



STRUCTURES
CLUSTER OF
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UNIVERSITÄT
HEIDELBERG
ZUKUNFT
SEIT 1386

Topological Data Analysis in Python

organized by:

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Homology

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Homology: For each dimension $d \geq 0$ assigns to a topological space a vector space

$$X \mapsto H_d(X)$$

and to a continuous map a linear map

$$(f: X \rightarrow Y) \mapsto (H_d(f): H_d(X) \rightarrow H_d(Y))$$

Homology

Algebraic Topology: Distinguishing topological spaces via algebraic invariants

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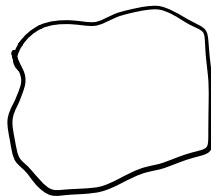
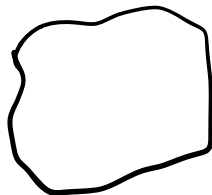
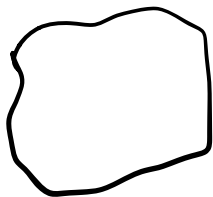
and to a continuous map a linear map

$$(f: X \rightarrow Y) \mapsto (H_d(f): H_d(X) \rightarrow H_d(Y))$$

Definition

$\beta_d(X) = \dim H_d(X)$ is called the d -th *Betti number* of X .

What homology can distinguish I

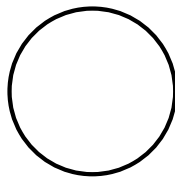


$$\beta_d(X \sqcup Y) = \beta_d(X) + \beta_d(Y).$$

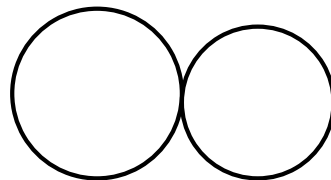
What homology can distinguish II



$$\beta_1 = 0$$



$$\beta_1 = 1$$



$$\beta_2 = 2$$

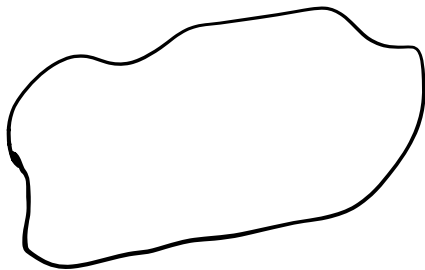
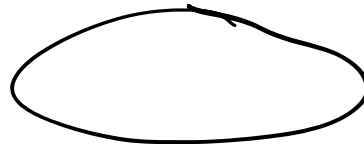
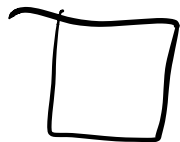
What homology can distinguish III



$$\beta_1 = 1 \quad \beta_2 = 0$$

$$\beta_1 = 0 \quad \beta_2 = 1$$

What homology cannot distinguish I



What homology cannot distinguish II



Homology in a nutshell

$\beta_d(X)$ is the number of d -dimensional holes in X .

Geometric Simplicial Complexes I

Definition

A *geometric n -simplex* is the convex hull of $n + 1$ affinely independent points in $\mathbb{R}^m$.



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If $\text{conv } X$ is a simplex and $Y \subseteq X$, then $\text{conv } Y$ is called a *face* of $\text{conv } X$.



Geometric Simplicial Complexes I

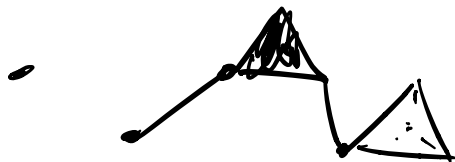
Definition

A *geometric n -simplex* is the convex hull of $n + 1$ affinely independent points in $\mathbb{R}^m$.

If $\text{conv } X$ is a simplex and $Y \subseteq X$, then $\text{conv } Y$ is called a *face* of $\text{conv } X$.

