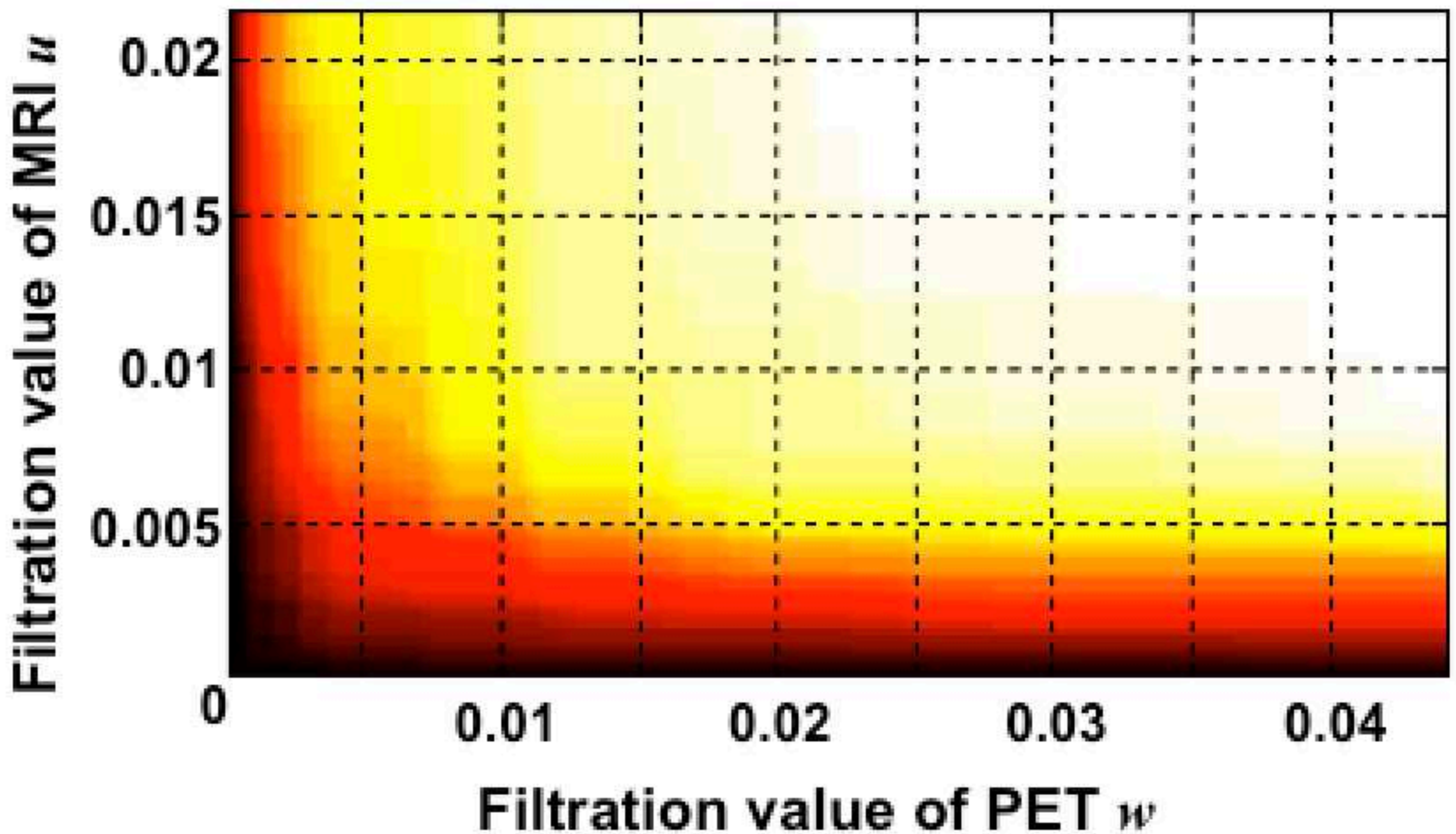
p-value<0.00001

More complex graph filtrations

◆ Human Brain Mapping 38:1387–1402 (2017) ◆

Integrated Multimodal Network Approach to PET and MRI Based on Multidimensional Persistent Homology

Hyekyoung Lee,[1,2] Hyejin Kang,[1,3] Moo K. Chung,[4,5] Seonhee Lim,[6] Bung-Nyun Kim,[7] and Dong Soo Lee[1,2*]



β_0 surface plot

Lee et al. 2017
HBM 38:1387-1402

Persistent Homology in Sparse Regression and Its Application to Brain Morphometry

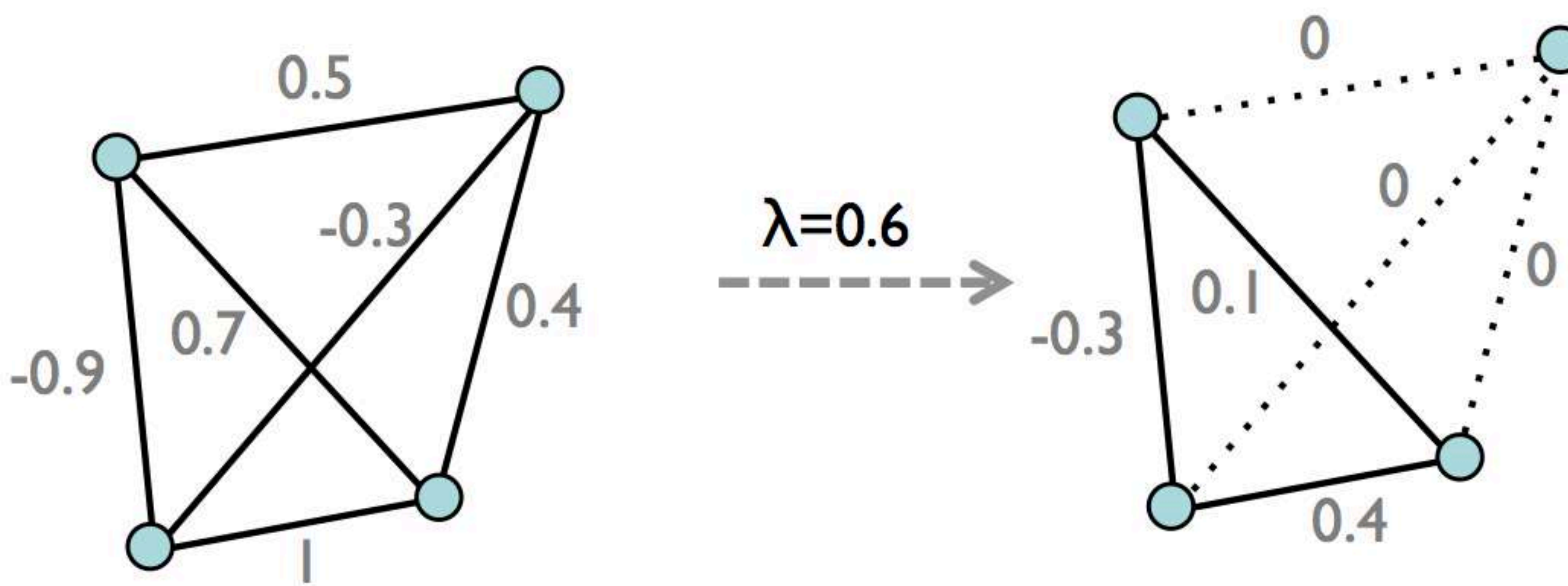
Moo K. Chung*, Jamie L. Hanson, Jieping Ye, Richard J. Davidson, and Seth D. Pollak

Abstract— tuning para How to choo difficult pro treating the persistent ho troduced ar in drastical soft-thresho used as mu (TBM) in cl have experi analyses re anatomical

Index Te mology, spa morphomet

nodeling the , [37], [38], his provides nivariate ap- ies, anatom- cal thickness re correlated], cross-cor- correlations, 6], [8], [30], es suffer the 73]. Specifi- y larger than mined linear icient and no

$$\widehat{\alpha} = \operatorname{argmin}_{\alpha} \ \frac{1}{2}\sum_{j}\sum_{k\neq j}\left\| x_j - \alpha_{jk}x_k \right\|^2 + \lambda\sum_{j,k}|\alpha_{jk}|$$

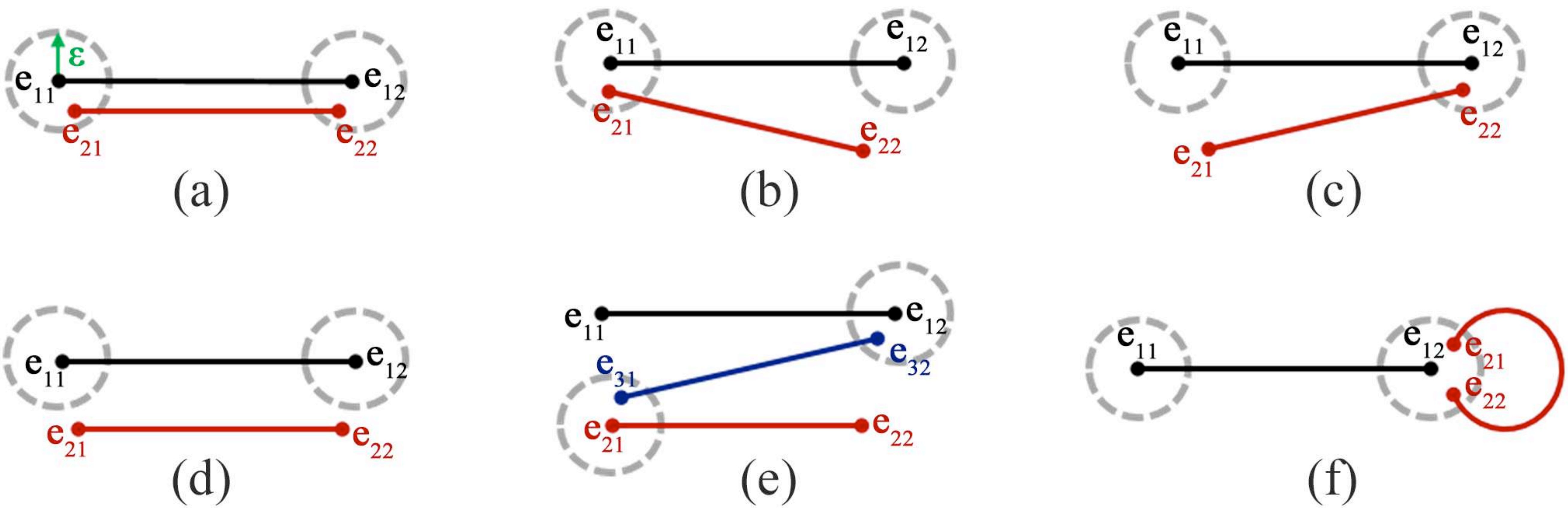


Chung et al. 2013 MICCAI 300-307

Chung et al. 2015 IEEE Transactions on Medical Imaging 34:1928-1939

Topological properties of the structural brain network constructed using the ε-neighbor method

