Brain network Modeling via Graph Filtration

Moo K. Chung

Department of Biostatistics and Medical Informatics
Waisman Laboratory for Brain Imaging and Behavior
University of Wisconsin-Madison

Department of Brain and Cognitive Sciences
Seoul National University
www.stat.wisc.edu/~mchung

Acknowledgement

Daniel J. Kelley, Nagesh Adluru, Kim M. Dalton,
Jamie Hanson, Andrew L. Alexander,
Seth Pollack, Richard J. Davidson
University of Wisconsin-Madison

Hyekyoung Lee, Hyejin Kang,
Boong-Nyun Kim, Dong Soo Lee
Seoul National University

Abstract

Brain connectivity has been usually modeled as a network graph. The whole brain region can be parcellated into disjoint regions, which serve as the nodes of the network. fMRI and DTI provide additional information of how one region is connected to another via a connectivity matrix. The connectivity matrix is then thresholded to produce a binarized adjacency matrix, which is further used in constructing a graph.

However, there is no gold standard for brain parcellation, which makes the identification of node depend on the choice of parcellation. Depending on the scale of parcellation, the parameters of graph, which characterize graph topology, vary considerably up to 95%. Another problem of the parcellation is the arbitrariness of thresholding connectivity matrix. The topological parameters such as sparsity and clustering coefficients change substantially depending on the level of threshold.

The problems of parcellation and the subsequent arbitrary thresholding can be avoided if we do not use any parcellation or thresholding in building the network. So the question is whether if it is possible to construct a network graph without the usual parcellation scheme. In this talk, we present a novel network graph modeling technique called the epsilon-neighbor and graph filtration methods that avoid parcellation and the subsequent thresholding of the connectivity matrix.

Motivation

Press Release • July 16, 2009

NIH Launches the Human Connectome Project to Unravel the Brain's Connections

The National Institutes of Health Blueprint for Neuroscience Research is launching a $30 million project that will use cutting-edge brain imaging technologies to map the circuitry of the healthy adult human brain. By systematically collecting brain imaging data from hundreds of subjects, the Human Connectome Project (HCP) will yield insight into how brain connections underlie brain function, and will open up new lines of inquiry for human neuroscience.

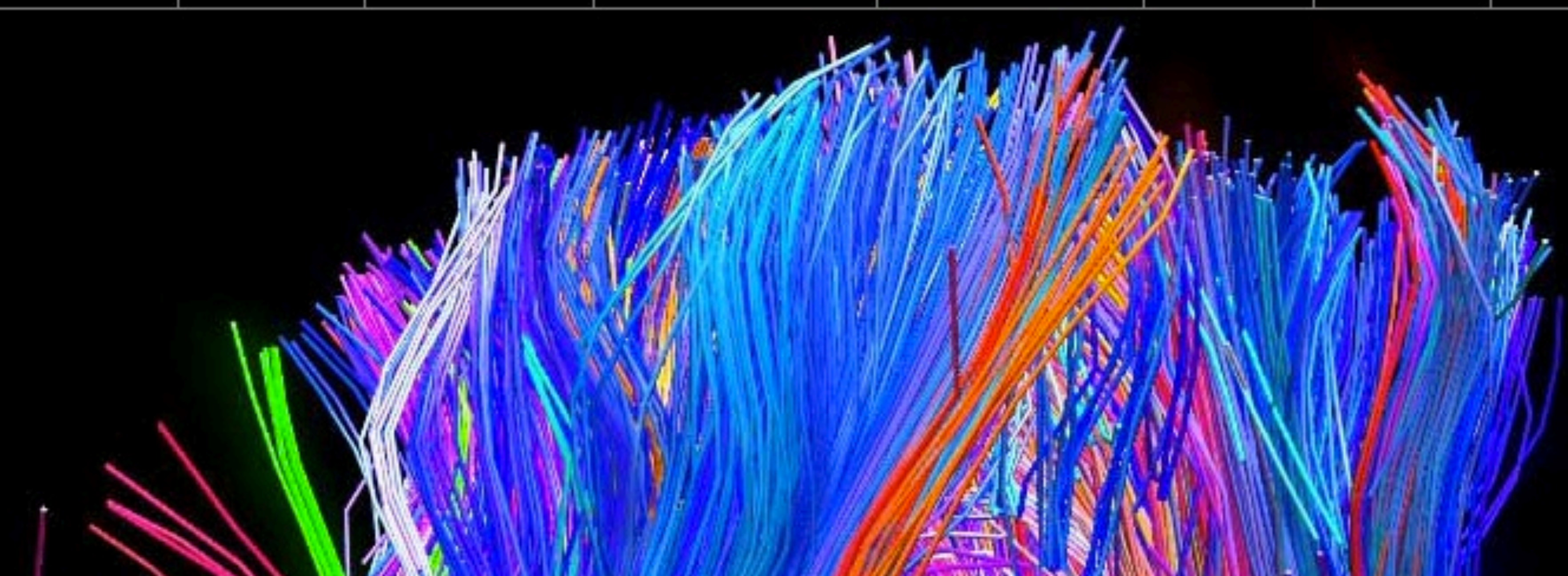
www.humanconnectomeproject.org

The NIH Human Connectome Project | Harvard/MGH-UCLA Consortium | WU-Minn Consortium | Neuroscience Blueprint

Human Connectome Project

Enter search keyword

Home | Overview | Collaborators | Publications | Data | Links | Contact



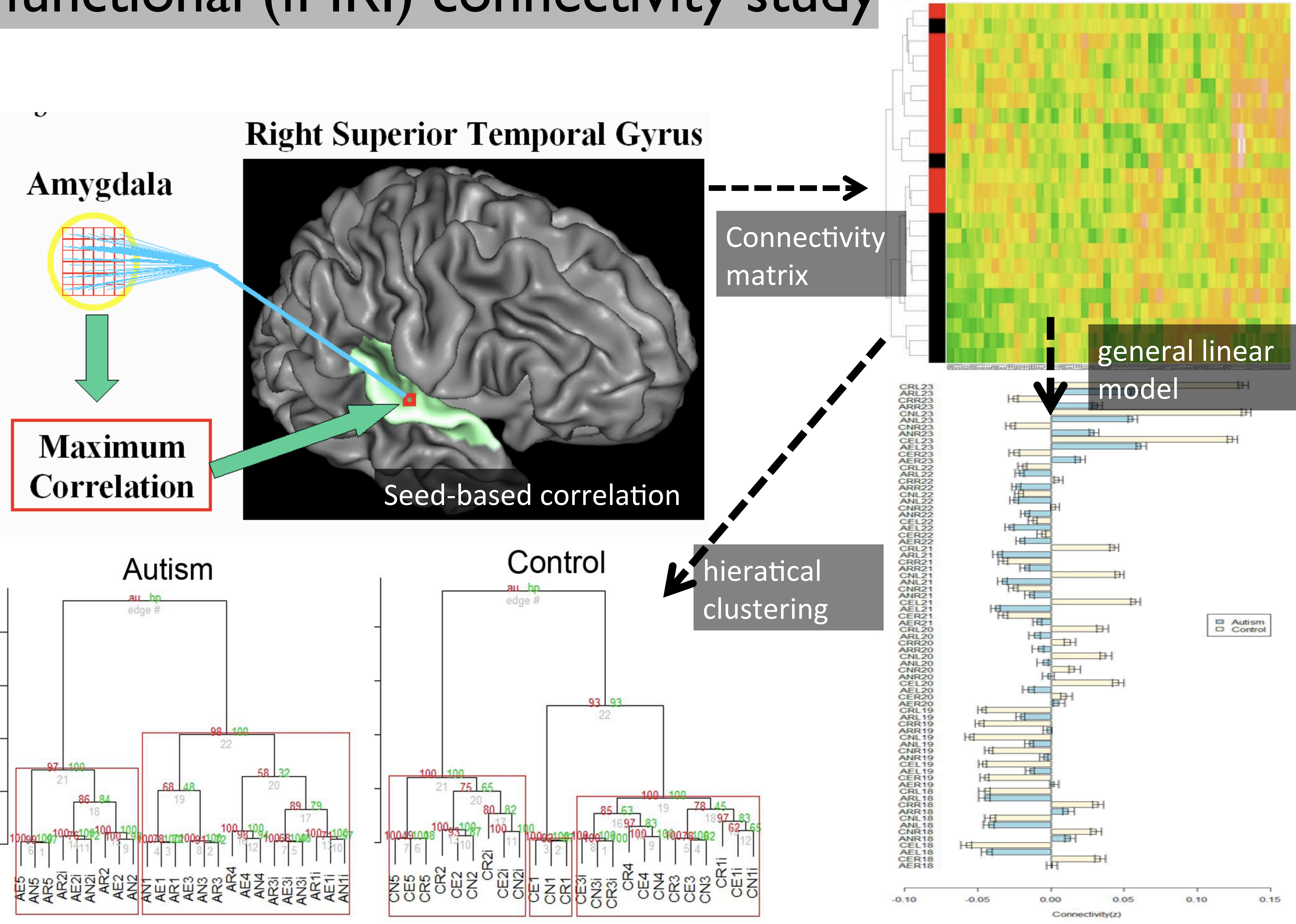
The Human Connectome Project

Navigate the brain in a way that was never before possible; fly through major brain pathways, compare essential circuits, zoom into a region to explore the cells that comprise it, and the functions that depend on it.

The Human Connectome Project aims to provide an unparalleled compilation of neural data, an interface to graphically navigate this data and the opportunity to

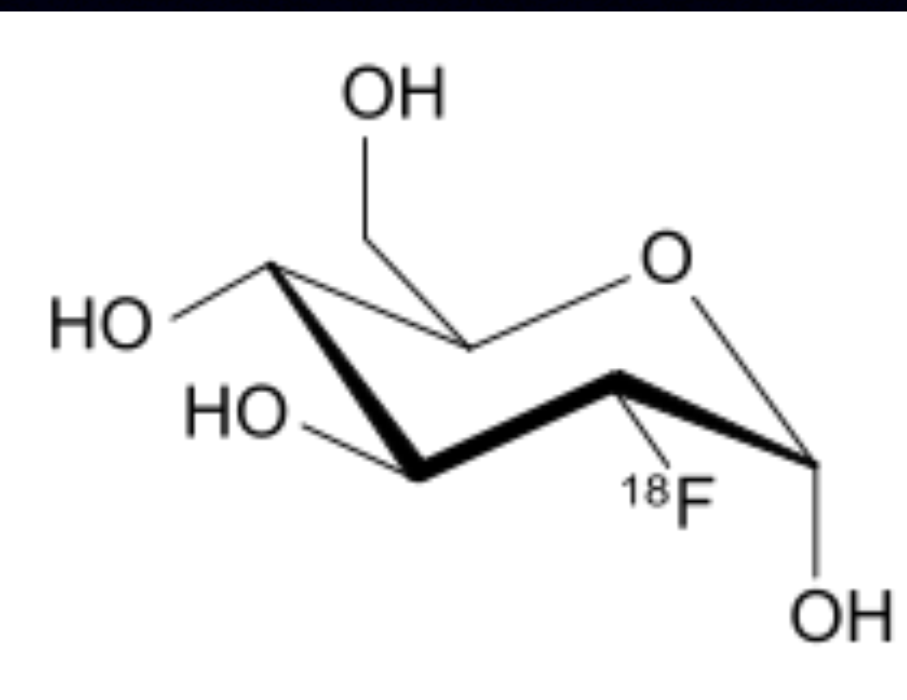
functional (fMRI) connectivity study

D.J. Kelley 2008 PhD thesis

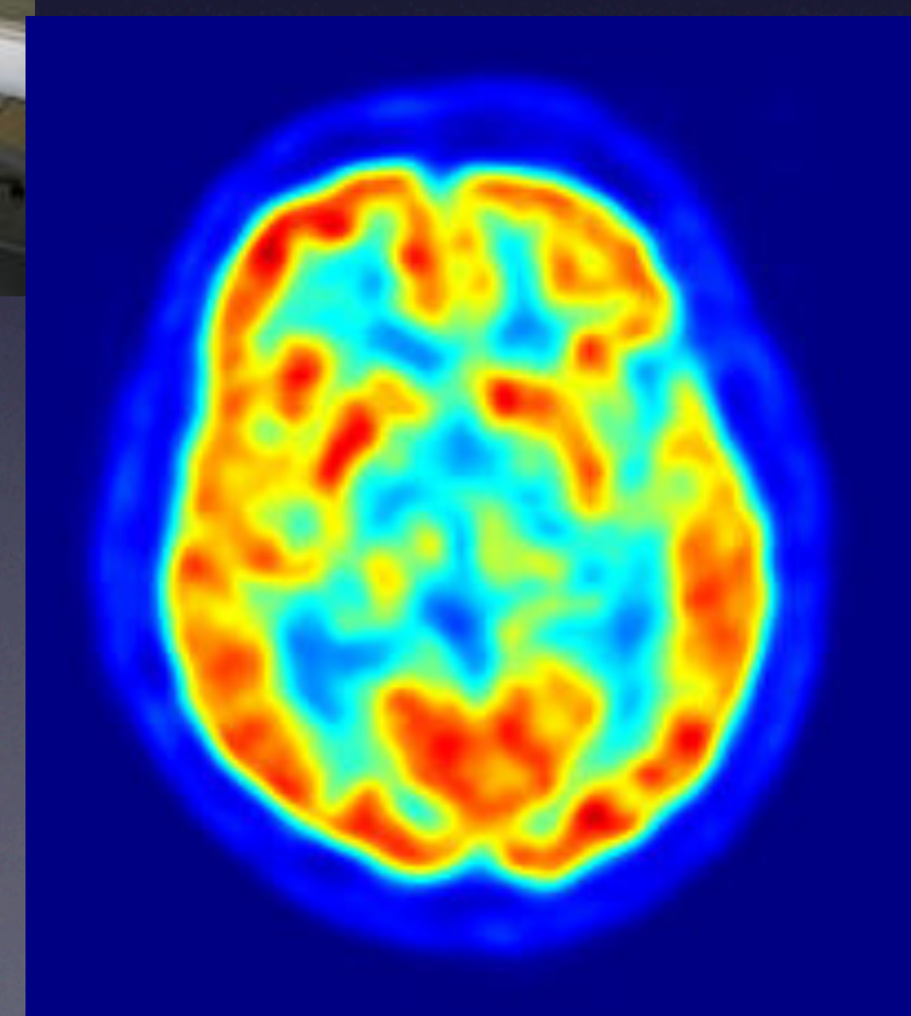


FDG-PET images

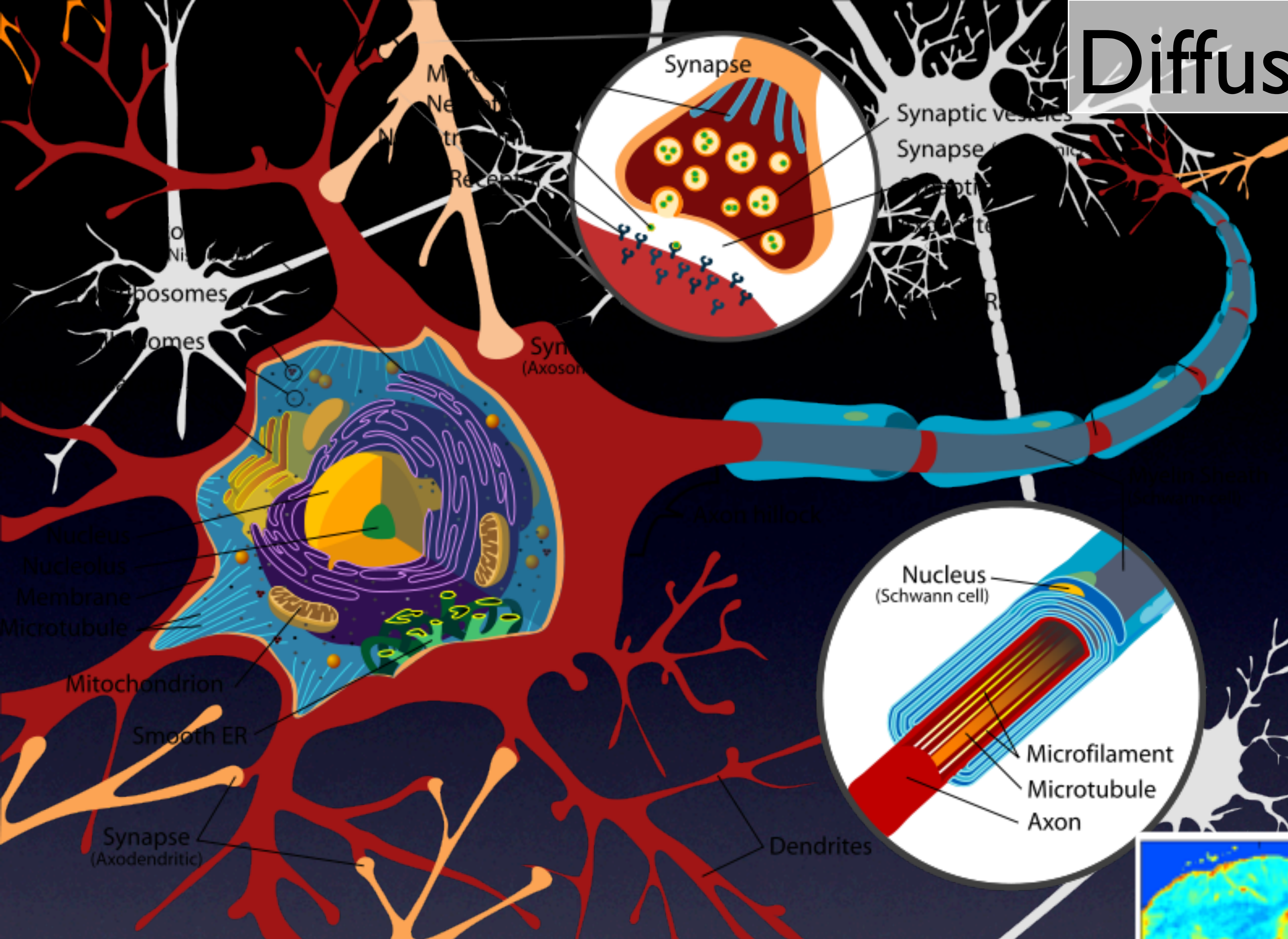
The PET scanner detects pairs of gamma rays emitted from a positron-emtting radioactive tracer.



^{18}F-FDG is the most widely used tracer used for measuring tissue metabolic activity, in terms of regional glucose uptake.

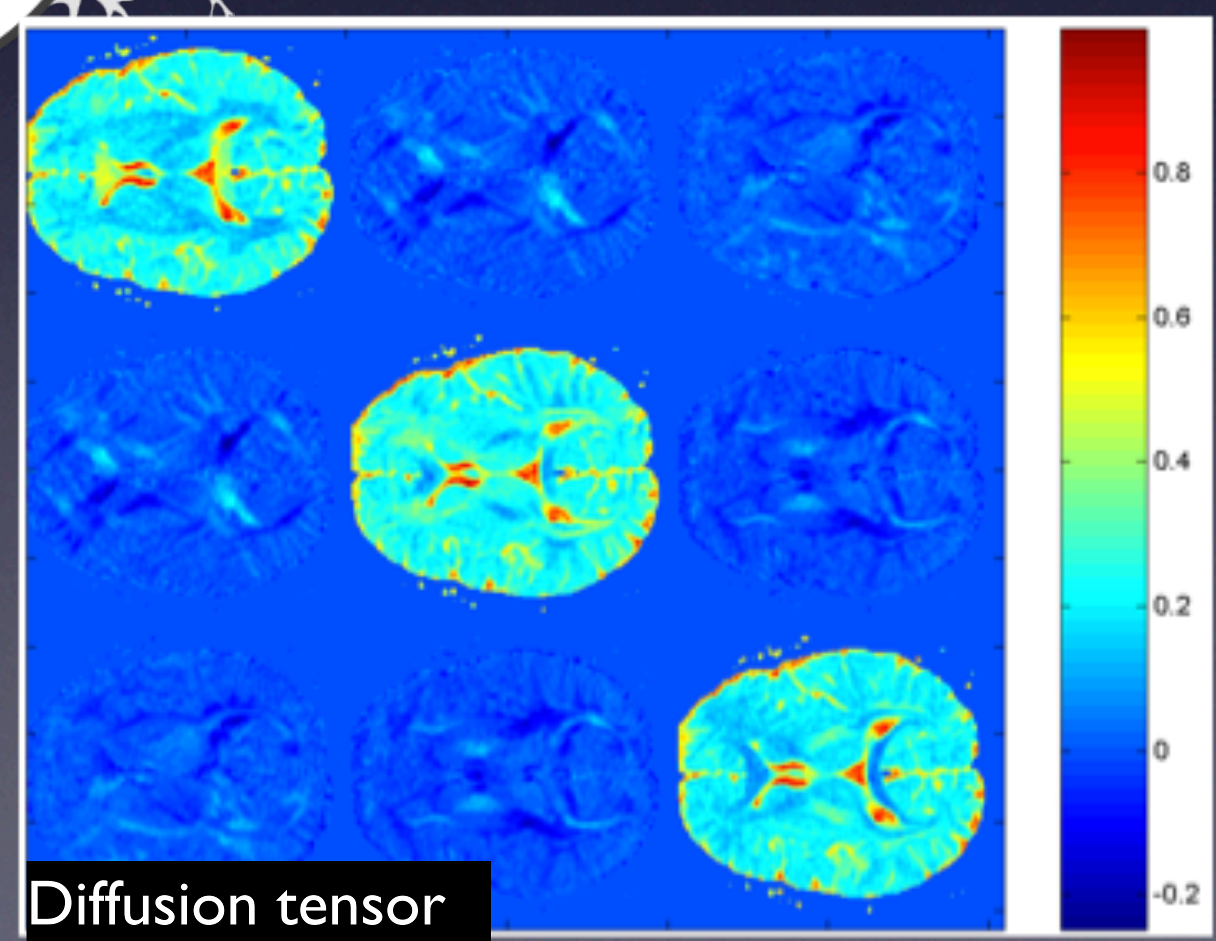


Diffusion Tensor Imaging



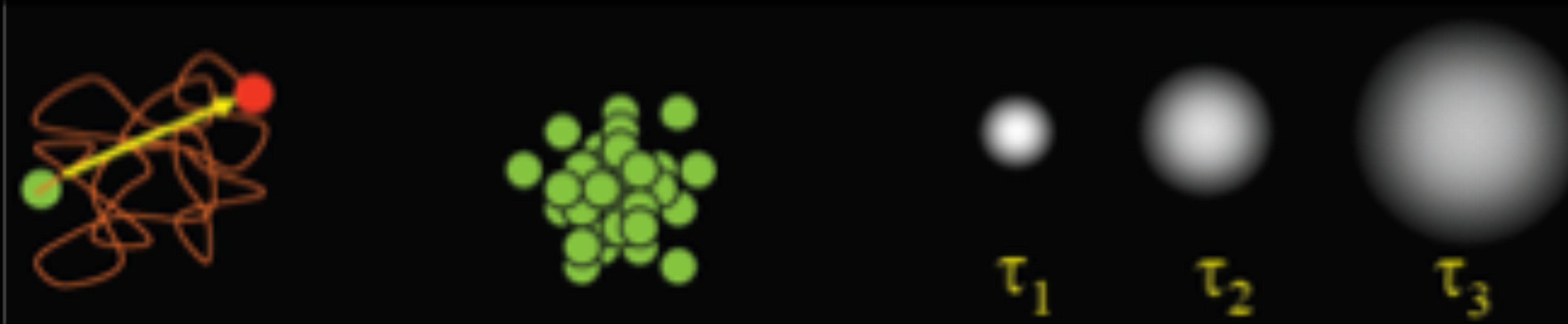
The movement of anisotropic water diffusion can be measured using DTI.

