



*The Waisman Laboratory  
for Brain Imaging and Behavior*



University of Wisconsin  
**SCHOOL OF MEDICINE  
AND PUBLIC HEALTH**

# Lecture 1 Simplicial homology and persistent homology

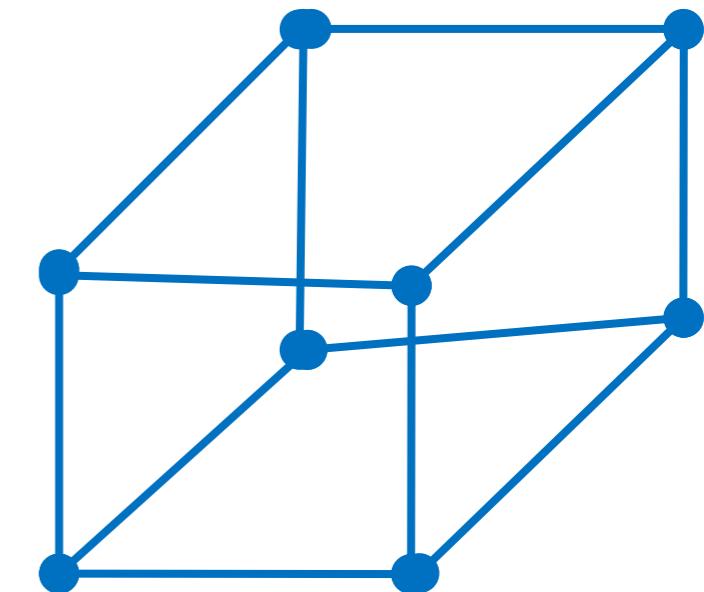
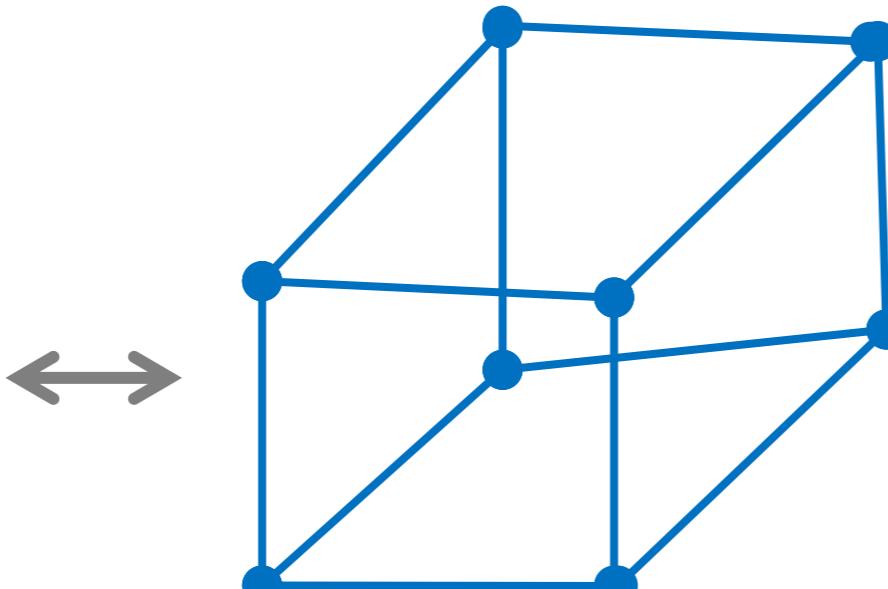
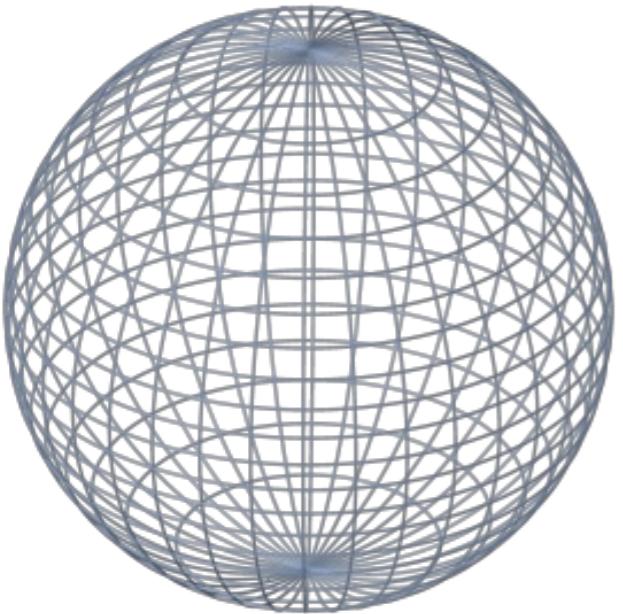
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University of Wisconsin-Madison

[www.stat.wisc.edu/~mchung](http://www.stat.wisc.edu/~mchung)

# Euler characteristic

Topologically equivalent  
Deformation-invariant



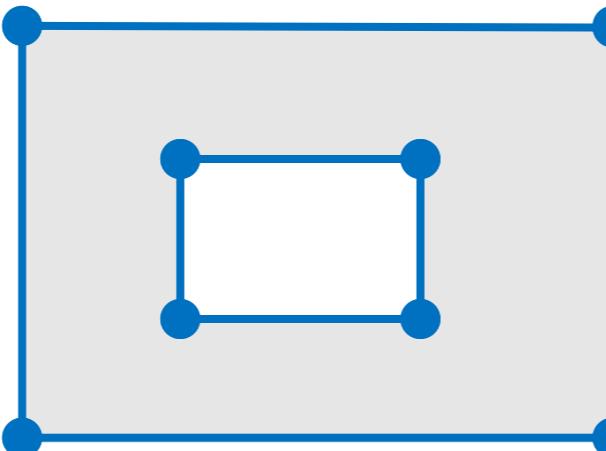
Sphere

$$\begin{aligned} \text{EC} &= N - E + F \\ &= 8 - 12 + 6 \\ &= 2 \end{aligned}$$

Solid ball

$$\begin{aligned} \text{EC} &= N - E + F - V \\ &= 8 - 12 + 6 - 1 \\ &= 1 \end{aligned}$$

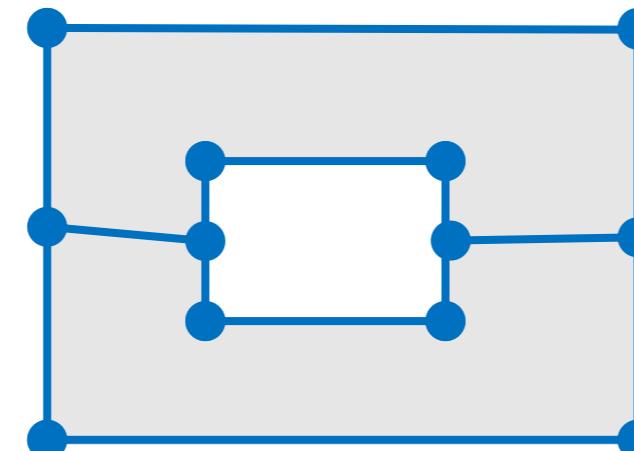
# Computing Euler characteristic by parts



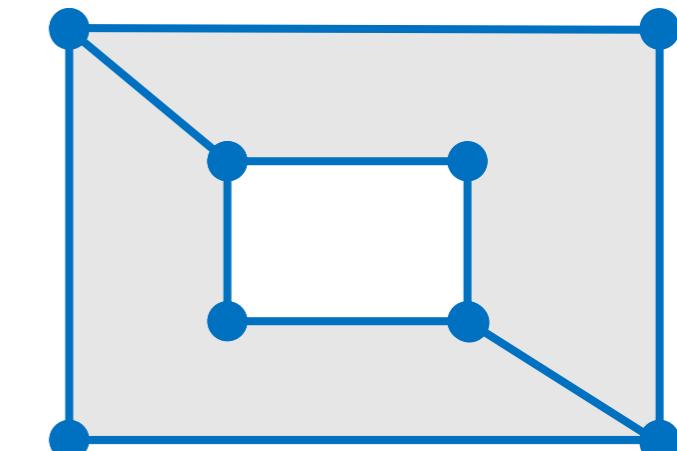
Cover an object  
with polyhedrons

Incorrect computation

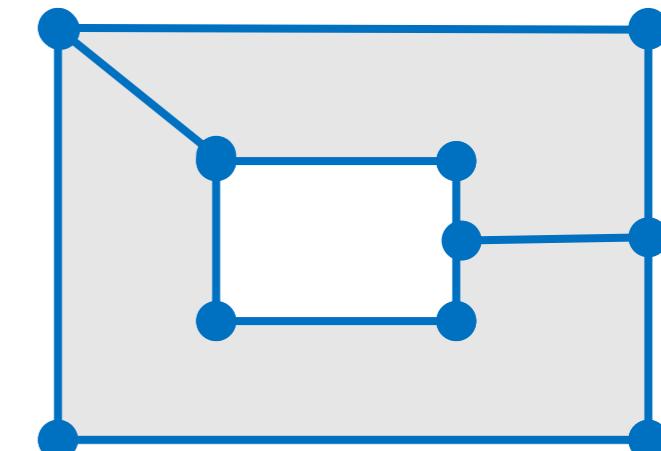
$$\begin{aligned} EC &= N - E + F \\ &= 8 - 8 + 1 \\ &= 1 \end{aligned}$$



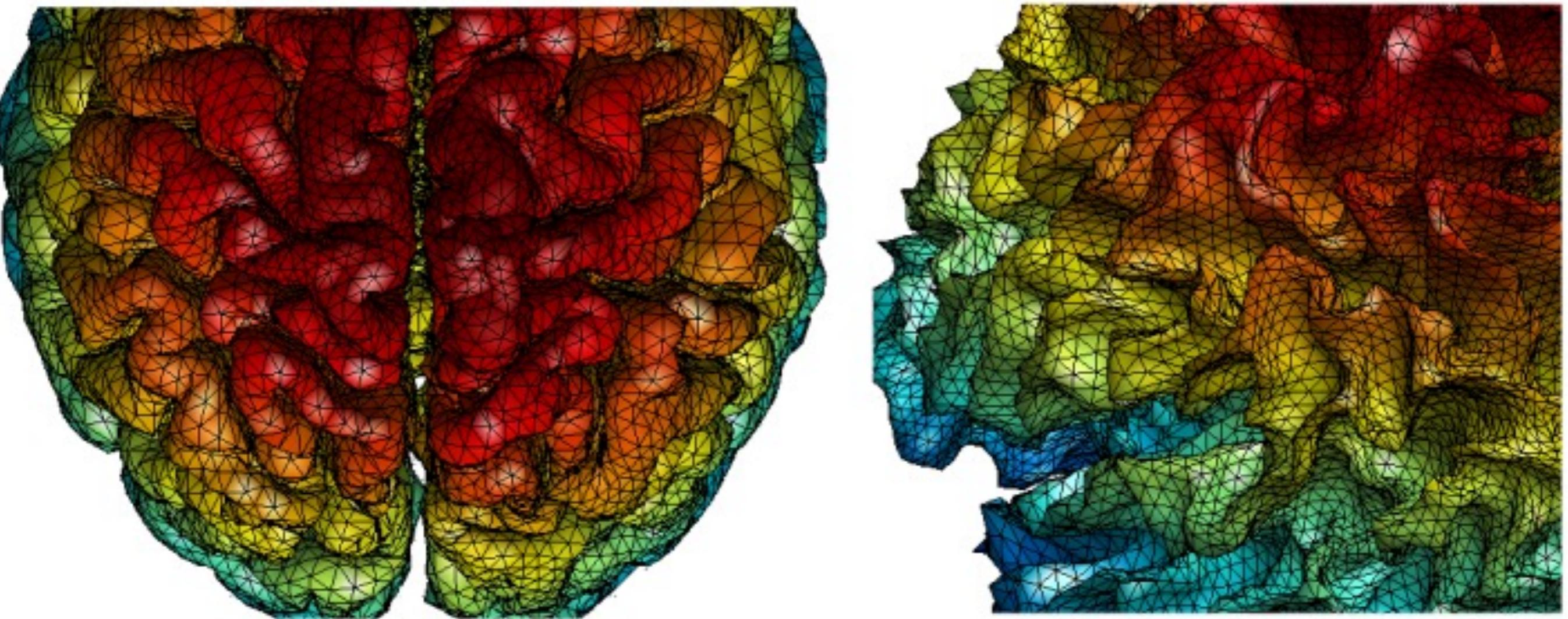
$$\begin{aligned} EC &= N - E + F \\ &= (8+4) - (8+6) + (1+1) \\ &= 0 \end{aligned}$$



$$\begin{aligned} EC &= N - E + F \\ &= 8 - (8+2) + (1+1) \\ &= 0 \end{aligned}$$



$$\begin{aligned} EC &= N - E + F \\ &= (8+2) - (8+4) + (1+1) \\ &= 0 \end{aligned}$$



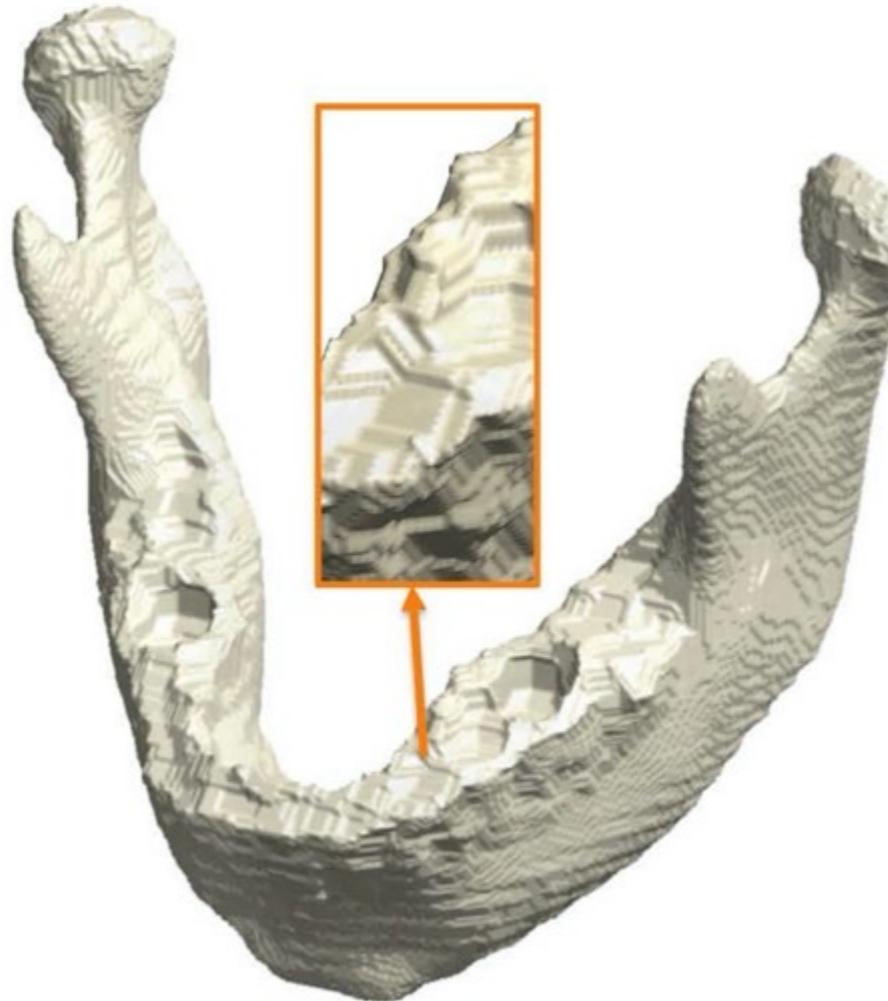
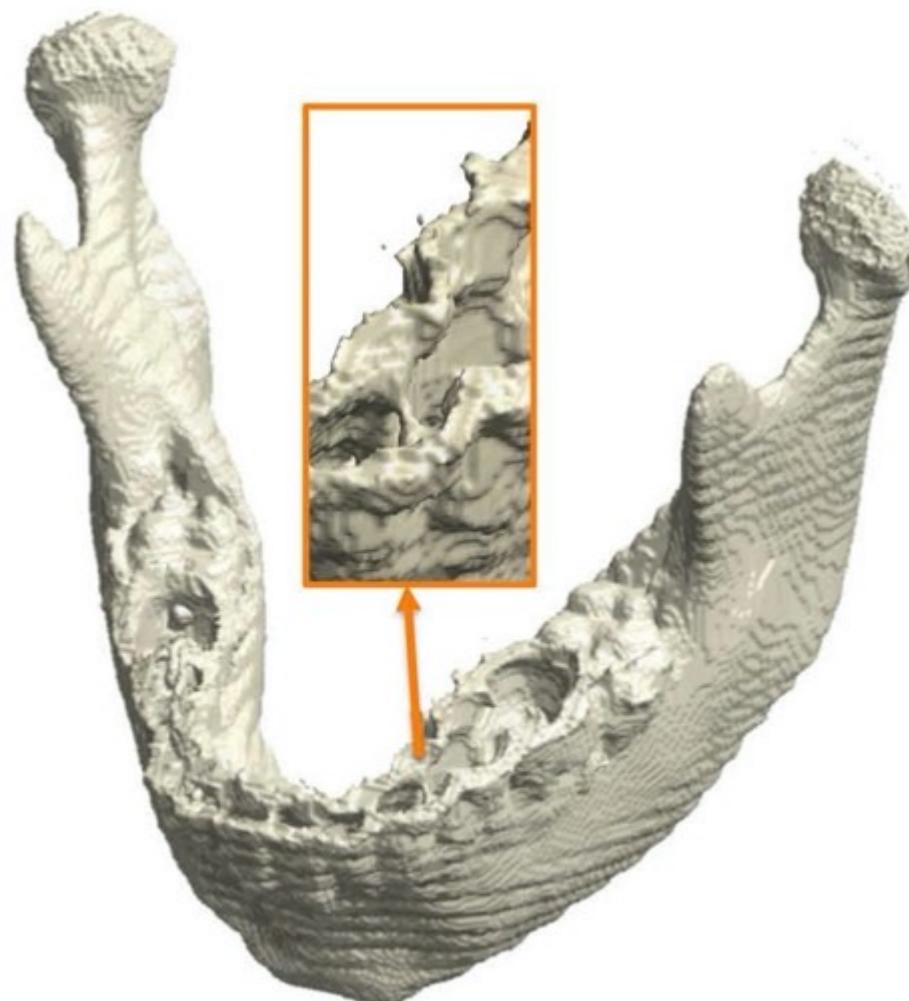
## Euler characteristic of a surface mesh from SurfStat

$N - E + F = 2$  for a surface topologically equivalent to a sphere. For each triangle, there are three edges. Since two adjacent triangles share the same edge, the total number of edges is  $E = 3F/2$ . Hence, we have  $F=2N - 4$  for a closed surface.



By checking the **Euler characteristic** of the binary volume of a mandible, holes in the binary volume can be detected. This process is necessary to make the mandible binary volume to be topologically equivalent to a solid sphere.

# Topology correction in segmentation



Hole & handles  
corrected using  
Euler characteristic

# Geometry to Topology

Gauss–Bonnet theorem The integral of the Gauss curvature on a 2D Riemannian manifold is  $2\pi\chi(\mathcal{M})$ , where  $\chi(\mathcal{M})$  is the Euler characteristic of  $\mathcal{M}$ .

# Keith Worsley's random field theory

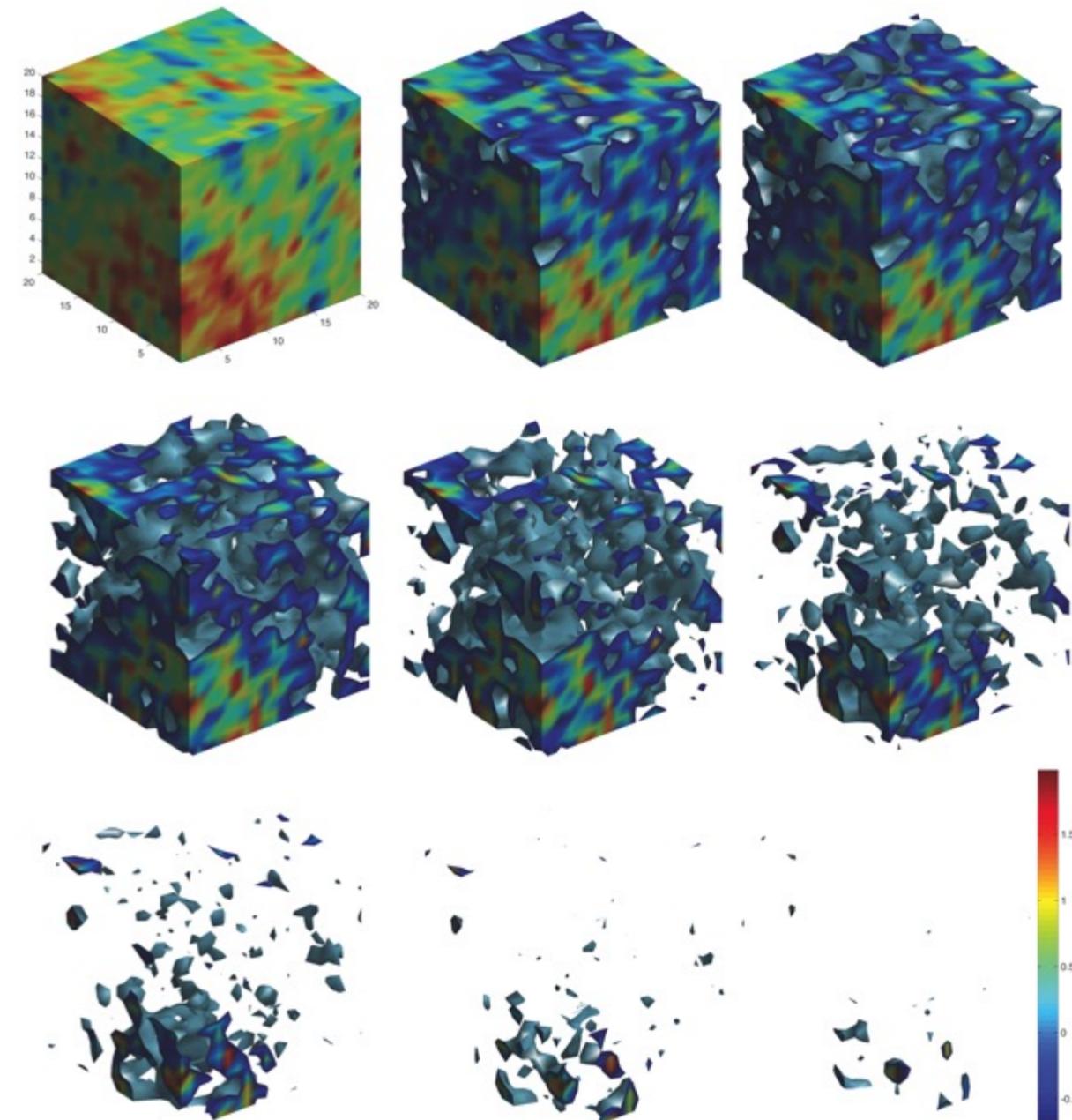
Random field, stochastic process

$$P\left(\sup_{x \in \mathbb{M}} T(x) > h\right)$$

$$A_h = \{x \in \mathbb{M} : T(x) > h\}$$

$$P\left(\sup_{x \in \mathbb{M}} T(x) > h\right) = \mathbb{E}\chi(A_h)$$

$$\chi(A_h) = \sum_j (-1)^j \beta_j(A_h)$$



Milnor 1963 Morse theory

Adler, 1994 The geometry of random fields

Worsley et al., 1996 Human Brain Mapping

# Matlab toolbox

## PH-STAT

Statistical Inference on Persistent Homology

<https://github.com/laplcebeltrami/PH-STAT>

# Topological Data Analysis

- Branch of data science that uses topology
- Study properties of data that remain invariant under continuous transformations
- Identify underlying patterns using topology