Min-Hee Lee, Dong Youn Kim, Moo K. Chung*, Andrew L. Alexander and Richard J. Davidson



Chung et al. 2011 SPIE 79624G

Lee et al. 2018 IEEE Biomedical Engineering

Degree-Based Statistic and Center Persistency for Brain Connectivity Analysis

Kwangsun Yoo,[1,2] Peter Lee,[1,2] Moo K. Chung,[3] William S. Sohn,[1]
Sun Ju Chung,[4] Duk L. Na,[5,6] Daheen Ju,[1] and Yong Jeong[1,2*]

Center persistency (CP)

each cluster. The CP is calculated by obtaining the sum of the weighted degrees for the entire possible range of thresholds.

$$\mathrm{CP}_{\mathrm{v_i}} = \int w_{\mathrm{v_i}}(s)ds \approx \sum_n w_{\mathrm{v_i}}(s)\Delta s$$

Yoo et al. 2017 Human Brain Mapping 38:165-181

Persistent homological network distances

Chung et al. 2017
[Topological distances beweeen brain networks, Connectomics in NeuroImaging (CNI) 10511:161-170]

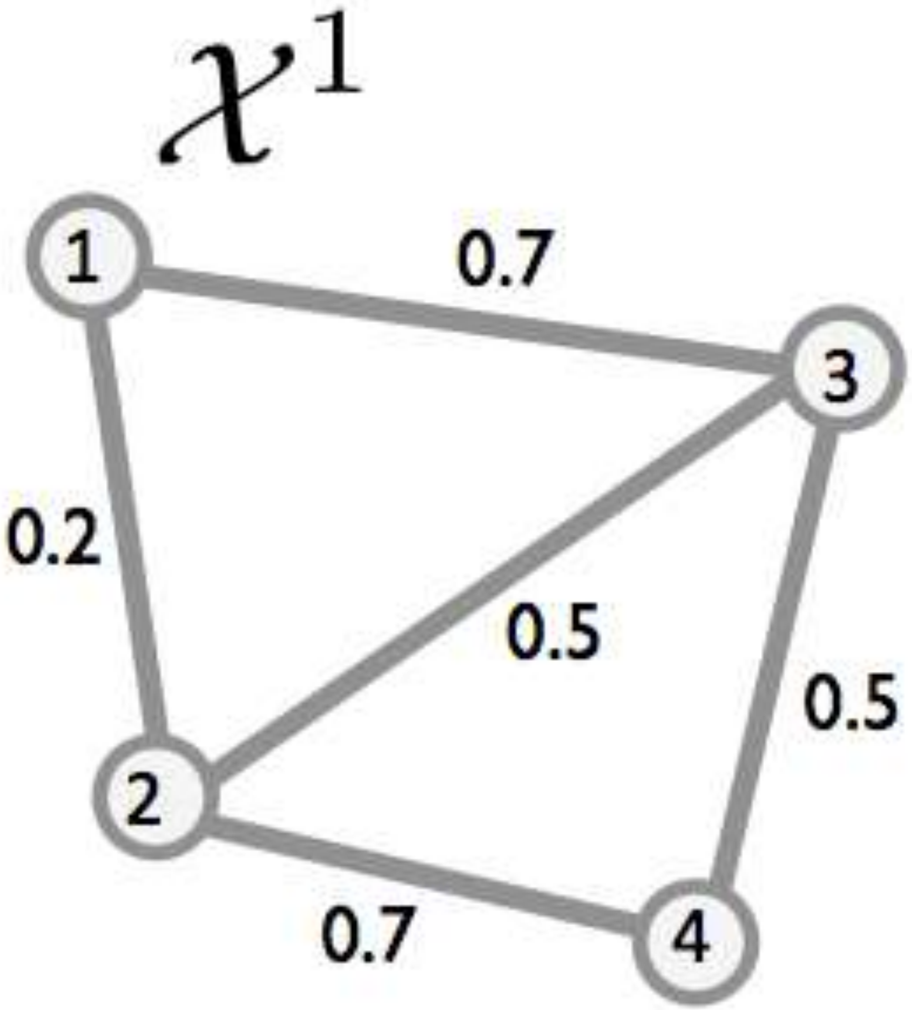
Matrix norm based distances

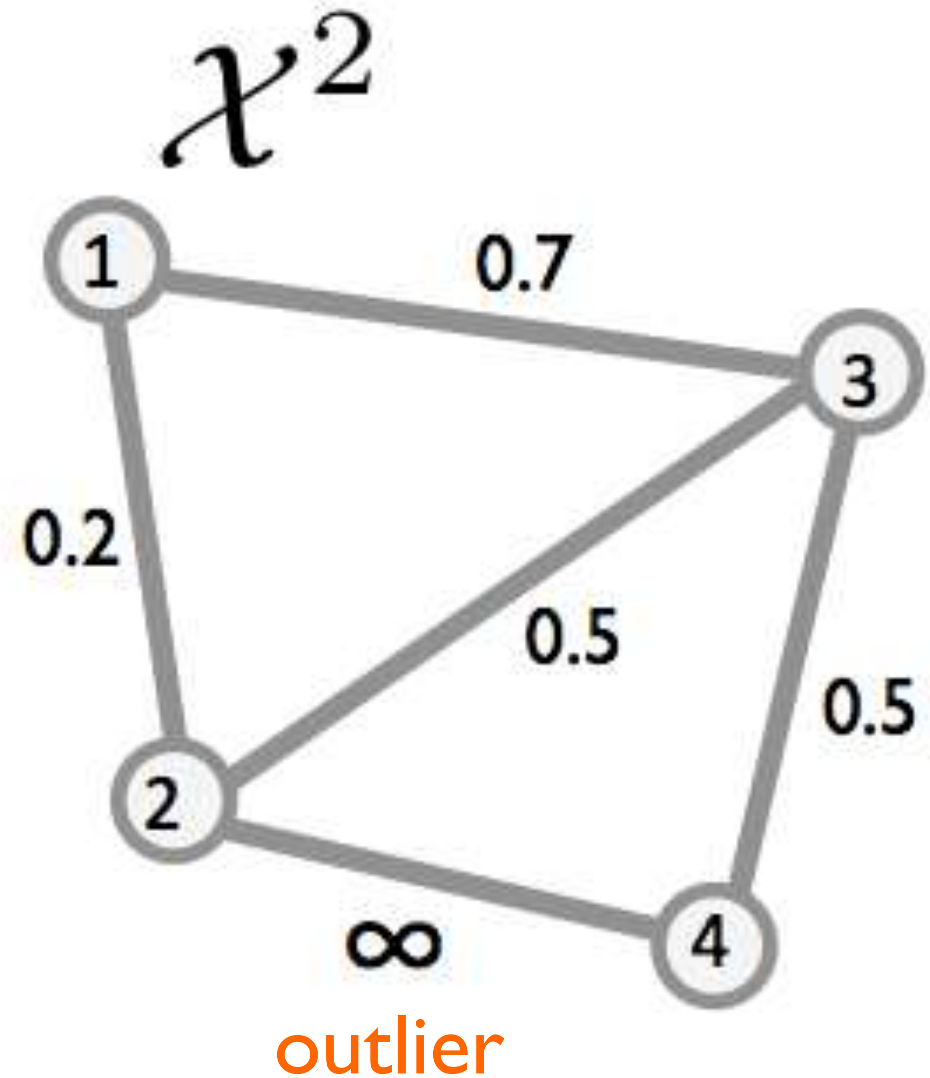
$$\mathcal{X}^1 = (V, w^1) \qquad \mathcal{X}^2 = (V, w^2)$$

$$D_l(\mathcal{X}^1, \mathcal{X}^2) = \Big(\sum_{i,j} |w^1_{ij} - w^2_{ij}|^l \Big)^{1/l}$$

$$D_\infty(\mathcal{X}^1, \mathcal{X}^2) = \max_{\forall i,j} |w^1_{ij} - w^2_{ij}|$$

Matrix norm fails!