The direction of neuronal filaments in the axon dictates the movement of water diffusion.

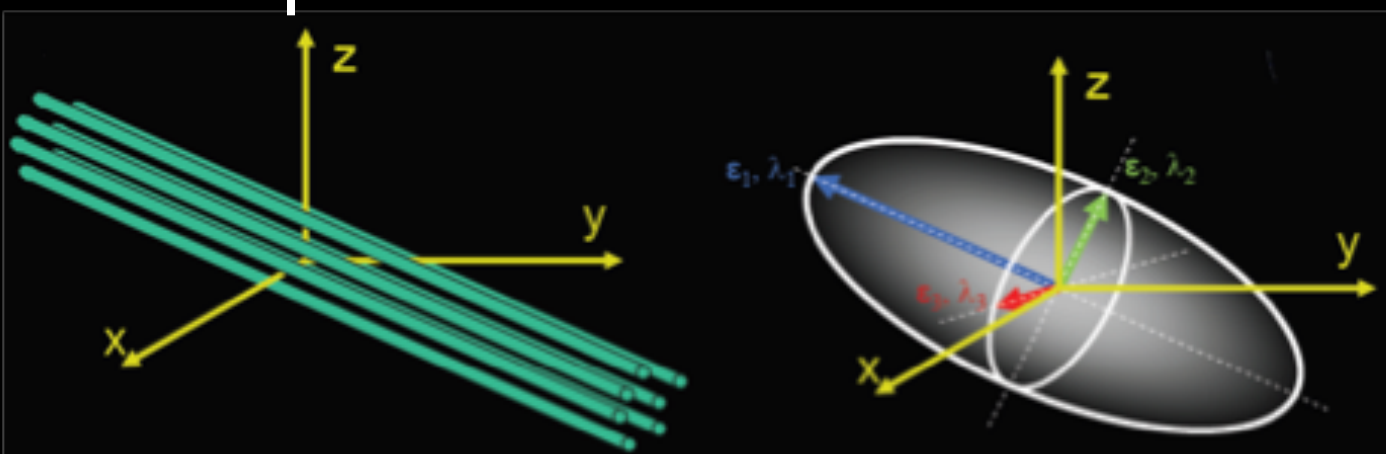


Diffusion Tensor

Mori and van Zijl NMR Biomed 2002



isotropic diffusion



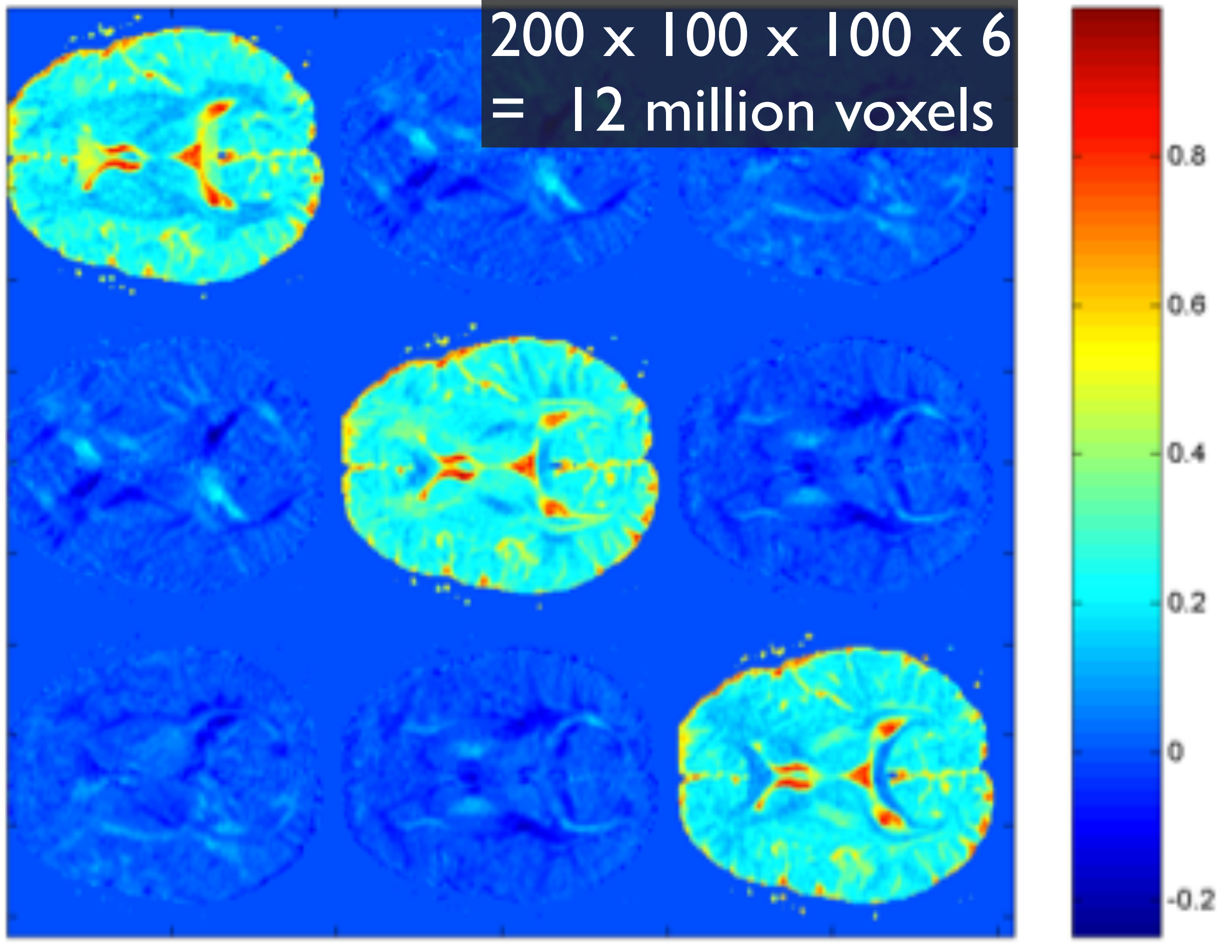
anisotropic diffusion

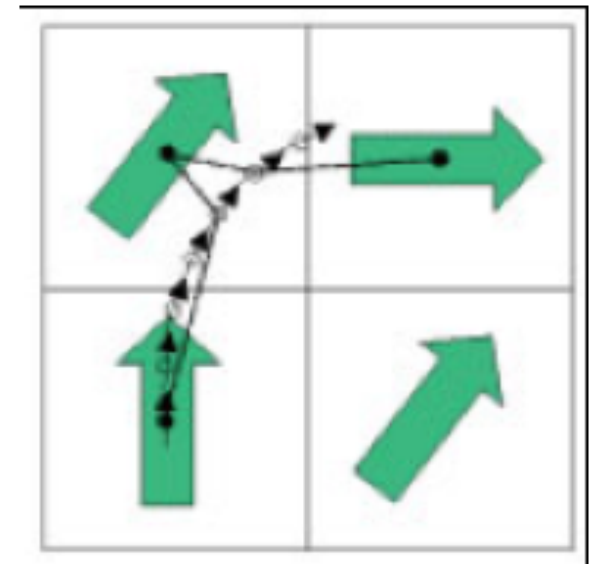
diffusion tensor

$$p(x \mid x_o, \tau) = \frac{1}{\sqrt{(4\pi\tau)^3 |\underline{D}|}} \exp\left(\frac{-(x - x_0)^T \underline{D}^{-1} (x - x_0)}{4\tau} \right)$$

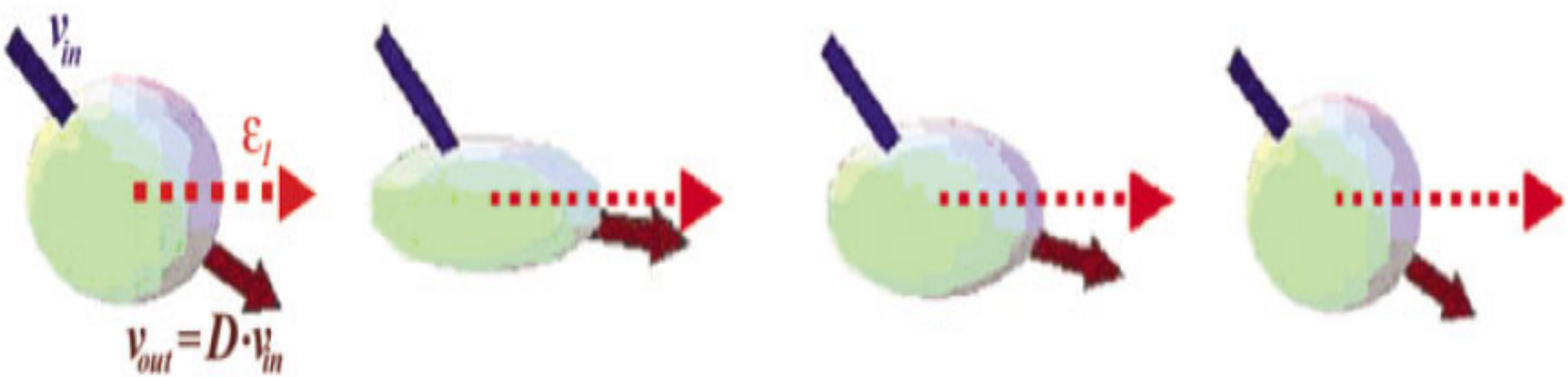
transition probability from x_0 to x

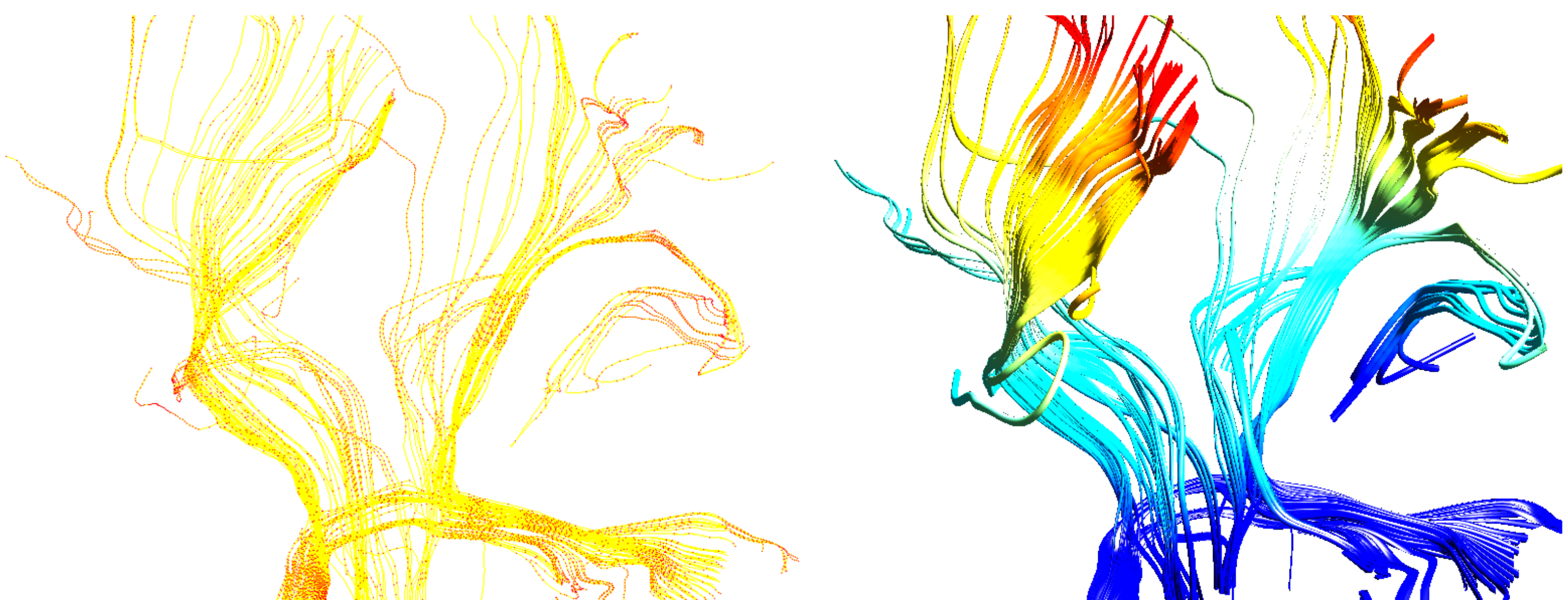
Fiber Tractography





TENsor Deflection (TEND) algorithm

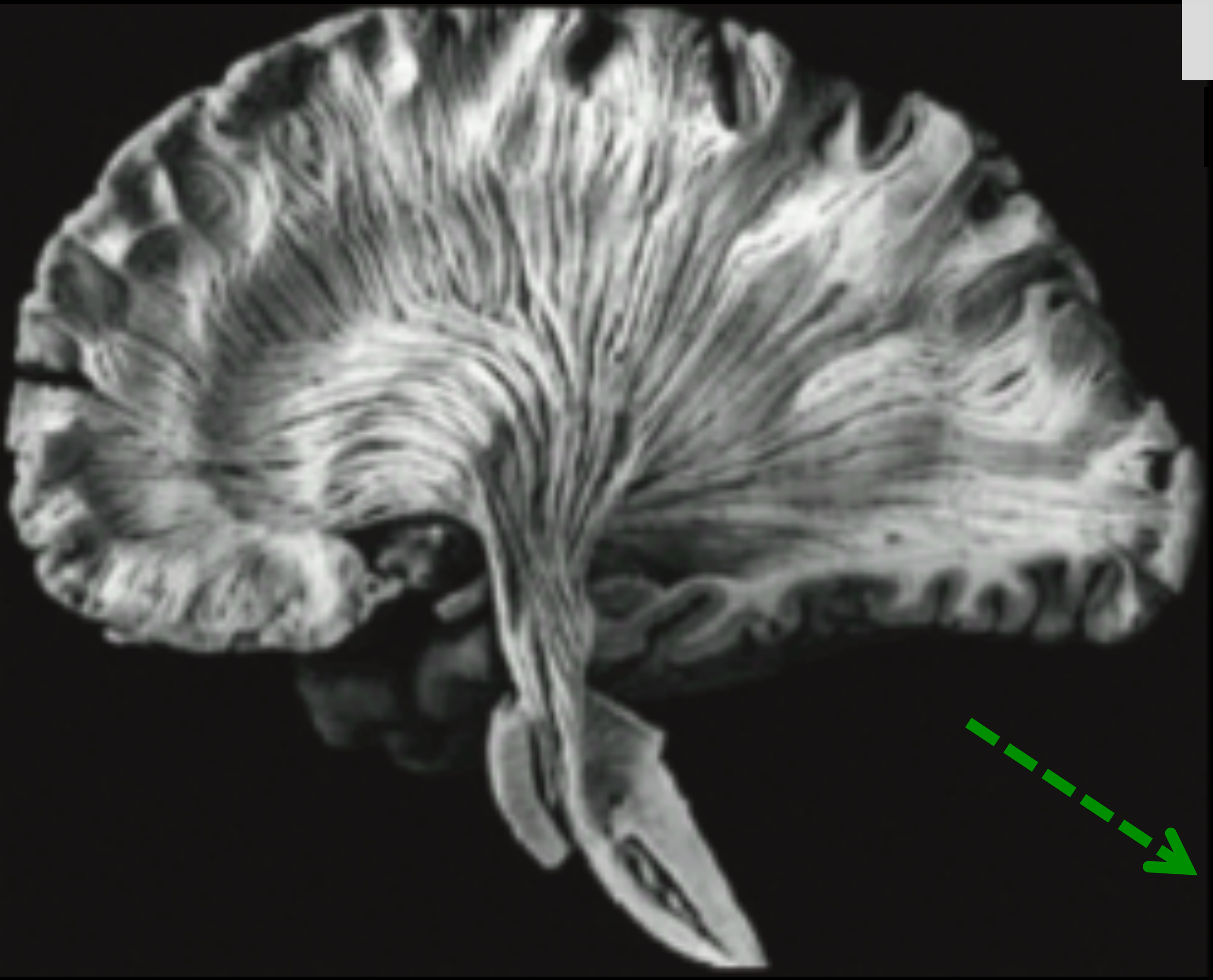




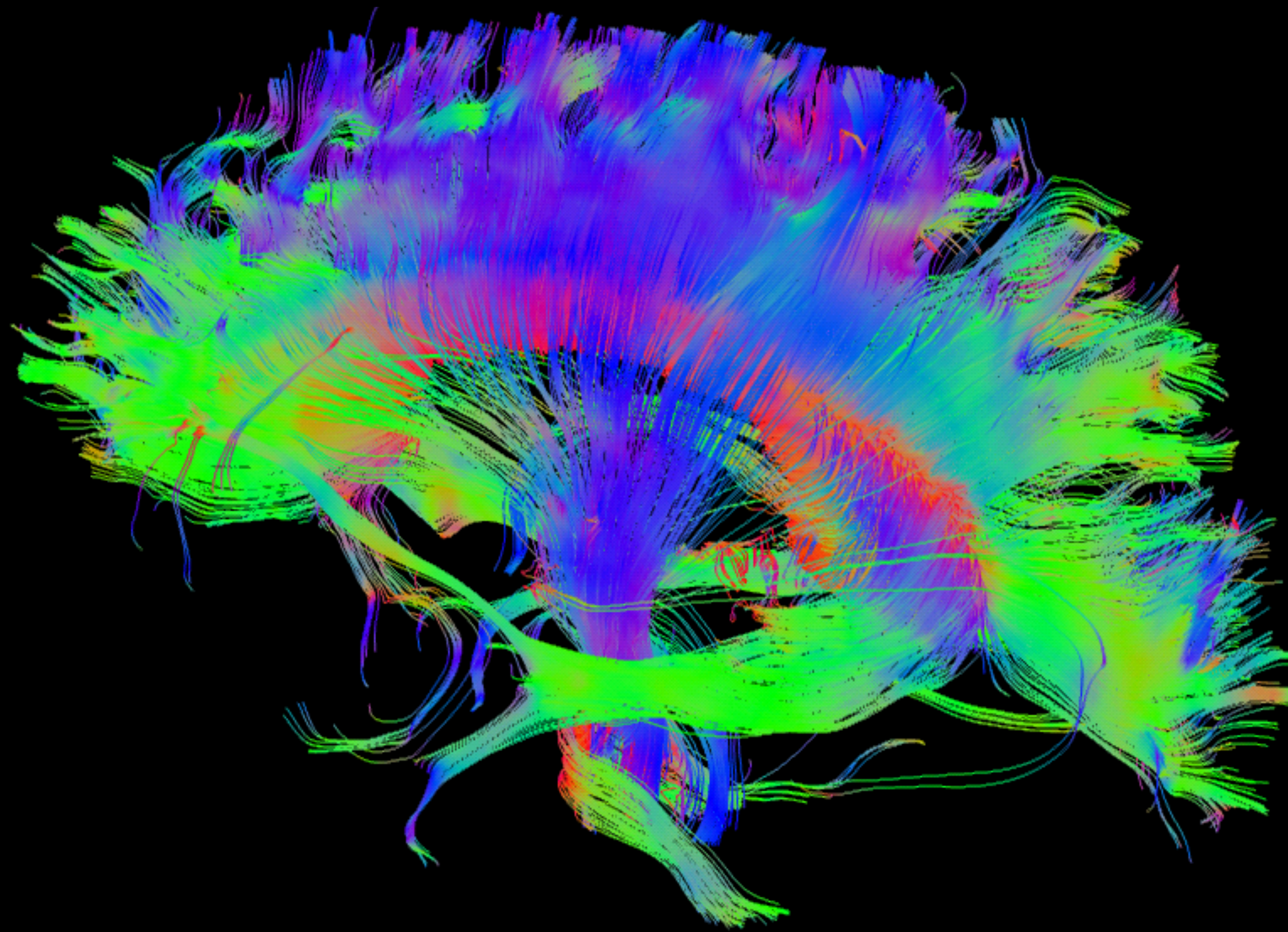
Second order Runge-Kutta algorithm with TEND