A *geometric simplicial complex* is a finite set K of simplices such that

- ▶ if $\sigma \in K$ and τ is a face of σ , then $\tau \in K$, and
- ▶ if $\sigma, \tau \in K$ and $\sigma \cap \tau \neq \emptyset$, then $\sigma \cap \tau$ is a face of σ and of τ .



Boundary matrix

Definition

Let $K = \{\sigma_1, \dots, \sigma_m\}$ be a simplicial complex. We define its *boundary matrix*

$D = (d_{i,j})$ as

$$d_{i,j} = \begin{cases} 1 & \text{if } \sigma_i \text{ is a } \textit{face} \text{ of } \sigma_j \text{ with } \dim \sigma_i = \dim \sigma_j - 1, \\ 0 & \text{otherwise.} \end{cases}$$

Boundary matrix

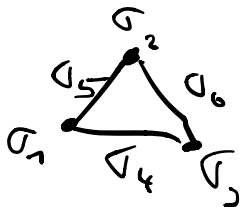
$$\overline{\mathbb{F}}_2 \quad 1+1=0$$

Definition

Let $K = \{\sigma_1, \dots, \sigma_m\}$ be a simplicial complex. We define its *boundary matrix* $D = (d_{i,j})$ as

$$d_{i,j} = \begin{cases} 1 & \text{if } \sigma_i \text{ is a boundary of } \sigma_j \text{ with } \dim \sigma_i = \dim \sigma_j - 1, \\ 0 & \text{otherwise.} \end{cases}$$

Example



$$\begin{matrix} & \sigma_1 & \sigma_2 & \sigma_3 & \sigma_4 & \sigma_5 & \sigma_6 \\ \begin{matrix} \sigma_1 \\ \sigma_2 \\ \sigma_3 \\ \dots \end{matrix} & \begin{pmatrix} 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \end{pmatrix} \end{matrix}$$

Matrix reduction I

Definition

Let $v = (v_1, \dots, v_m)^T$ be a column vector. We define

$$\text{pivot } v = \max\{i \in \{1, \dots, m\} \mid v_i \neq 0\}.$$

$$\begin{pmatrix} 0 \\ 1 \\ 0 \end{pmatrix}$$

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If M is a matrix, we write m_j for its j -th column and $\text{cols } M$ for the set of all its non-zero columns.

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We say that M is *reduced* if $\text{pivot } m_j = \text{pivot } m_k$ implies $m_j = m_k$ for all $m_j, m_k \in \text{cols } M$.

pivot m_k

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Example

Reduced: $\begin{pmatrix} 0 & 1 & 1 \\ 1 & 0 & 0 \\ 0 & 0 & 1 \end{pmatrix}$

Not reduced: $\begin{pmatrix} 0 & 0 & 1 \\ 1 & 0 & 1 \\ 0 & 1 & 1 \end{pmatrix}$

Matrix reduction II

Definition

Let M be a matrix. We say that (R, V) is a *reduction* of M if R is reduced, V is upper-triangular and invertible and we have $R = MV$.

Matrix reduction II

Definition

Let M be a matrix. We say that (R, V) is a *reduction* of M if R is reduced, V is upper-triangular and invertible and we have $R = MV$.

Input: M

Output: (R, V) reduction of M

$R \leftarrow M$

$V \leftarrow I$

while $\exists i < j$ with pivot $R_i = \text{pivot } R_j$ **do**

$R_j \leftarrow R_j + R_i$

$V_j \leftarrow V_j + V_i$

end while

return (R, V)

Matrix reduction III

$$\begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 1 \\ 0 & 1 & 1 \end{pmatrix} \rightsquigarrow \begin{pmatrix} 1 & 0 & 1 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \end{pmatrix} \rightsquigarrow \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \end{pmatrix}$$

Theorem

Let $K = \{\sigma_1, \dots, \sigma_m\}$ be a simplicial complex with boundary matrix D . Let (R, V) be a reduction of D . Then

$$\beta_d(K) = \#\{i \mid R_i = 0, i \notin \text{pivots } R, \dim \sigma_i = d\}.$$