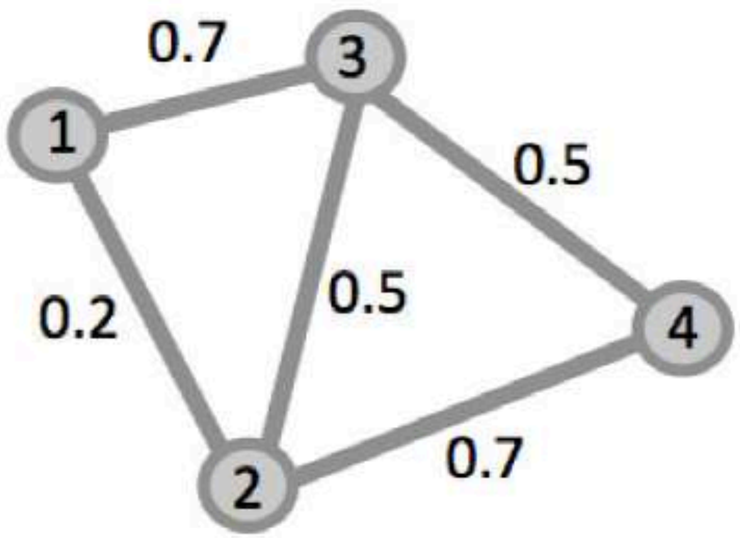


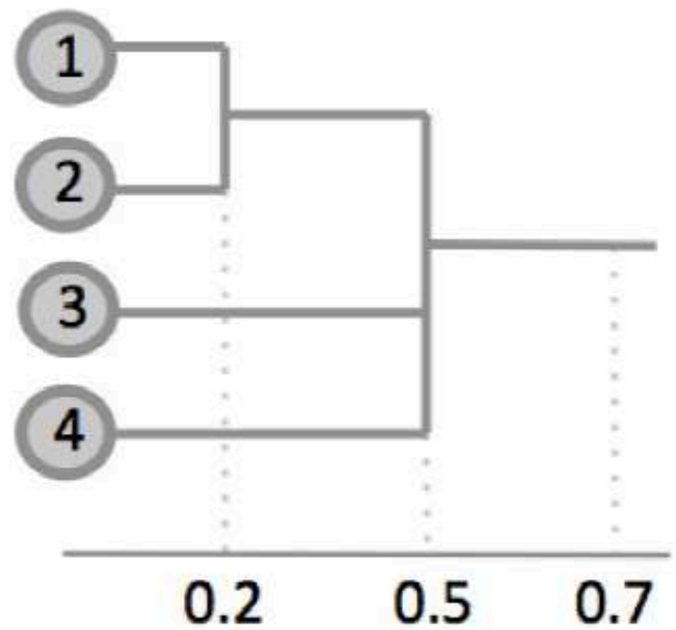
$$D_l(\mathcal{X}^1, \mathcal{X}^2) = \infty \qquad D_\infty(\mathcal{X}^1, \mathcal{X}^2) = \infty$$

Gromov-Hausdorff distance

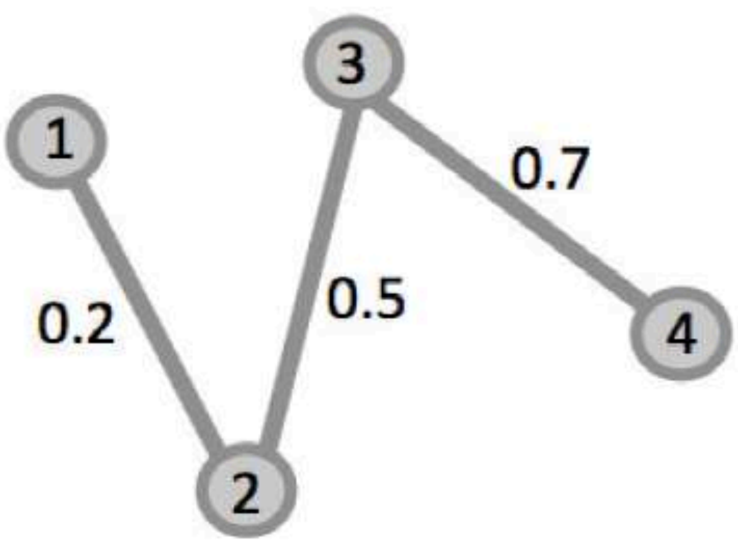
Lee et al., 2011 MICCAI 6892:302-309
Lee et al. 2012 IEEE Transactions on Medical Image 31:2267-2277

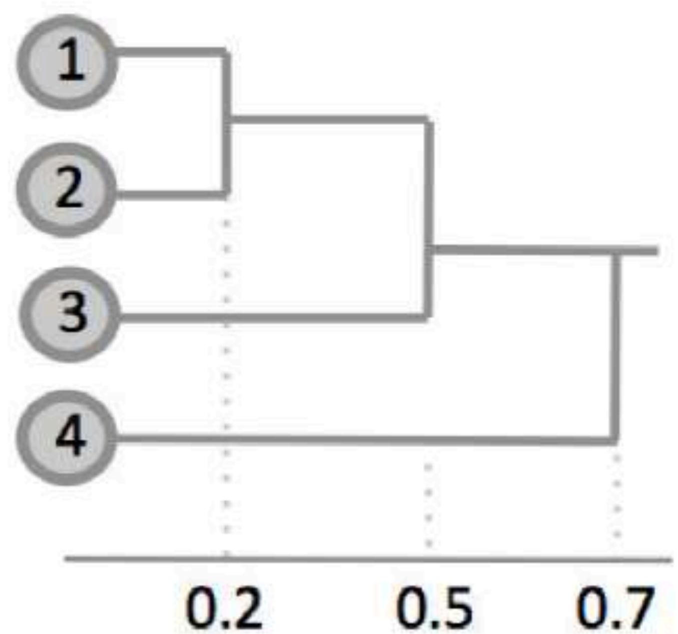
Single linkage distance (SLD)





$$
\begin{matrix}
0 & 0.2 & 0.5 & 0.5 \\
0.2 & 0 & 0.5 & 0.5 \\
0.5 & 0.5 & 0 & 0.5 \\
0.5 & 0.5 & 0.5 & 0
\end{matrix}
$$





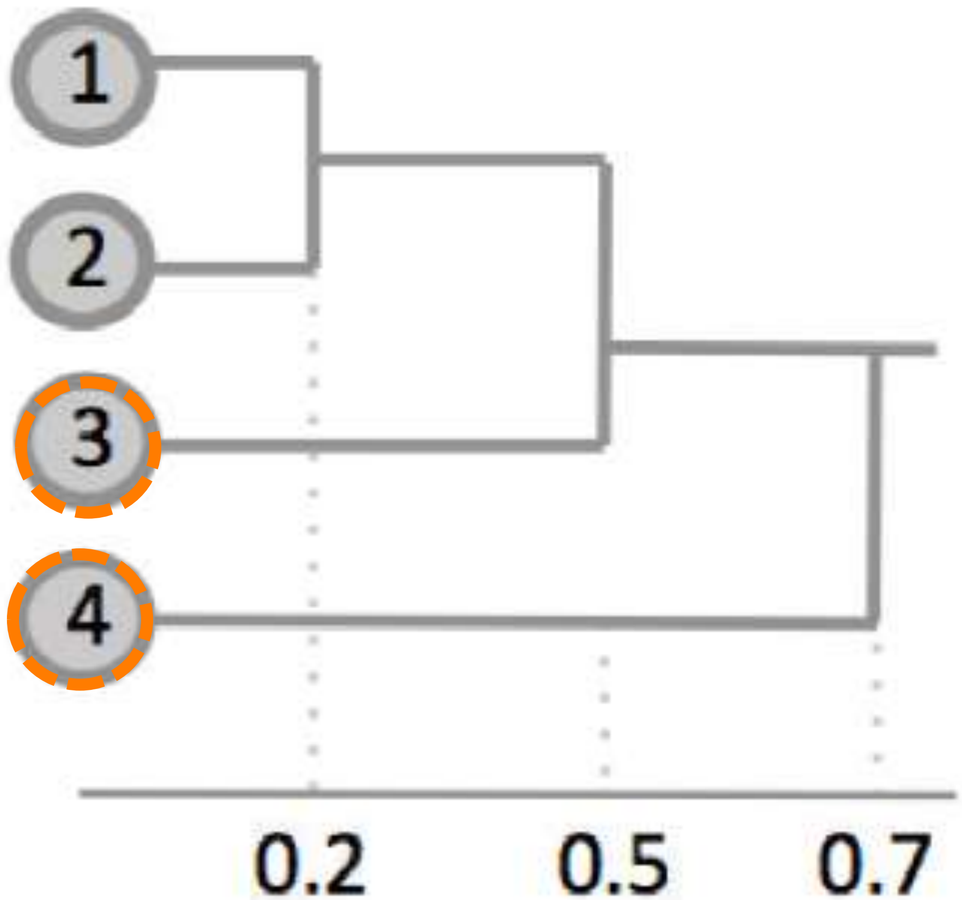
$$
\begin{matrix}
0 & 0.2 & 0.5 & 0.7 \\
0.2 & 0 & 0.5 & 0.7 \\
0.5 & 0.5 & 0 & 0.7 \\
0.7 & 0.7 & 0.7 & 0
\end{matrix}
$$

dendrogram

SLD $s = (s_{ij})$

Single linkage distance (SLD)