Lazar et al., HBM 2003

White Matter Fibers in Brain



Postmortem



Half million tracts
600MB image per subject

MATLAB DEMO

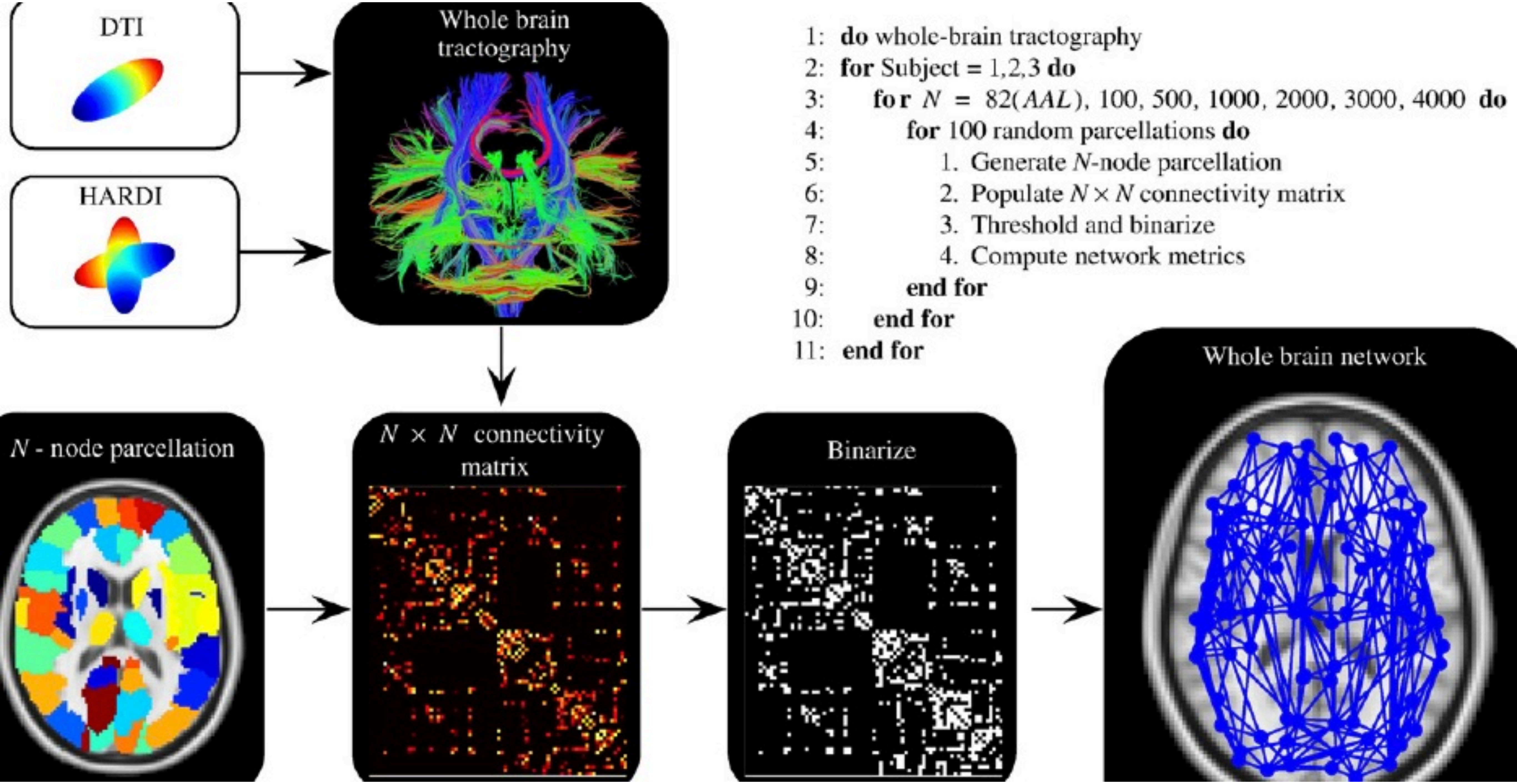
White matter fibers

/adjacency.matrix/matlab/DEMO.2011.07.09.IMSchina.m

Traditional Methods

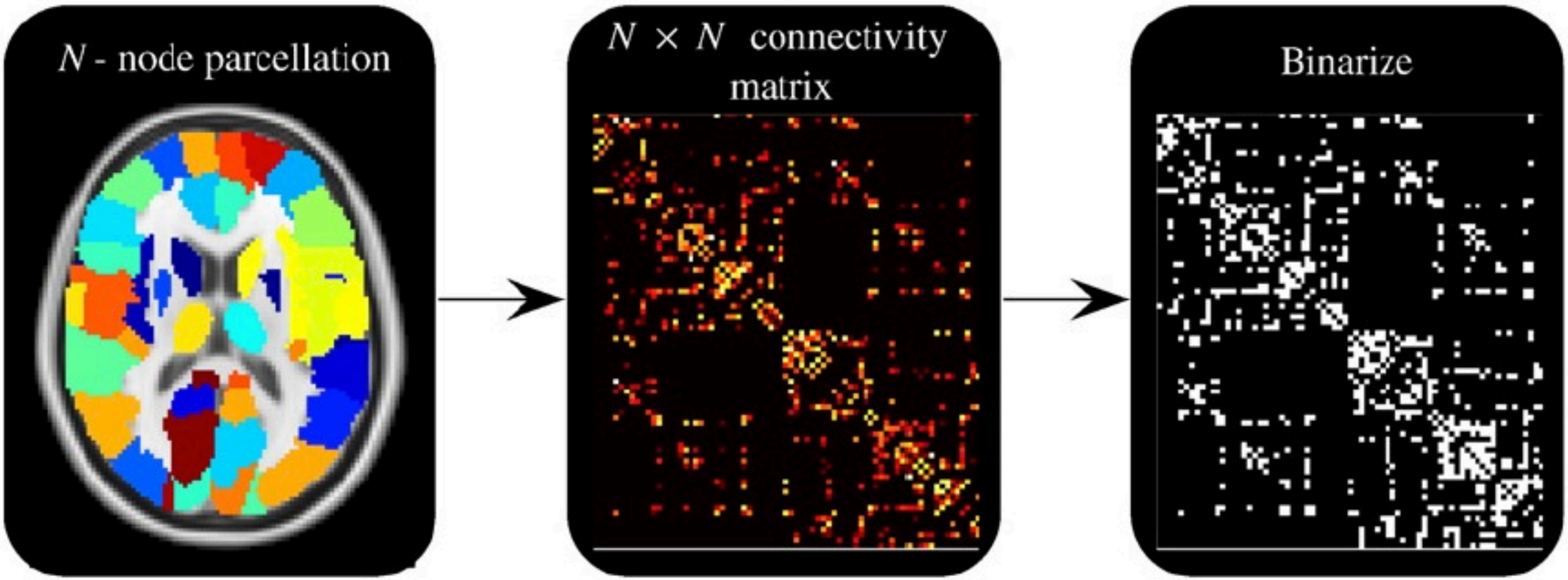
(90% of approaches)

Traditional brain network modeling flow



Zalesky et al. NeuroImage 2010

Two problems with the standard method



Parcellation

70-100 regions

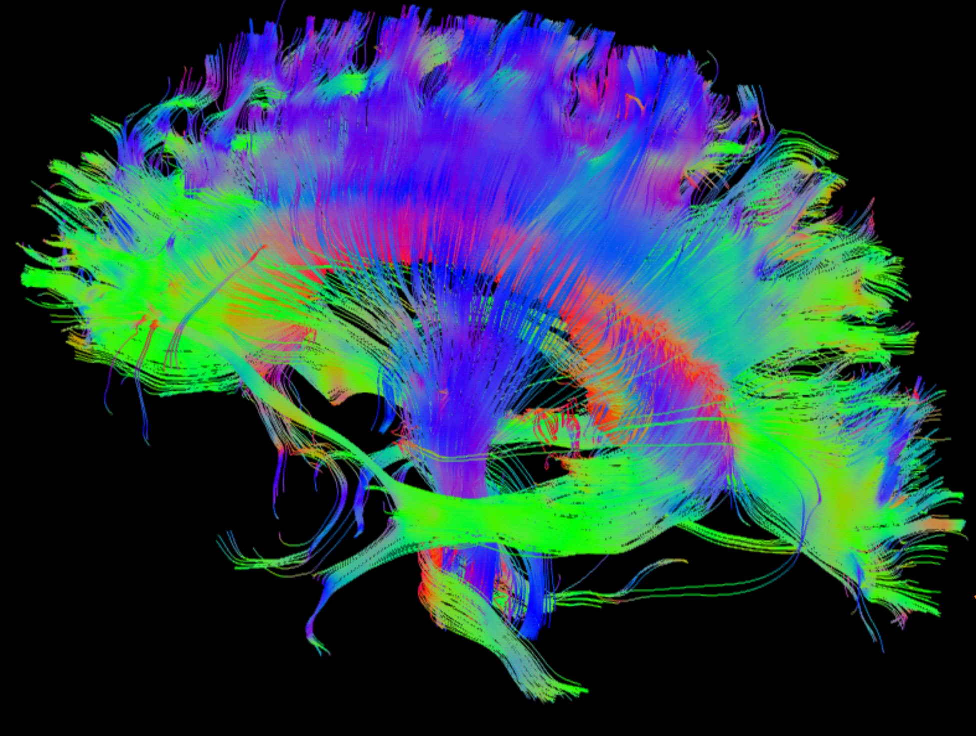
Arbitary thresholding

Brain Network Modeling without parcellation and thresholding

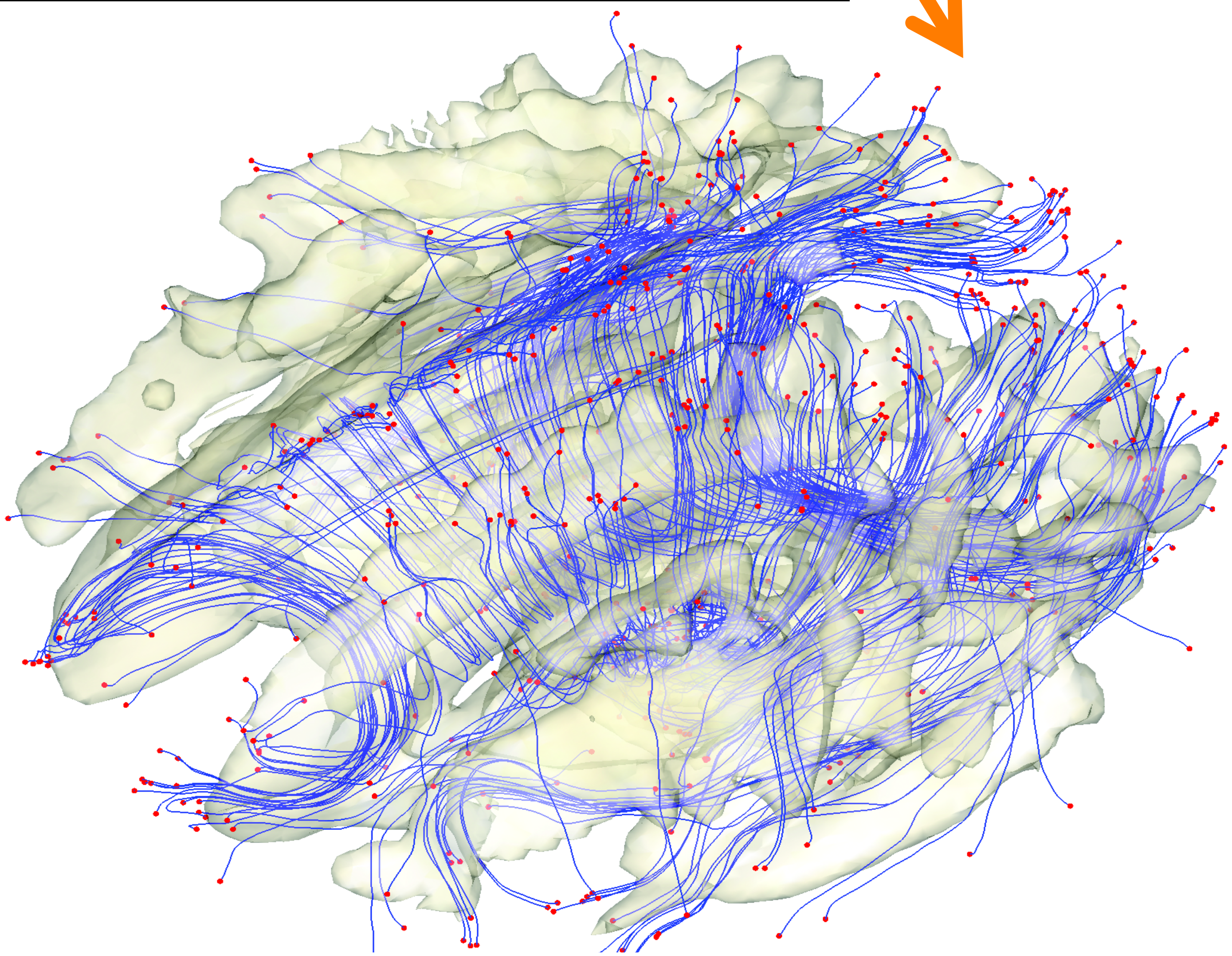
Epsilon-neighbor method

A different simplex construction technique

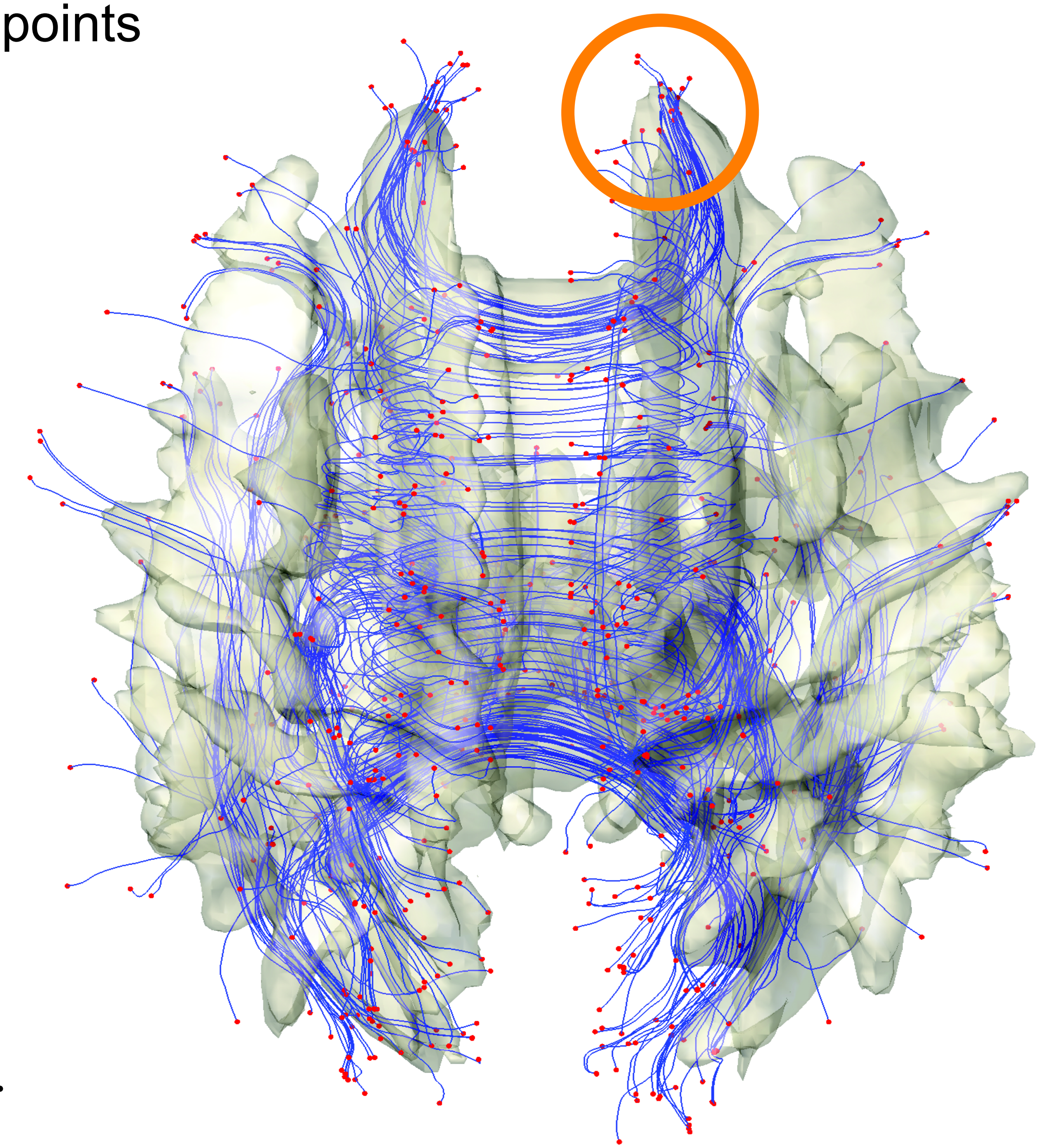
ε-neighbor graph simplication



Identify end points

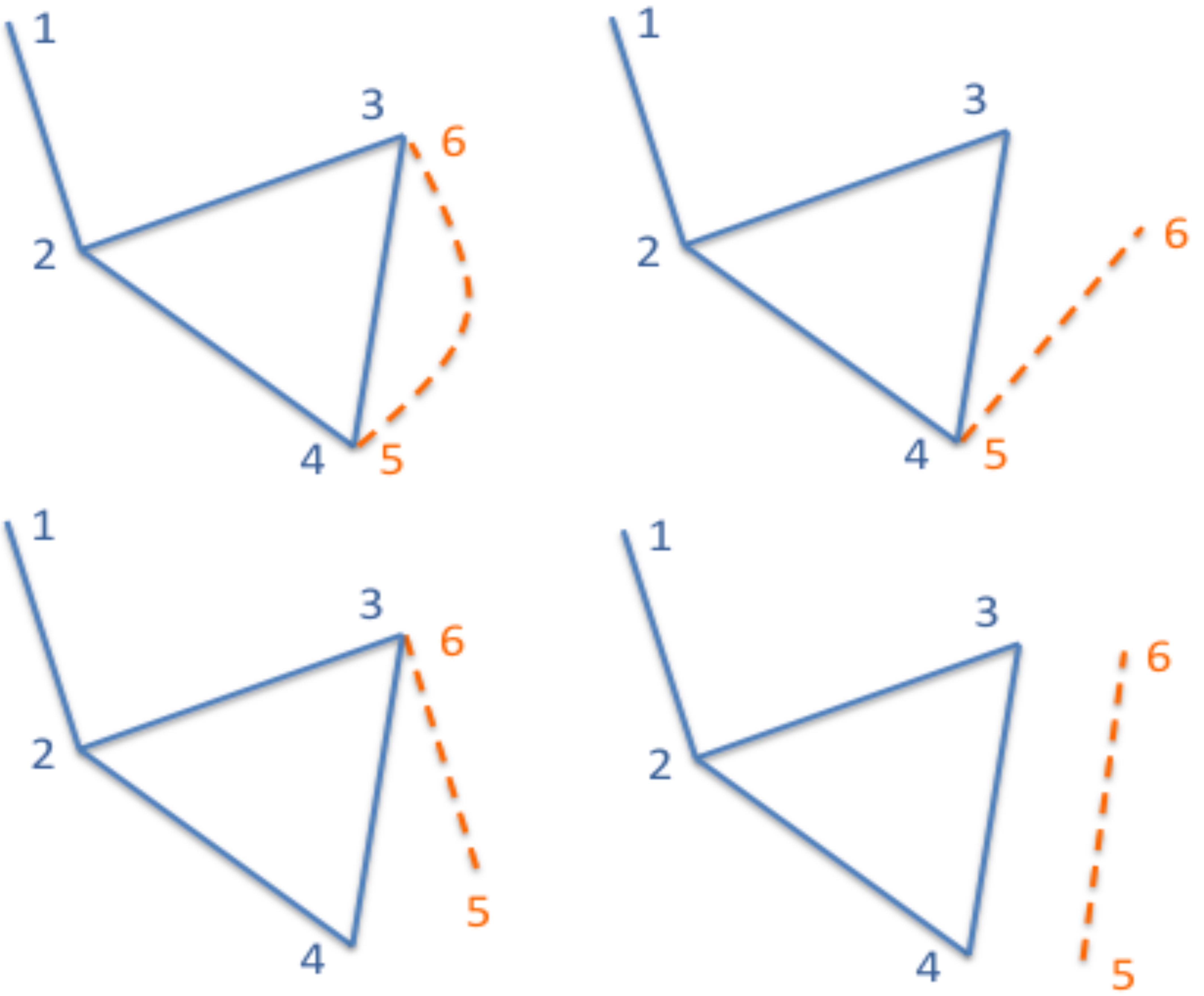


All points in the ε-neighbor are identified as a single node in a graph



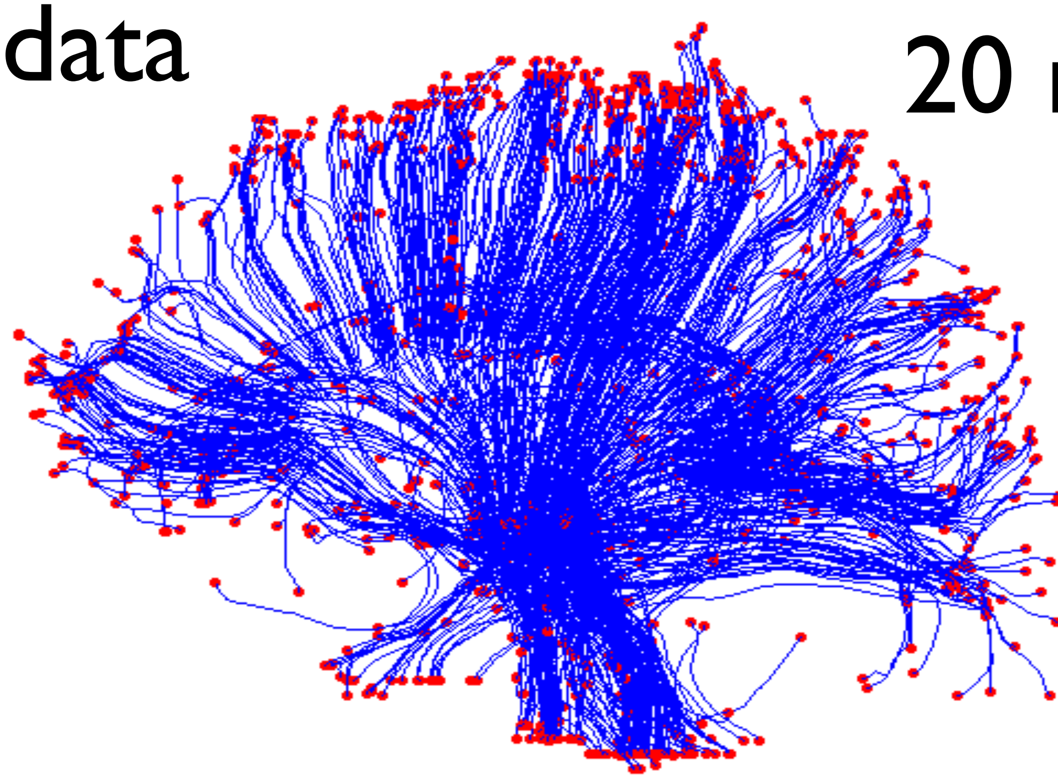
The first data-driven DTI structural network construction framework without any parcellation.