# Persistent Homology

- Captures the topological features of data across different scales
- More persistent topological features → signal
- Less persistent topological features → noise
- Multiscale approach

## *References*

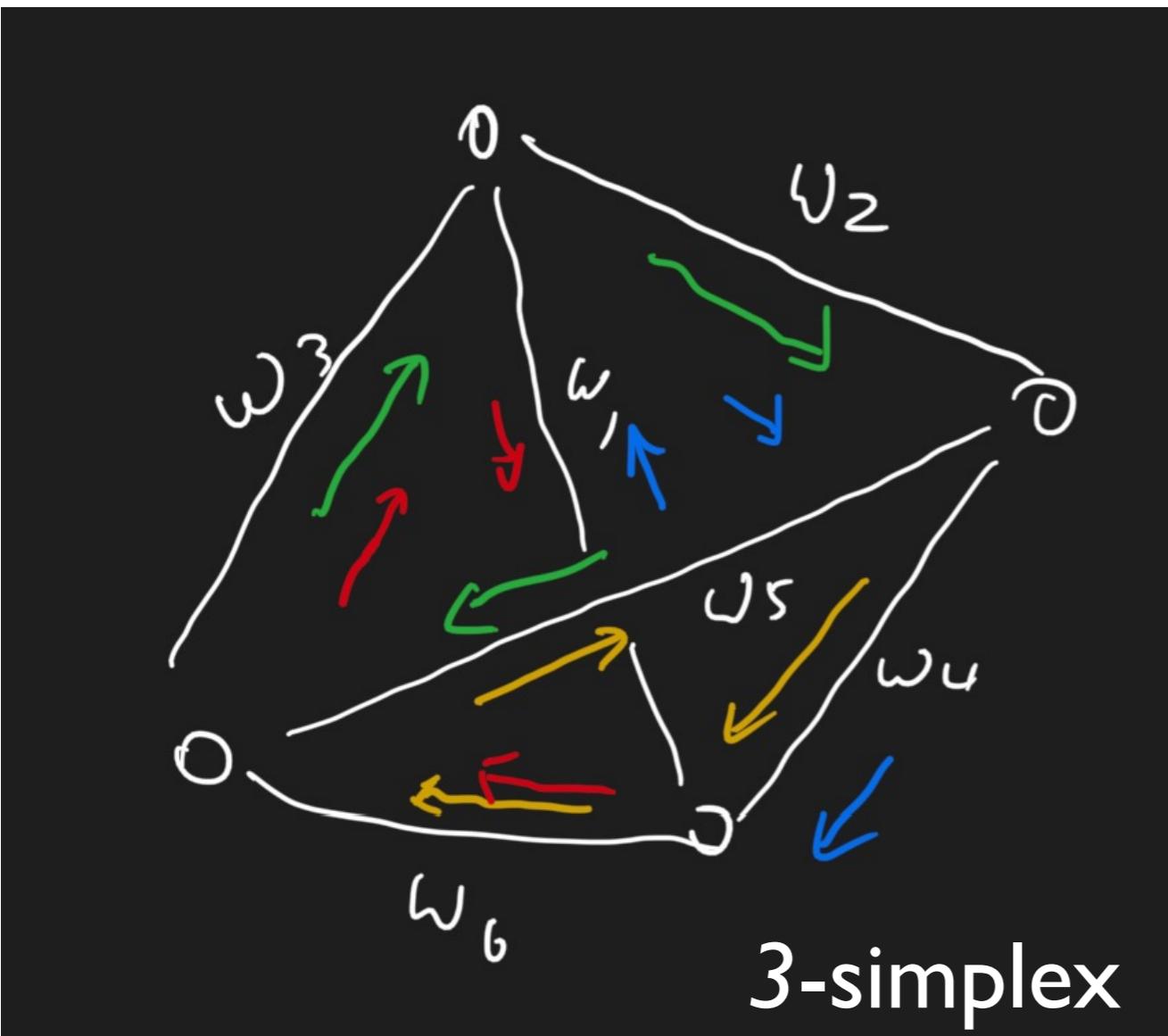
Gunnar Carlsson 2009, A User's Guide to Topological Data Analysis

Herbert Edelsbrunner and John L. Harer  
Computational Topology: An Introduction 2010,  
American Mathematical Society

Chung et al. 2020 Review: Toplogical distance and losses in brain networks arXiv:2102.08623

# $n$ -simplex

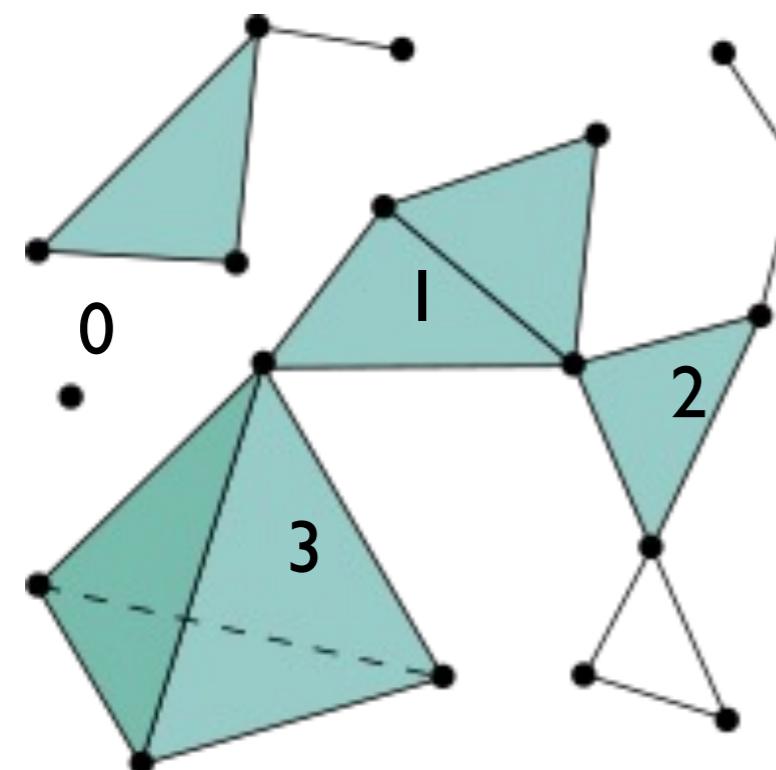
The basic building block of persistent homology  
The smallest convex set containing  $n+1$  points



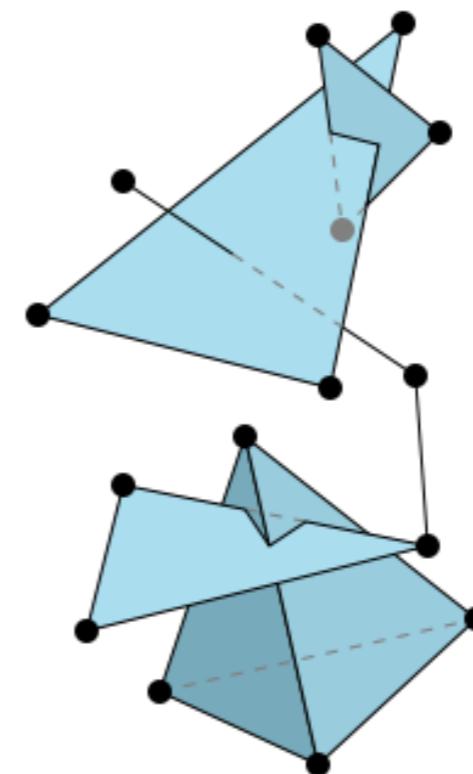
$$\sum_{i=0}^n x_i = 1, x_i \geq 0$$

# Simplicial complex

A simplicial complex is a set composed of points, line segments, triangles, and their n-dimensional counterparts.



Simplicial complex

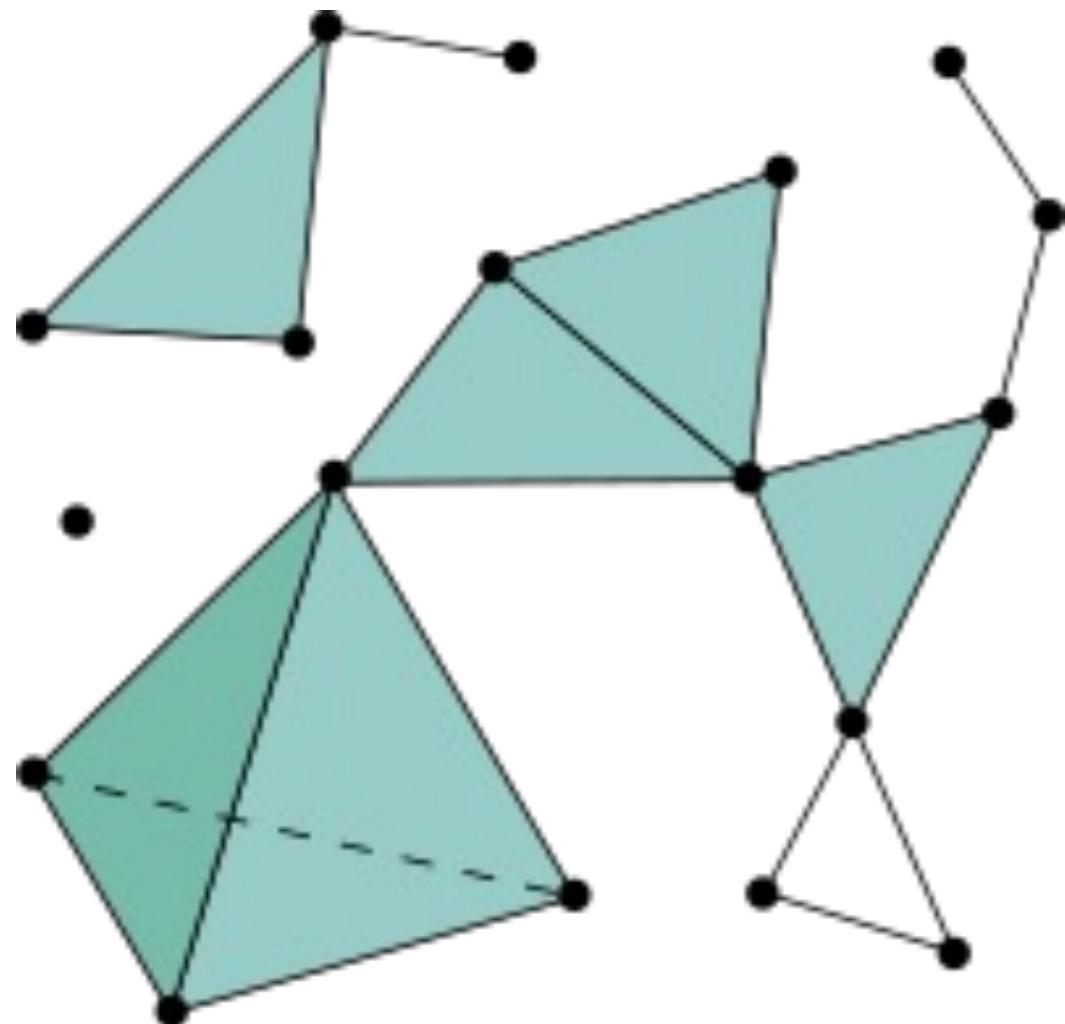


Not simplicial complex

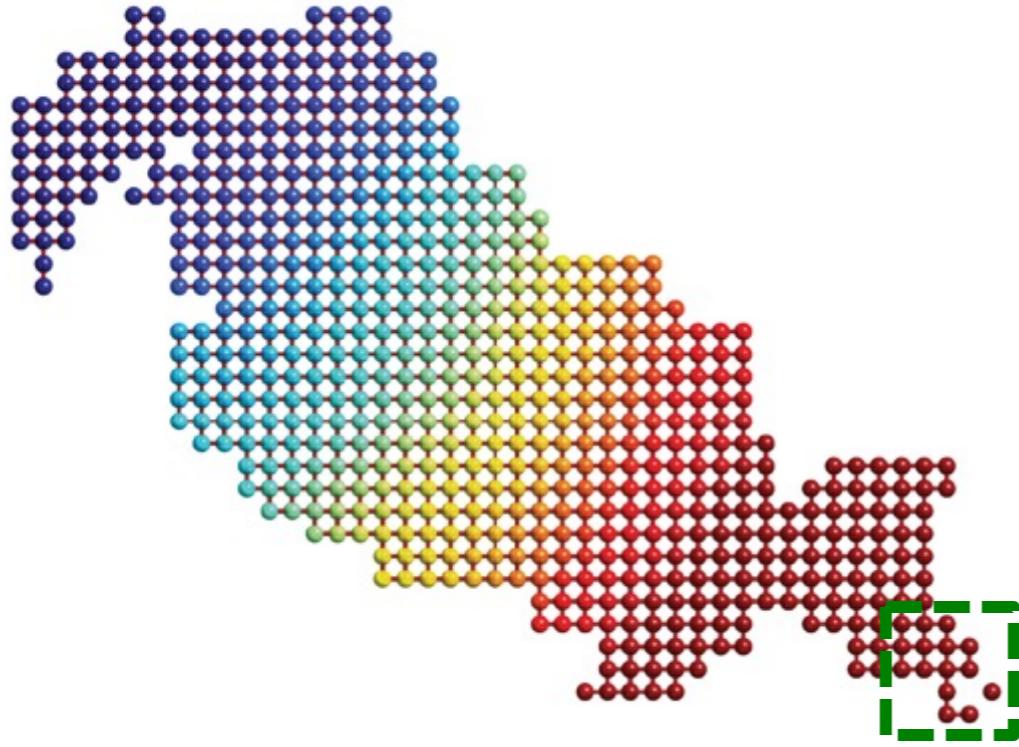
*Ex.* surface mesh, graphs (including hypergraphs), networks

## k-skeleton

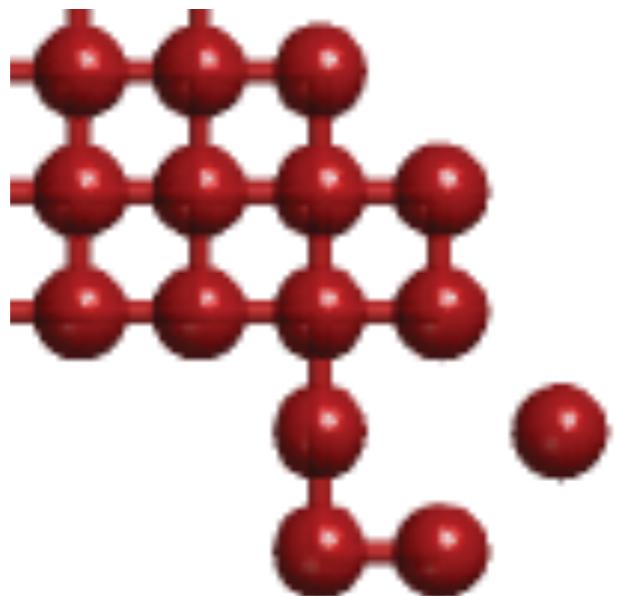
A simplicial complex consisting of points and line segments only → graphs & network



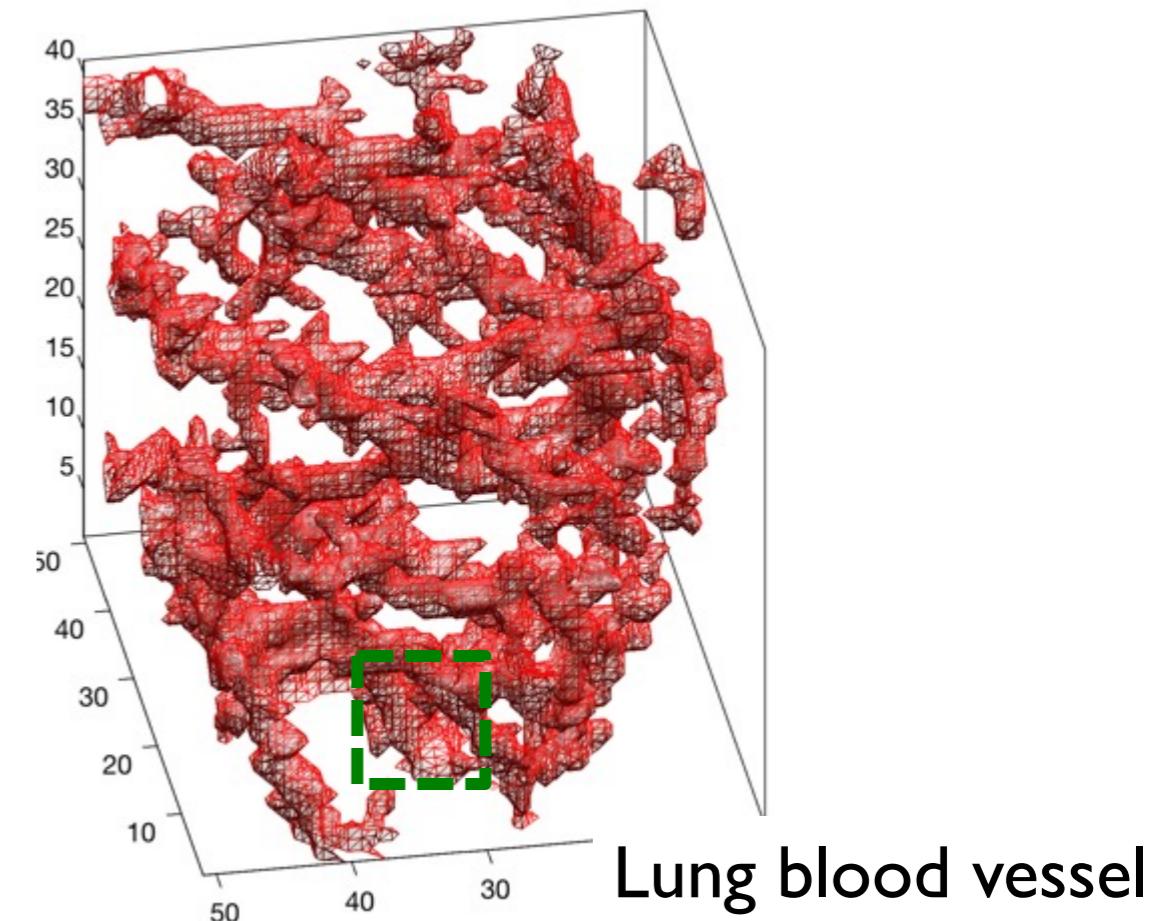
# Cubical complex (2D or 3D images)



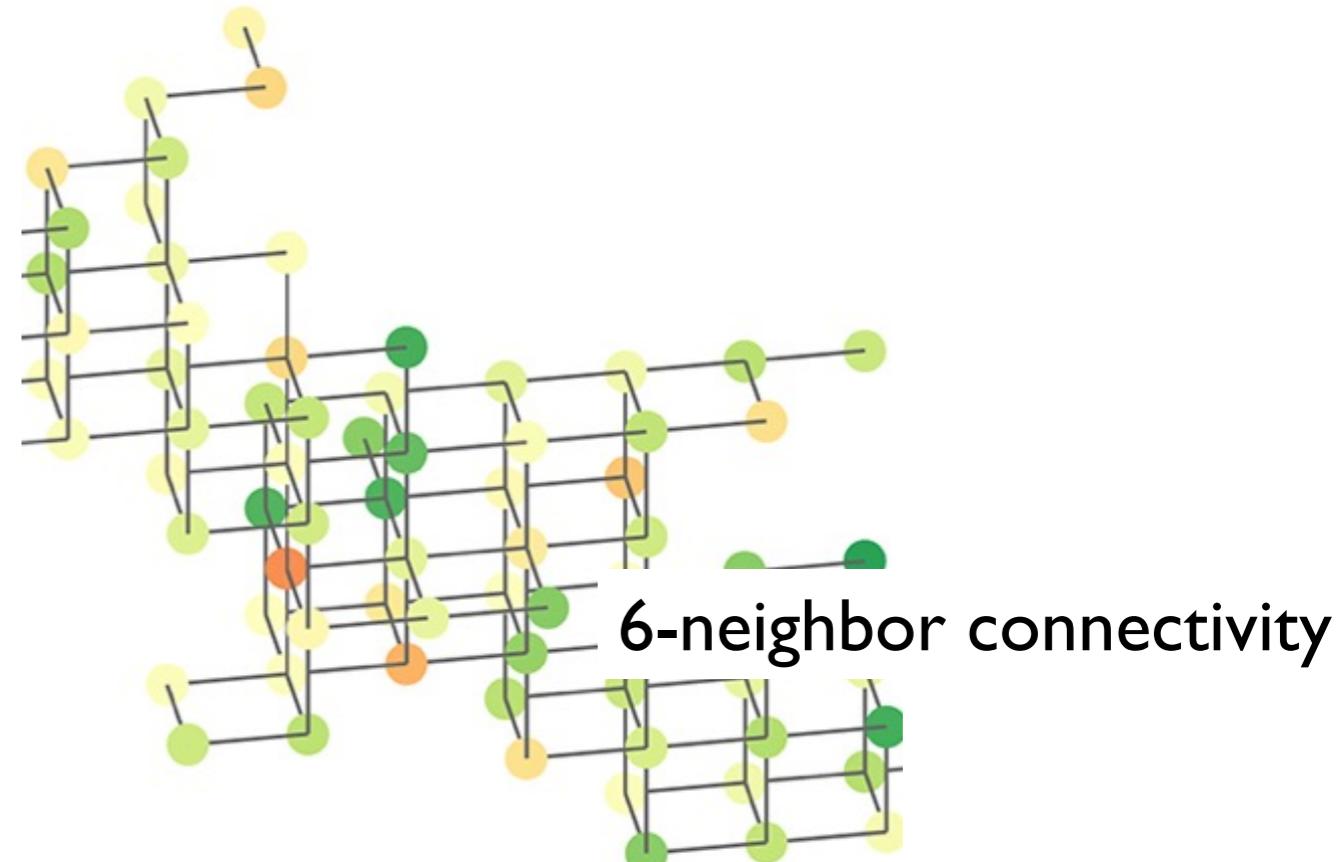
Left central gyrus



4-neighbor connectivity



Lung blood vessel



6-neighbor connectivity

Betti numbers  $\beta_i$

# of i-dimensional  
holes/loops

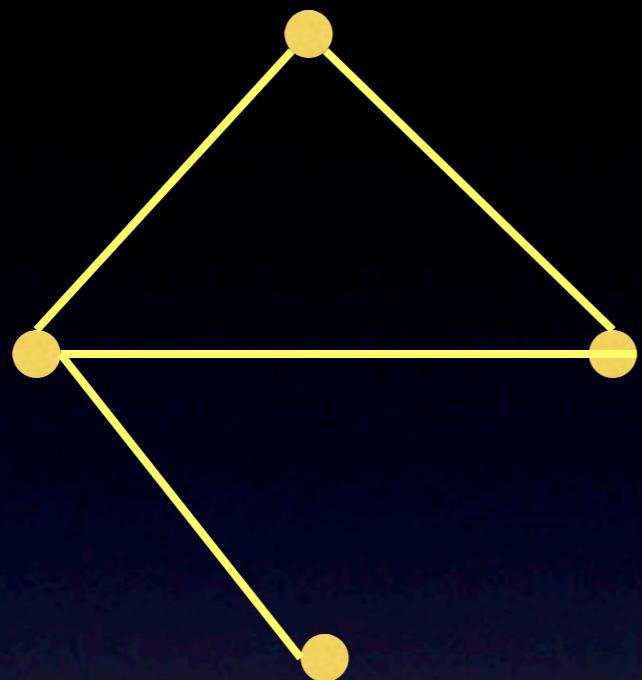


$\beta_0 = \# \text{ of}$   
connected  
components = 3

$\beta_1 = \# \text{ of cycles}$   
= 1

Euler characteristic:  $\chi = 3 - 1 = 2$

Betti numbers  $\beta_i$  # of i-dimensional holes/loops



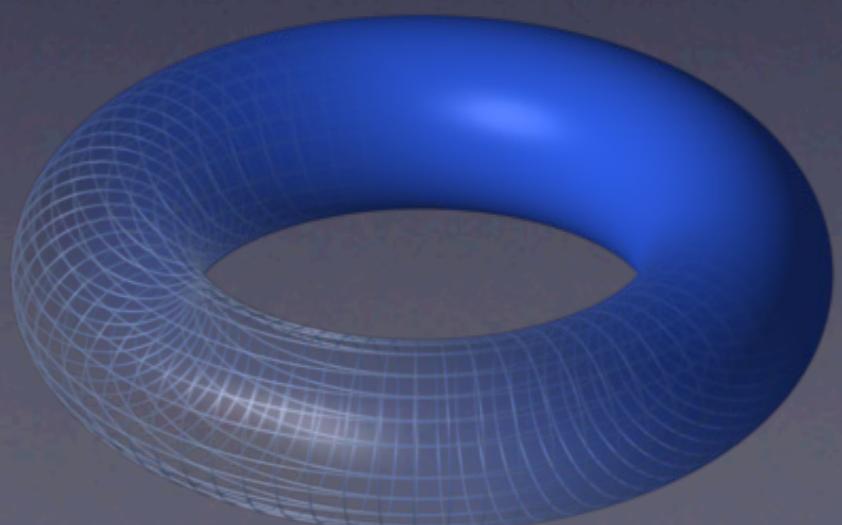
$\beta_0 = \# \text{ of connected components} = 3$   
 $\beta_1 = \# \text{ of 1D holes} = 1$   
 $\beta_2 = \# \text{ of 2D cavities} = 0$