ultrametric $\quad s_{ij} \leq \max(s_{ik}, s_{kj})$

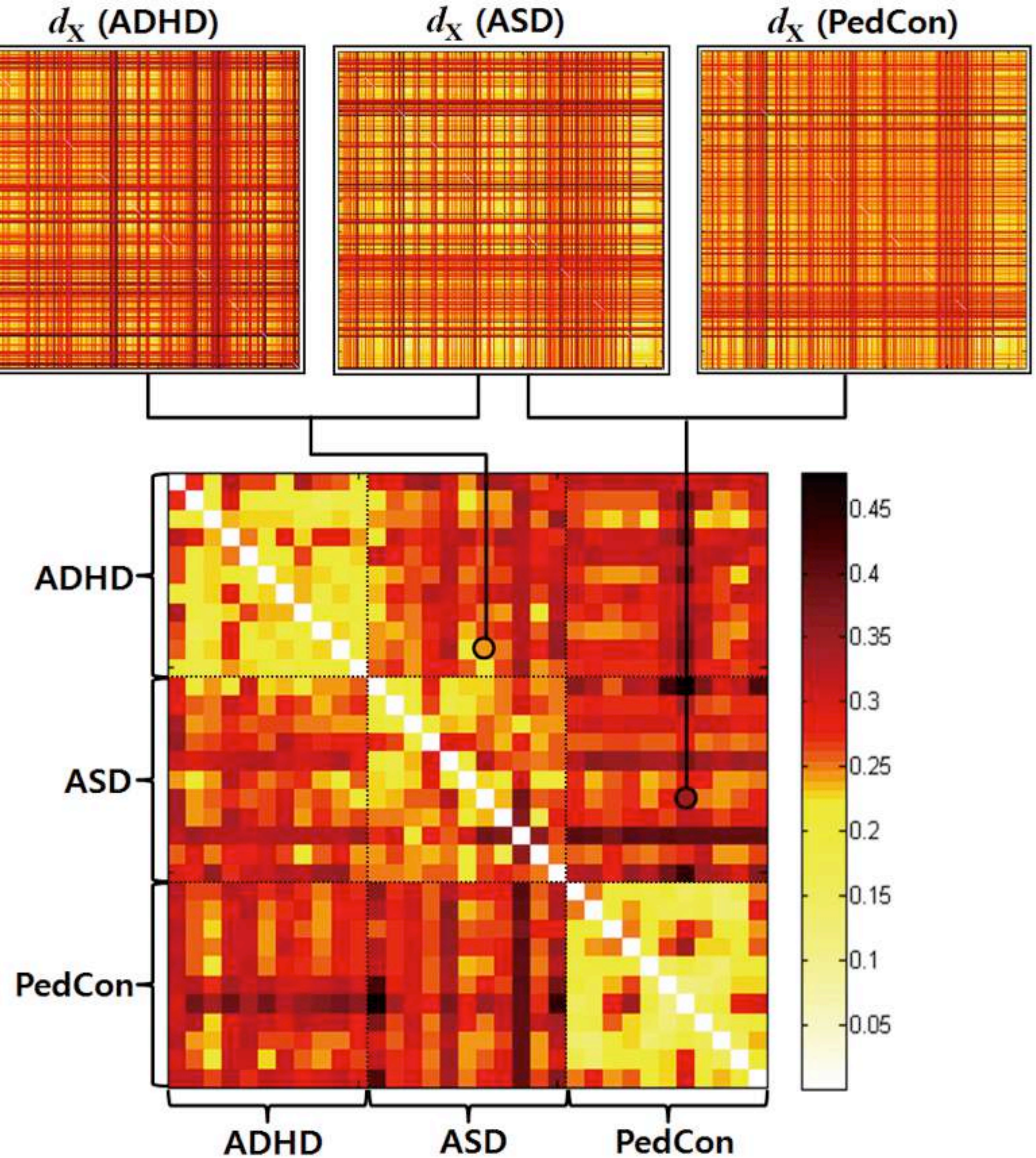


$$\begin{array}{cccc} 0 & 0.2 & 0.5 & 0.7 \\ 0.2 & 0 & 0.5 & 0.7 \\ 0.5 & 0.5 & 0 & 0.7 \\ 0.7 & 0.7 & 0.7 & 0 \end{array}$$

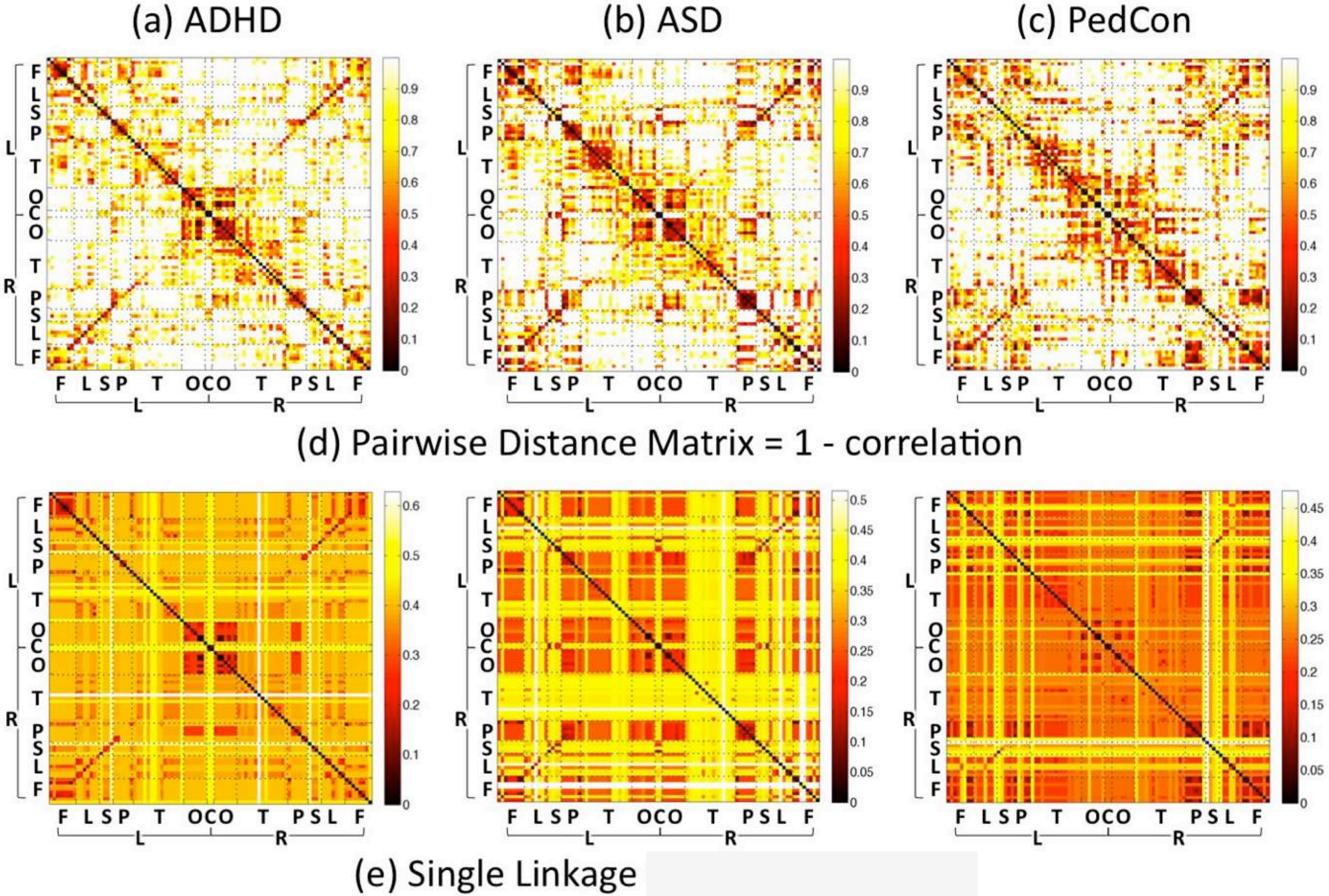
Gromov-Hausdorff distance between networks

Single linkage distance

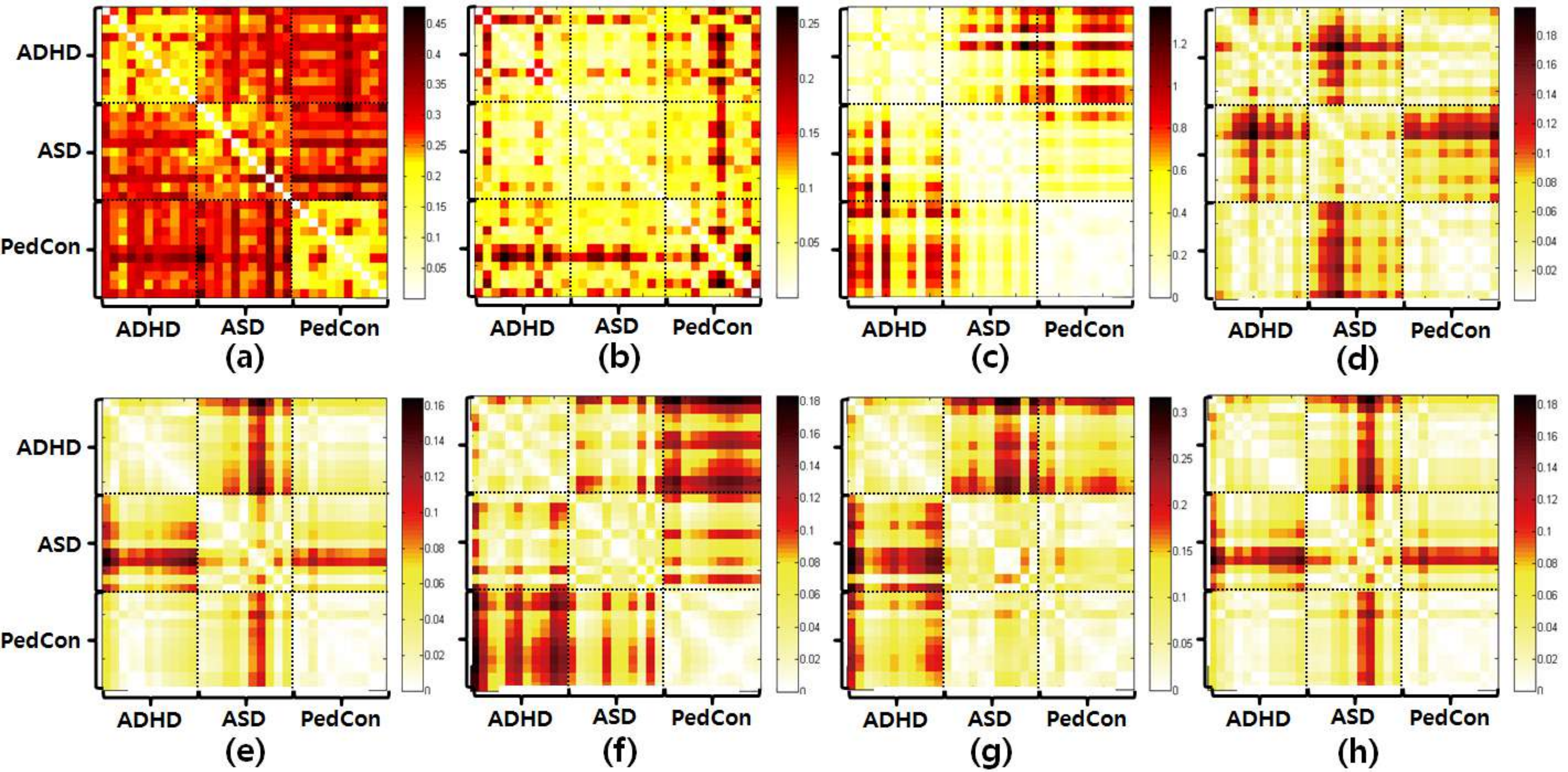
$$D_{GH}(\mathcal{D}^1, \mathcal{D}^2) = \frac{1}{2} \max_{\forall i,j} |s^1_{ij} - s^2_{ij}|$$