Iterative graph construction

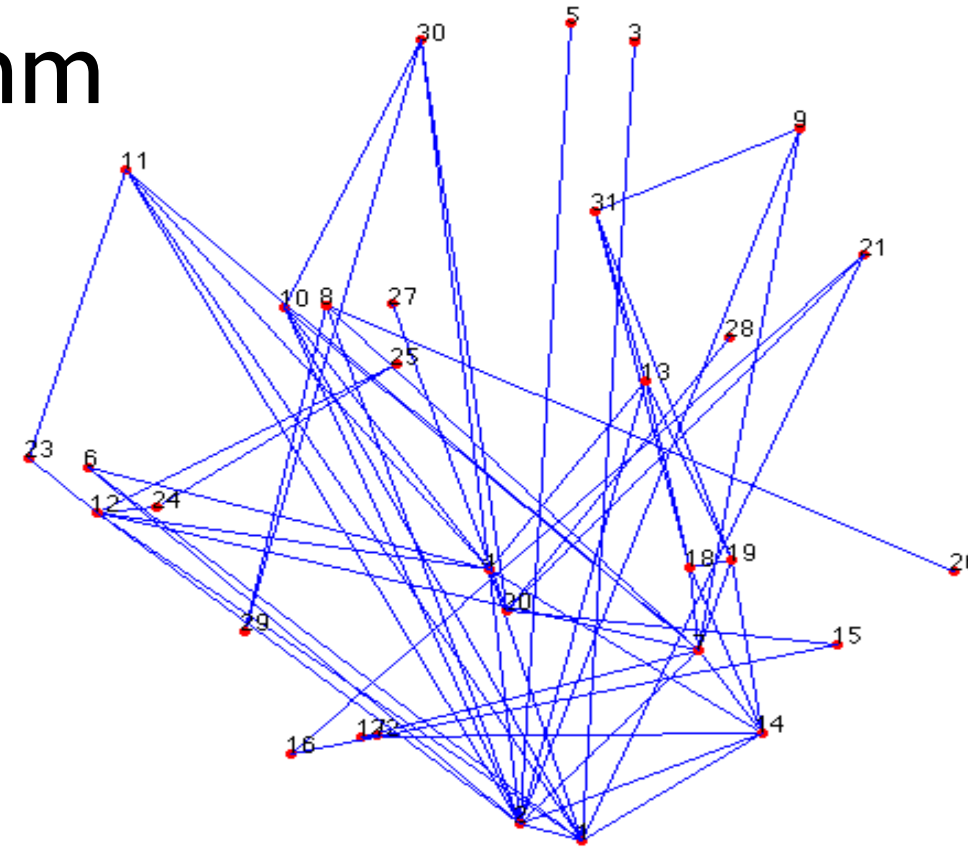


ε-neighbor graphs with different ε

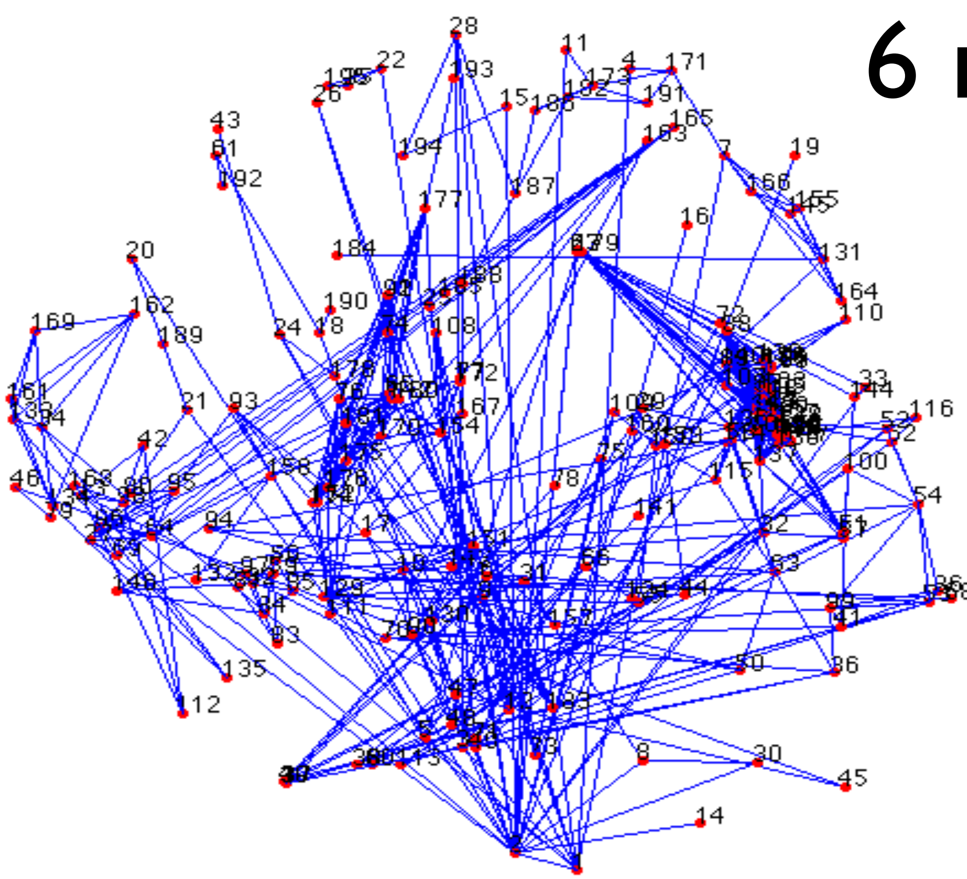
original data



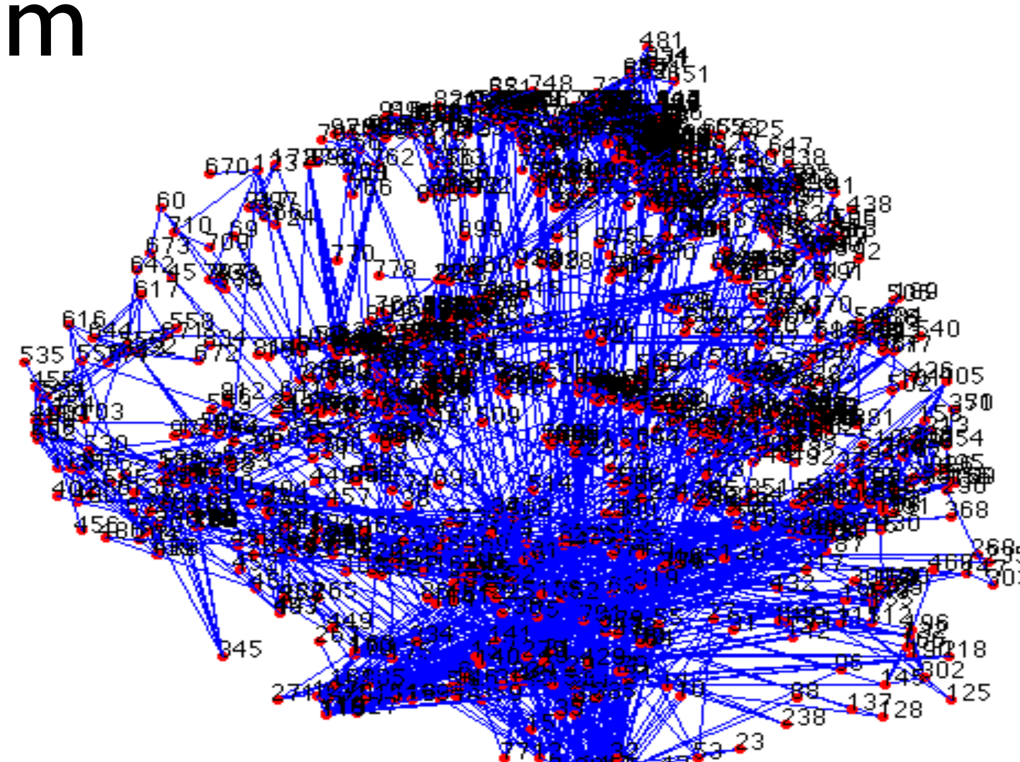
20 mm



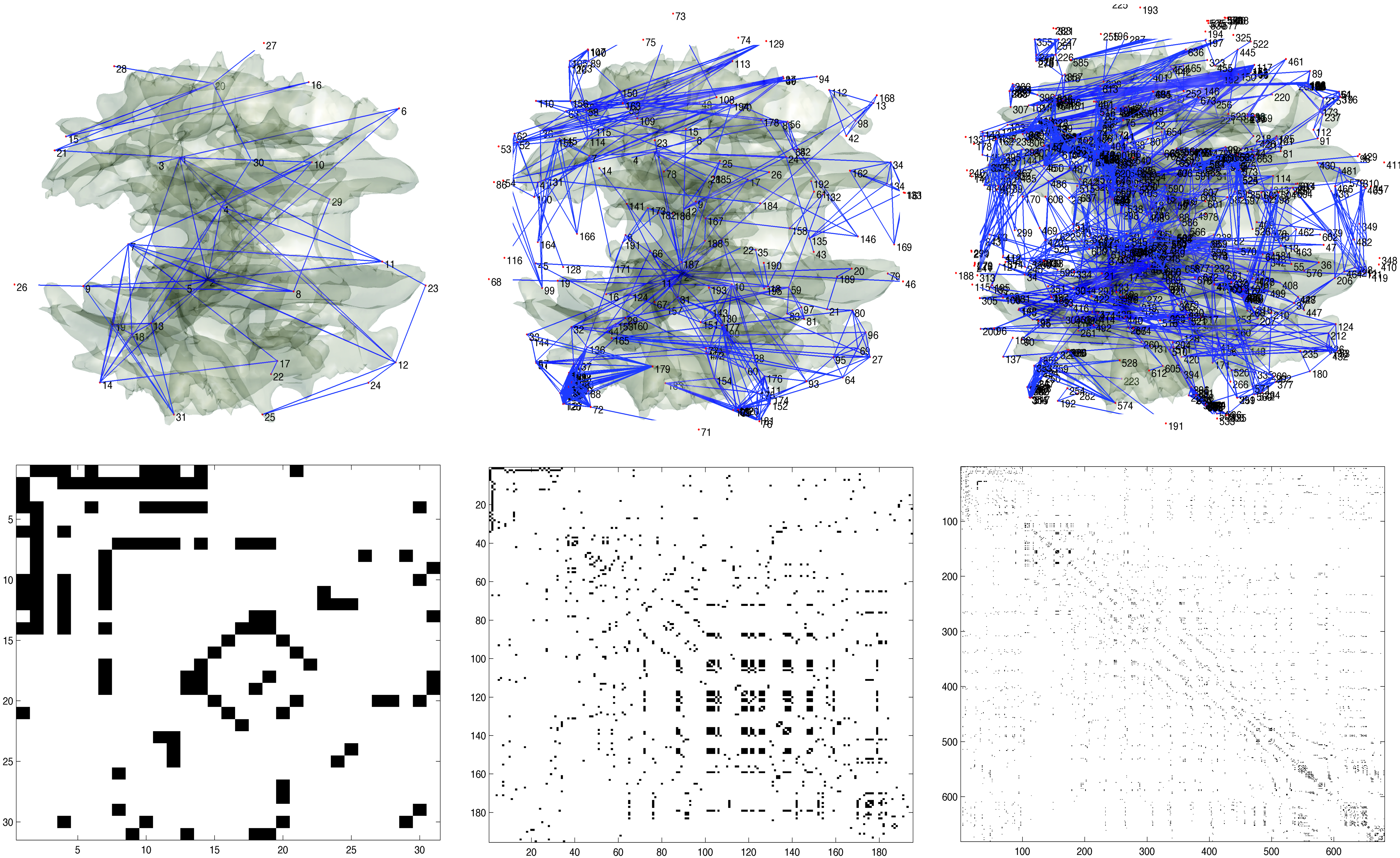
10 mm



6 mm



Adjacency matrix



MATLAB DEMO

Epsilon Neighbor method

/adjacency.matrix/matlab/DEMO.2011.07.09.IMSchina.m

Application to autism

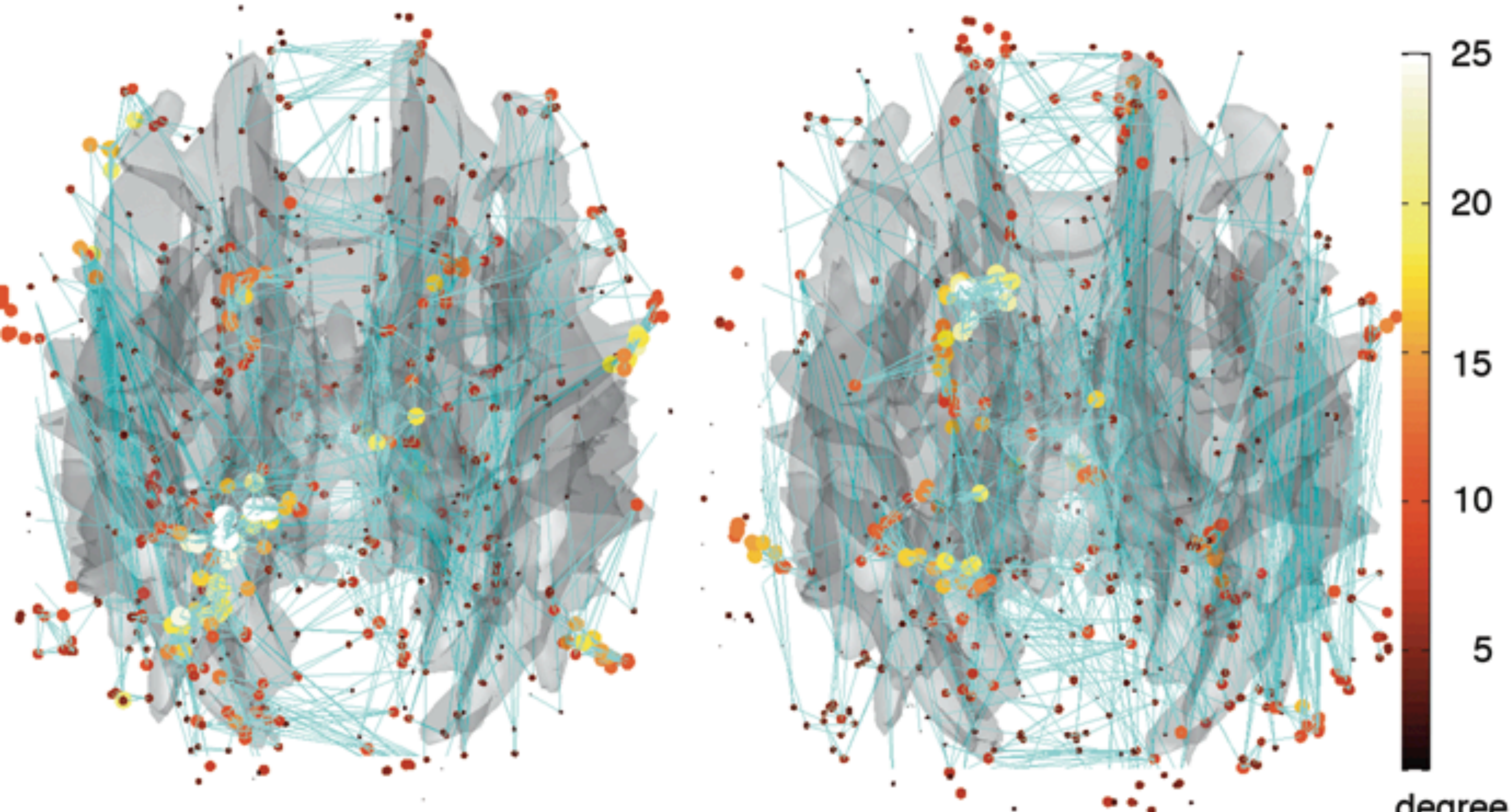
Autistic children (n=17)

Control subjects (n=14)

Matched for age, handedness, IQ and head size

Abnormal connectivity in autism ?