Betti-number representation:  
 $(3, 1, 0, 0, \dots)$

Euler characteristic:

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

$\beta_0 = 1, \beta_1 = 2, \beta_2 = 1$   
 $(1, 2, 1, 0, 0, \dots)$



# Filtration



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

Sequence of nested objects or vector spaces



Extract persistent homological features

Persistent diagram, barcodes

Hierarchical  
nestness does  
not imply  
robustness



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

Sequence of nested objects or vector spaces



To have robustness, you need monotone feature

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

# Morse Filtration

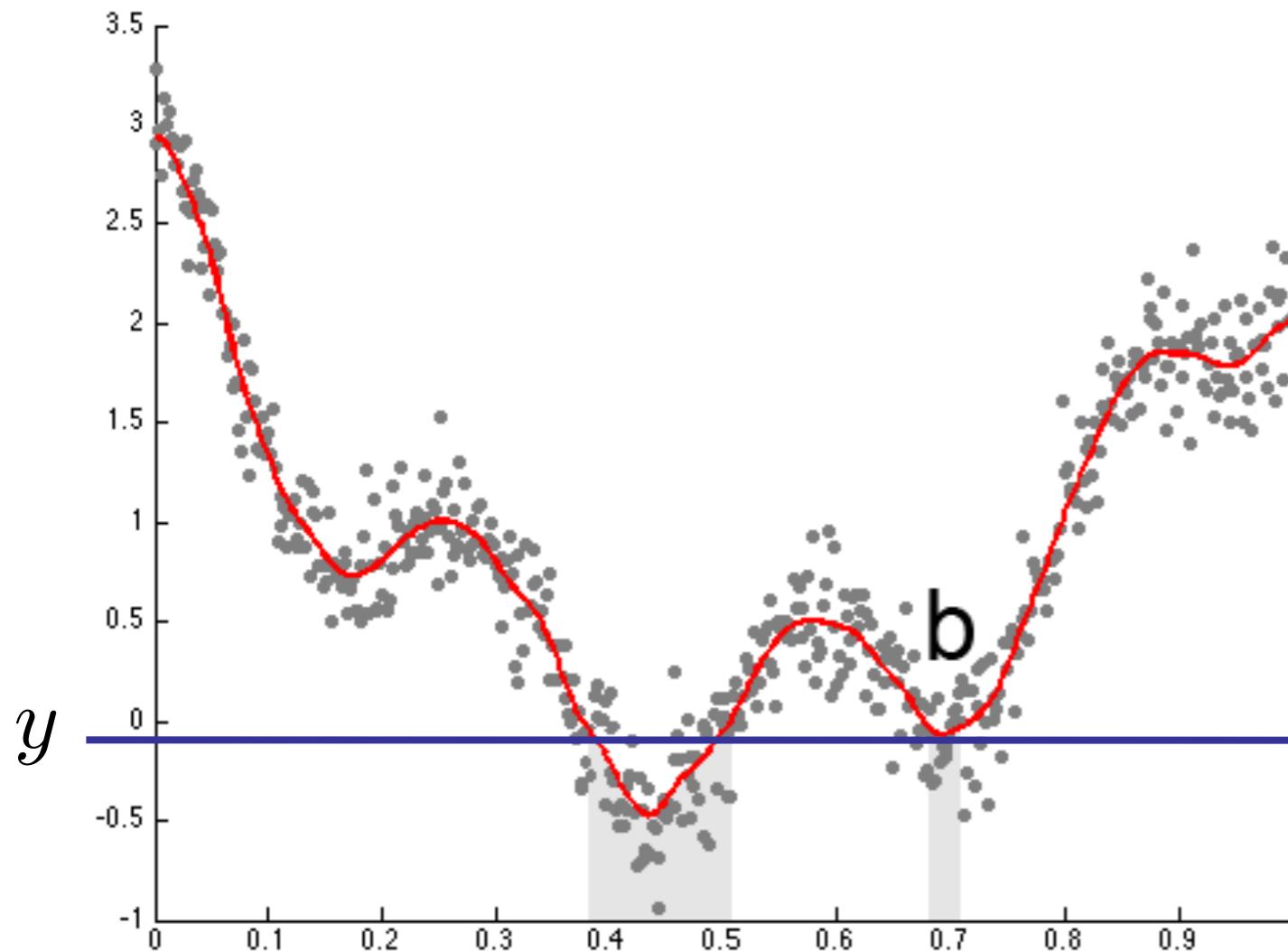
Most useful in functional and  
time series data

# Morse theory for functional data

$$Y = \mu + \epsilon$$

Chung et al., 2009 *Information Processing in Medical Imaging (IPMI)* 5636:386-397.

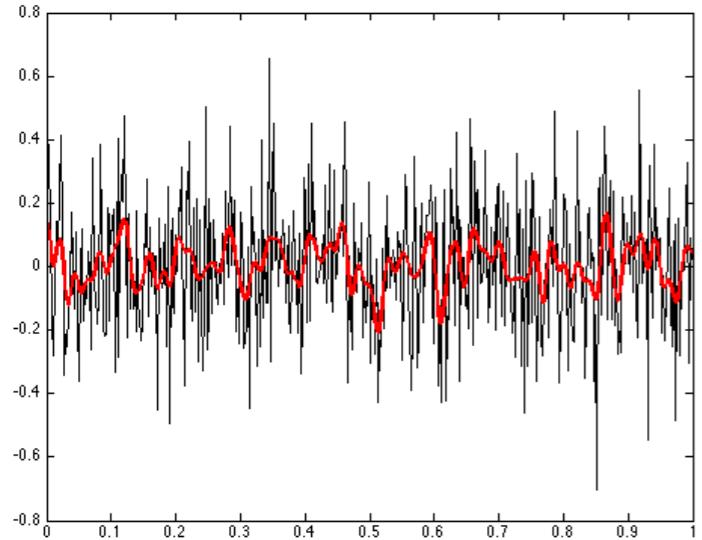
Unknown signal  $\mu$  is assumed to be a Morse function: all critical values are unique.



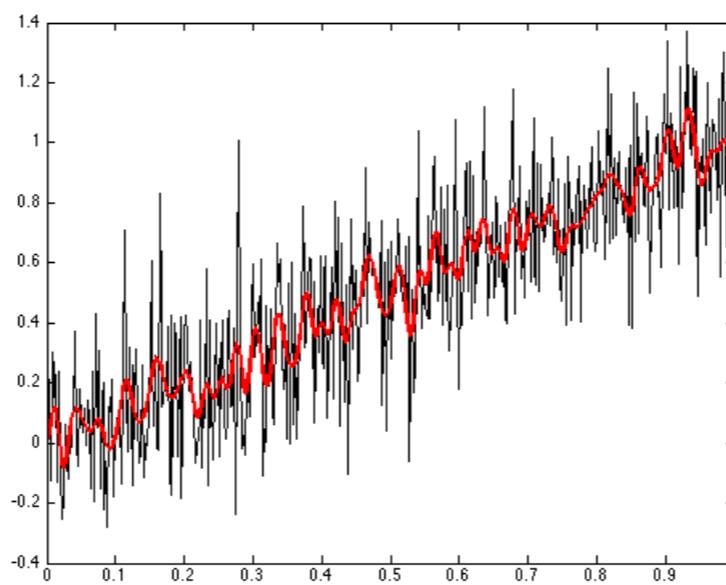
Sublevel set  
 $R(y) = \mu^{-1}(-\infty, y]$

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

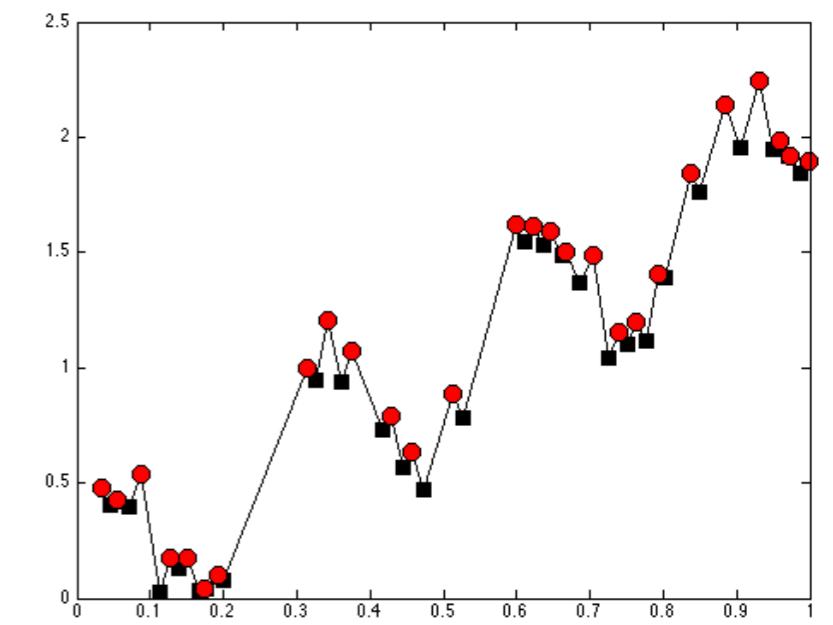
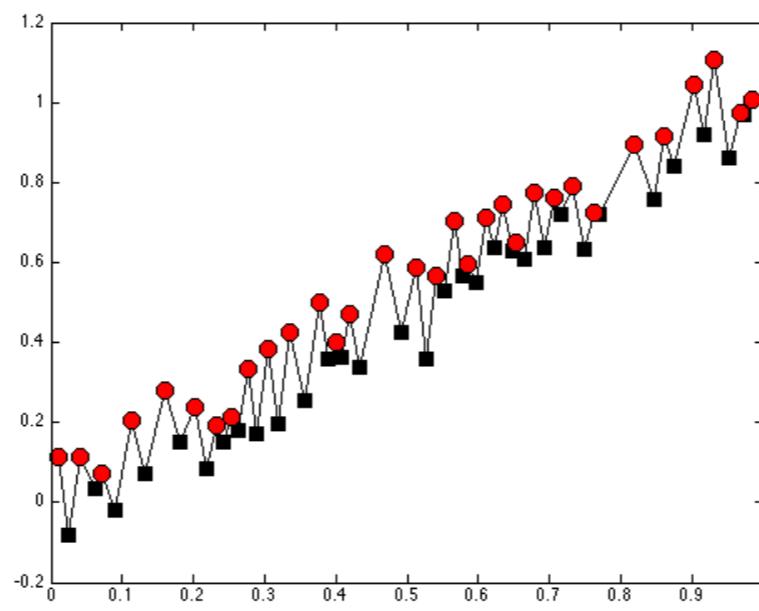
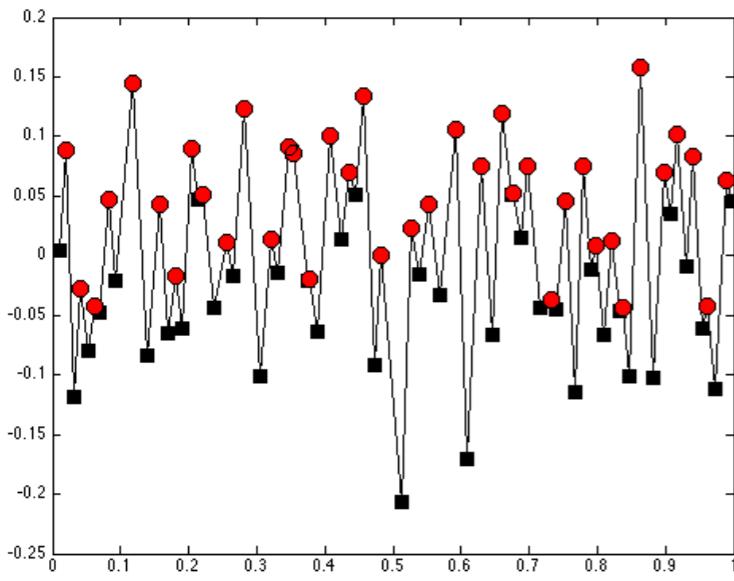
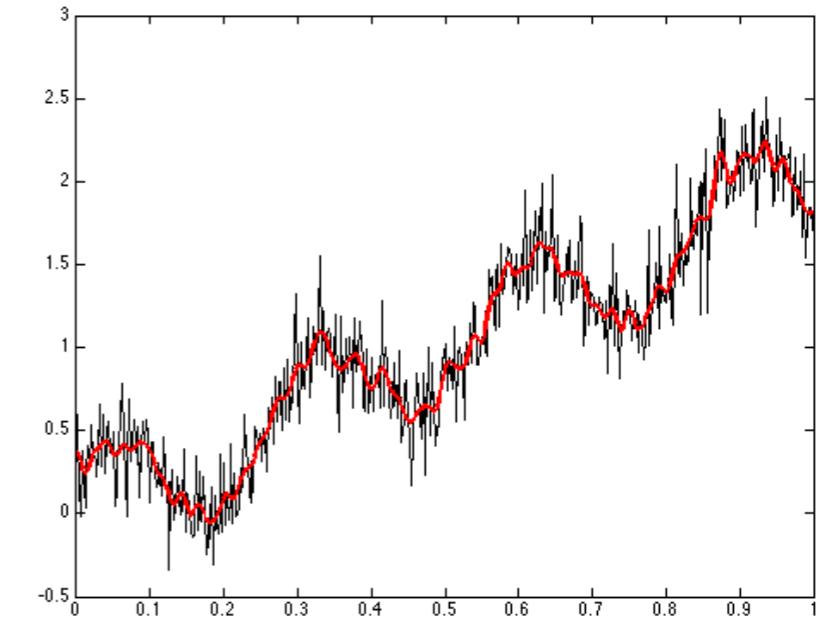
# Critical values capture the pattern of signal changes



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



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



# Morse filtration

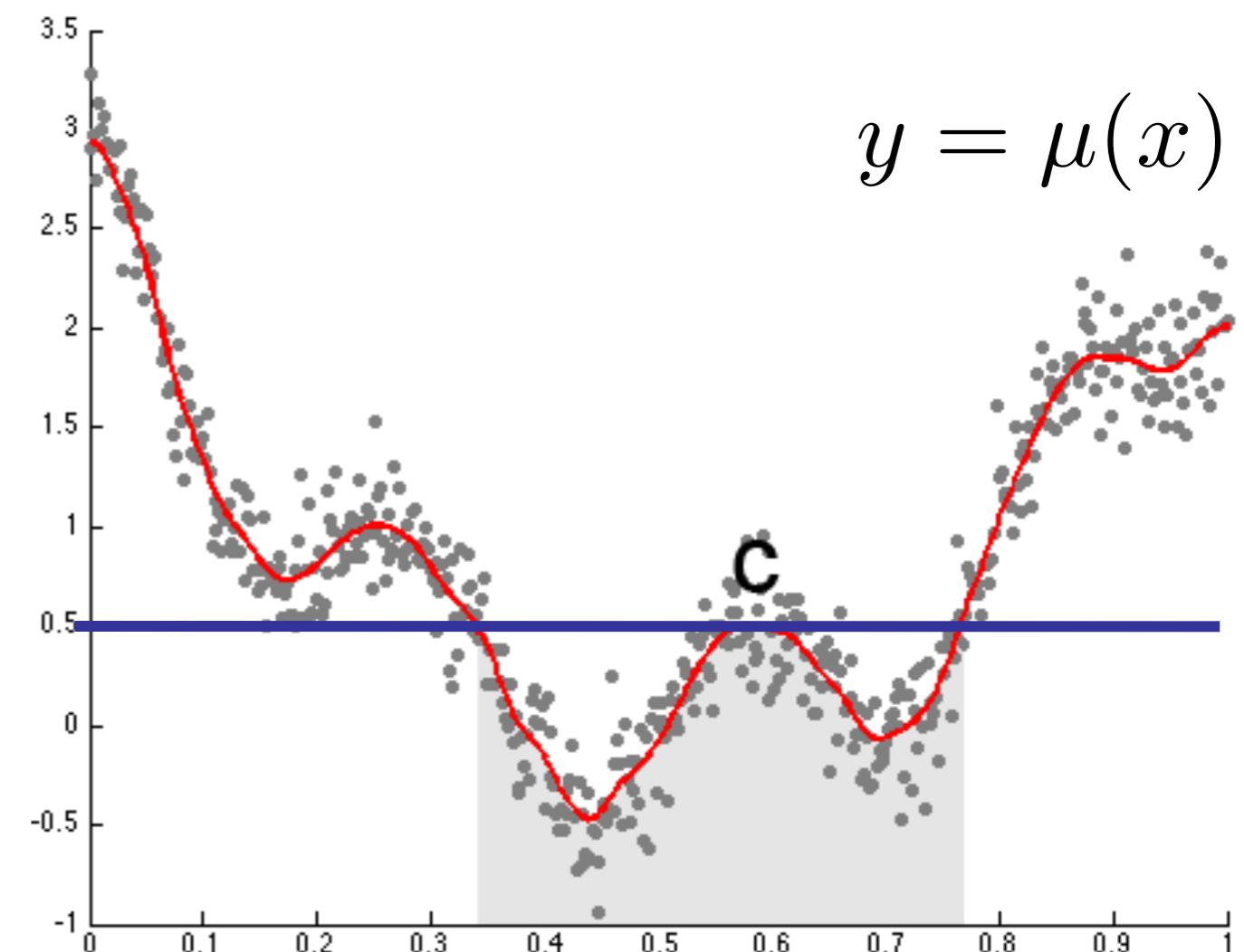
Consider a sublevel set

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

For critical values

$$b < c$$

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

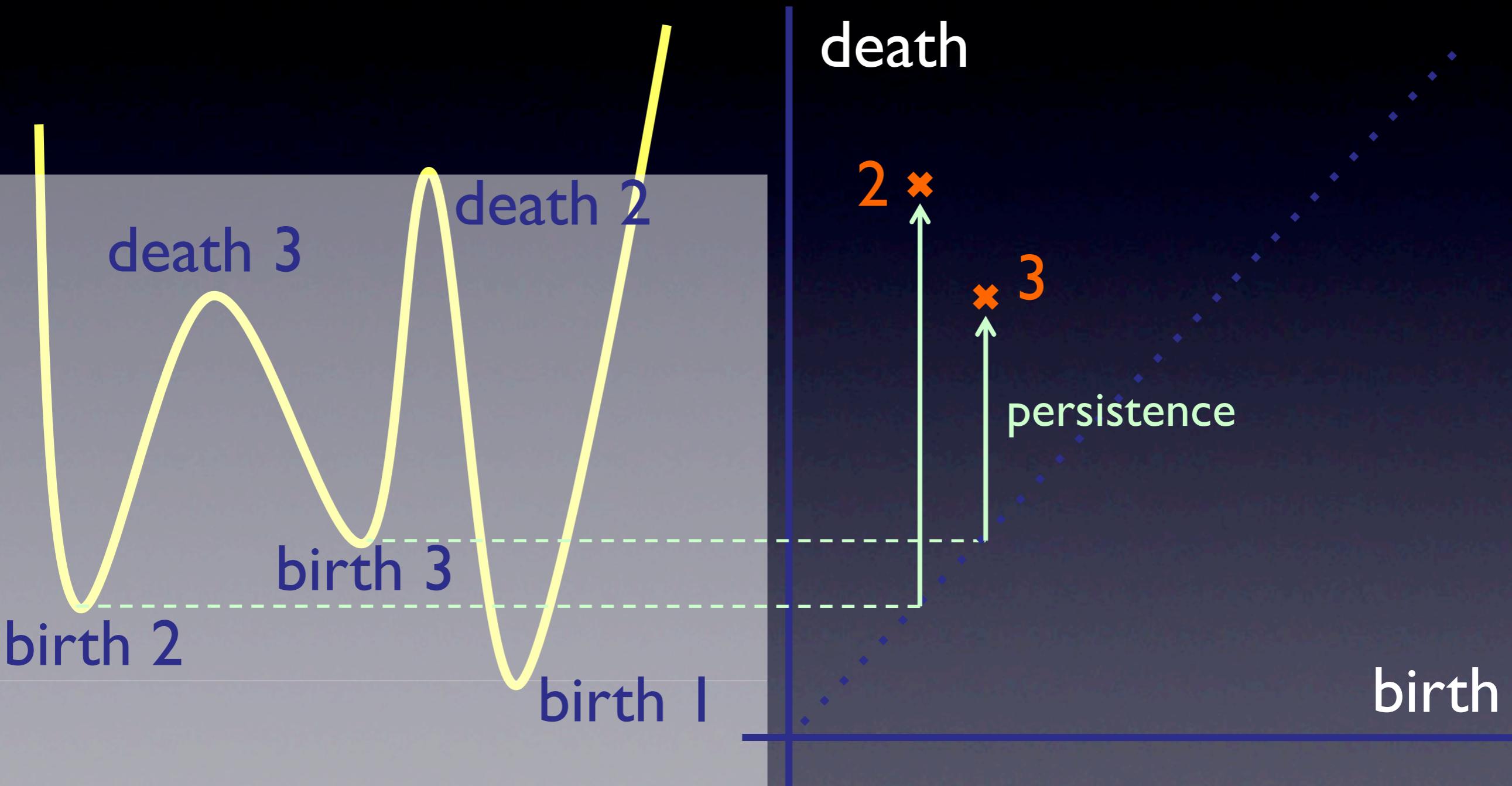


# of connected components

$$\#R(b) = \#R(c) - 1$$

# Persistence Diagram (PD)

$O(n \log n)$



Pair the time of death with the time of the closest earlier birth.  
Birth I is paired to infinity or ignored.