Connectivity matrix of brain network

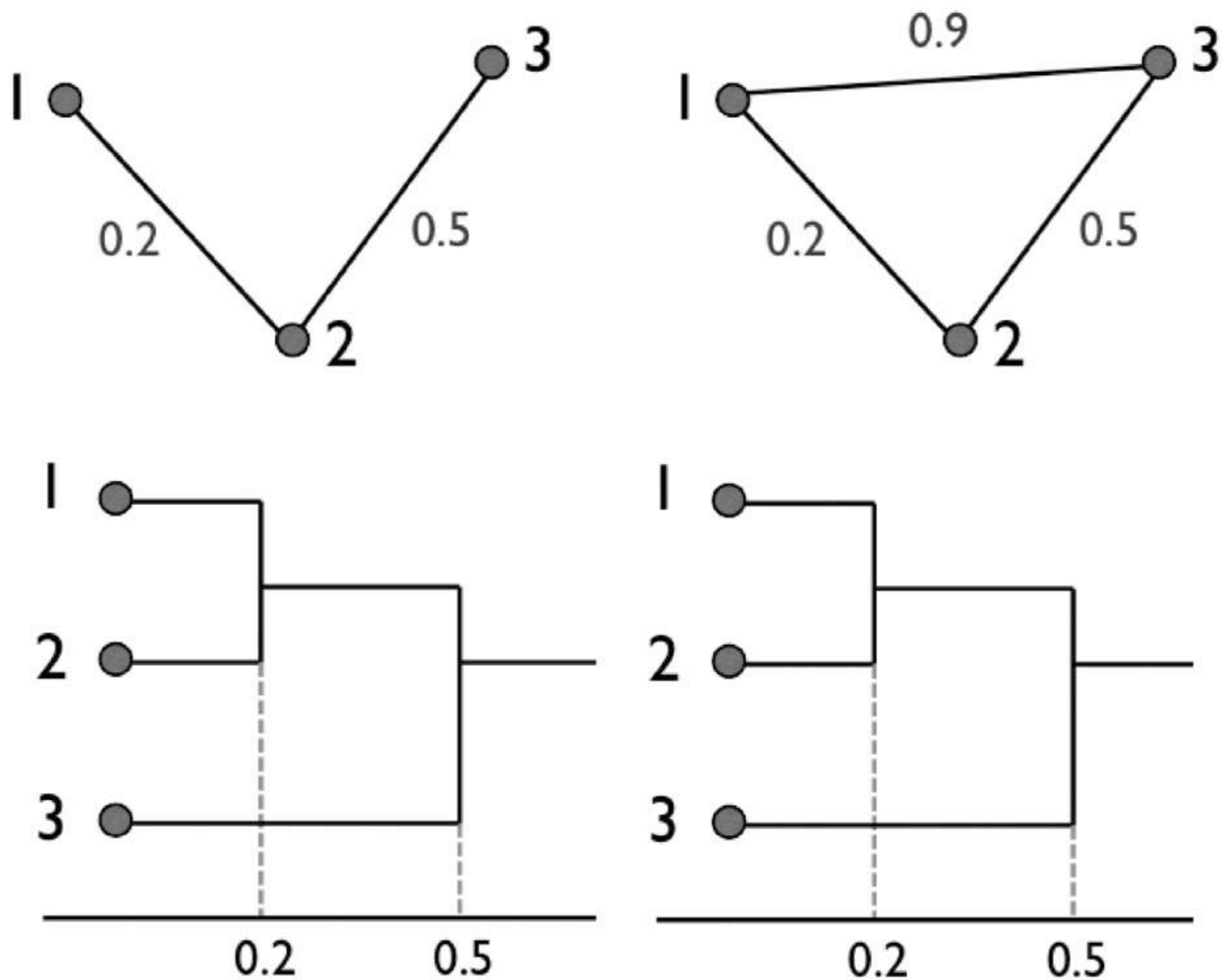


Clustering accuracy on PET correlation network



	GH	bottleneck	slope	modularity	clustering coeff.	char. path length	small-worldness	transitivity
avg.	0.9630	0.5112	0.8306	0.6106	0.6118	0.6558	0.6349	0.5512
std.	0.0655	0.0827	0.1428	0.0761	0.1341	0.1027	0.1065	0.1353

Limitation of GH-distance

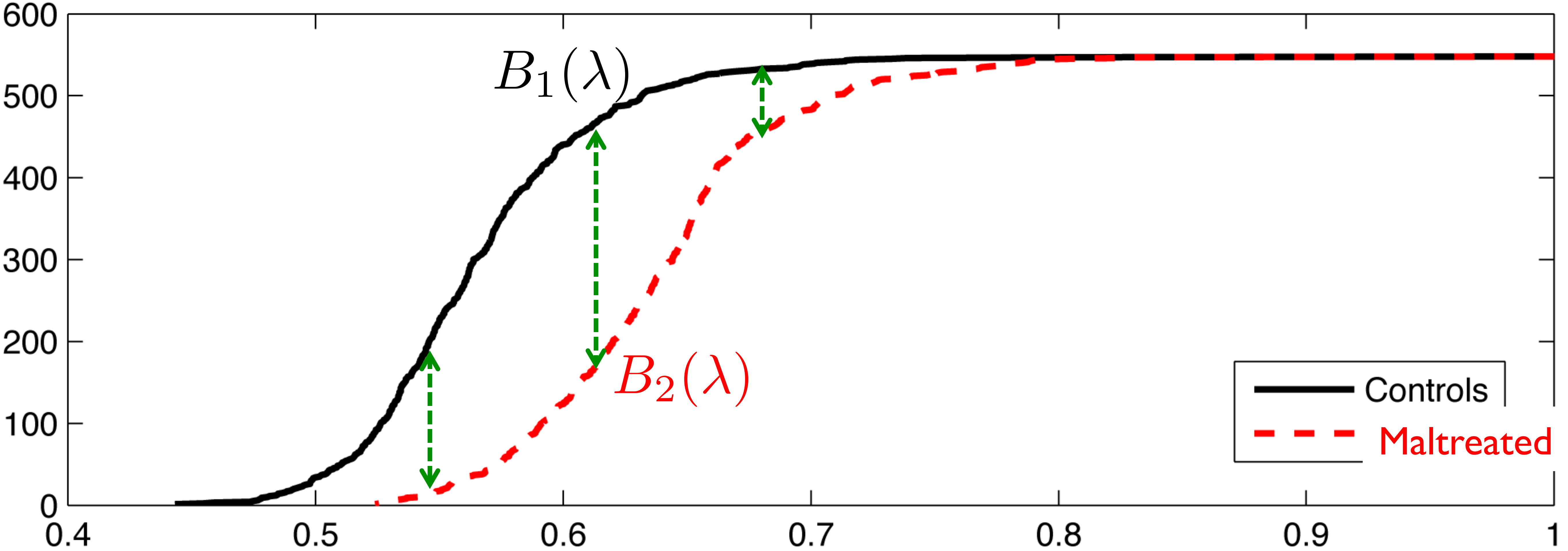


Need to design new topological distances

Kolmogorov-Smirnov (KS) distance

Chung, M.K. et al. 2017
[Exact topological inference for paired brain networks via persistent homology. Information Processing in Medical Imaging (IPMI) 10265:299-310]