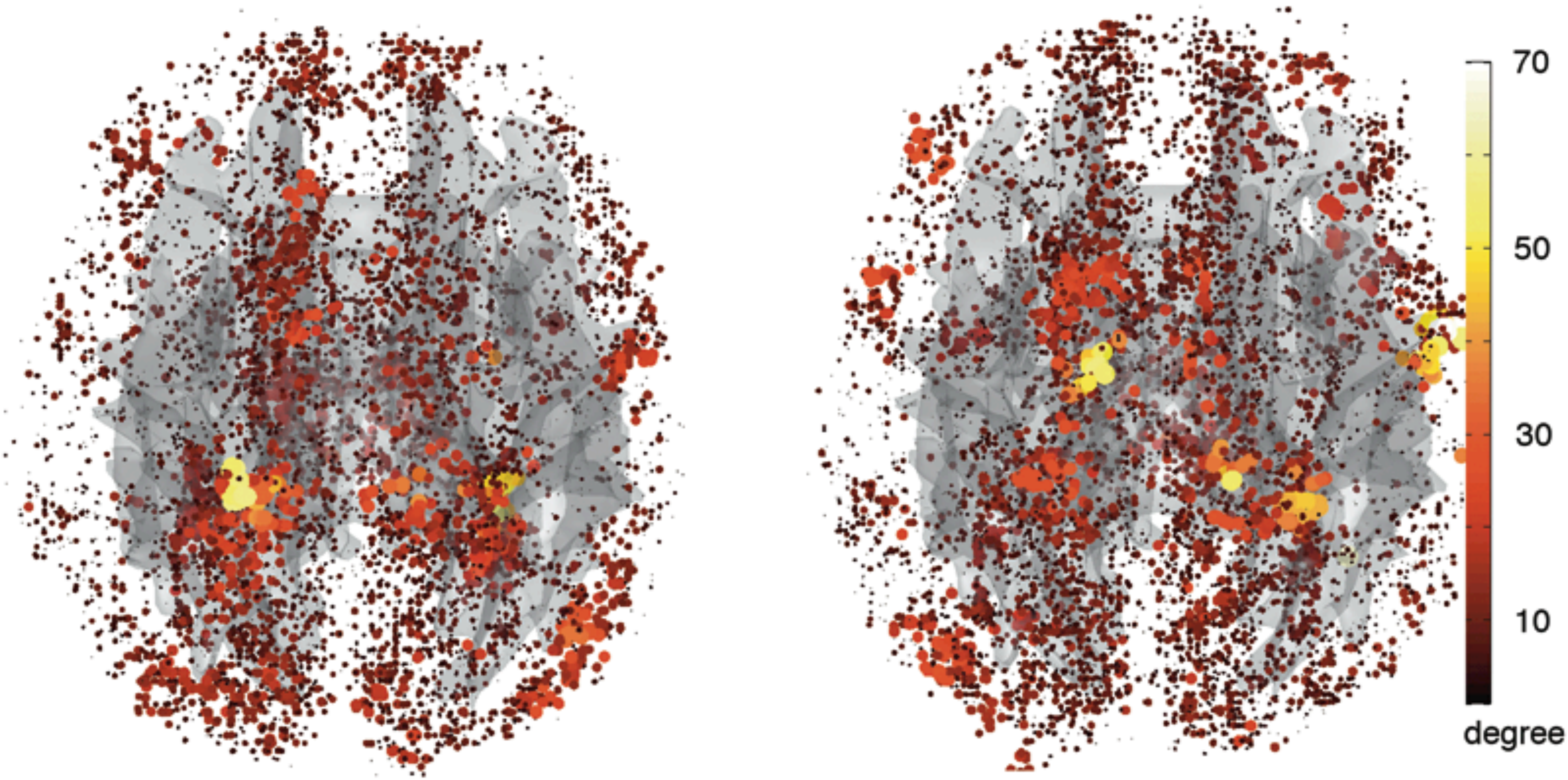
Degree of nodes for a single subject



control #001 autism #120

Local inference on degree

Superimposition of every subjects

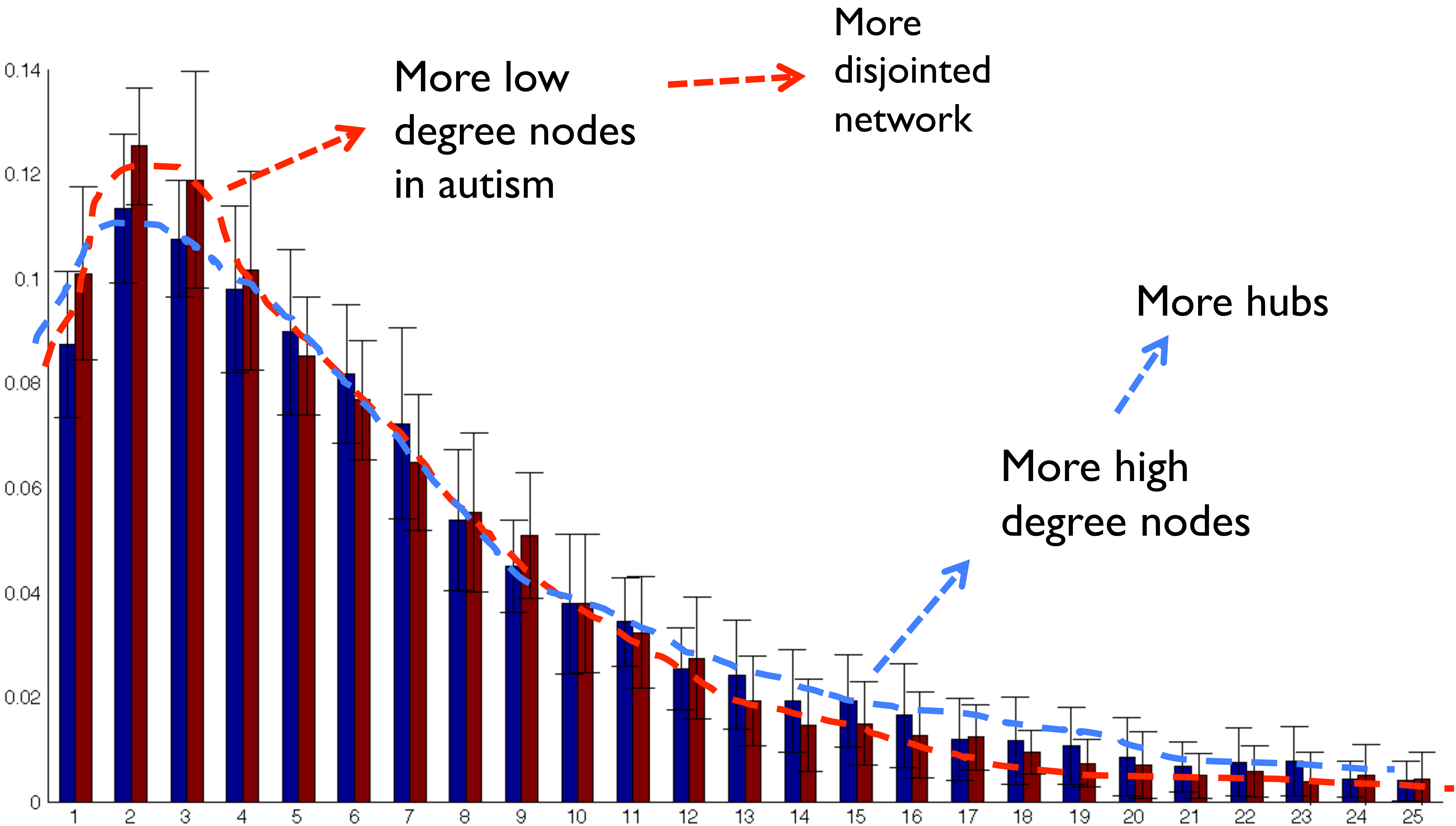


Control

Autism

Degree distribution

red: autism
blue: control



pvalues = 0.024, 0.015 and 0.080 for degrees 1, 2 and 3.

Introduction to

Graph Filtration

Filtration on ε-neighbor graphs

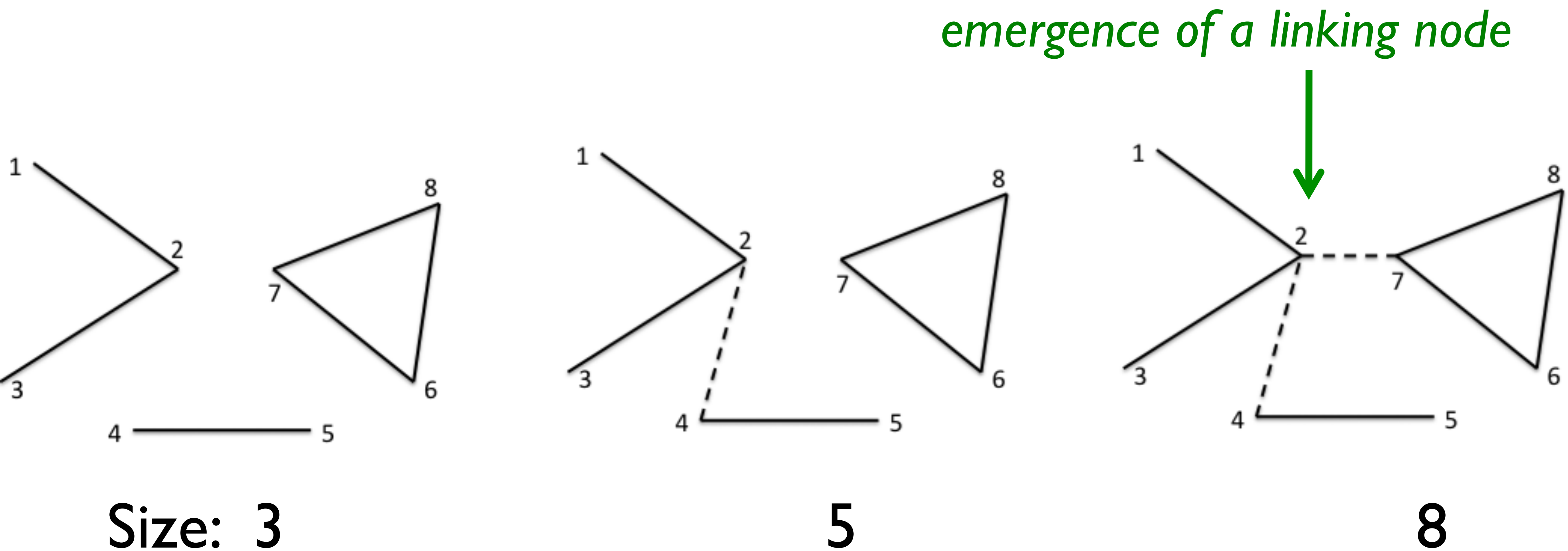
ε-neighbor graph at the *i*-th iteration $\mathcal{G}_i$

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

The size of the *i*-th graph is an increasing function:

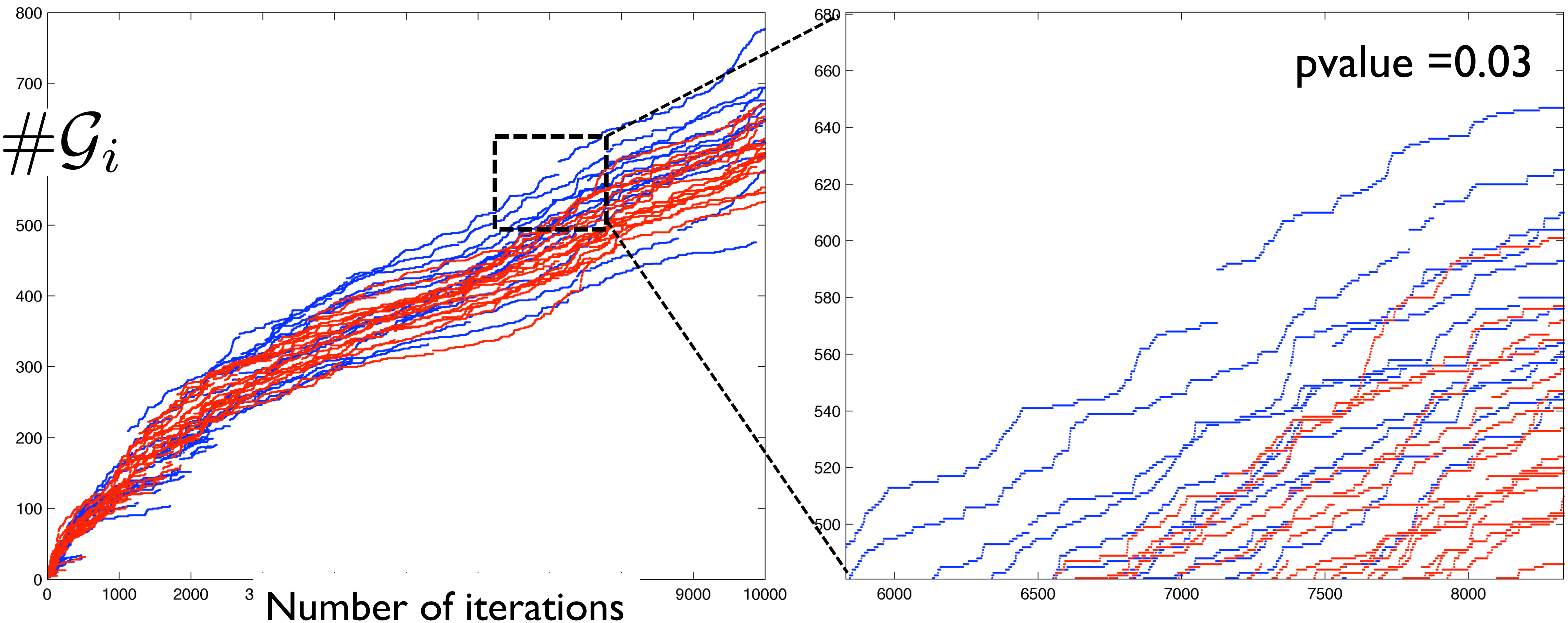
$$\#\mathcal{G}_1 < \#\mathcal{G}_2 < \#\mathcal{G}_3 < \cdots$$

The size of the largest connected component



Network growth rate difference

Control=blue
Autism=red



The brain network in control subjects merges to a single component faster than other populations.

Introduction to

Persistence Homology

Images as random fields

$$f_i(x) = \mu(x) + \epsilon_i(x)$$

i-th measurement signal random field

Signal detection as an inference problem

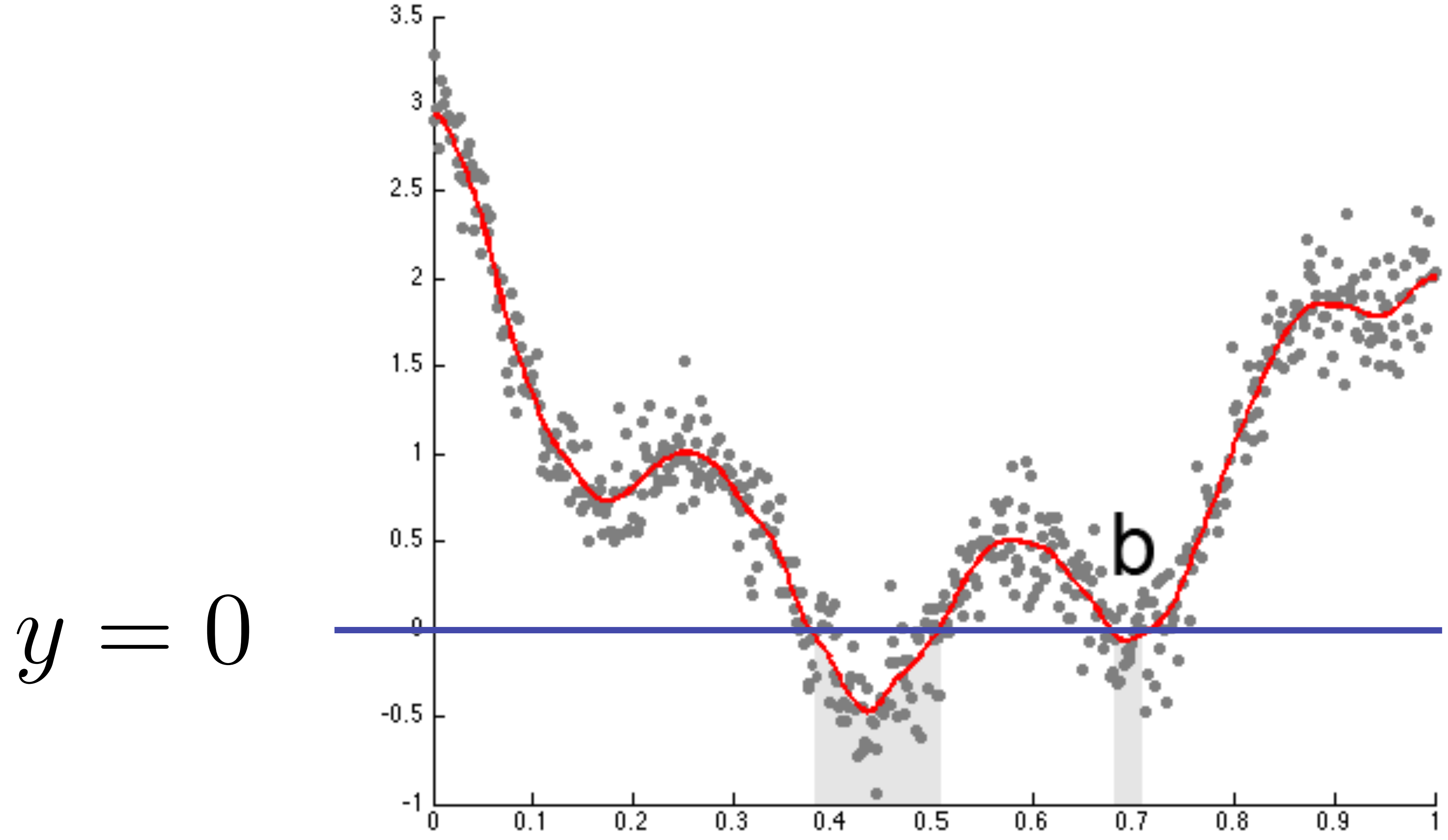
$$H_0(x) : \mu(x) = 0 \text{ vs. } H_1(x) : \mu(x) > 0$$

for all *x* for some *x*

Morse Theory

Assume underlying measurement f_i to be a Morse function (all critical values are unique).

Define a sublevel set $R(y) = f_i^{-1}(-\infty, y]$



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

Local min: $h_1, \cdots, h_n$

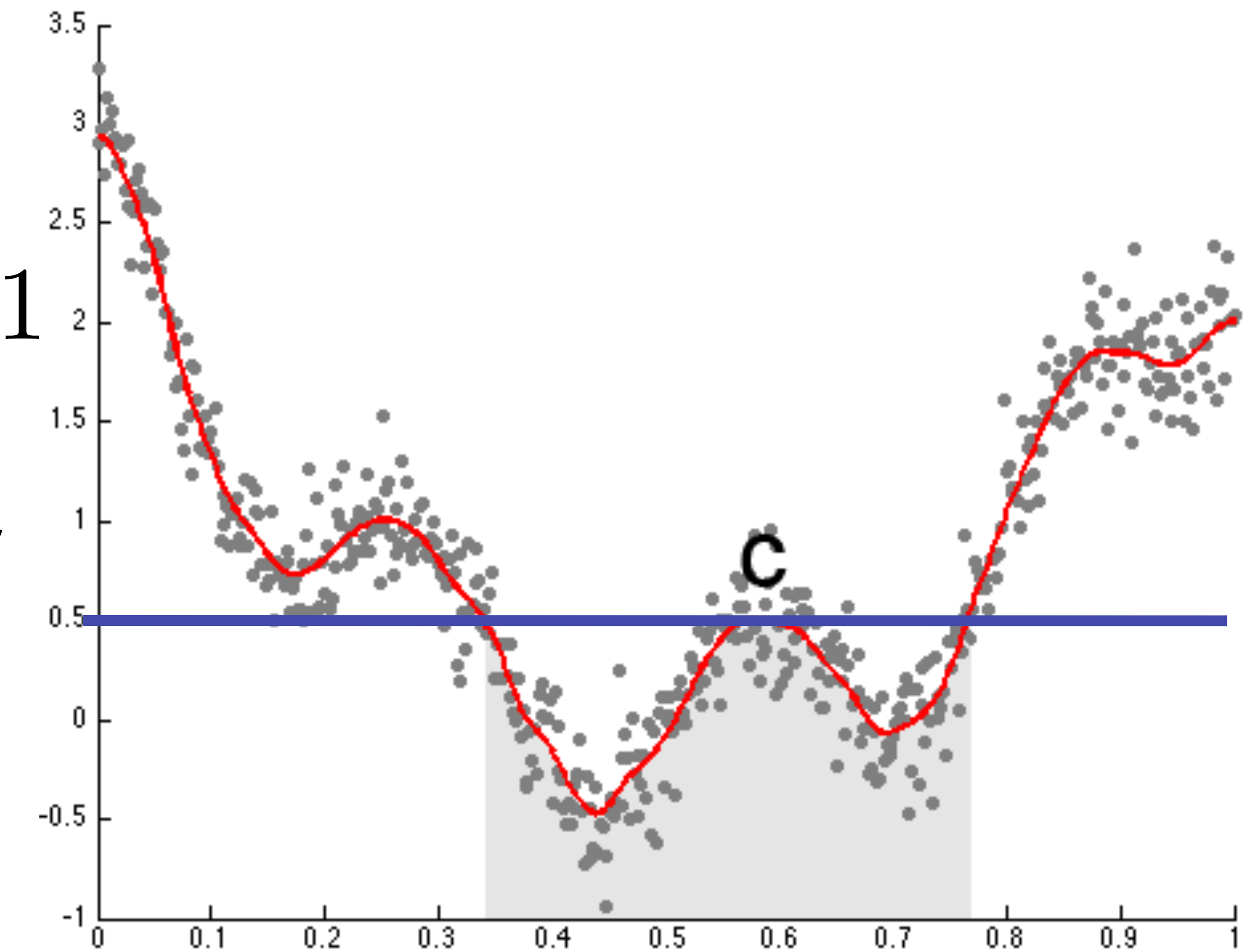
Birth:

$$\#R(h_i - \epsilon) = \#R(h_i) - 1$$

Local max: $g_1, \cdots, g_n$

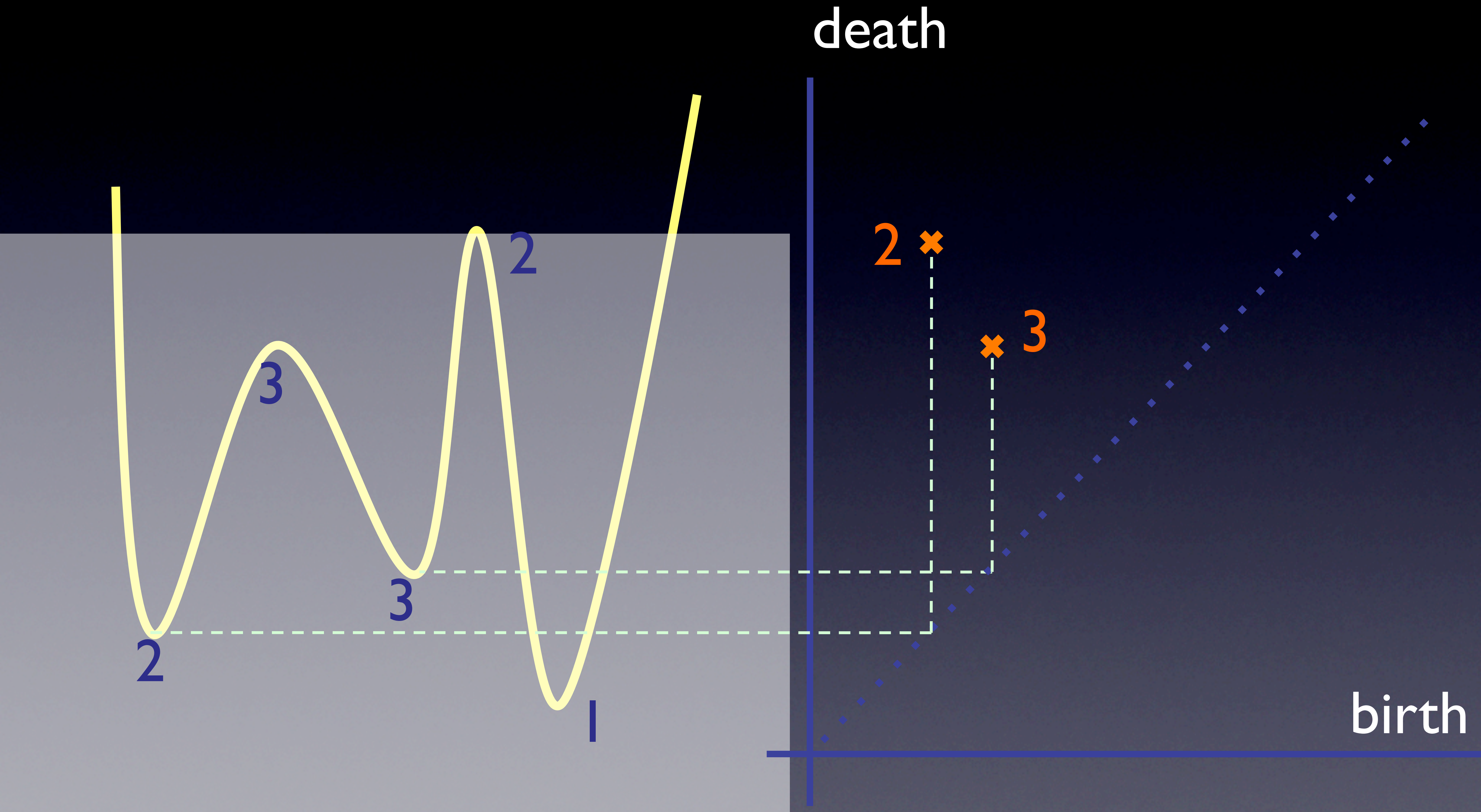
Death:

$$\#R(g_i - \epsilon) = \#R(g_i) + 1$$



Topological characteristic of sublevel set is completely characterized by tabulating the occurrence of critical values.