# Pairing Brackets

((((0)(0)(0 ((0 0))) 00000((((0))))

((((0)(0)(0 ((0 0))) 00000((((0))))

((((0)(0)(0 ((0 0))) 00000((((0))))

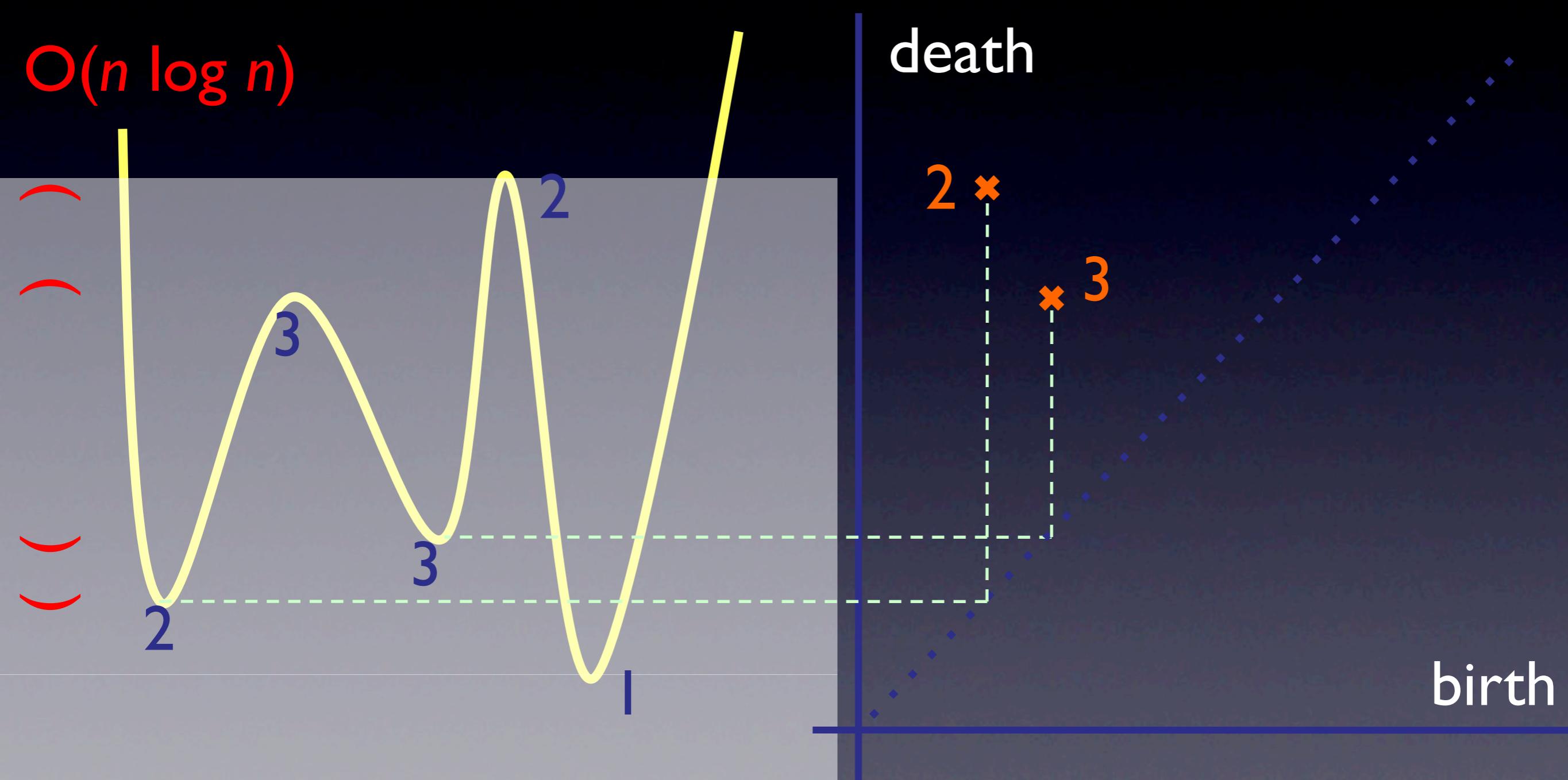
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# Persistence Diagram (PD)



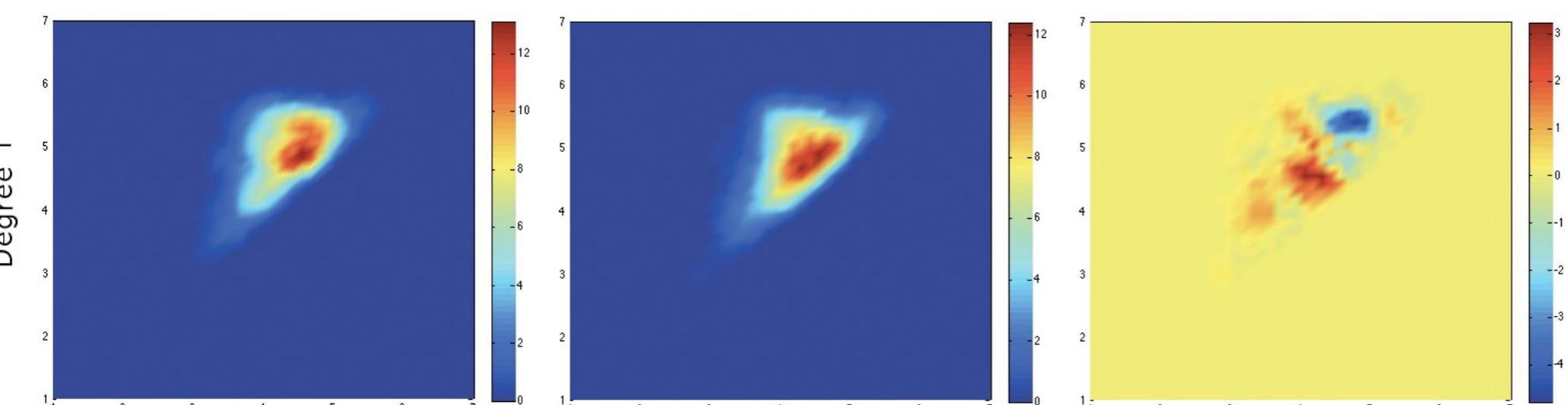
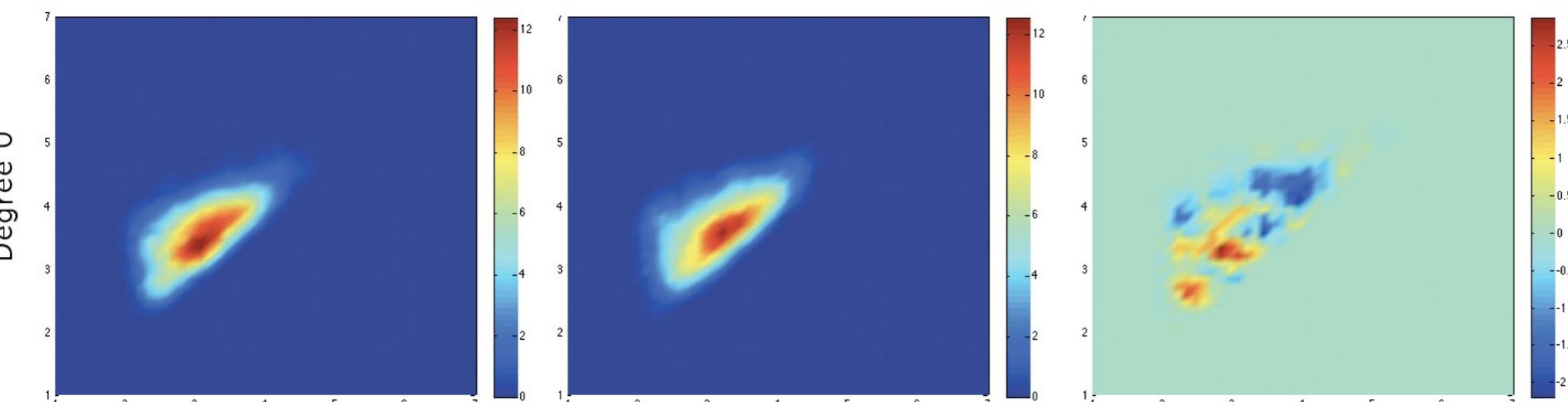
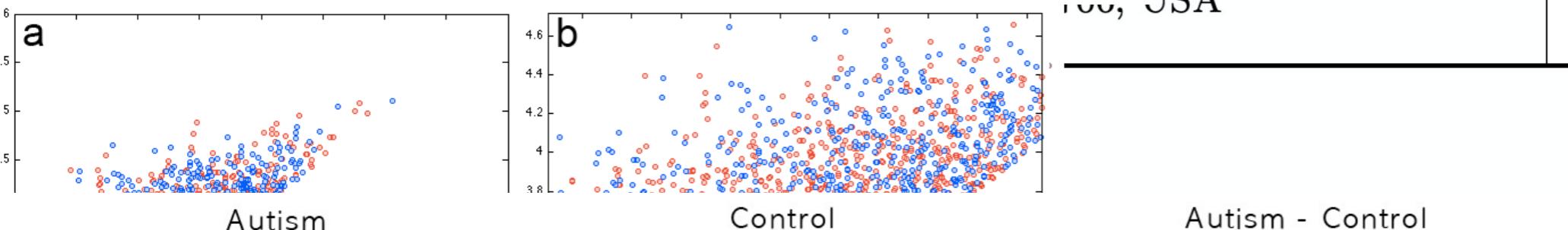
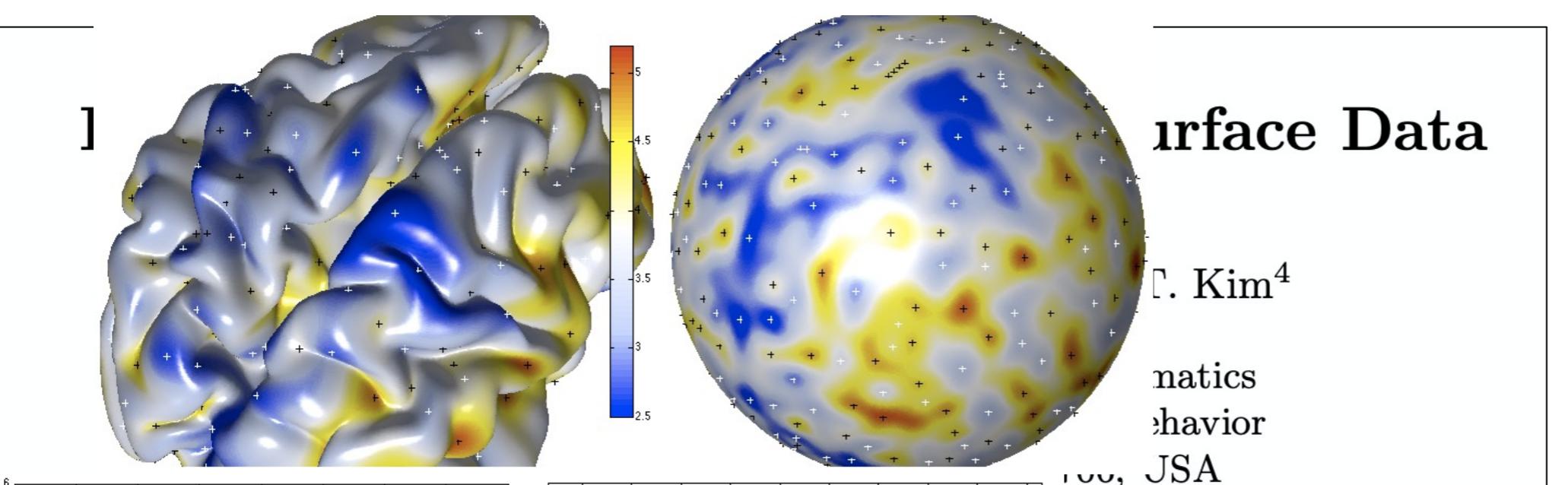
Pair the time of death with the time of the closest earlier birth

Chung et al., 2009  
Information Processing  
in Medical Imaging  
(IPMI) 5636:386-397.

## Surface Data

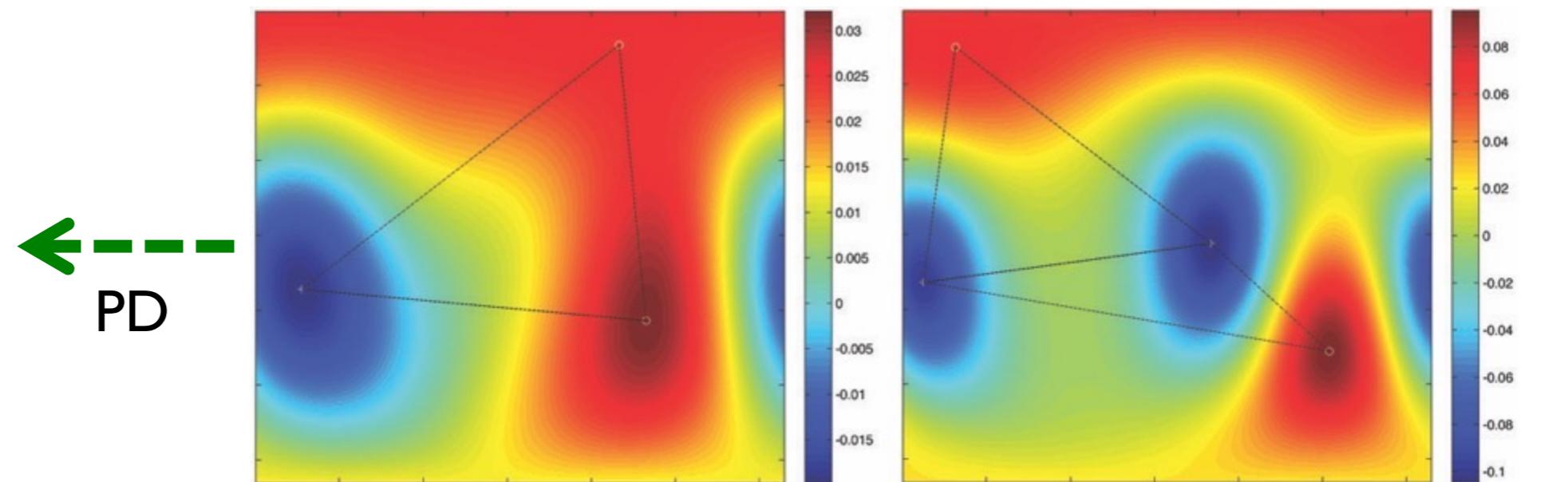
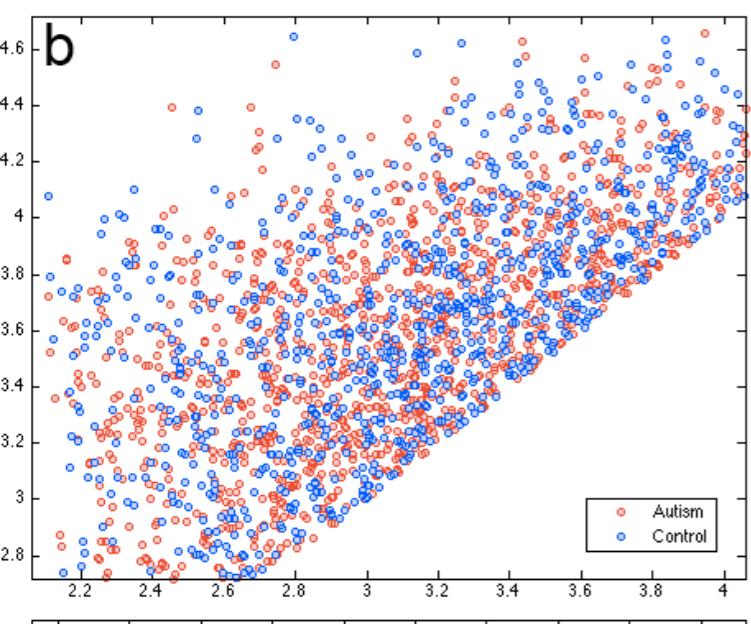
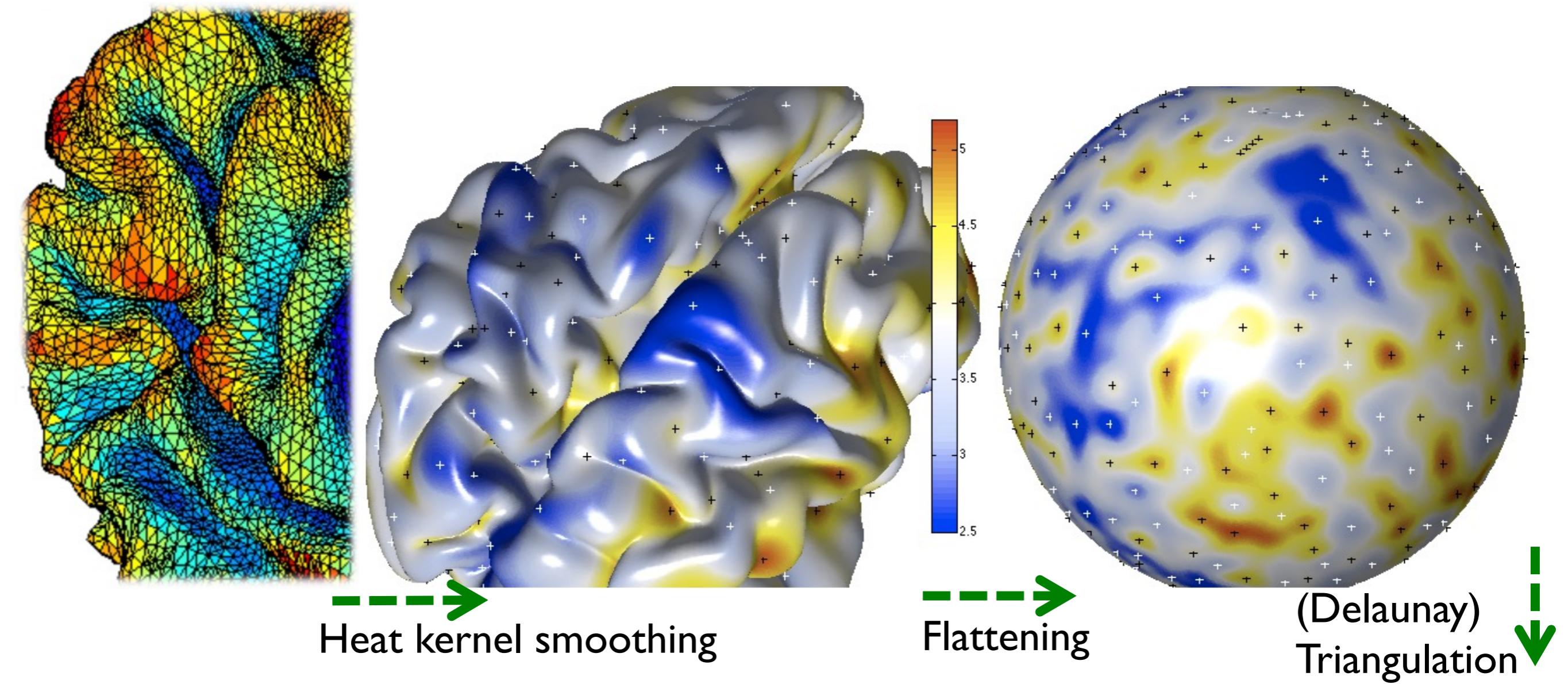
T. Kim<sup>4</sup>

mathematics  
behavior  
JSA



*First persistent  
homology study  
applied to medical  
imaging*

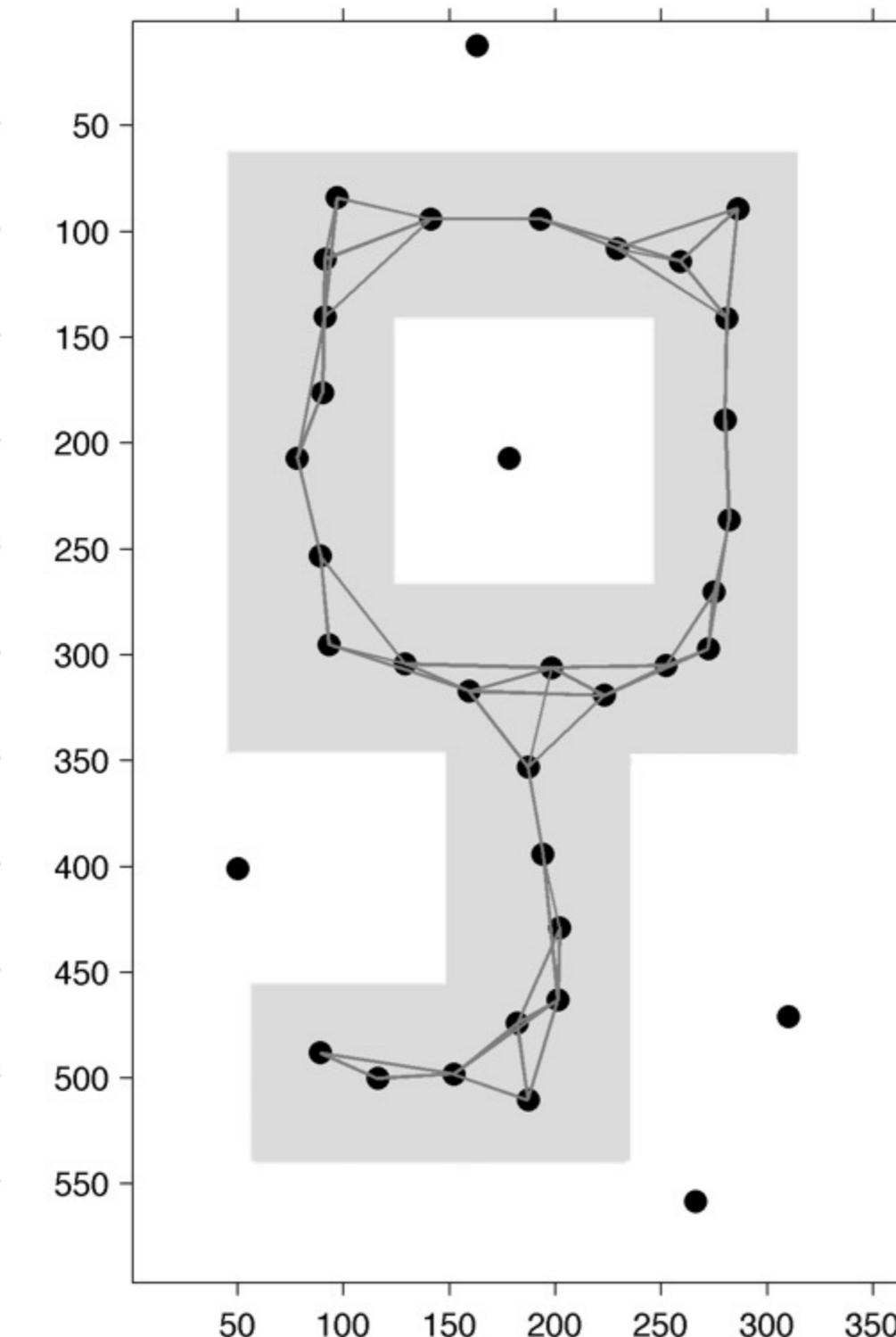
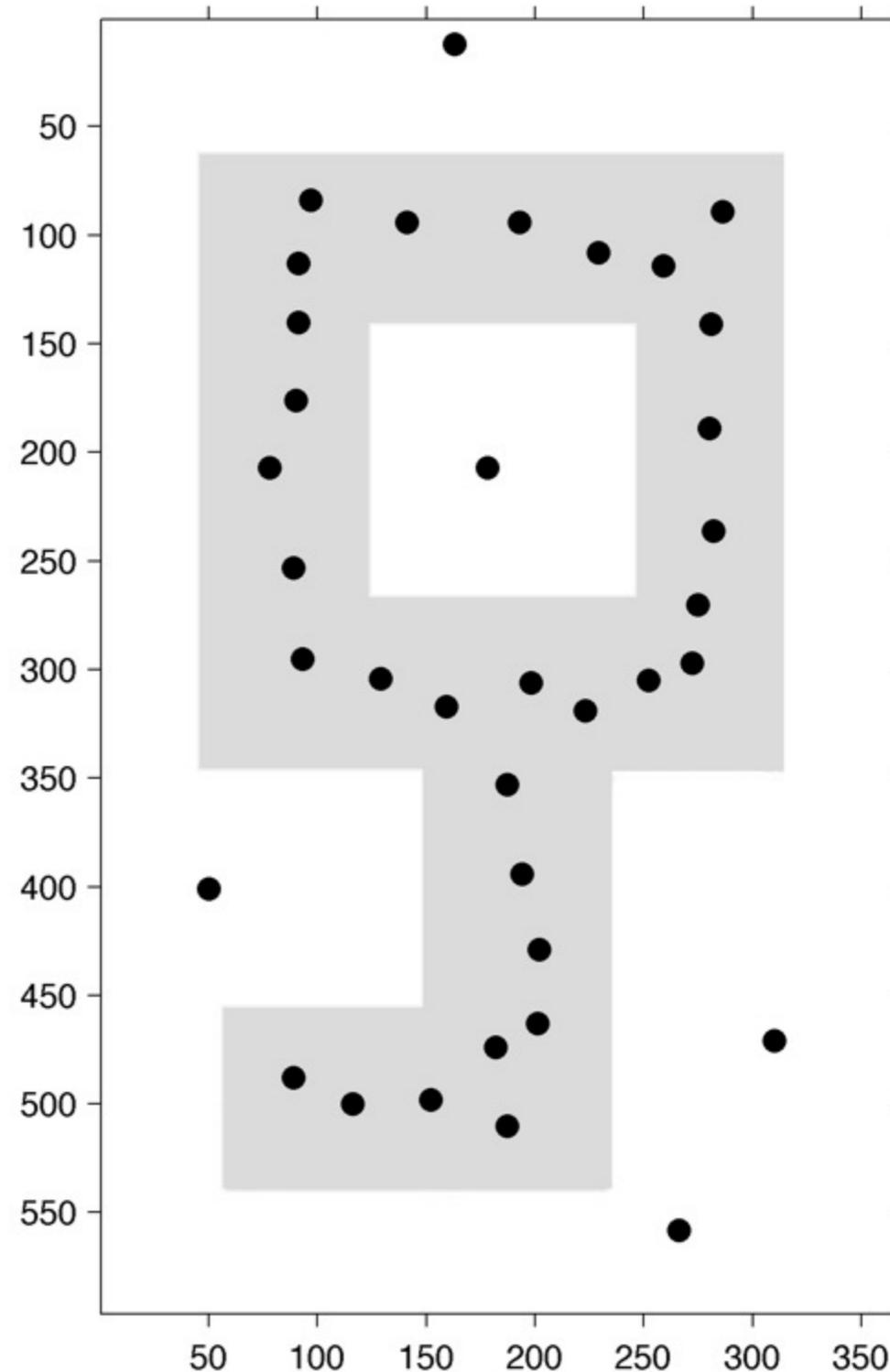
# Persistent homology on cortical manifolds