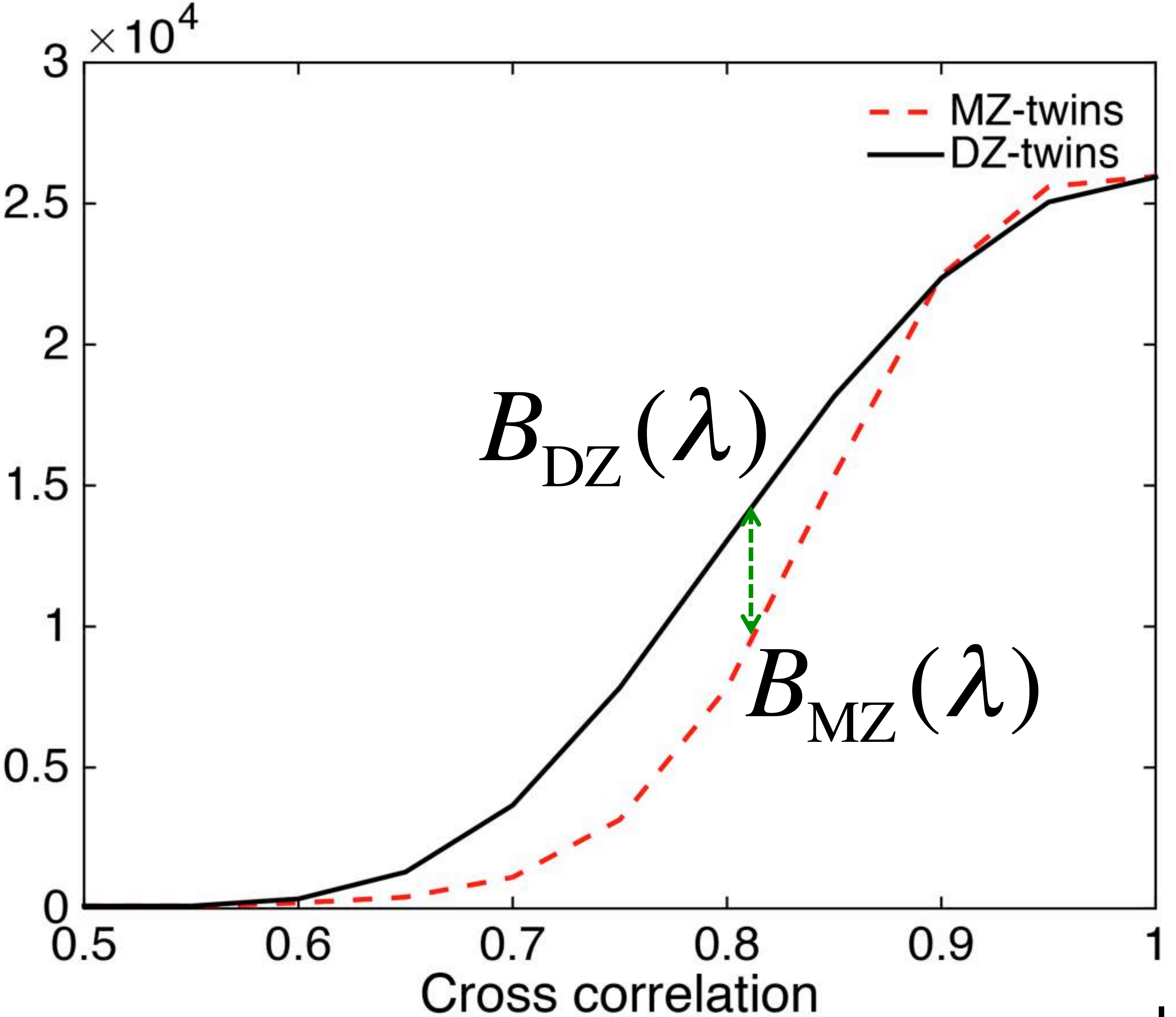
Betti-0 plot on FA correlations



KS-distance: $\max_{\lambda} |B_1(\lambda) - B_2(\lambda)|$

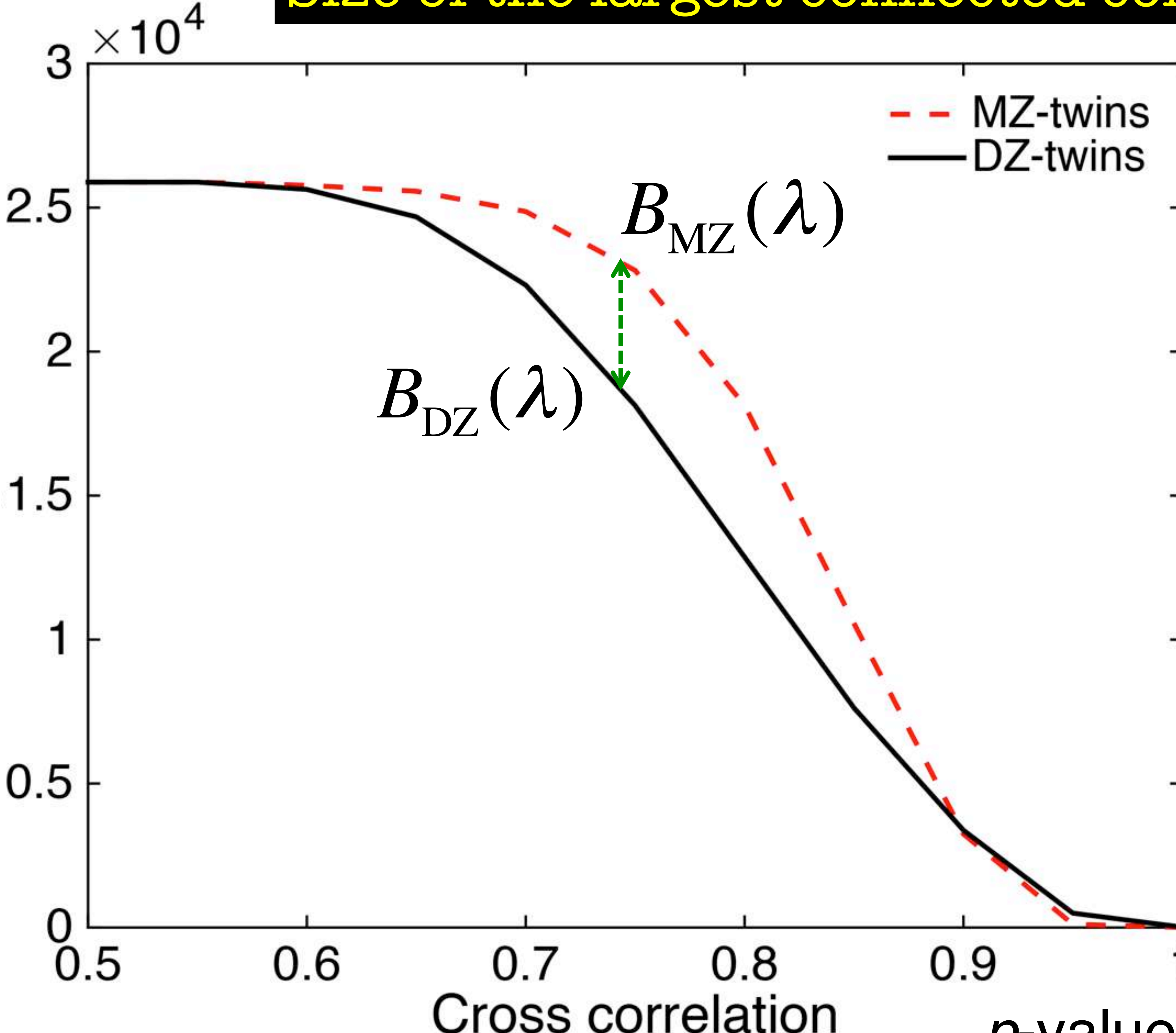
p-value <0.0001

Number of connected components



p-value < 0.0002

Size of the largest connected component



p-value < 0.0001

Exact permutation test

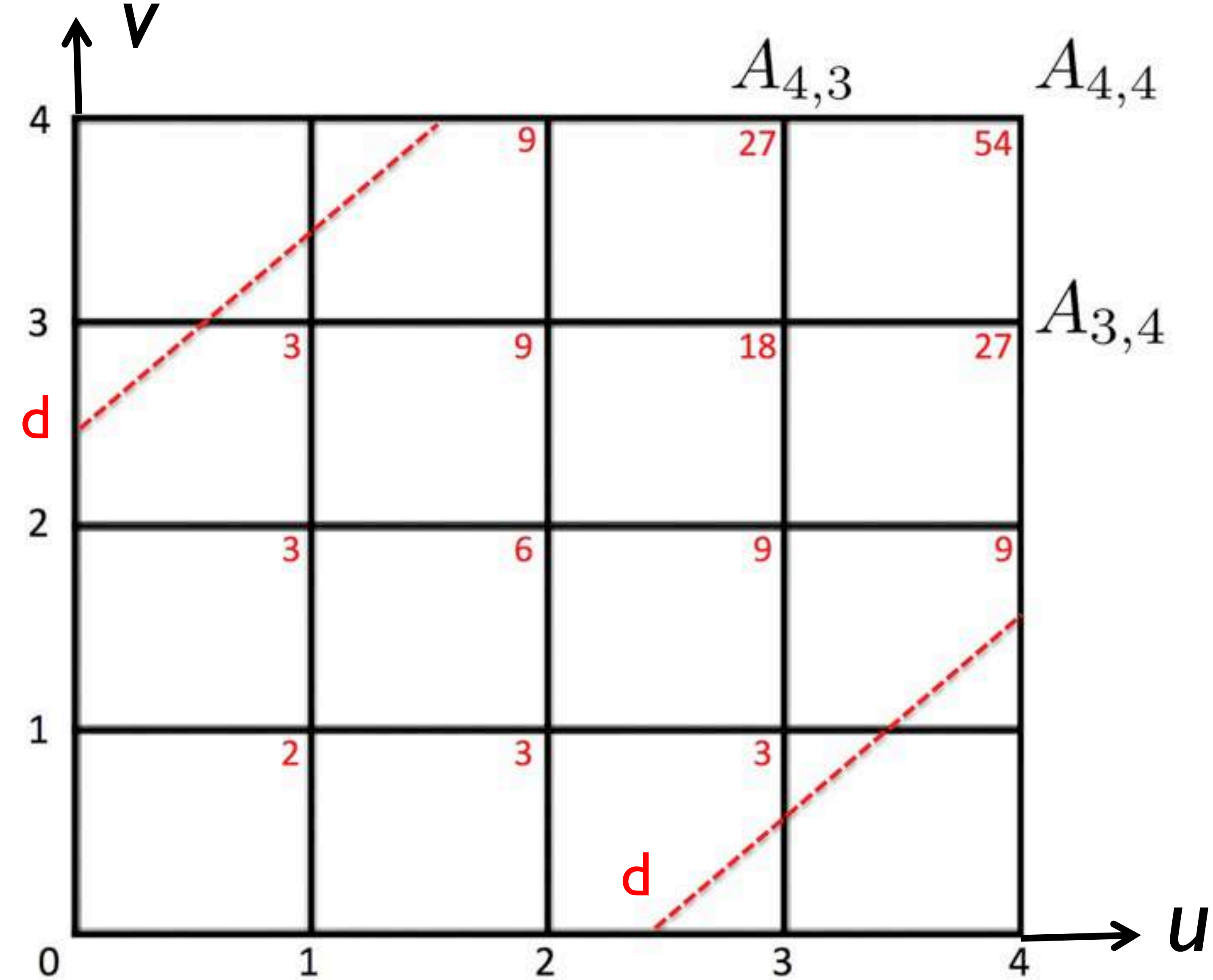
Theorem 1.

$$D_q = \sup_{1 \le j \le q} \left| B(G^1_{\lambda_j}) - B(G^2_{\lambda_j}) \right|$$