Tabulation is done by persistence diagram



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

Example: 2D functional measurement on a manifold

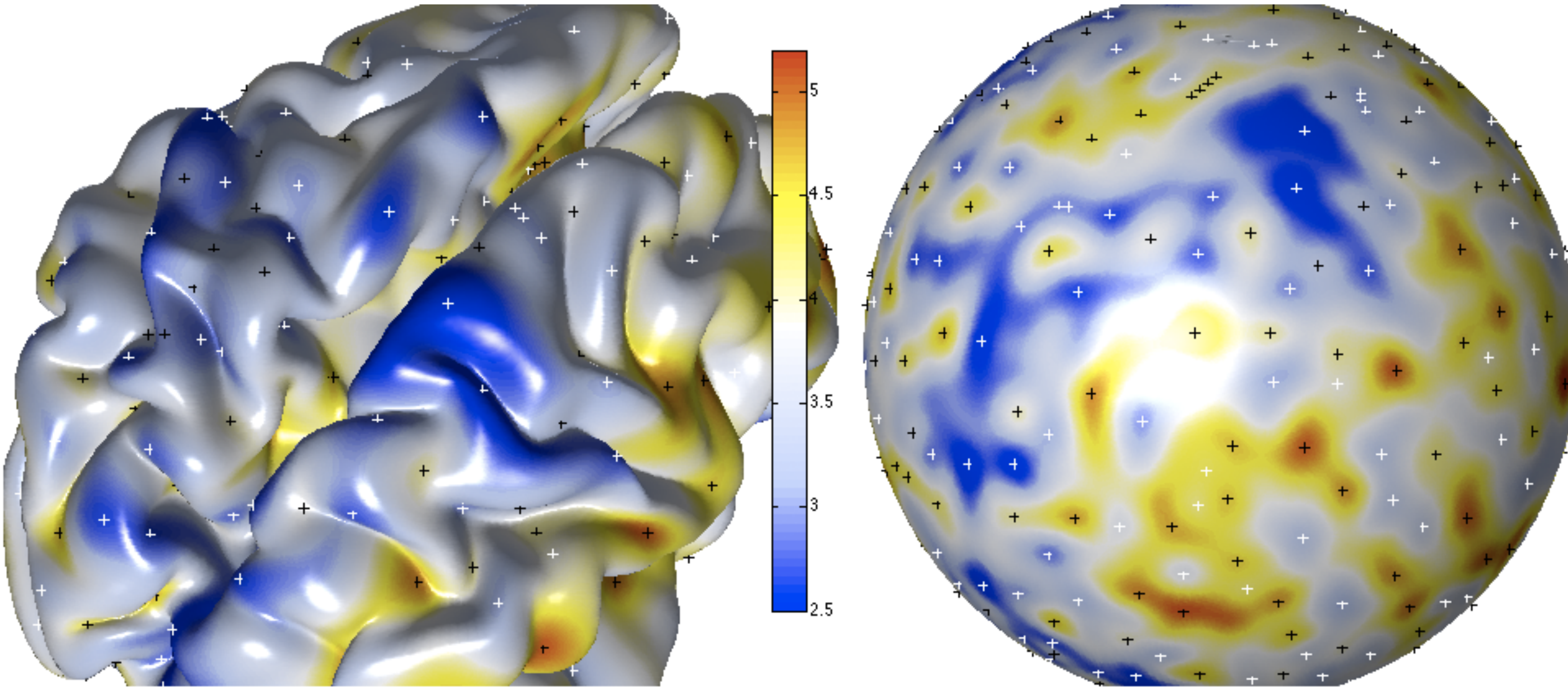
Persistence Diagrams of Cortical Surface Data

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

[1] Department of Biostatistics and Medical Informatics
[2] Waisman Laboratory for Brain Imaging and Behavior
University of Wisconsin, Madison, WI 53706, USA
[3] Department of Mathematics
Cleveland State University, Cleveland, Ohio 44115, USA
[4] Department of Mathematics and Statistics
University of Guelph, Guelph, Ontario N1G 2W1, Canada
mkchung@wisc.edu

Information Processing in Medical Imaging (IPMI). 2009

Rips complex of functional data

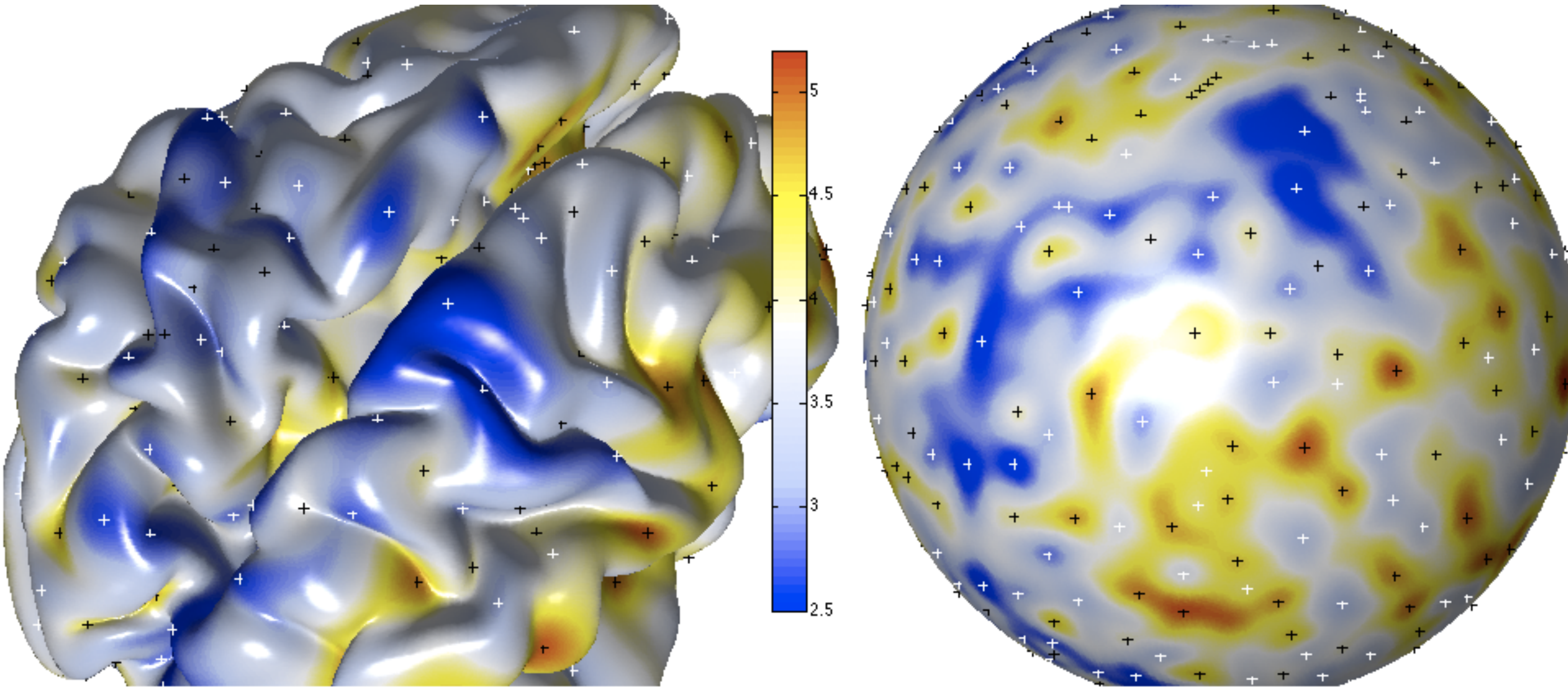


White cross = min, black cross = max

Saddle points are left out

Chung et al. IPMI 2009

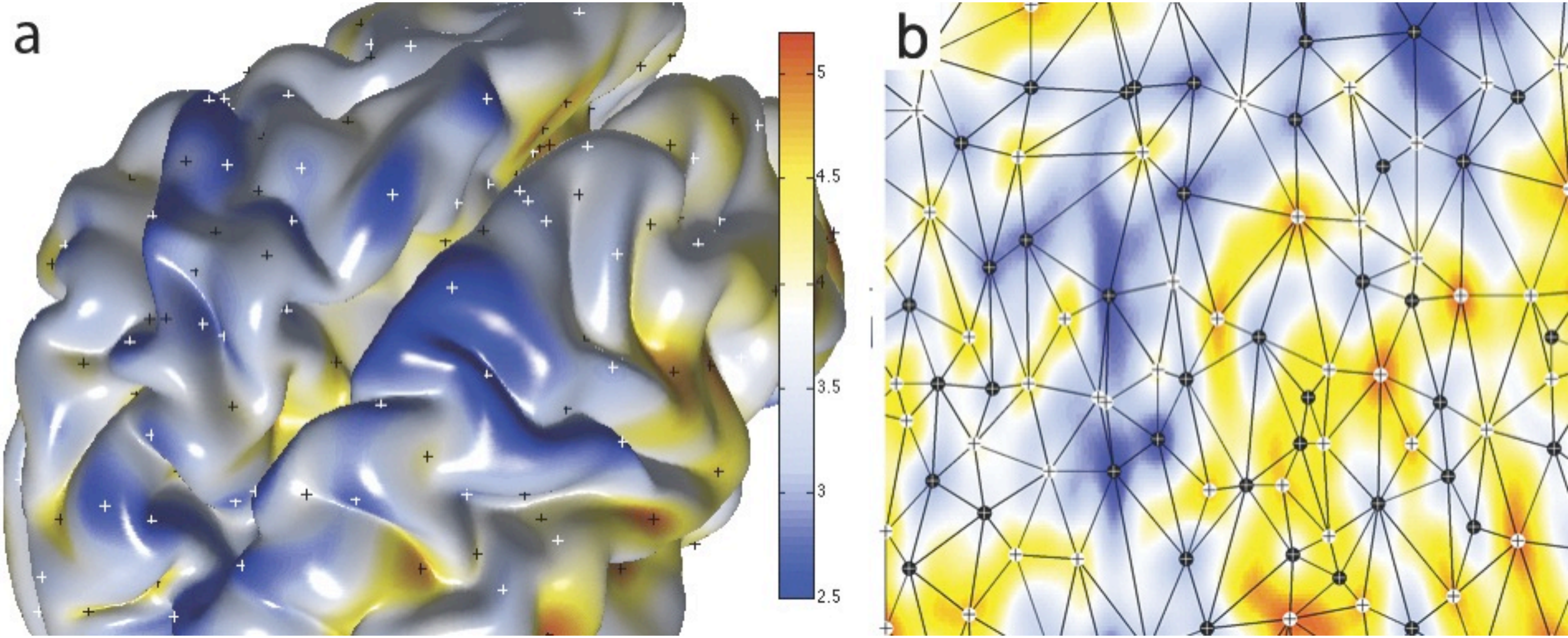
Critical values on cortical thickness



Chung et al. IPMI 2009
Chung et al. MICCAI 2009
Pachauri et al. IEEE TMI 2011

White cross = min
black cross = max

Other construction technique: Delaunay triangulation



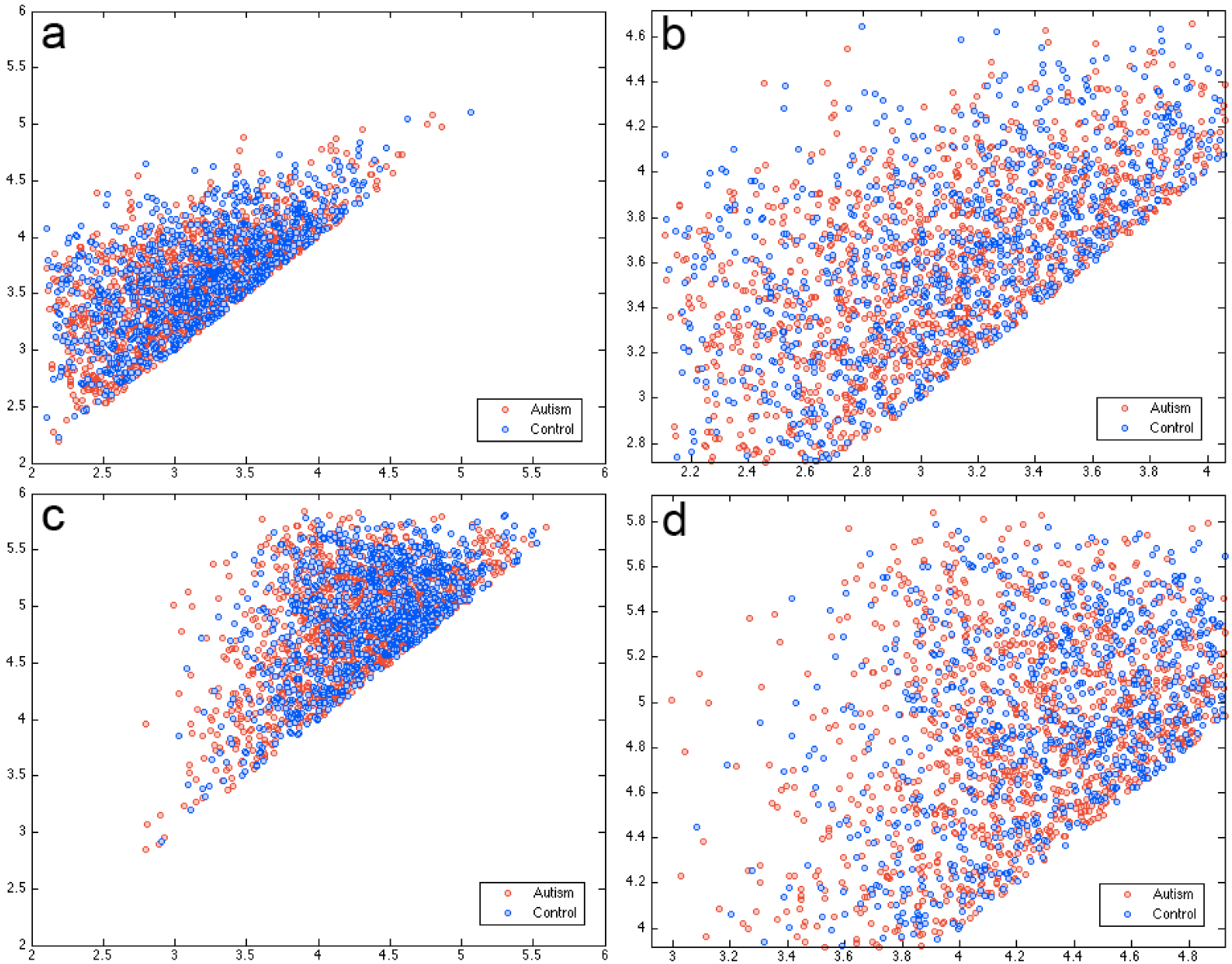
Chung et al. MICCAI 2009

Persistence Diagrams

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

degree 0
pairing of saddle points to minimums

degree 1
pairing of saddle points to maximums



Bar Codes

Persistence diagram is
too hard to interpret.

/adjacency.matrix/matlab/DEMO.2011.07.09.IMSchina.m

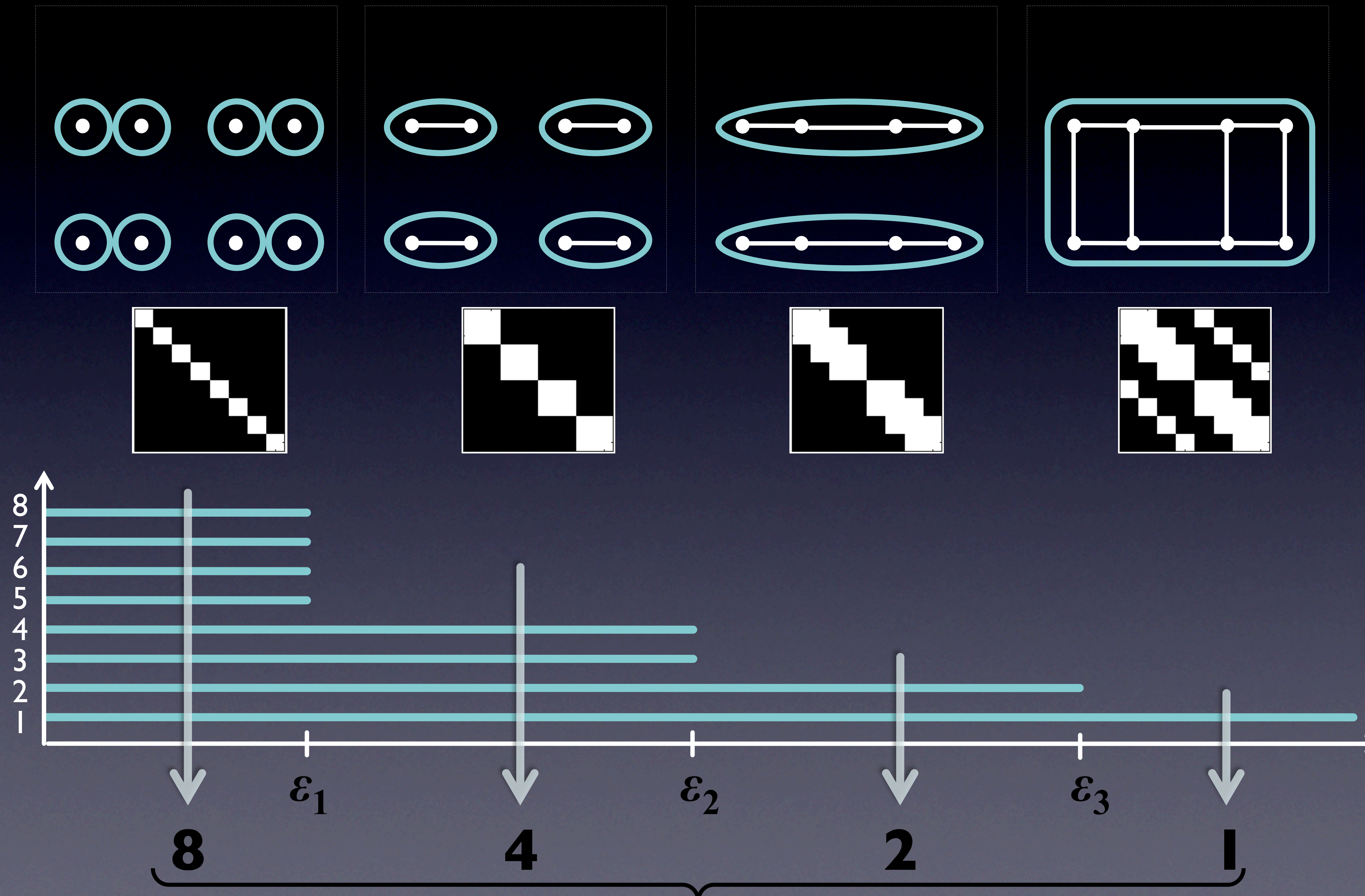
MATLAB DEMO

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

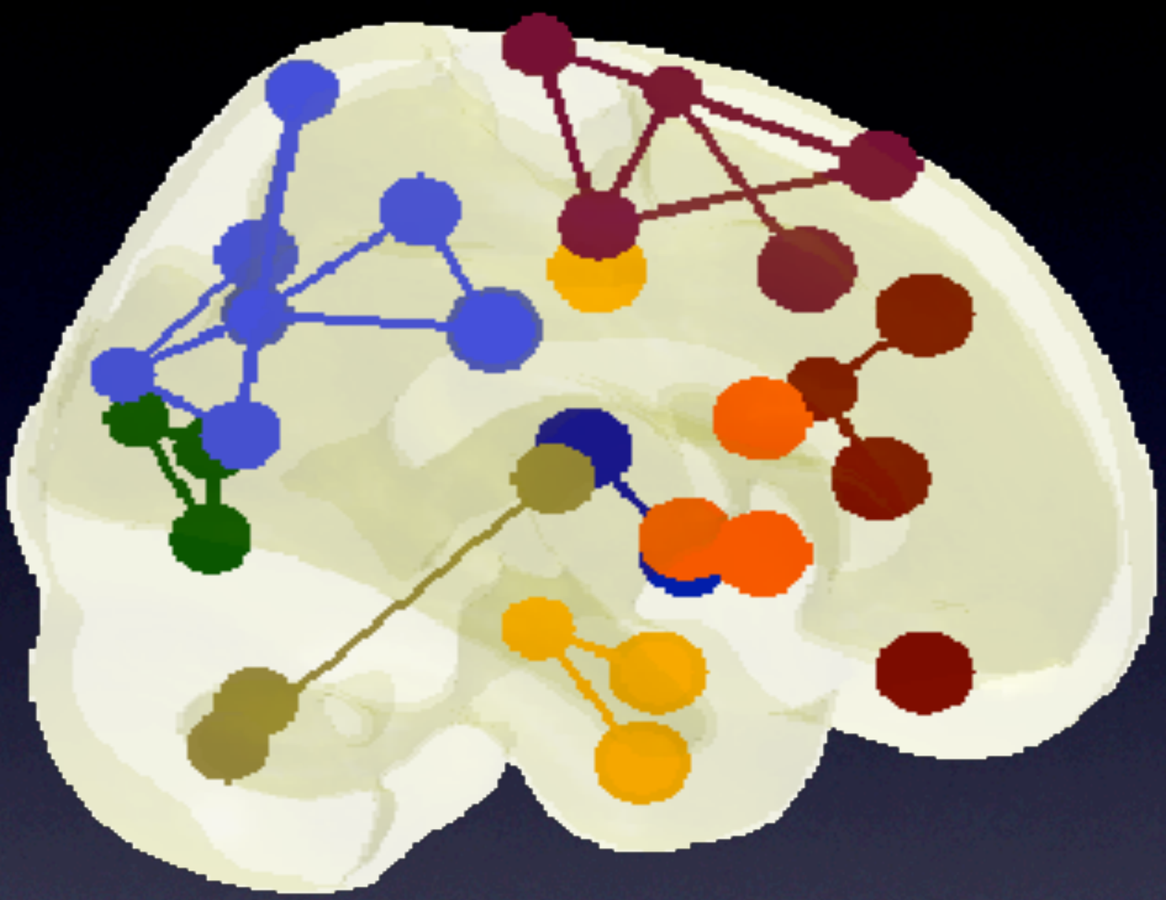
/adjacency.matrix/matlab/DEMO.2011.07.09.IMSchina.m