# Rips filtrations

# 1-skeleton of point cloud data

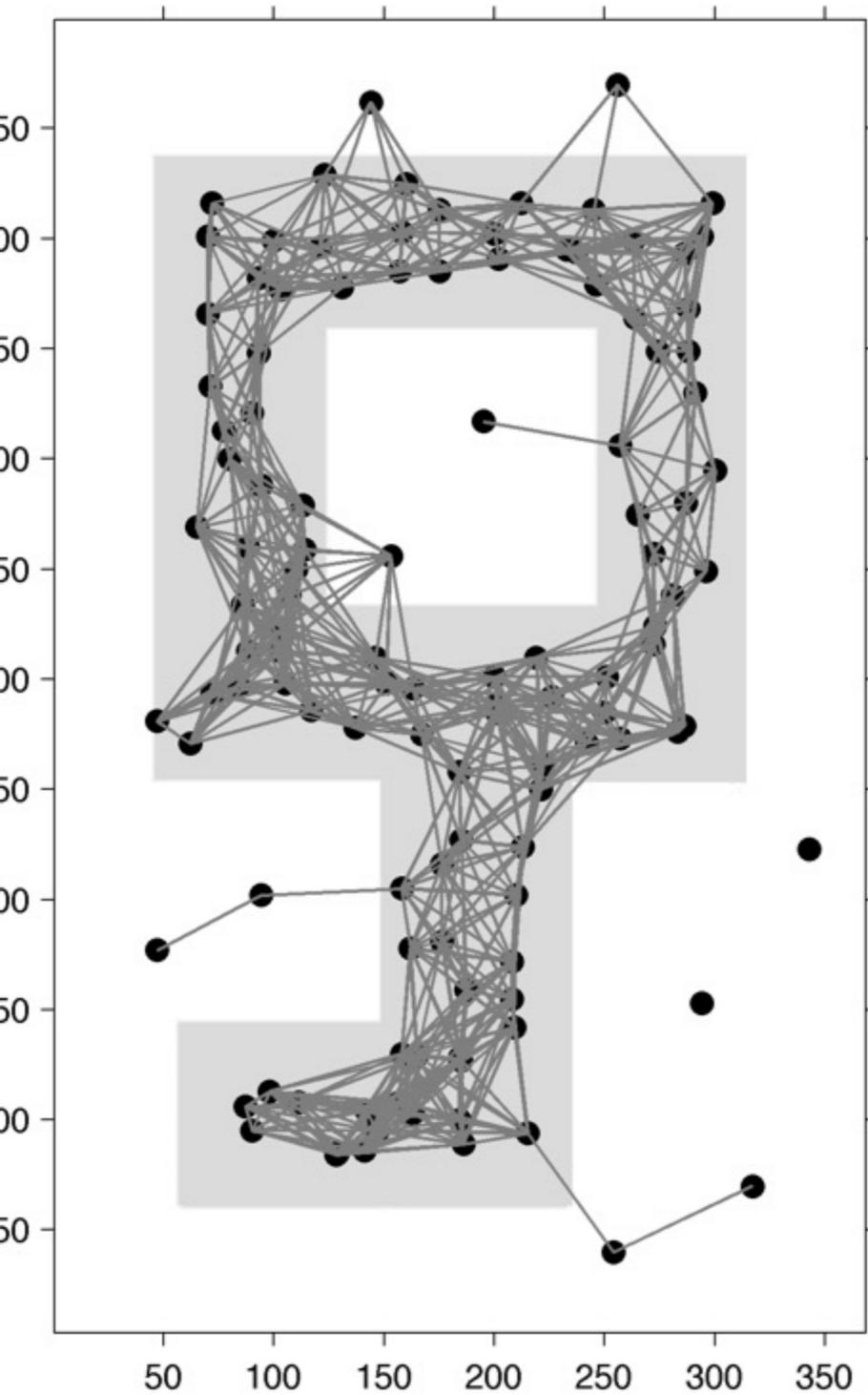
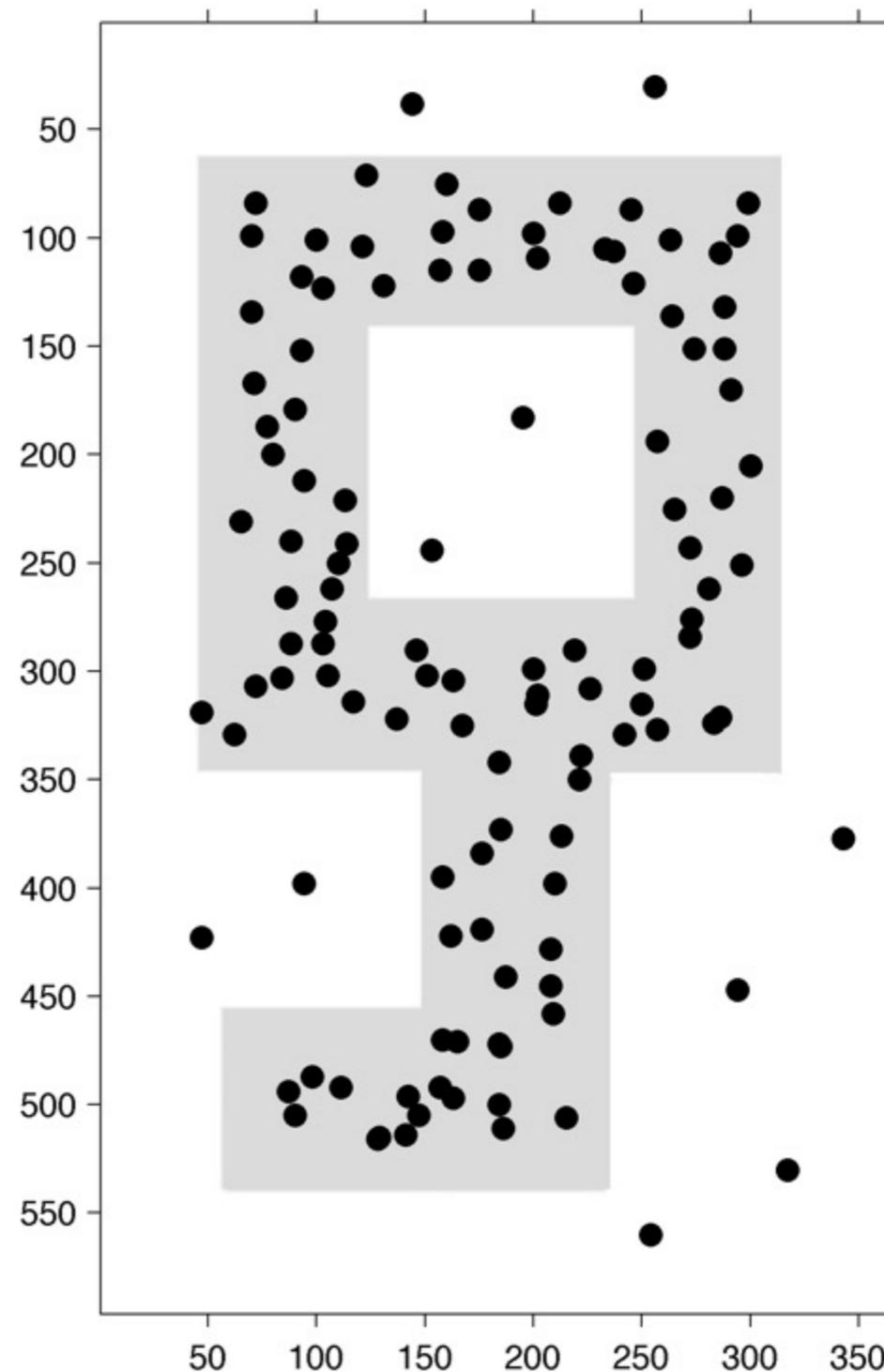
$\varepsilon = 70\text{mm}$



Recovering underlying topology

# 1-skeleton of point cloud data

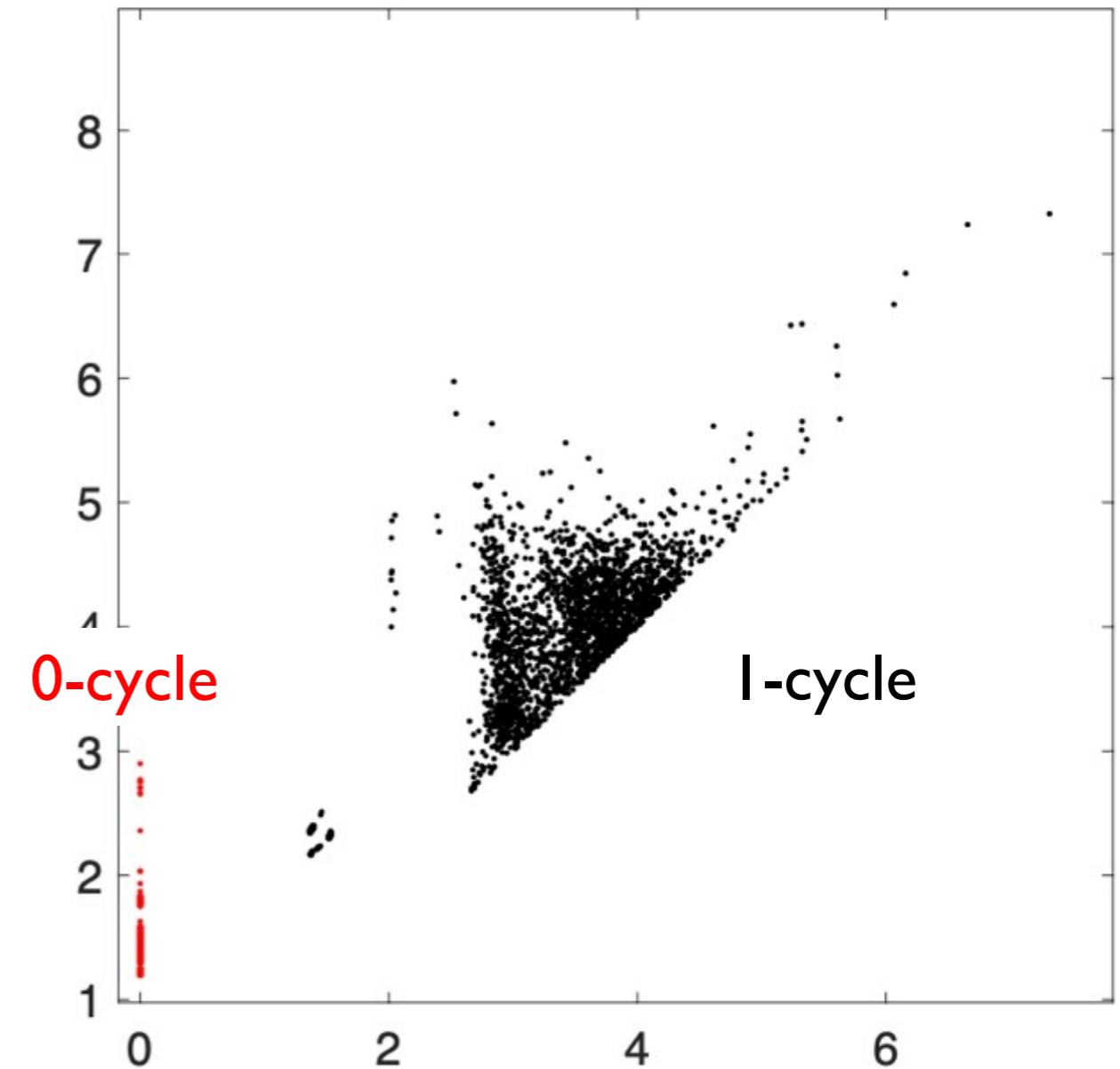
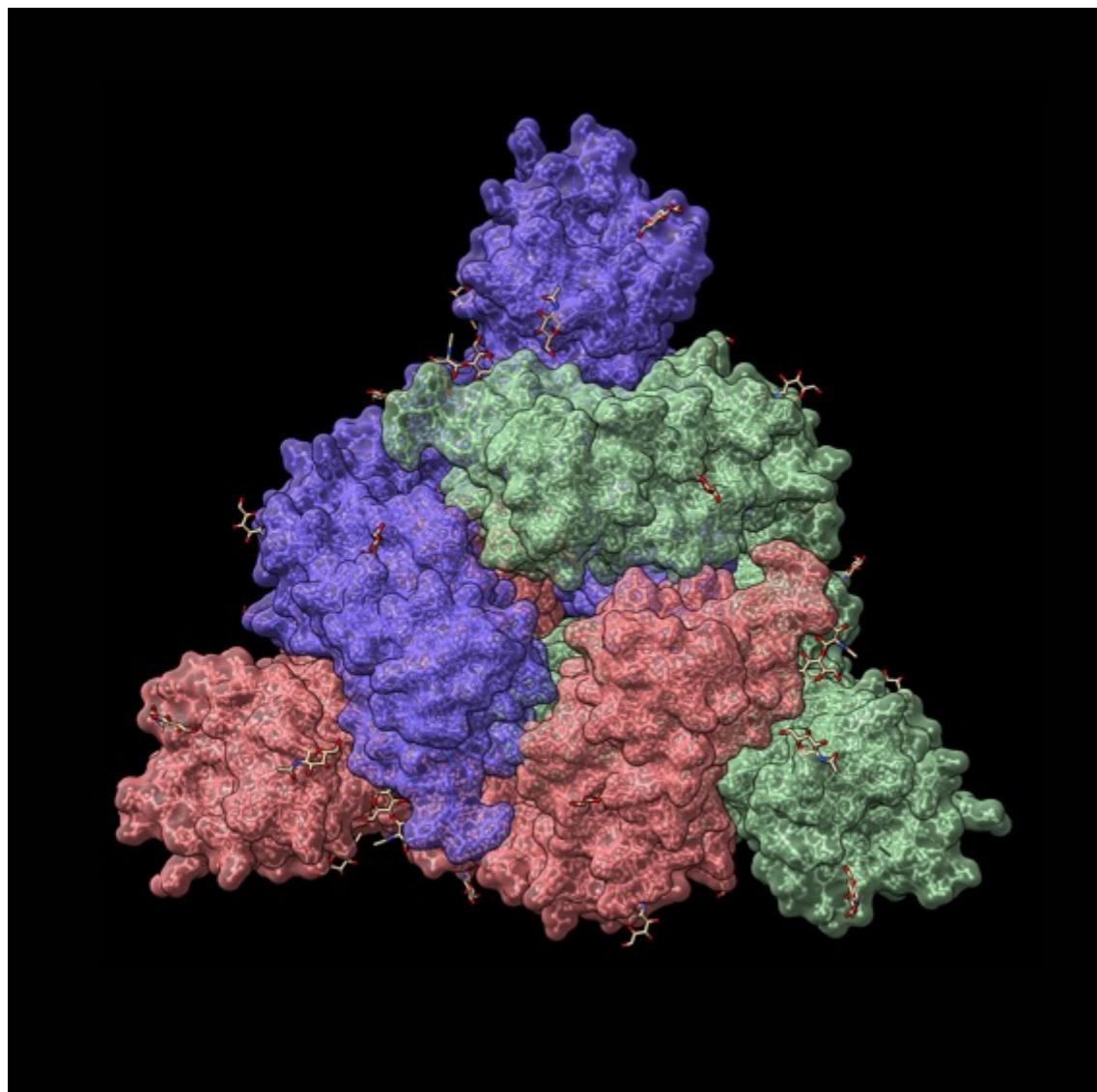
$\epsilon = 70\text{mm}$



Better approach: perform kernel smoothing and then Morse filtration

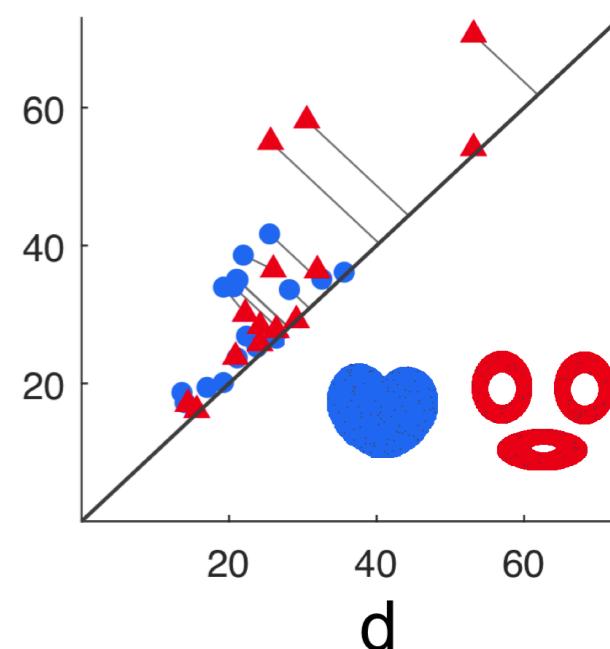
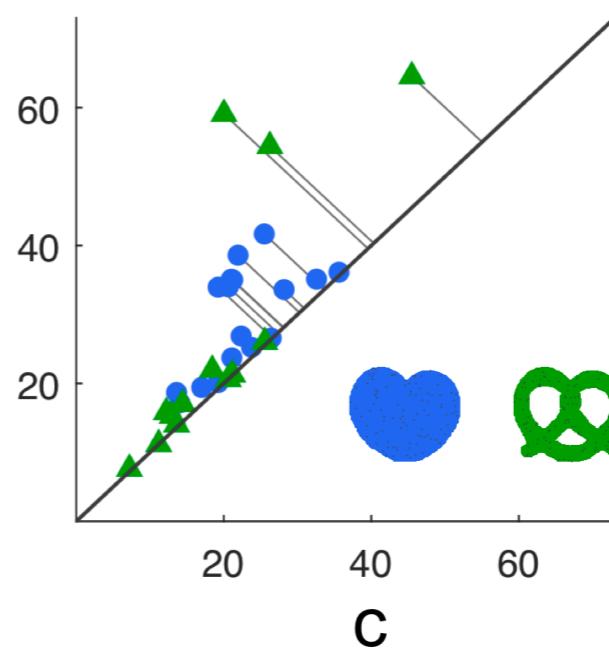
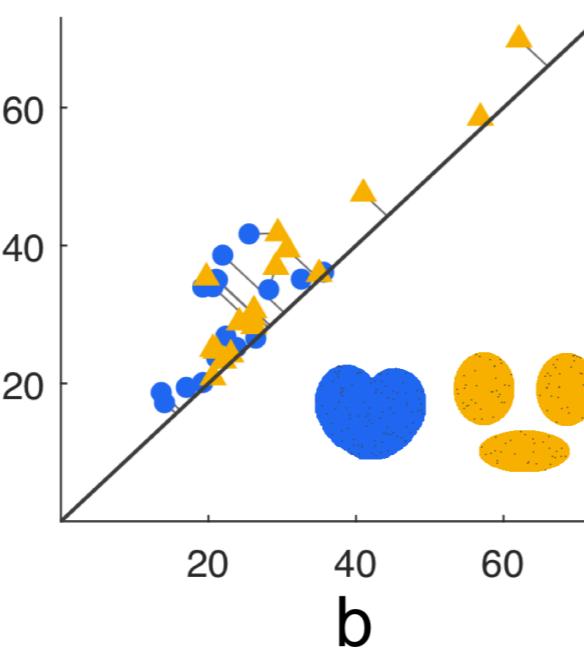
# Persistence Diagram (PD) of a protein molecule