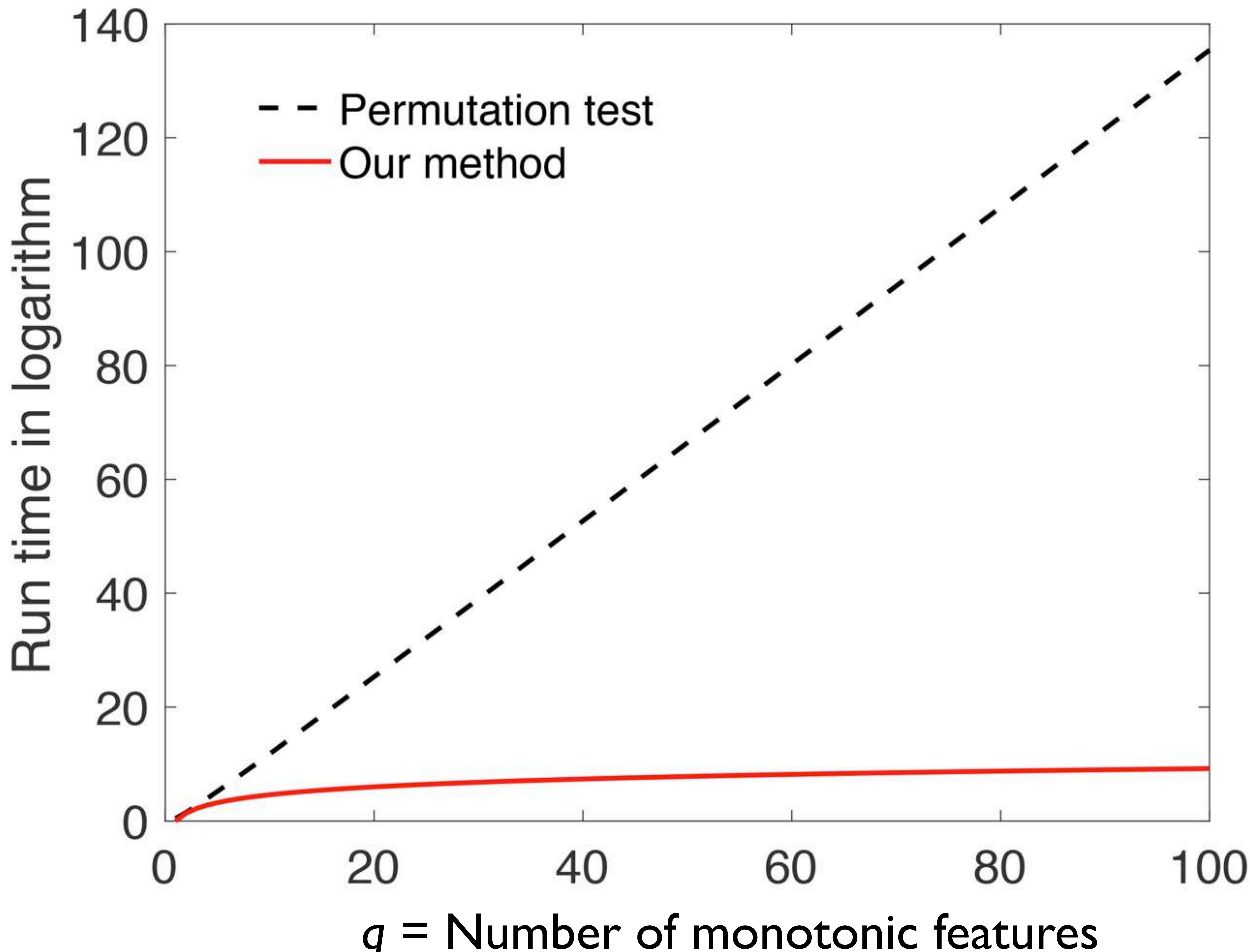
$$P(D_q \ge d) = 1 - \frac{A_{q,q}}{\binom{2q}{q}}$$

$$A_{u,v} = A_{u-1,v} + A_{u,v-1}$$

$$|u - v| < d$$



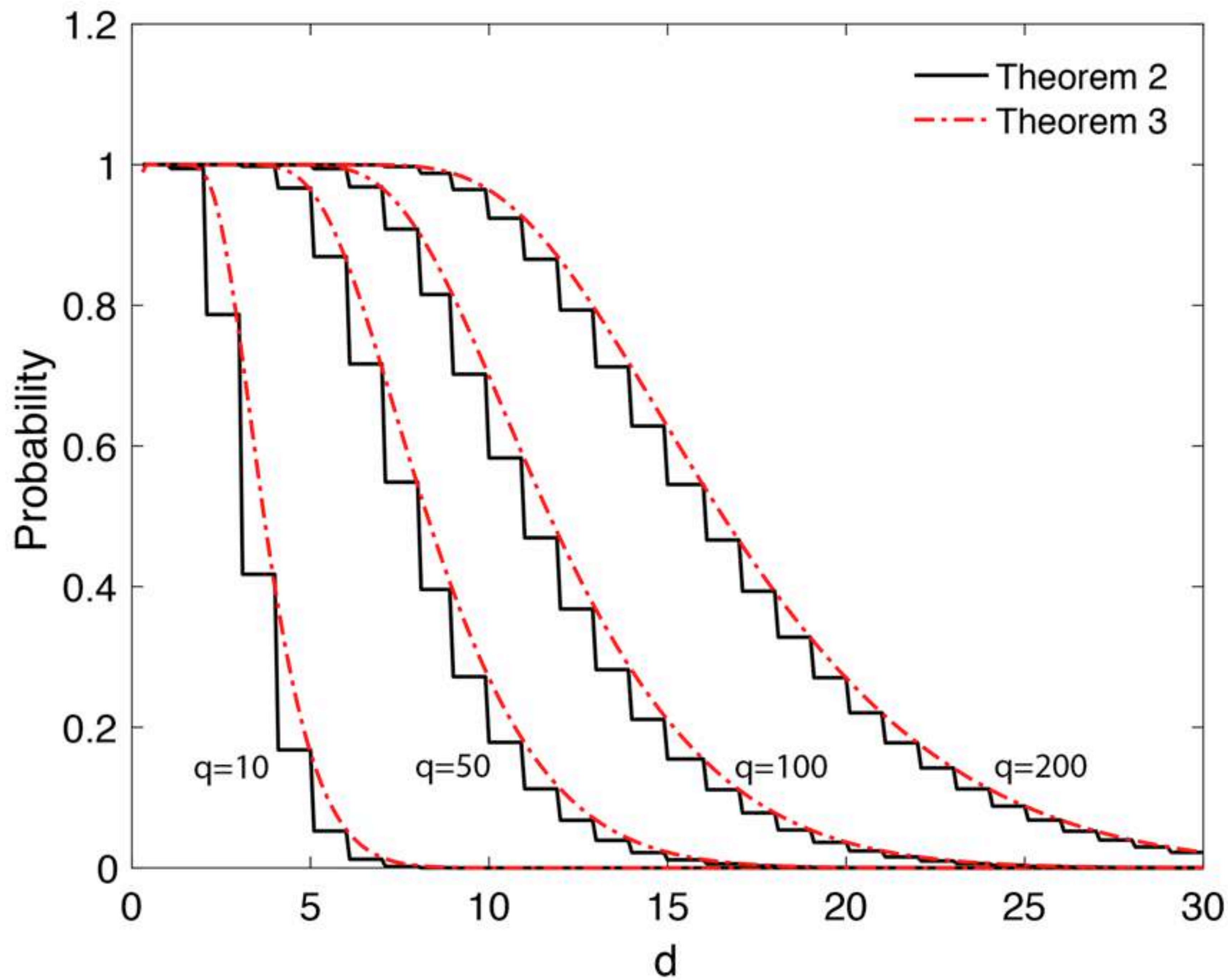
MATLAB codes: www.stat.wisc.edu/~mchung/twins



Permutation test
Our method
Run time in logarithm
0
20
40
60
80
100
120
140
0
20
40
60
80
100
q = Number of monotonic features

Theorem 2.

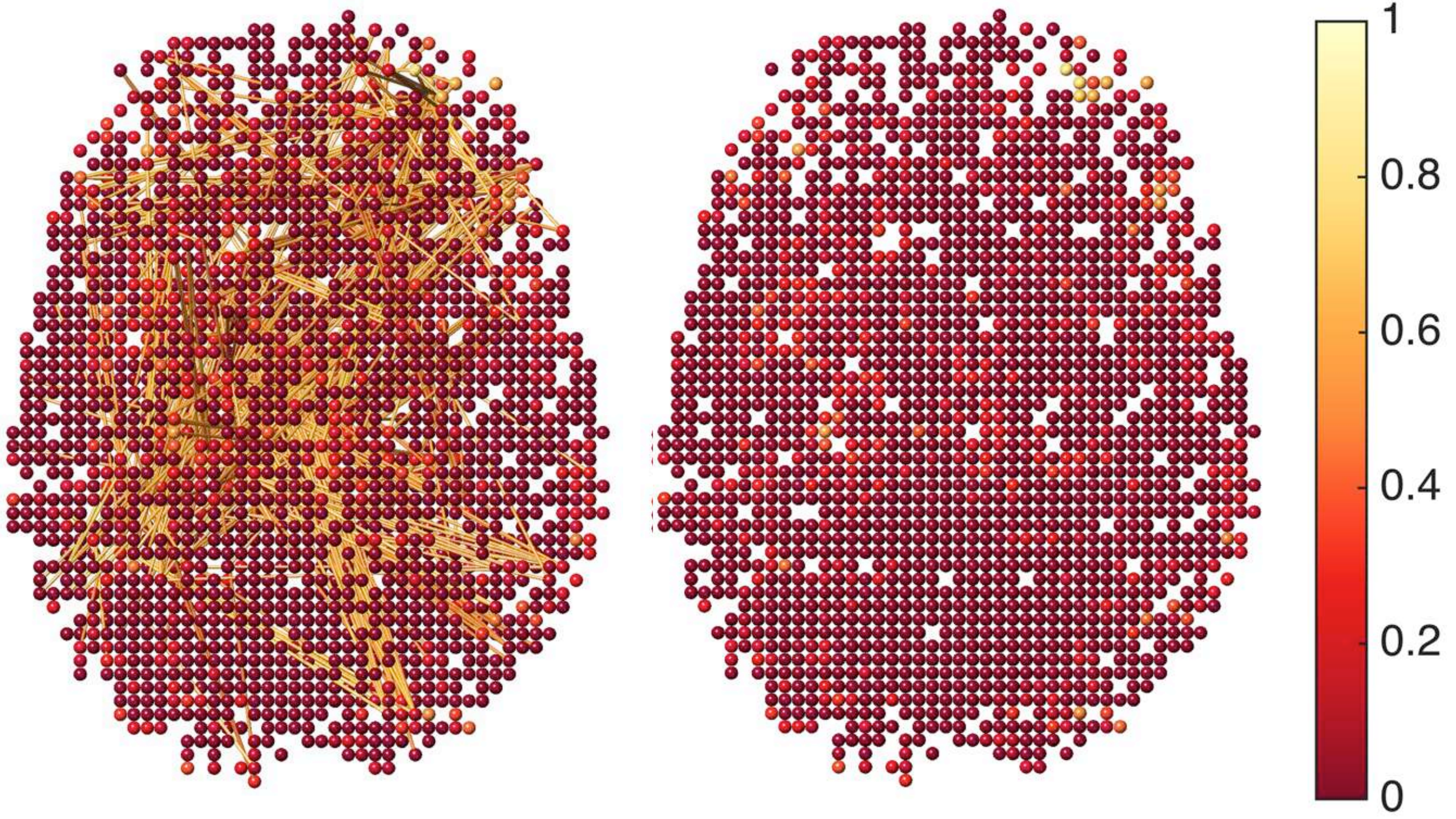
$$\lim_{q\to\infty} P\left(D_q/\sqrt{2q} \geq d\right) = 2\sum_{i=1}^{\infty}(-1)^{i-1}e^{-2i^2d^2}$$