Rips Complex

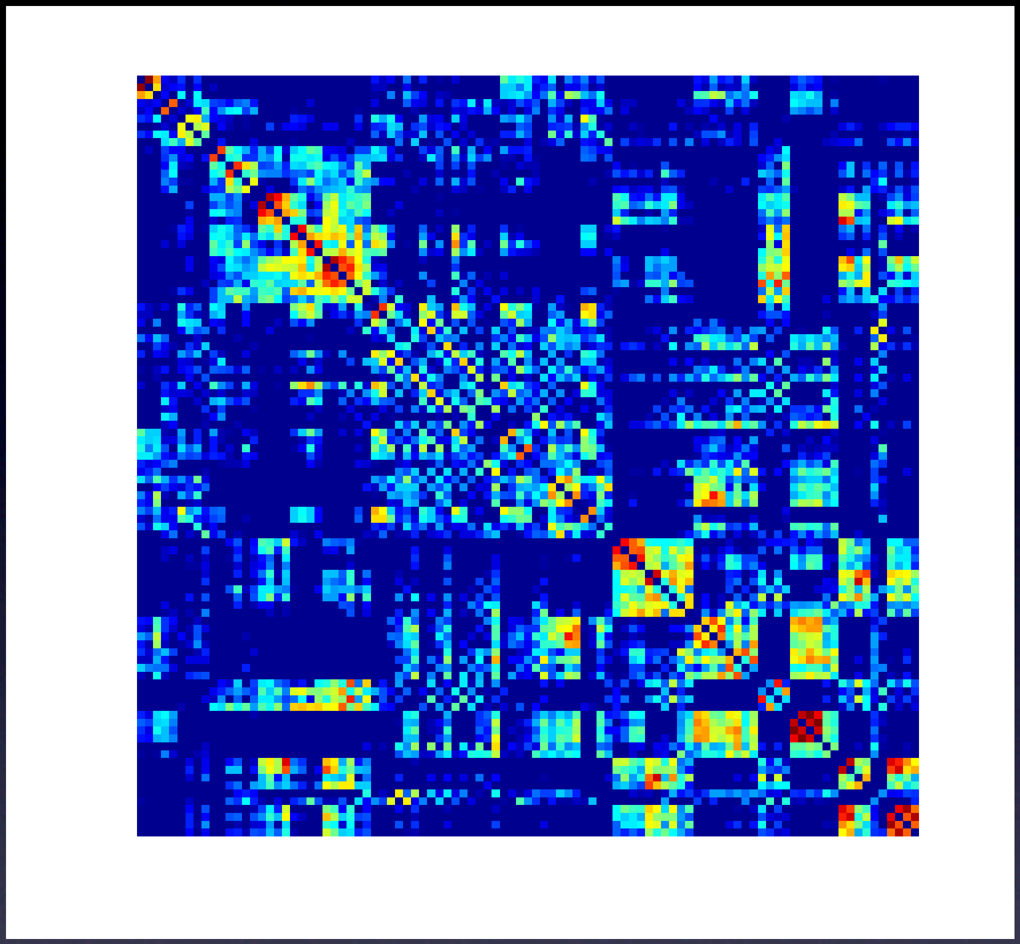
0-th Betti number over epsilon



Bar codes for brain network



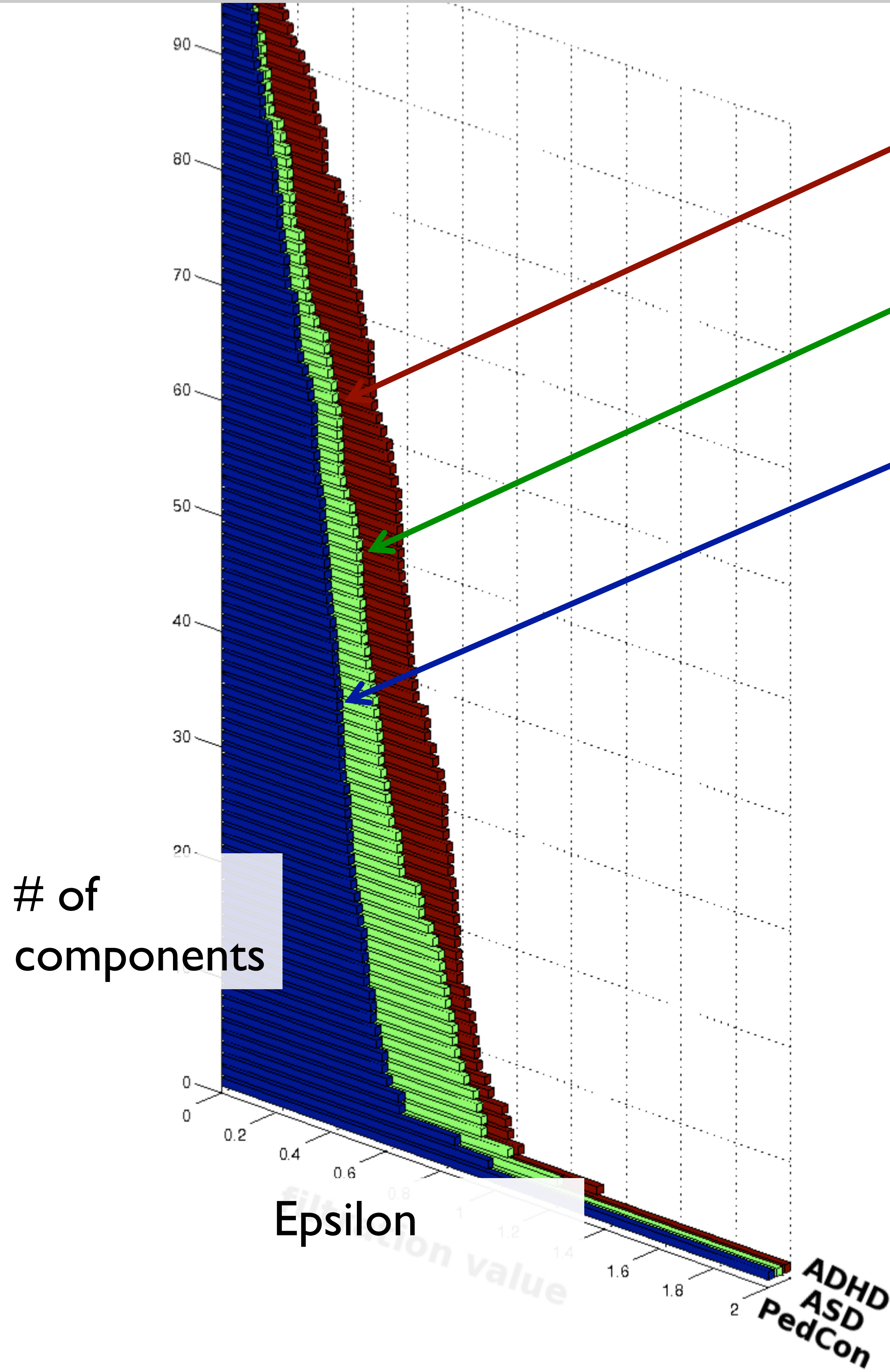
PET measures on nodes



Correlation

Distance = 1- correlation

Bar code on graph filtration



24 attention deficit hyperactivity disorder (ADHD) children

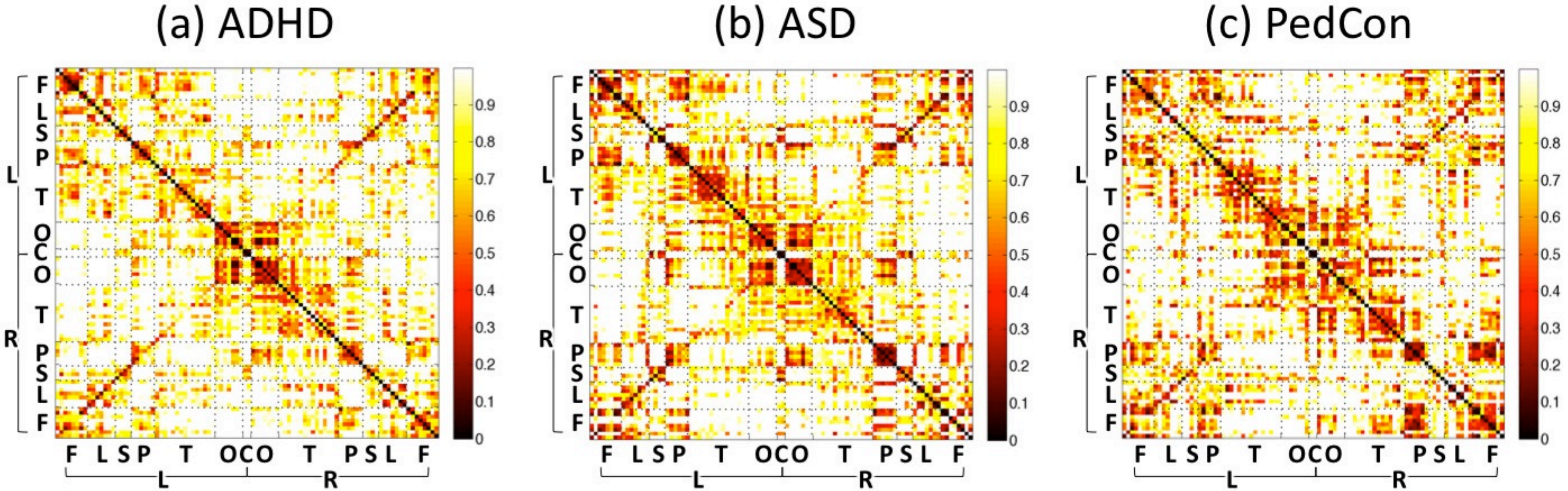
26 autism spectrum disorder (ASD) children

11 pediatric control subjects

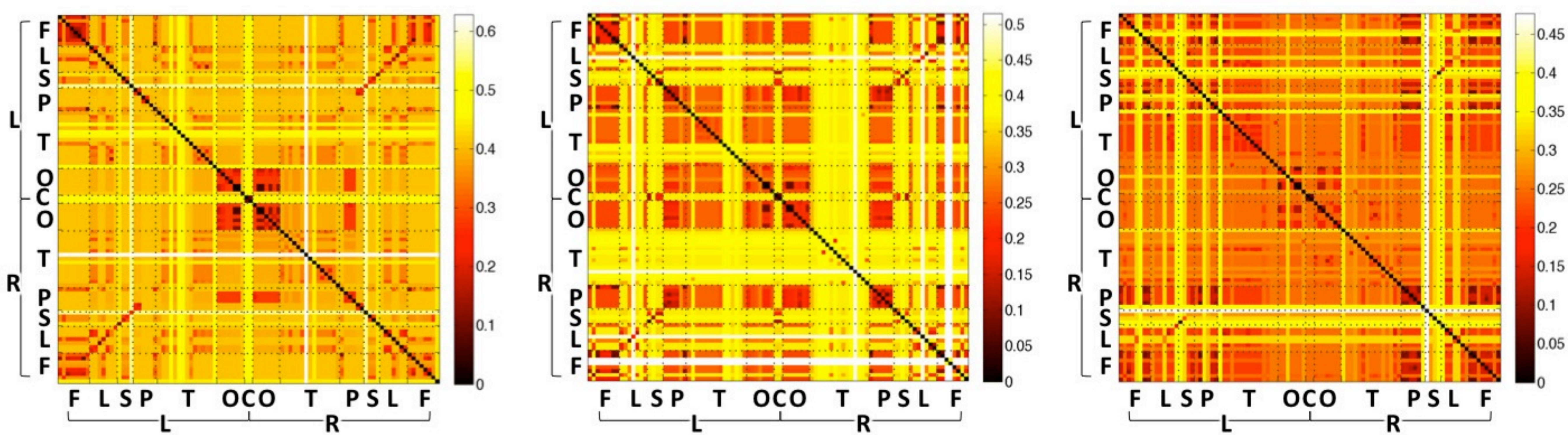
The brain network in control subjects merges to a single component faster than other populations!

Lee et al., 2011. ISBI

Connectivity matrix of brain network



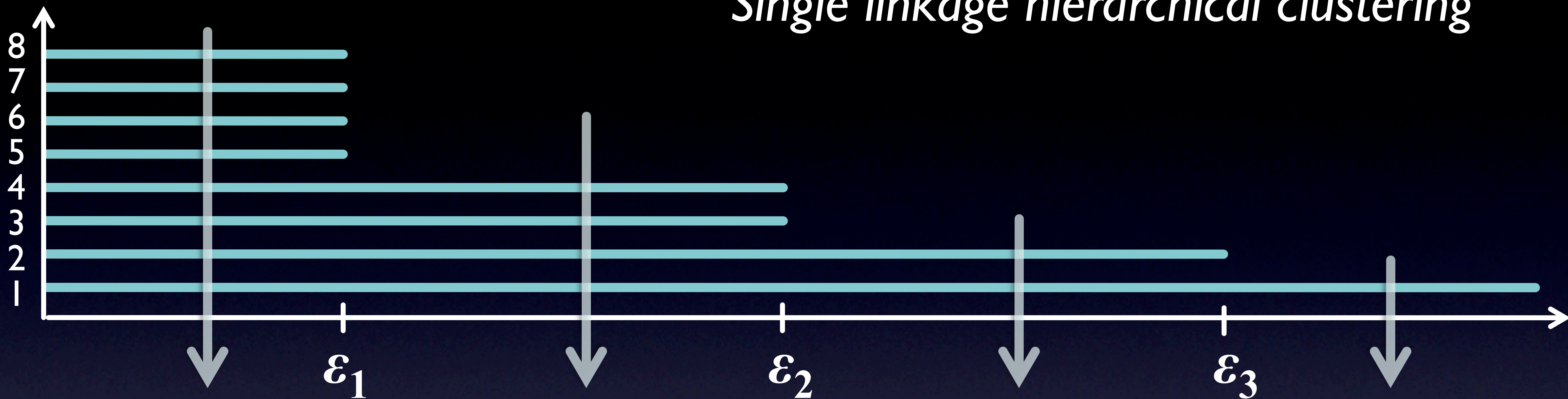
(d) Pairwise Distance Matrix = 1 - correlation