Rips filtration on distance between 8000 atoms

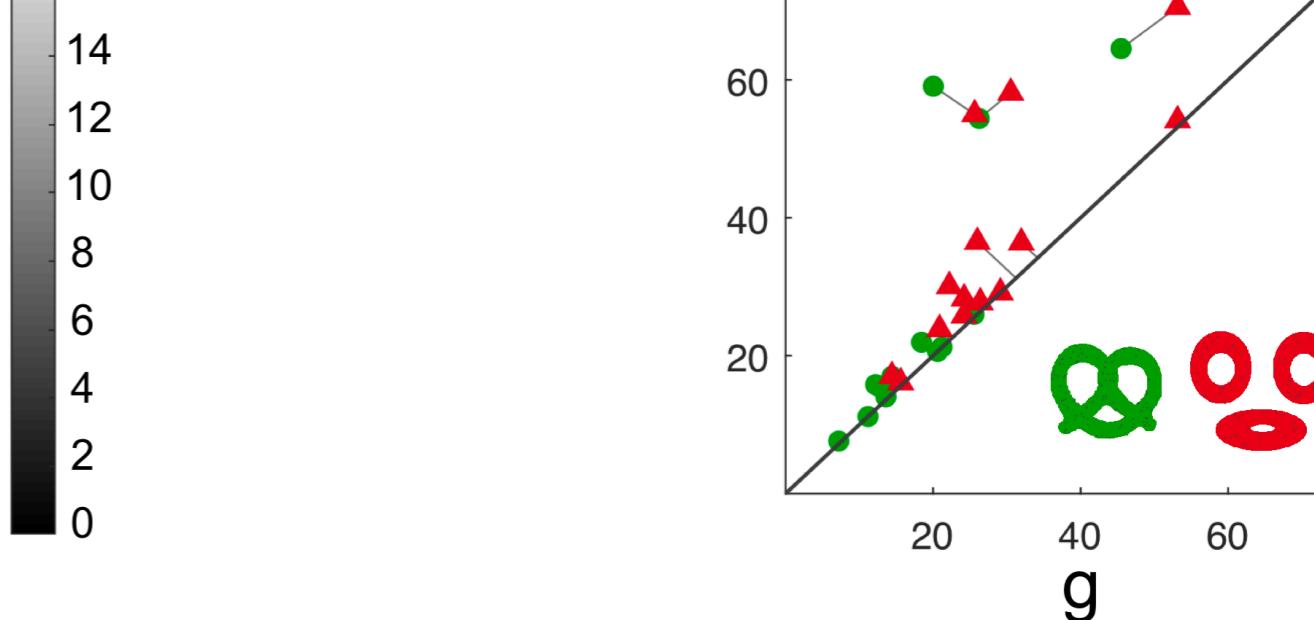
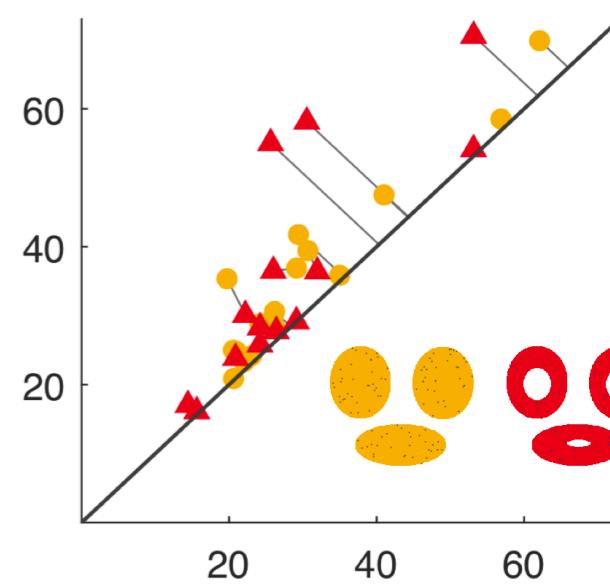
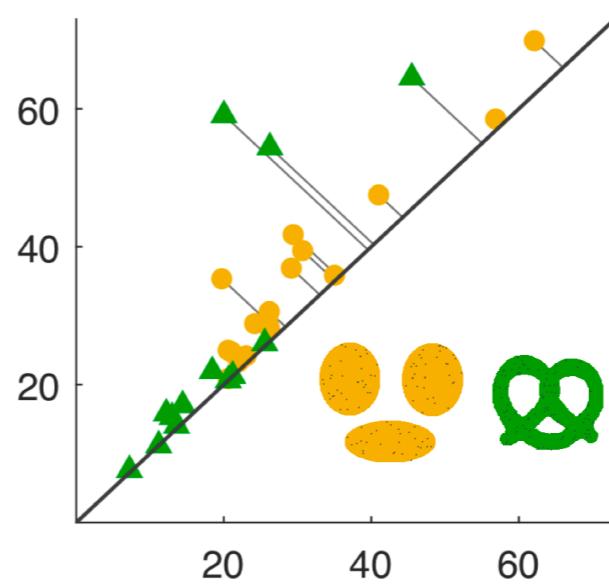
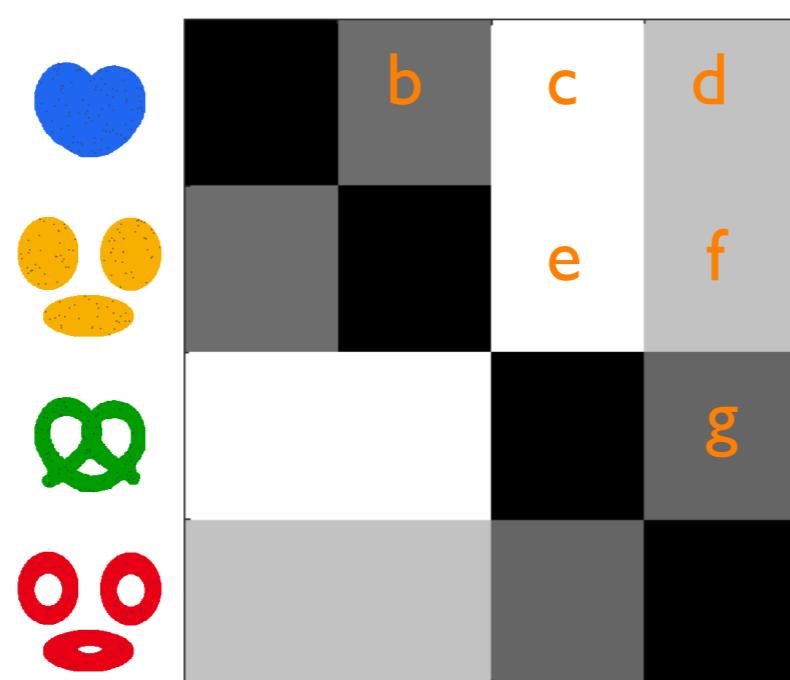


Extremely slow computation → Simply use graph filtration

# Bottleneck distance



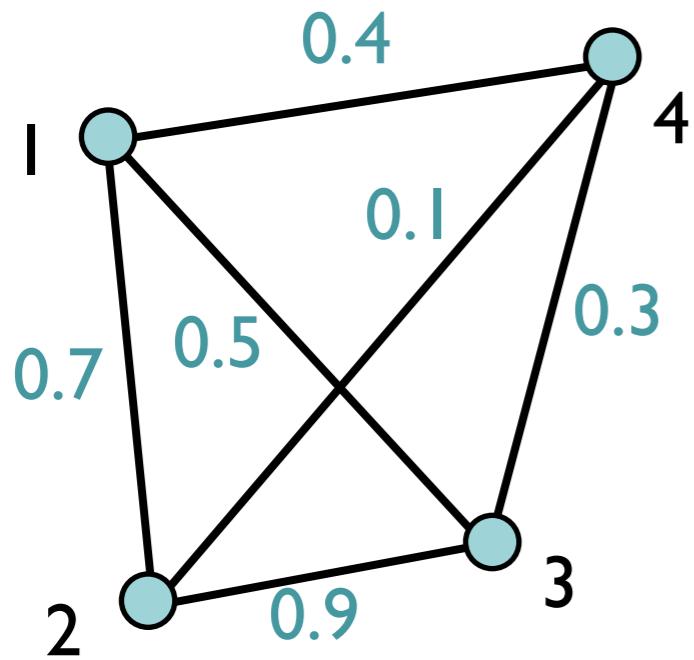
For definition, simply  
read the assigned reading PDF



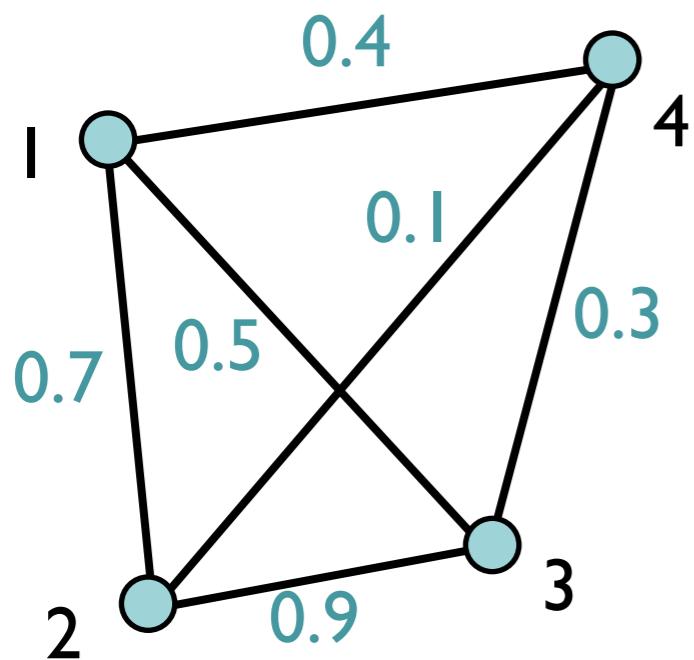
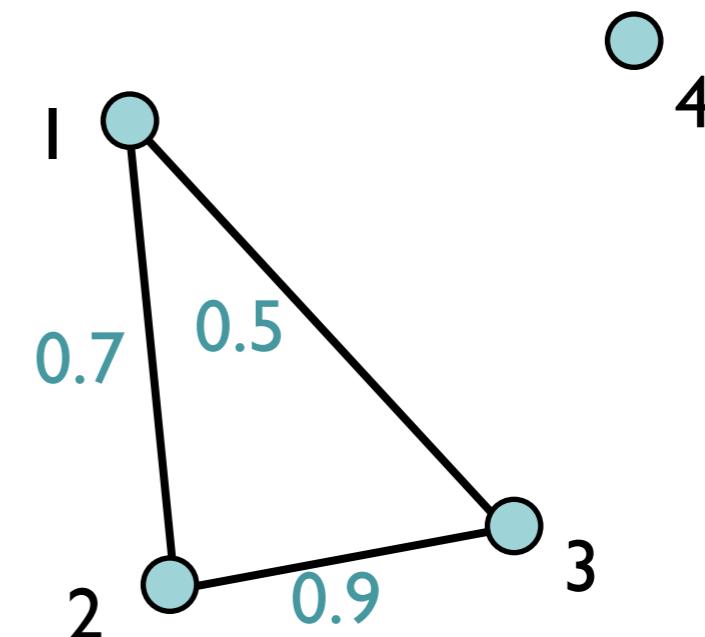
# What is wrong with the arbitrary thresholding?

Edge weight  $\rho_{ij}$  between node  $i$  and  $j$

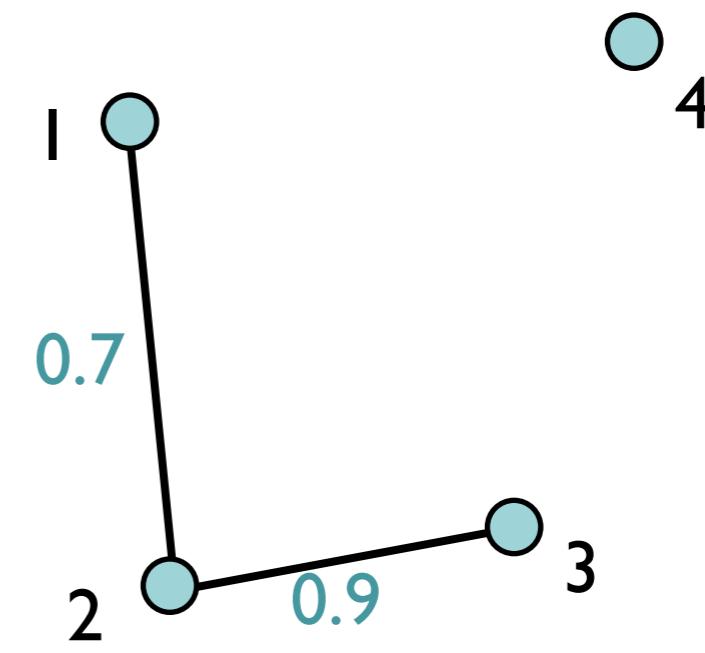
→ Connectivity matrix  $\rho = (\rho_{ij})$



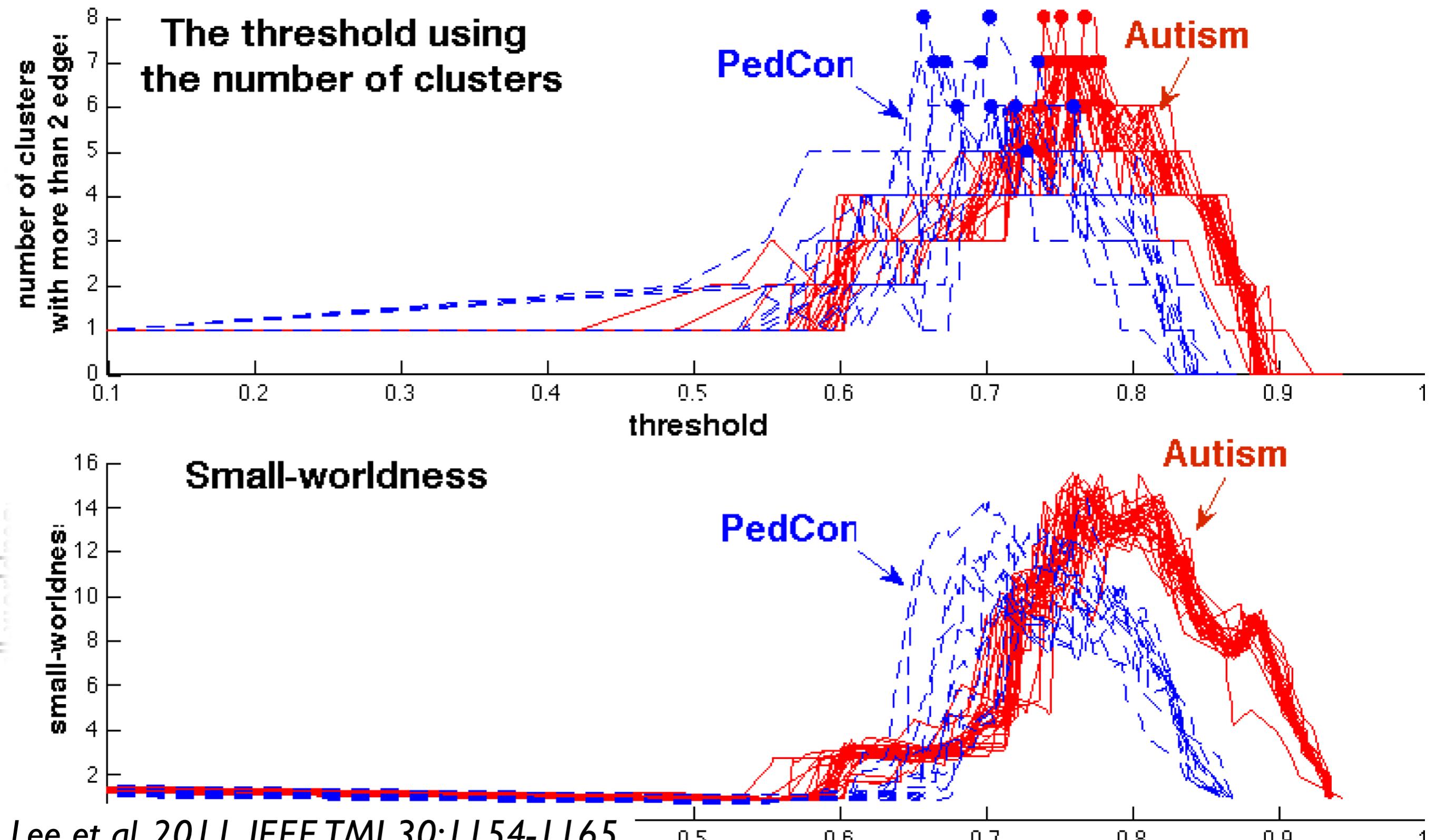
Threshold at 0.5



Threshold at 0.7



# Single threshold often suboptimal → TDA-based network analysis



# Graph filtrations

Baseline filtration for brain networks first introduced in

Lee et al. 2011 MICCAI 302-309

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

# Rips filtration

vs.

# graph filtration

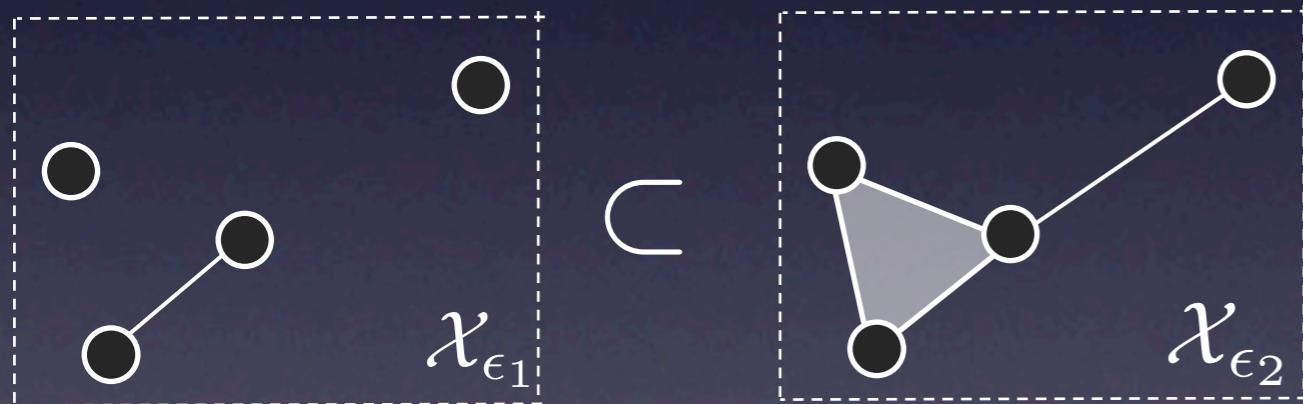
Metric space

$$\mathcal{X} = (V, w) \quad w = (w_{ij})$$

Node set      Metric

$$w_{ik} < w_{ij} + w_{jk}$$

Rips complex = Simplicial complex



Rips filtration

$$\mathcal{X}_{\epsilon_0} \subset \mathcal{X}_{\epsilon_1} \subset \mathcal{X}_{\epsilon_2} \subset \dots$$

for increased radius

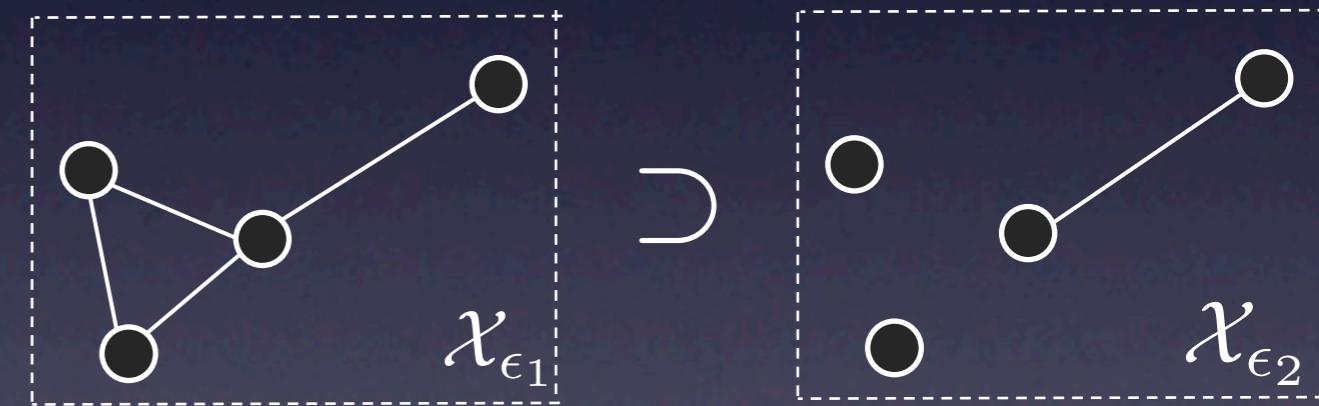
$$\epsilon_0 < \epsilon_1 < \epsilon_2 < \dots$$

Weighted graph

$$\mathcal{X} = (V, w) \quad w = (w_{ij})$$

Node set      Edge weight

Binary graph: 1-skeleton



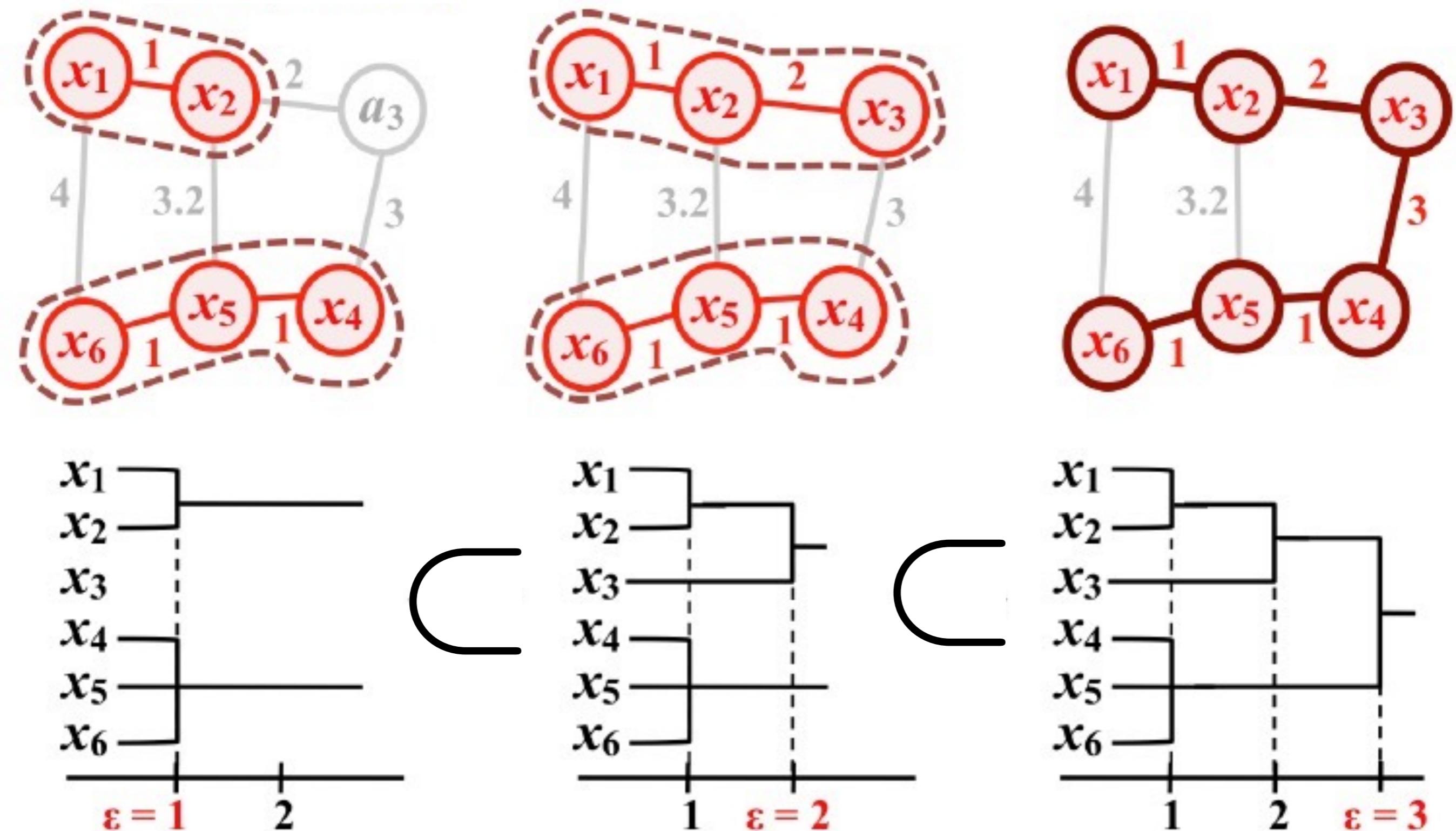
Graph filtration

$$\mathcal{X}_{\epsilon_0} \supset \mathcal{X}_{\epsilon_1} \supset \mathcal{X}_{\epsilon_2} \supset \dots$$

for increased edge weights

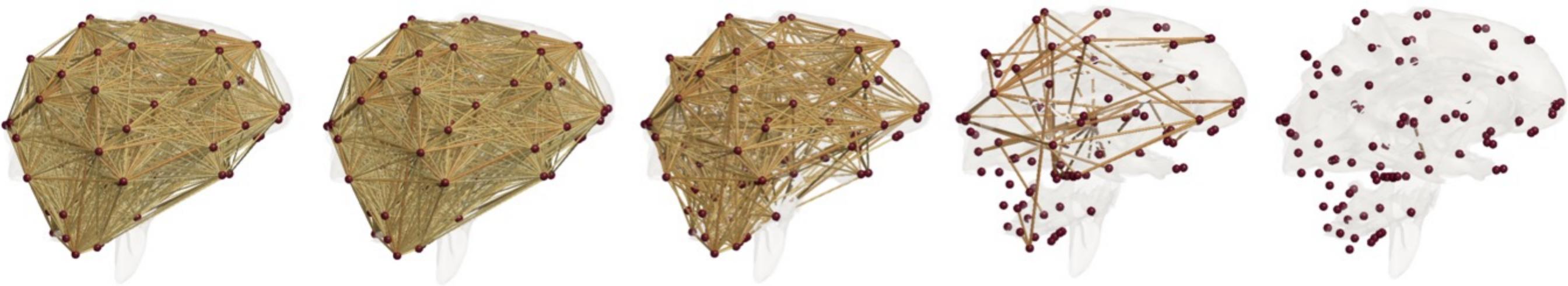
$$\epsilon_0 < \epsilon_1 < \epsilon_2 < \dots$$