MATLAB codes:
www.stat.wisc.edu/~mchung/twins

Validations

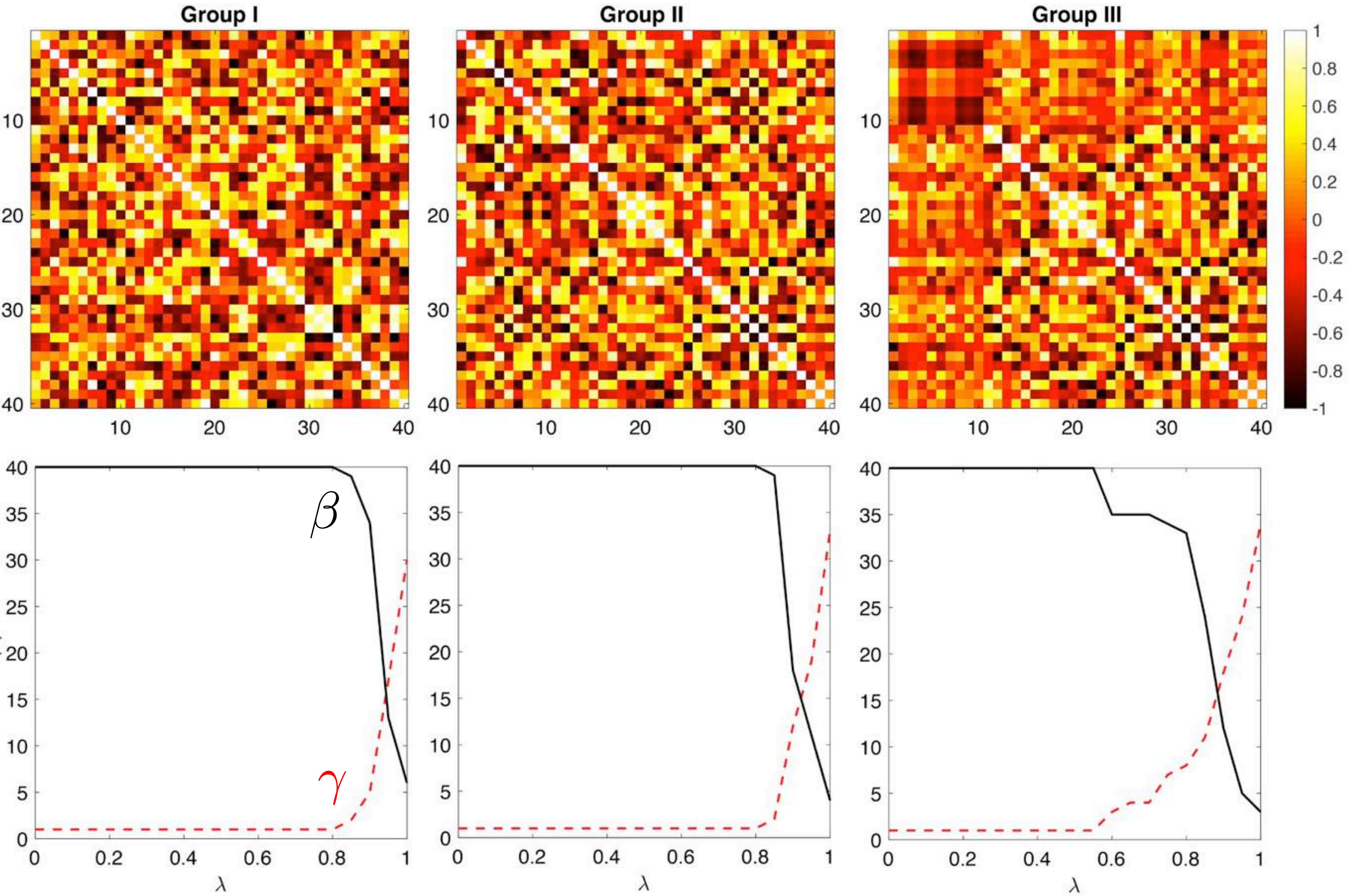
Null data check:
Network of random pairs in two group comparison



parameter 0.5

parameter 0.7

Random graph simulations



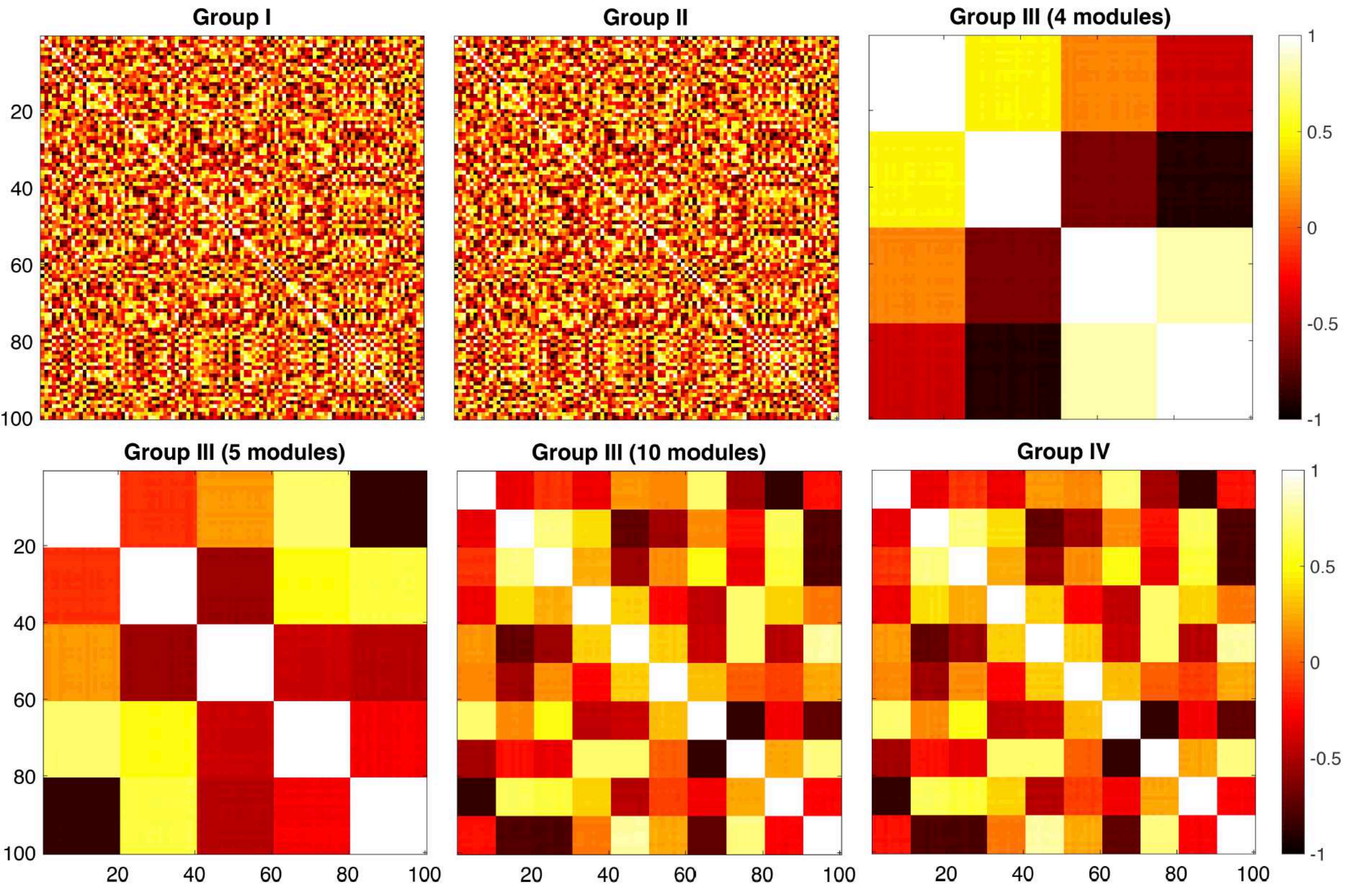
Simulating modular structure

$$\mathbf{x}_i = N(0, I)$$

$$\mathbf{y}_i = 0.5\mathbf{x}_{ci+1} + N(0, \sigma^2 I)$$

module size:
c number of nodes

Simulations on modular structures



p-values on network distances

	Modules	L_1	L_2	L_∞	GH	KS (β_0)	KS (γ)
No diff.	0 vs. 0	0.93	0.93	0.93	0.87	1.00	1.00
	4 vs. 4	0.89	0.89	0.90	0.86	0.87	0.88
Diff.	4 vs. 5	0.14	0.06	0.03	0.29	0.07^{**}	0.07^{**}
	5 vs. 10	0.47	0.19	0.10	0.33	0.01	0.06^{*}

$*$ = $\times 10^{-3}$

$**$ = $\times 10^{-4}$