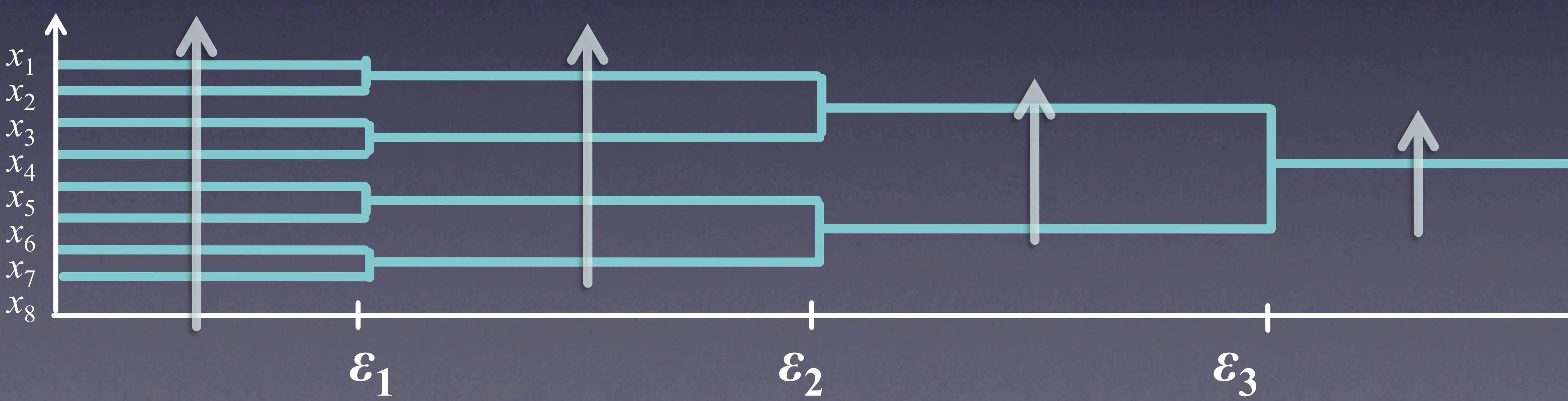
(e) Single Linkage Connectivity matrix

Permuted bar code = Dendrogram

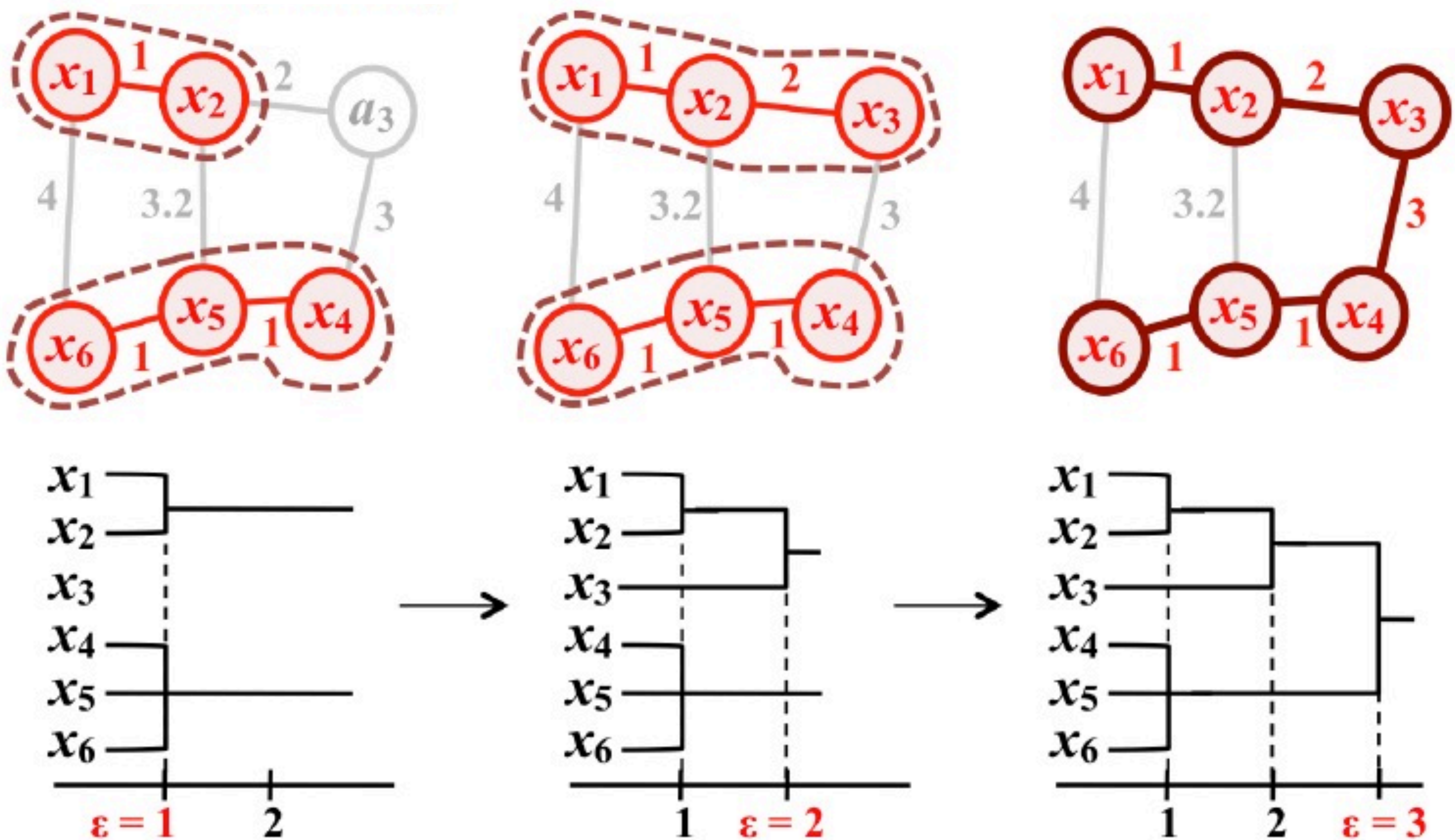
Single linkage hierarchical clustering



Rearrange the barcode according to the node index

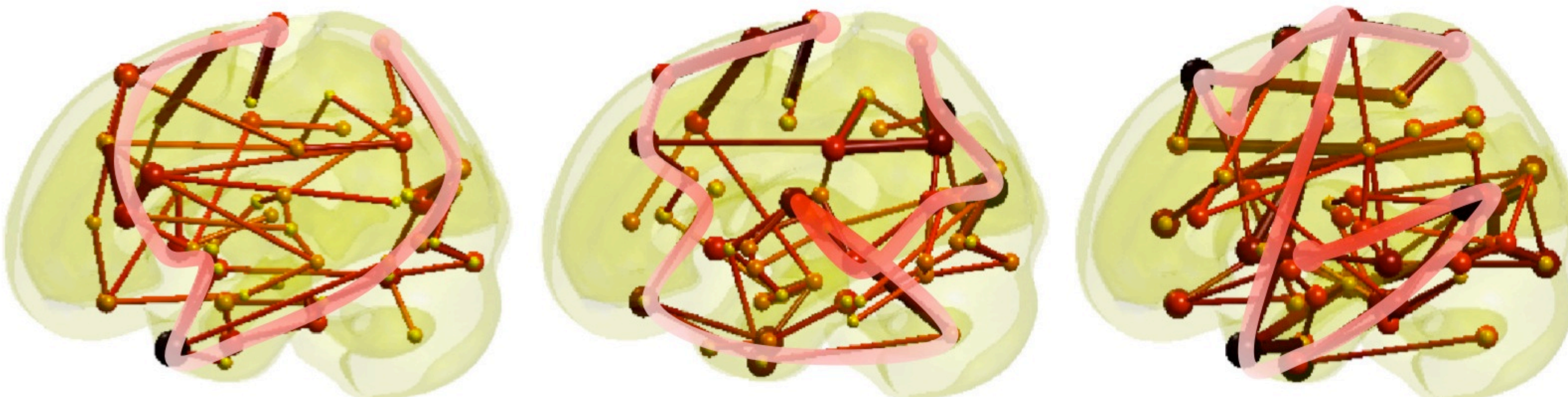


Network filtration = dendrogram construction



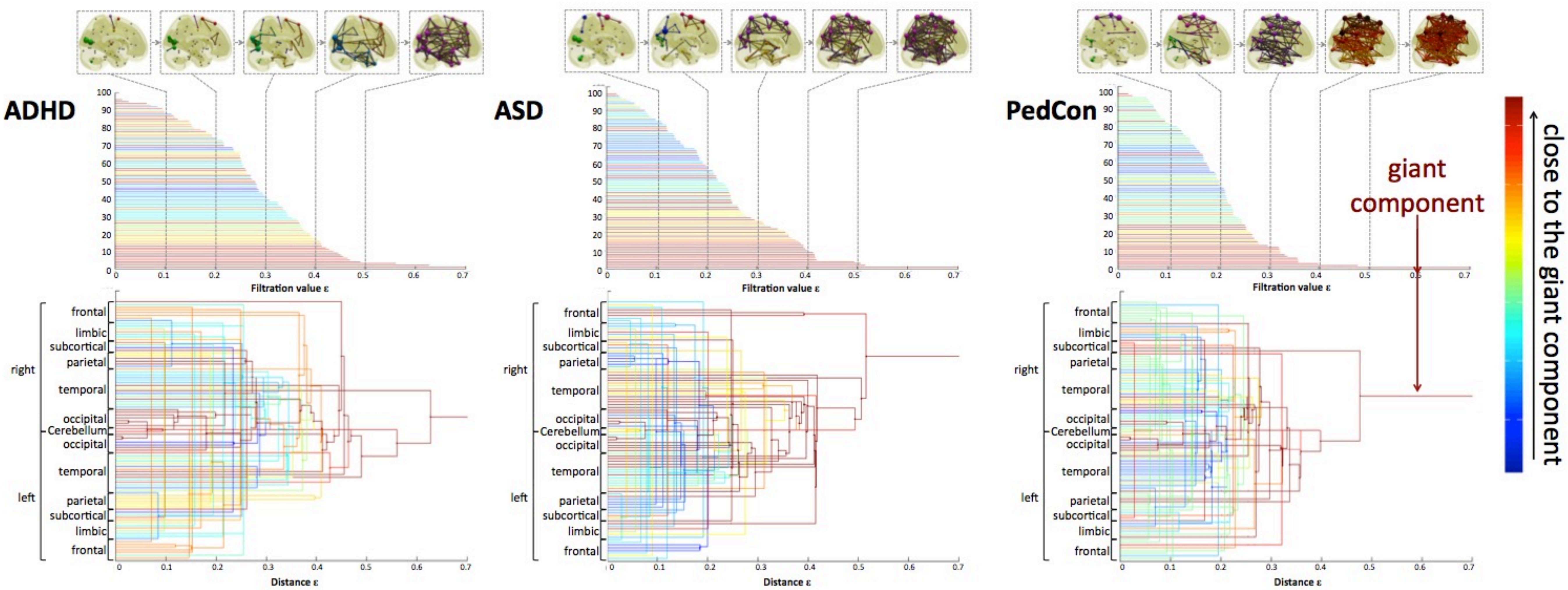
MICCAI 2011 Oral presentation

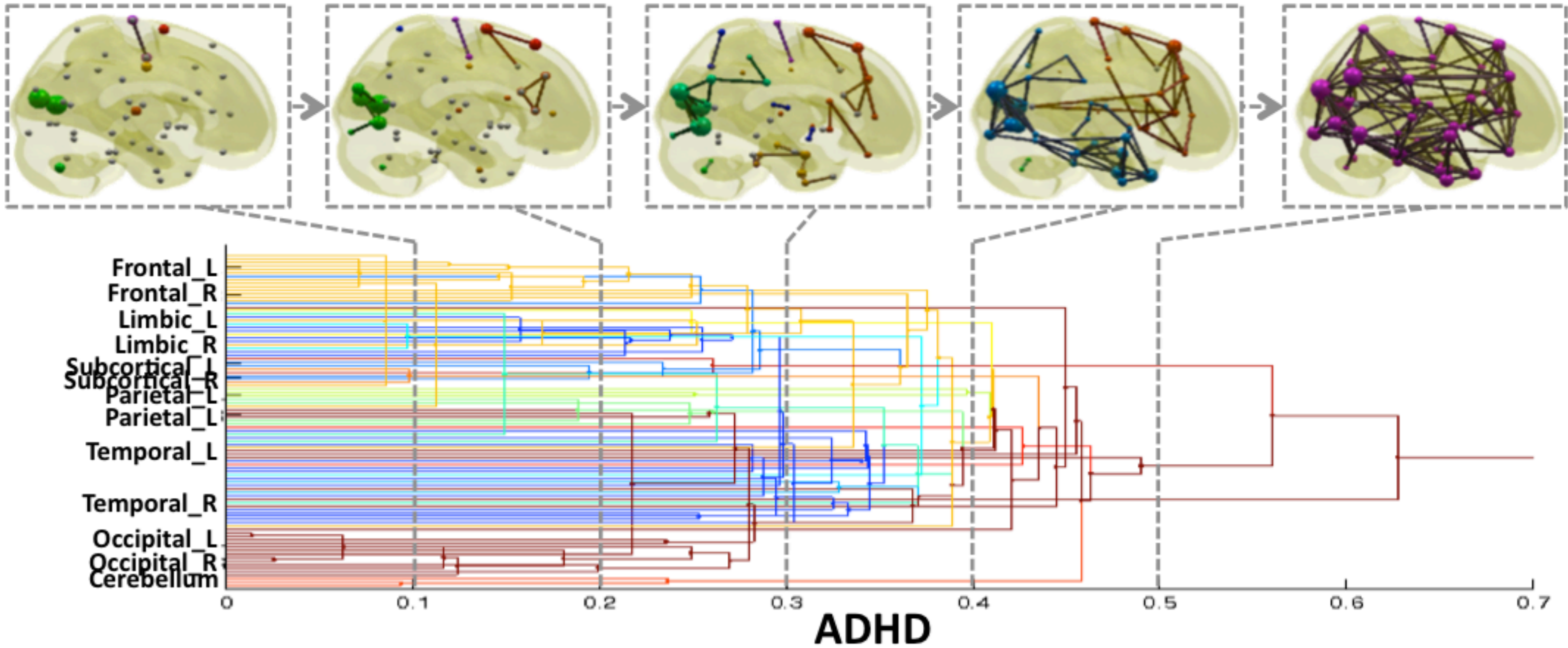
Minimum spanning tree = dendrogram



(a) ADHD (b) ASD (c) PedCon

Bar code and dendrogram difference





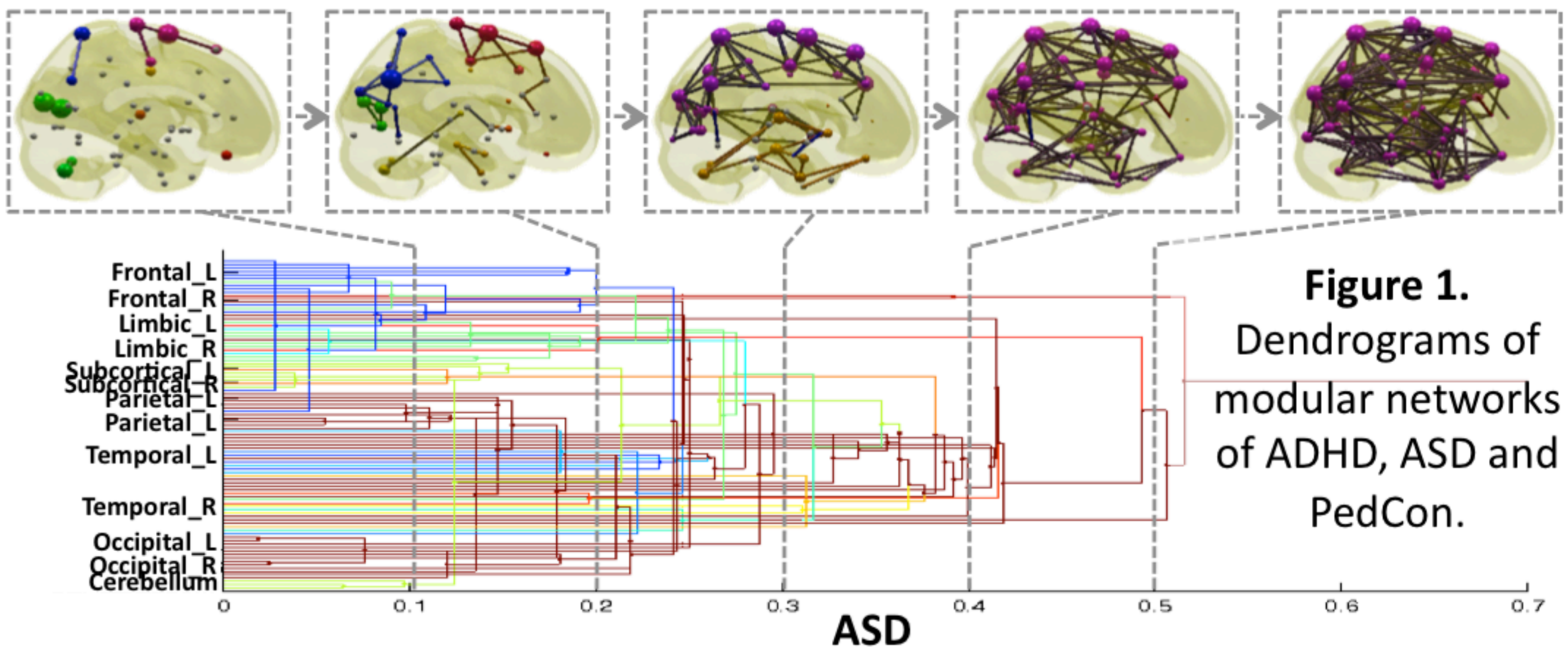
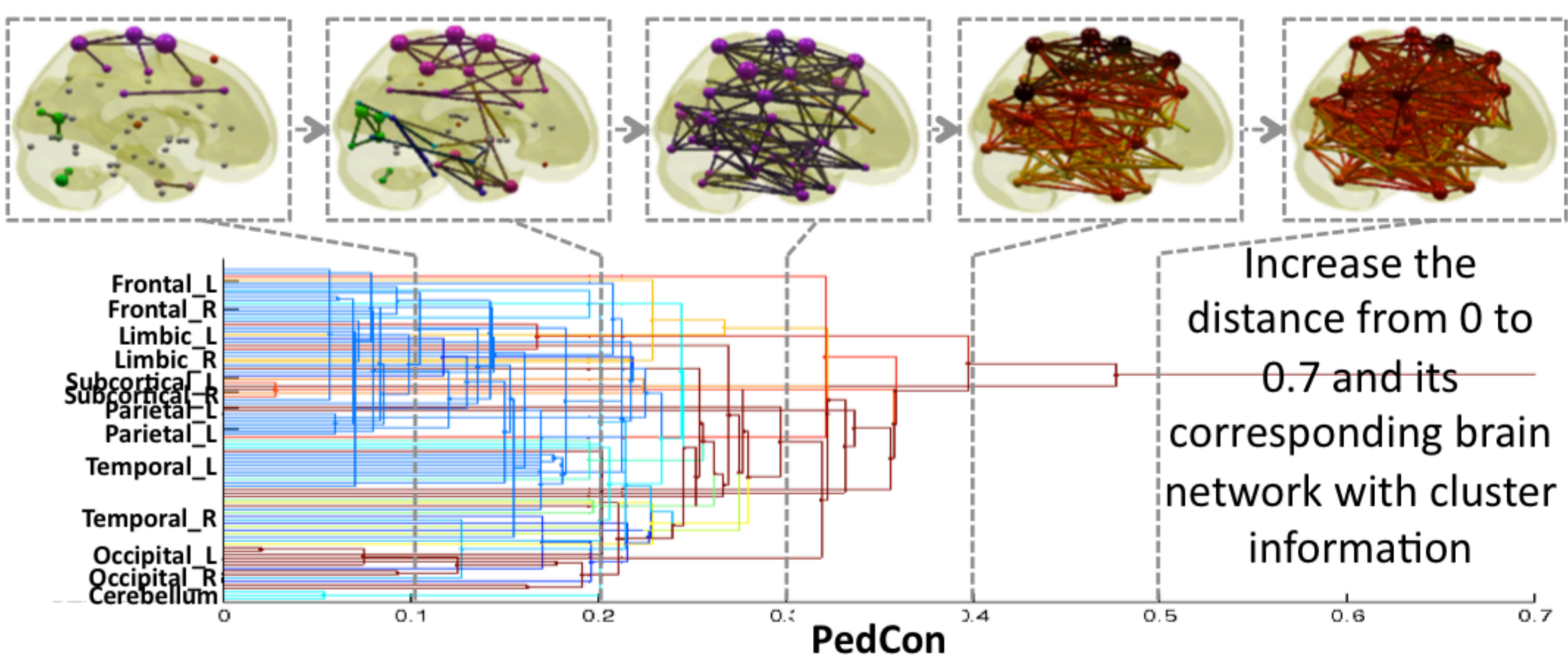
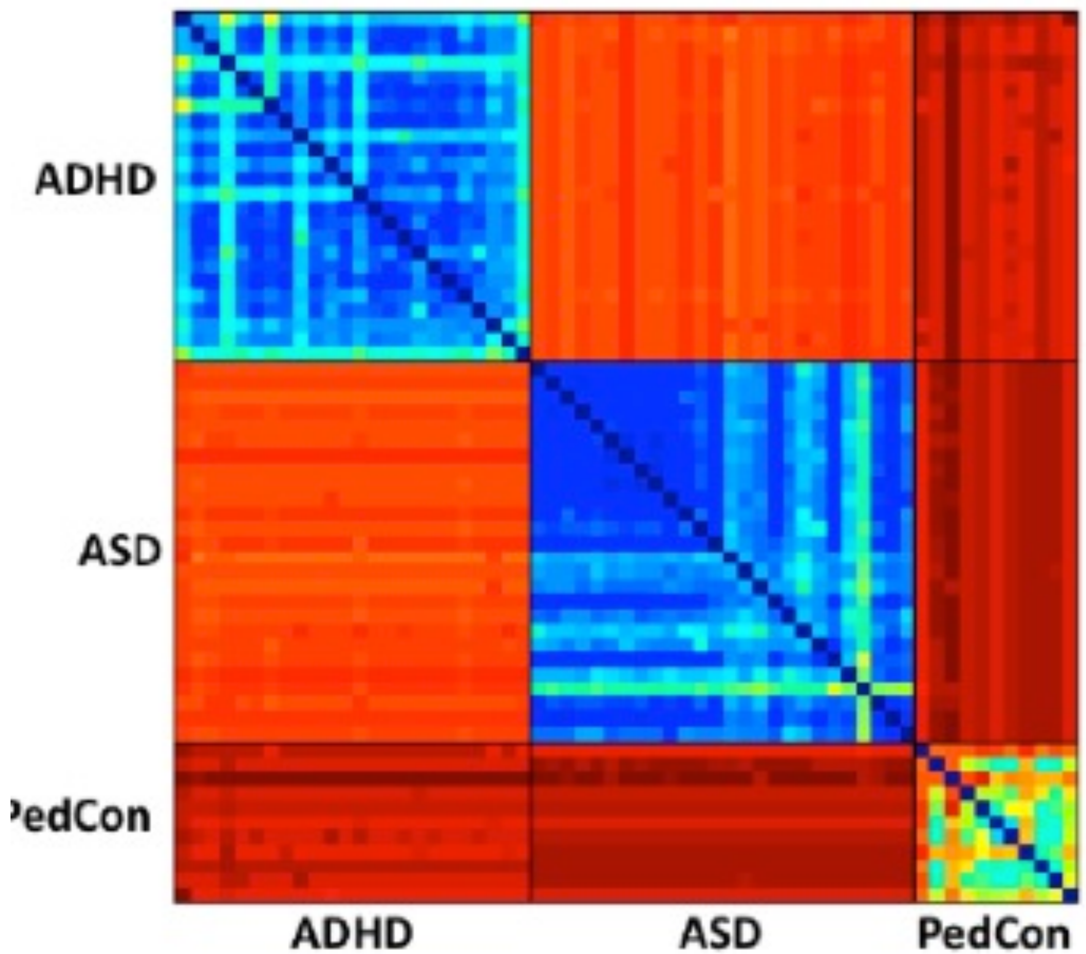


Figure 1. Dendrograms of modular networks of ADHD, ASD and PedCon.



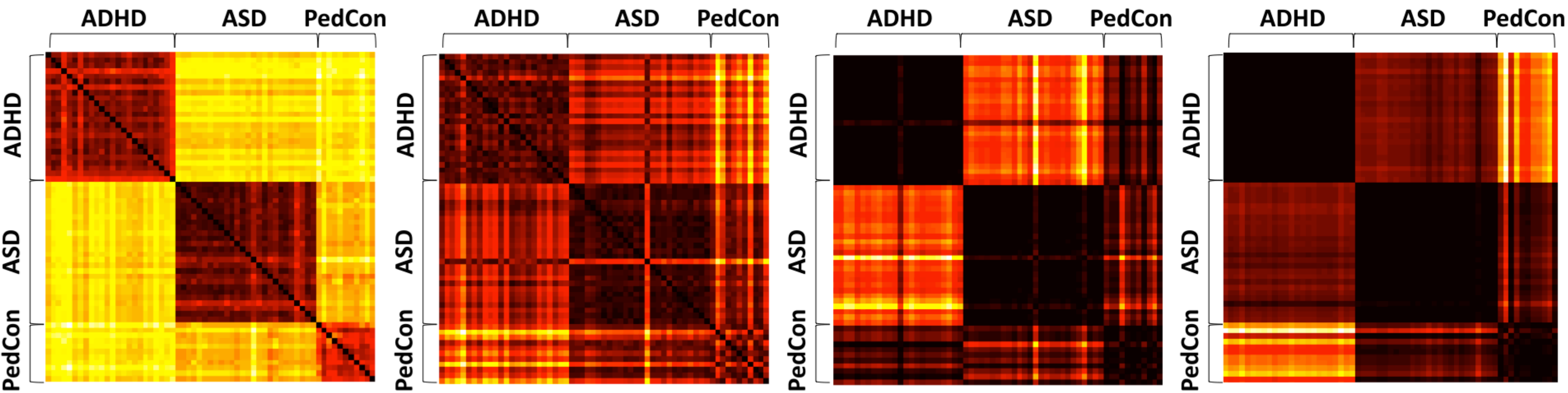
Increase the distance from 0 to 0.7 and its corresponding brain network with cluster information



Gromov-Hausdorff distance

Lee et al. 2011. HBM (selected for oral)

Classification Accuracy

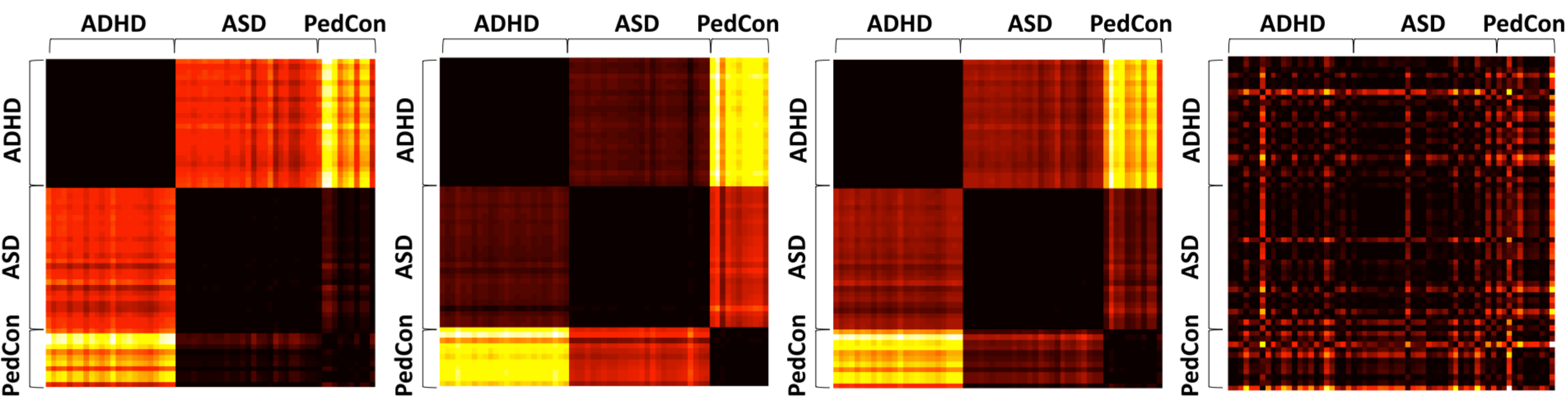


(a) GH distance
cluster_acc = 100 %
|w-b| = 0.4904

(b) Bottleneck distance
cluster_acc = 52.46 %
|w-b| = 0.1879

(c) Assortativity
cluster_acc = 77.05 %
|w-b| = 0.2982

(d) Betweenness Centrality
cluster_acc = 83.61 %
|w-b| = 0.2321



(e) Clustering Coefficient
cluster_acc = 85.25 %
|w-b| = 0.3382

(f) Characteristic Path Length
cluster_acc = 100 %
|w-b| = 0.3015

(g) Small-worldness
cluster_acc = 100 %
|w-b| = 0.2867

(h) Modularity
cluster_acc = 45.90 %
|w-b| = 0.0274

Thank you

Papers and MATLAB codes can be downloaded from www.stat.wisc.edu/~mchung