# Graph filtration=single linkage clustering



# Graph filtrations on resting-state fMRI

MZ-twins



0.1

0.2

0.3

0.4

0.5

DZ-twins



0.1

0.2

0.3

0.4

0.5

# Advantage of 1-skeleton over Rips-complex

Easy biological interpretation

Betti numbers are monotone over filtration

Robustness

Easier statistical inference

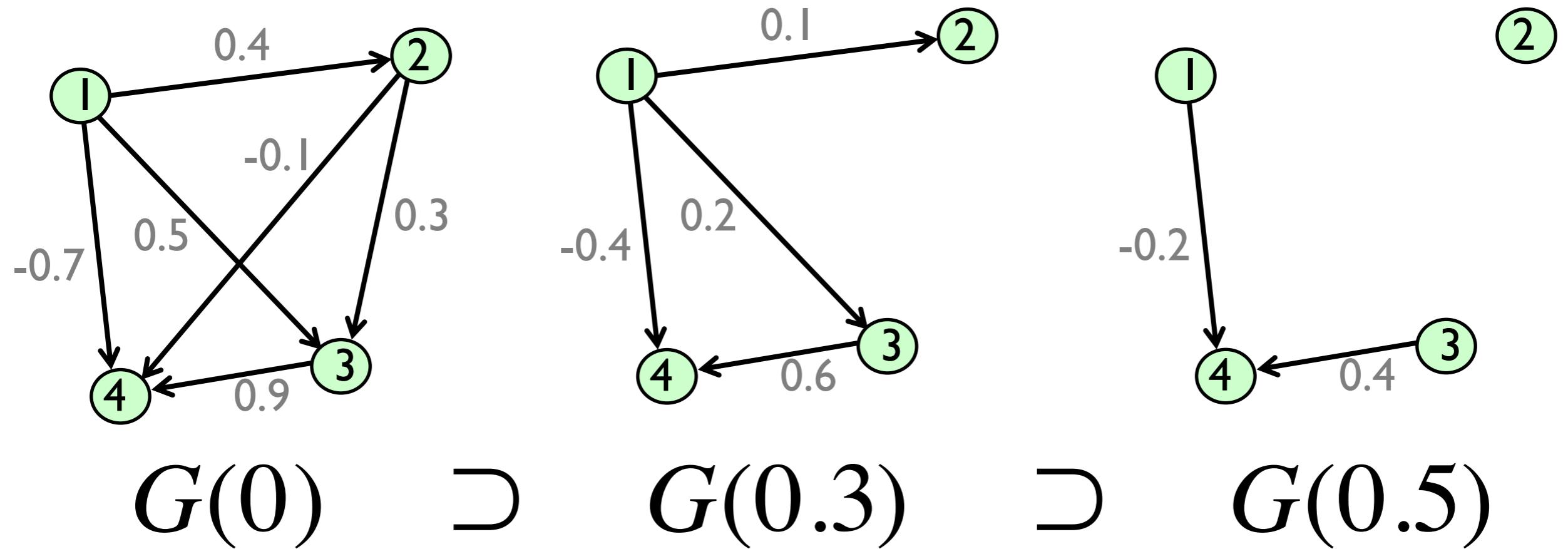
# Graph filtration (filtration on 1-skeleton)

Rips filtration is computationally expensive:

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

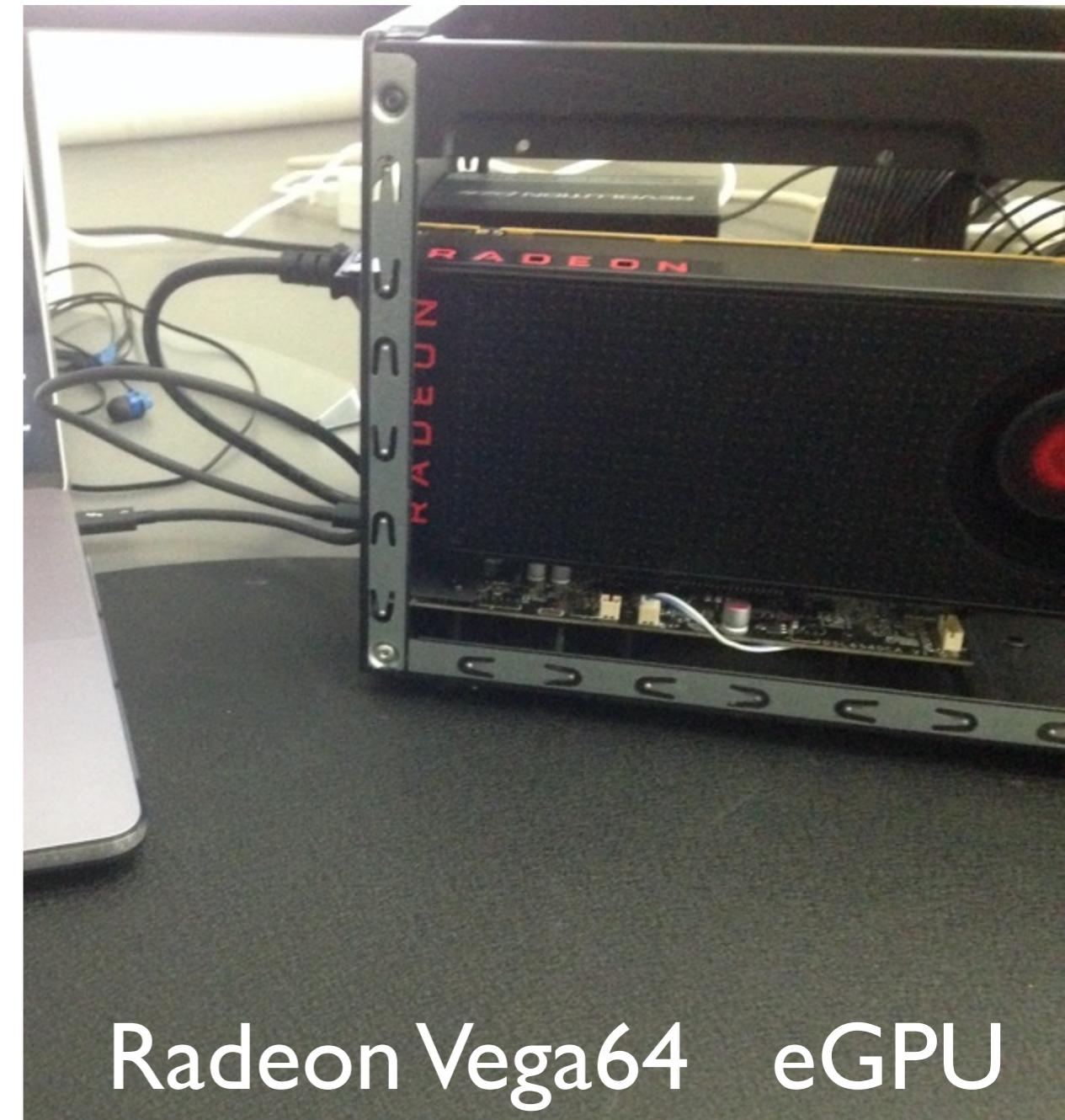
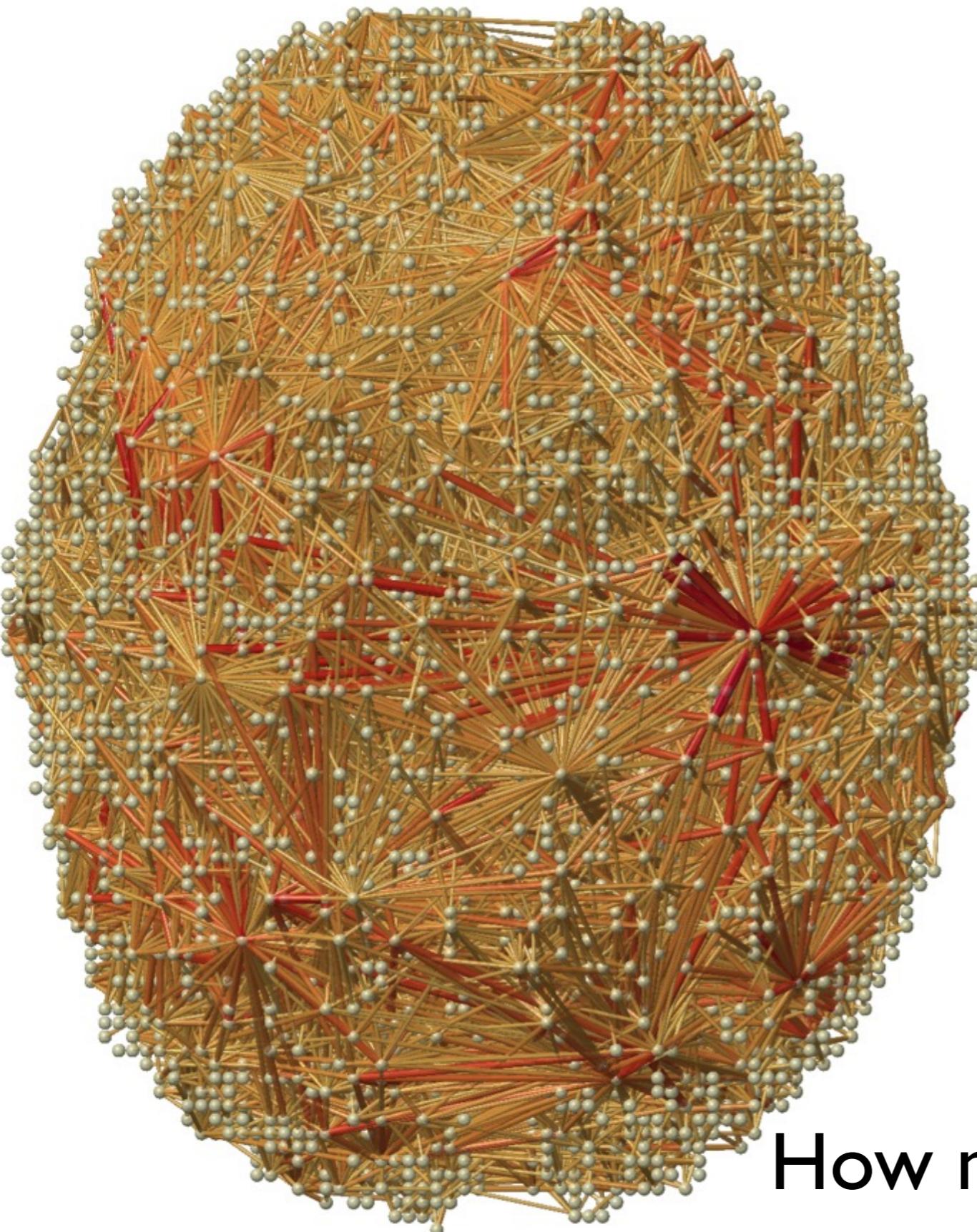
For 1-skeleton, graph filtration is  $O(n \log n)$  for both 0-th and 1-st Betti number.

# Graph filtration on directed graphs



Building persistent homology on directed graphs  
is not trivial and important → [Research project](#)

How to compute the number of cycles in big network data?



Radeon Vega64 eGPU

How many cycles in the network?

# Betti numbers

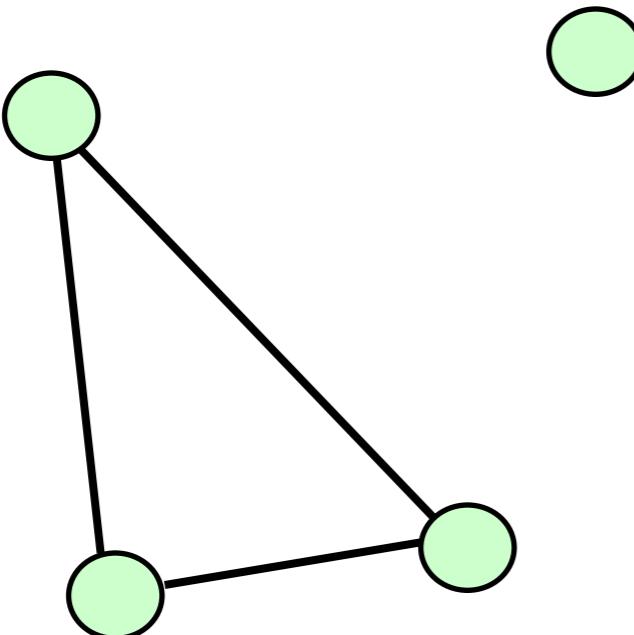
# Monotonicity of Betti-0 plot

## Monotonicity of $\beta_0$

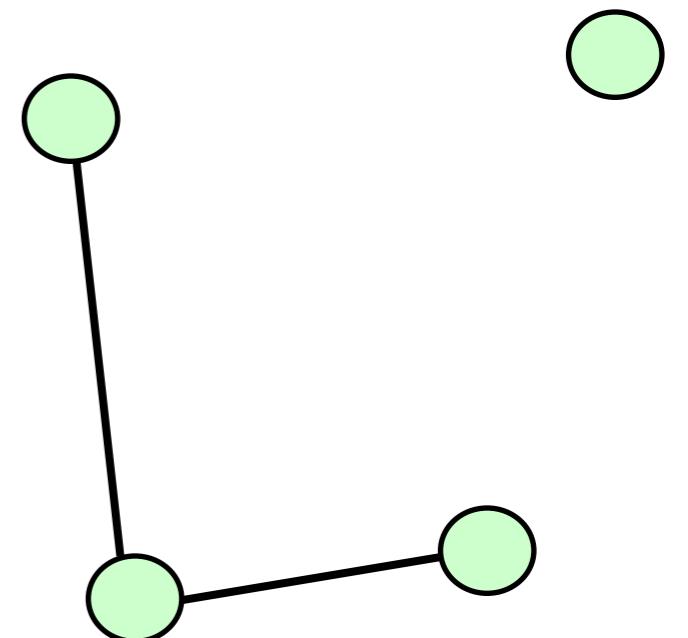
The **deletion** of edge **increases** the the number of connected components by at most 1.

$\beta_0$  increases by 0 or 1.

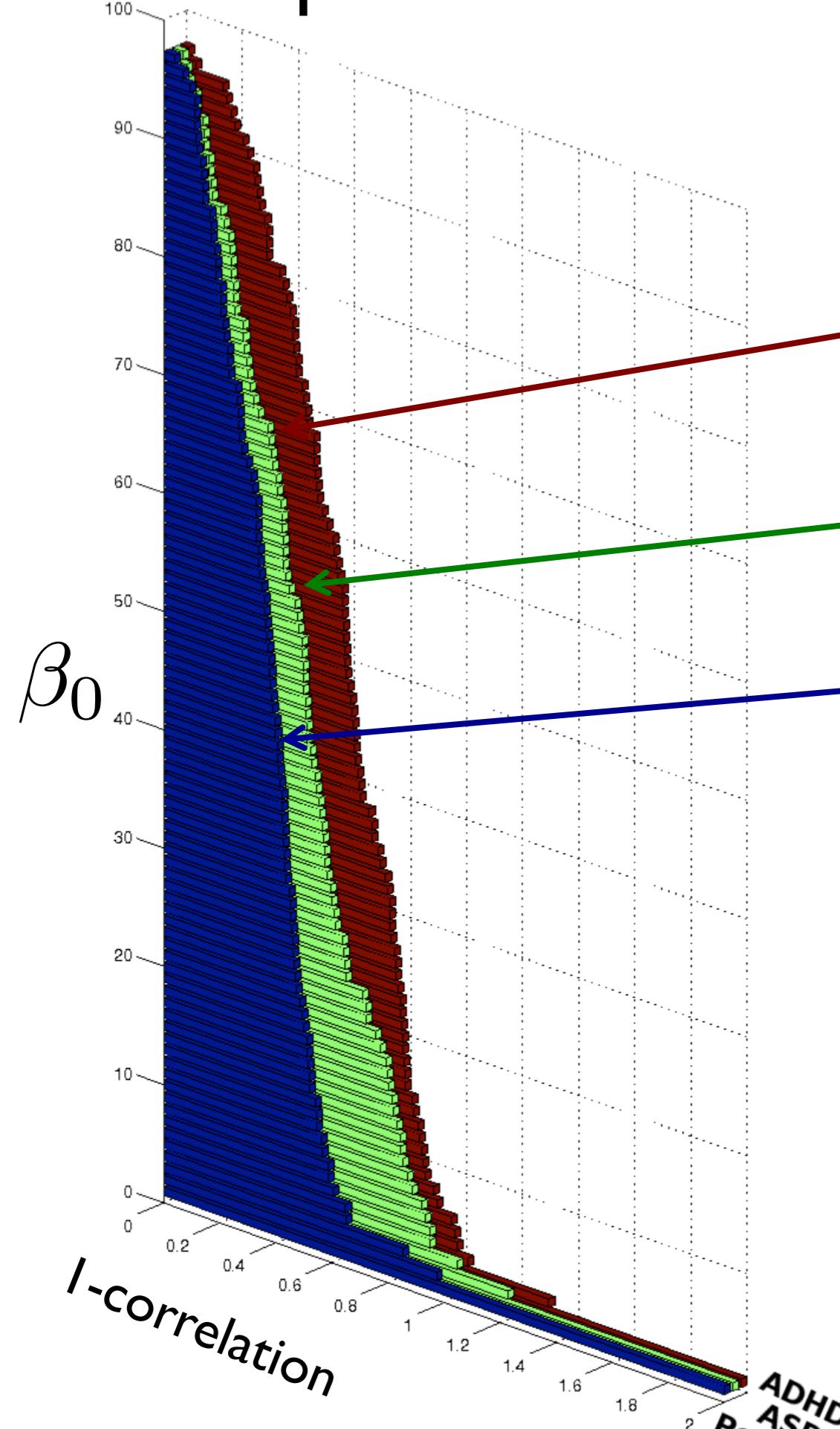
Case 1



Case 2



# 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

# Monotonicity of Betti-1 plot

Monotonicity of  $\beta_1$ :

The **deletion** of edge (in the filtration download) decreases the the number of **cycles** by at most 1.  
 $\beta_1$  decreases by 0 or 1.

Euler characteristic  
for  $l$ -skeleton:

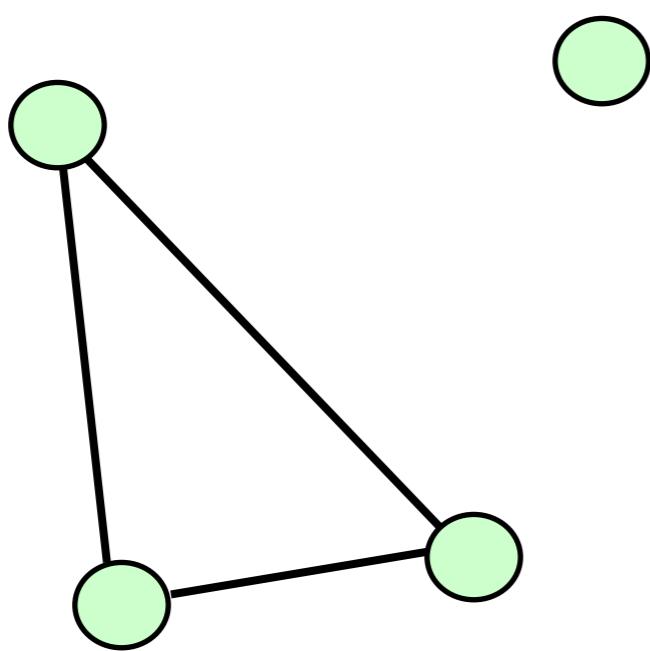
$$\chi = \beta_0 - \beta_1 = p - q$$

$\uparrow$        $\uparrow$   
nodes    edges

$$\beta_1 = \beta_0 - p + q$$

$\uparrow$        $\uparrow$        $\uparrow$        $\uparrow$   
-l, 0    0, +l    fixed    -l

# How Betti numbers change over downward graph filtration



$$\beta_0 = 2$$

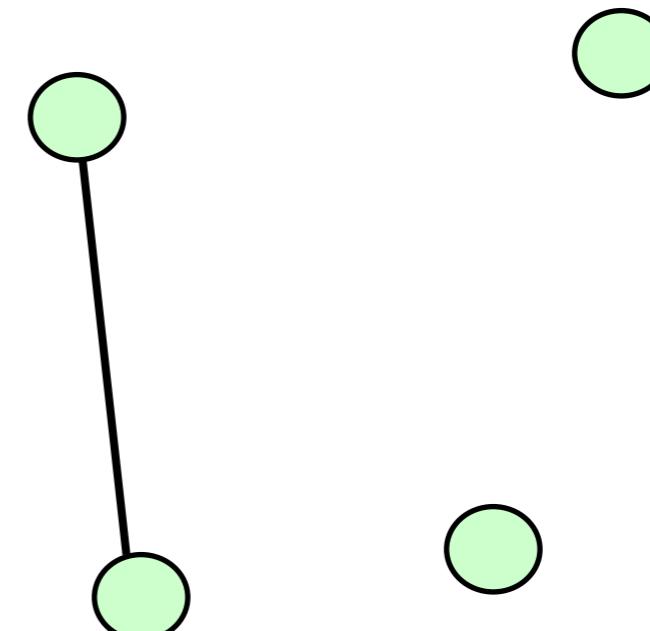
$$\beta_0 - \beta_1 = 1$$

$$\beta_1 = 1$$

$$p = 4$$

$$p - q = 1$$

$$q = 3$$



$$\beta_0 = 3$$

$$\beta_0 - \beta_1 = 3$$

$$\beta_1 = 0$$

$$p = 4$$

$$p - q = 3$$

$$q = 1$$

# Computation of Betti-plots in practice

Computation of  $\beta_0$ : Many existing algorithms. Can use a built-in function in MATLAB.

```
[beta_0, S] = graphconncomp(adj)
```

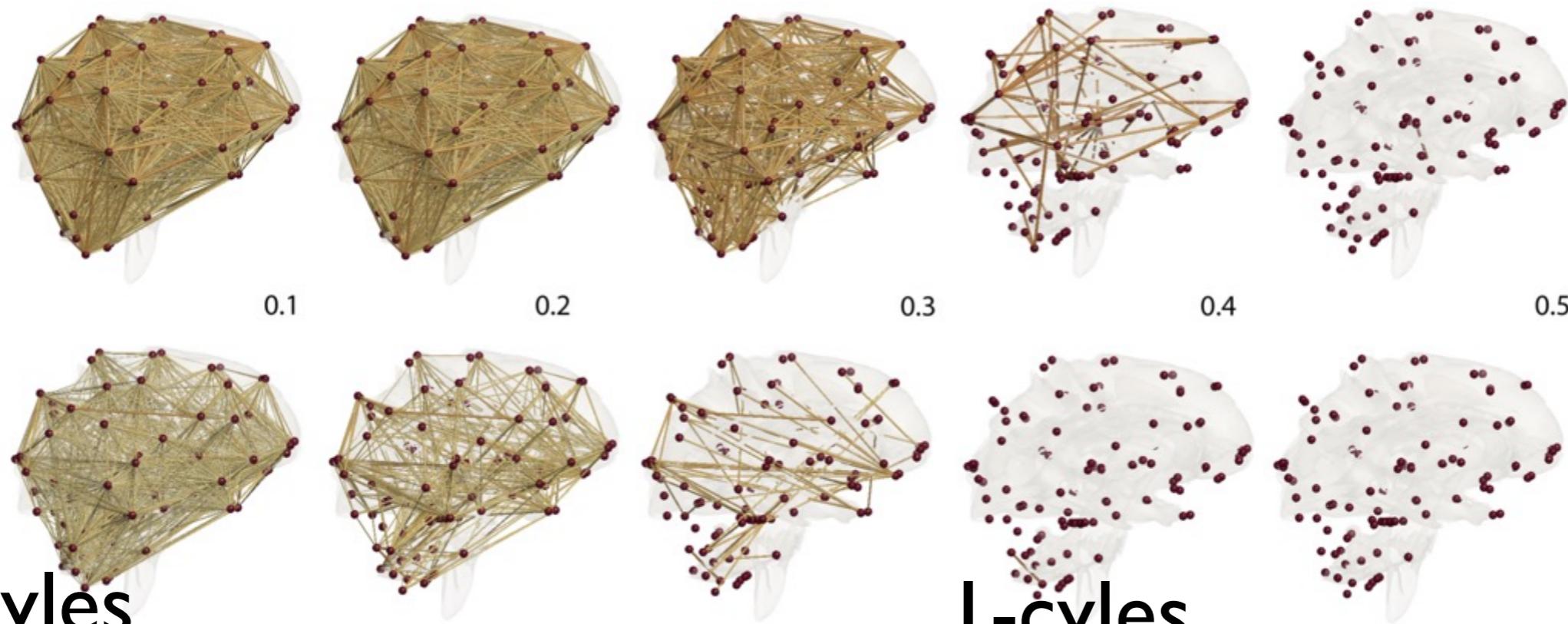
Computation of  $\beta_1$ : As a function of  $\beta_0$

$$\beta_1 = \beta_0 - p + q$$

```
q=sum(sum(adj))/2;  
beta_1 = beta_0 - p + q;
```

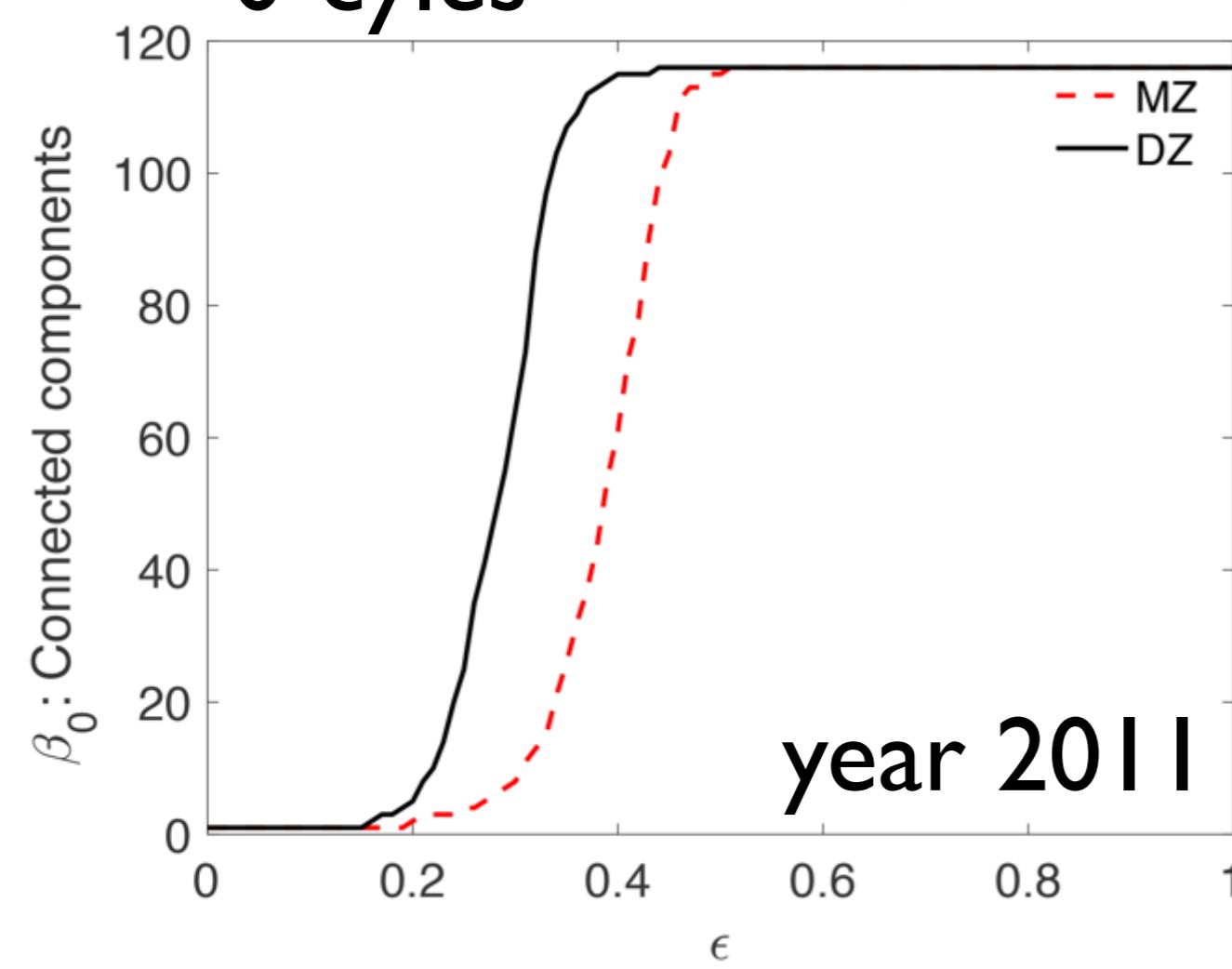
This is not efficient. Need an incremental algorithm that updates as we delete one edge at a time.

# Betti-plots in 116 nodes network

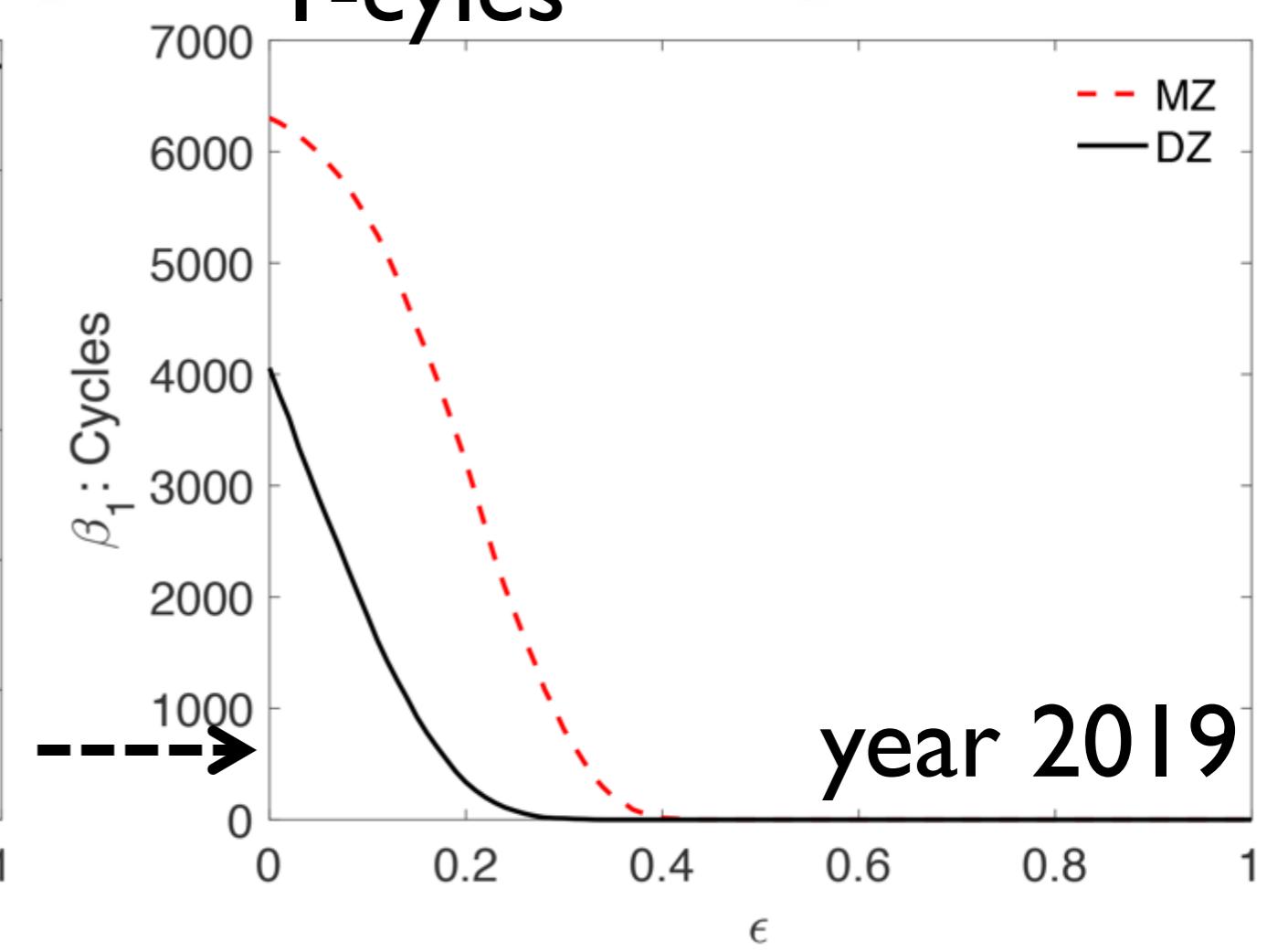


0-cyles

1-cyles



year 2011

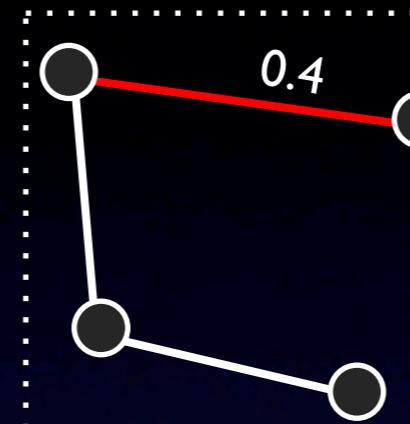
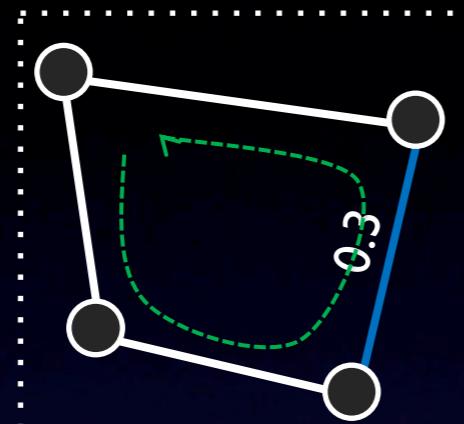
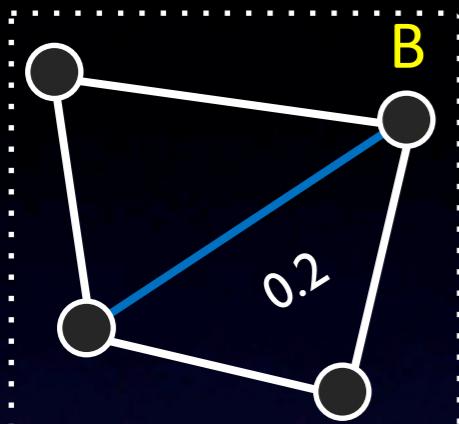


year 2019

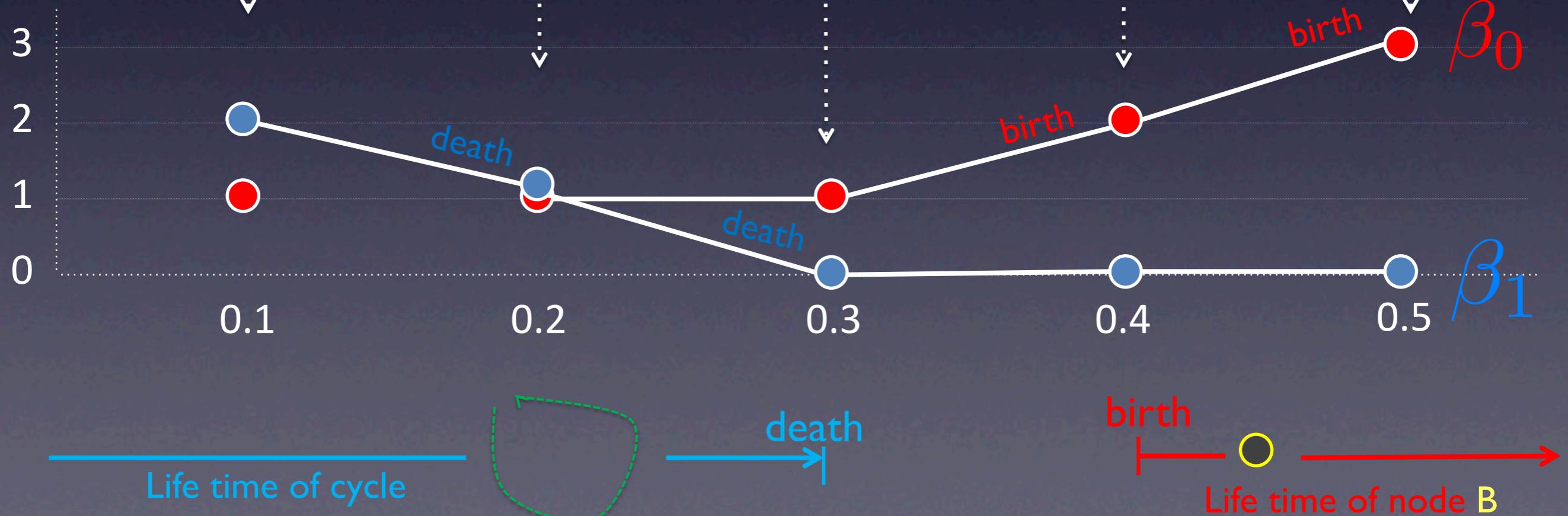
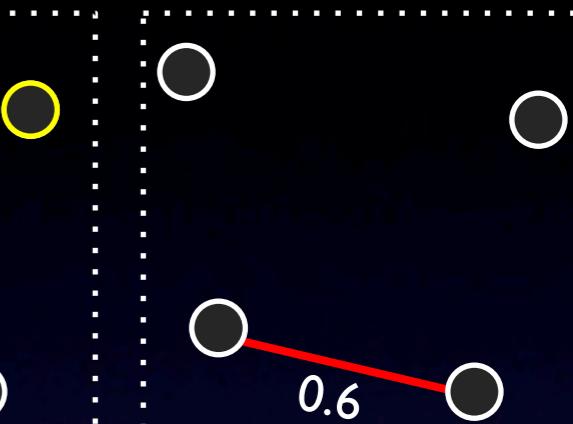
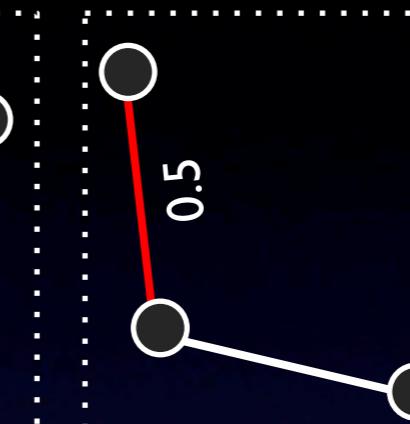
# Birth and death decomposition

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

Edges destroy cycles

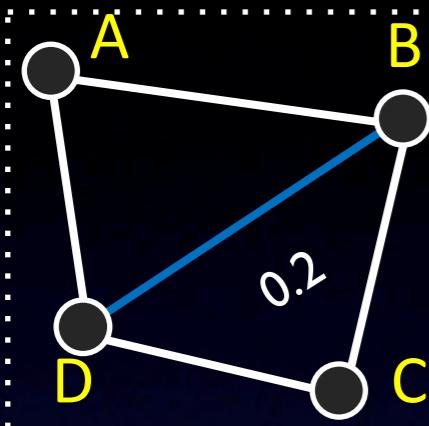


Edges create components

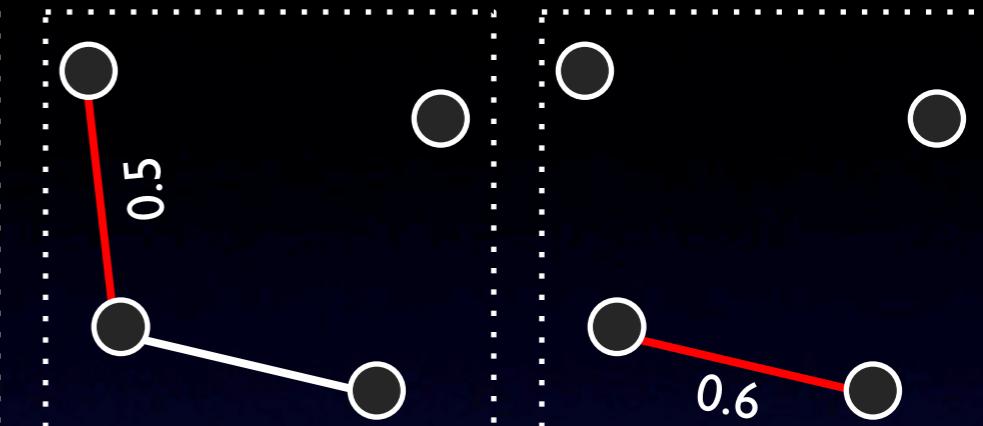
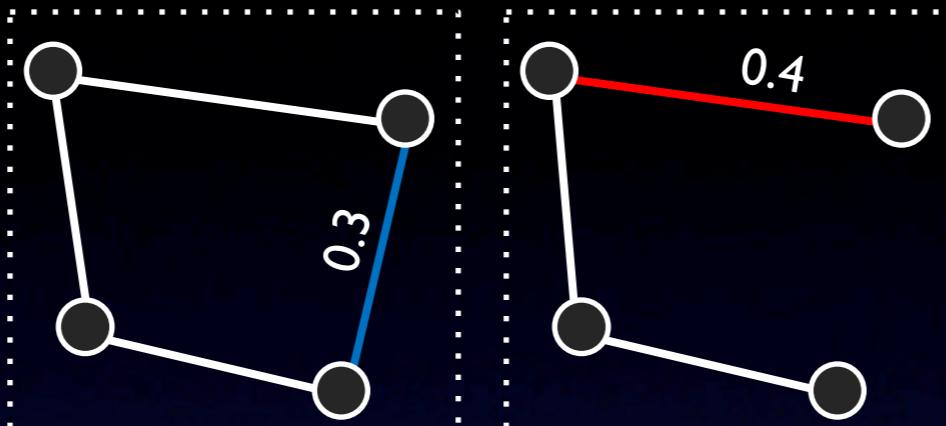


# Theorem Birth & death sets partition the edge set

$E_1$  Edges destroy cycles



$E_0$  Edges create components

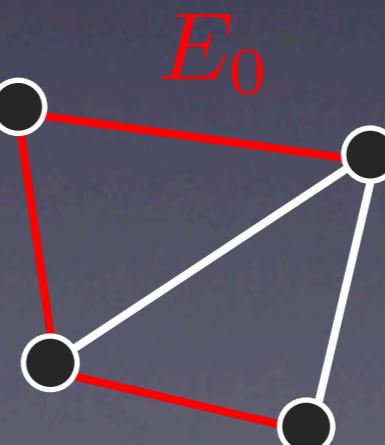
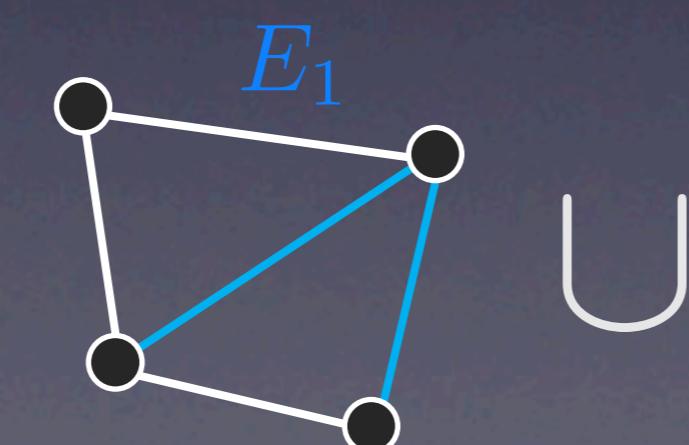
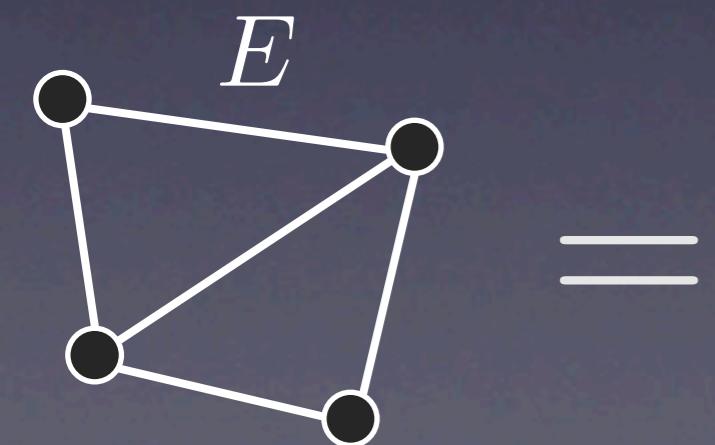


$$\#(E_1) = 1 + \frac{|V|(|V| - 3)}{2}$$

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

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

Maximum  
spanning  
tree



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