Computing homology I

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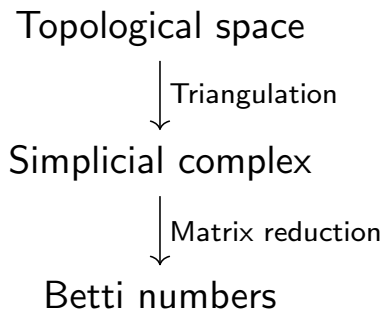
Example



$$D = \left(\begin{array}{ccc|ccc} 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & \vdots & \vdots & 0 & 1 & 1 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \end{array} \right) \sim R = \left(\begin{array}{ccc|ccc} \vdots & \vdots & \vdots & 1 & 1 & 0 \\ \vdots & \vdots & \vdots & 0 & 1 & 1 \\ \vdots & \vdots & \vdots & 0 & 0 & \vdots \\ \vdots & \vdots & \vdots & 0 & 0 & \vdots \\ \vdots & \vdots & \vdots & 0 & 0 & \vdots \end{array} \right) \leftarrow \{ \}$$

i with $R_i = 0$

$\dim = 0 \rightarrow \textcircled{1} 2, 3, \textcircled{6} \leftarrow \dim = 1$ Pivots R : 2, 3



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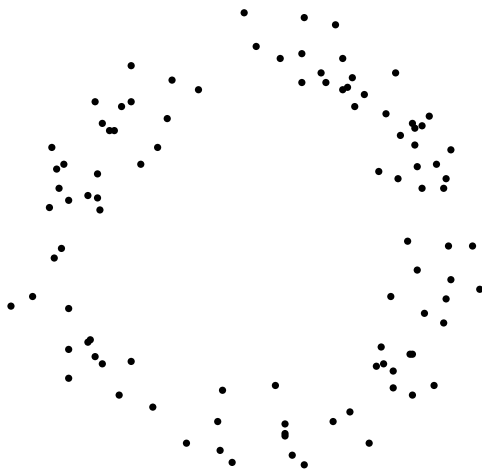
Homology of Spaces

Homology of Data

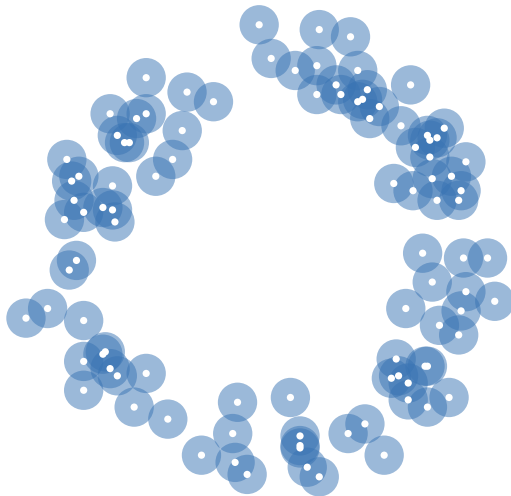
Ripser

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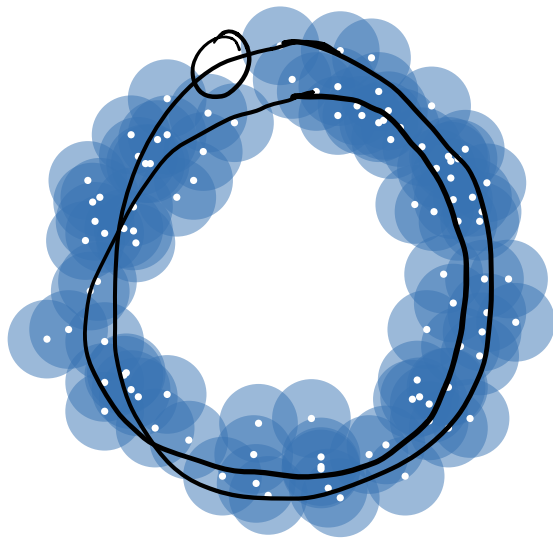
Manifold recovery I



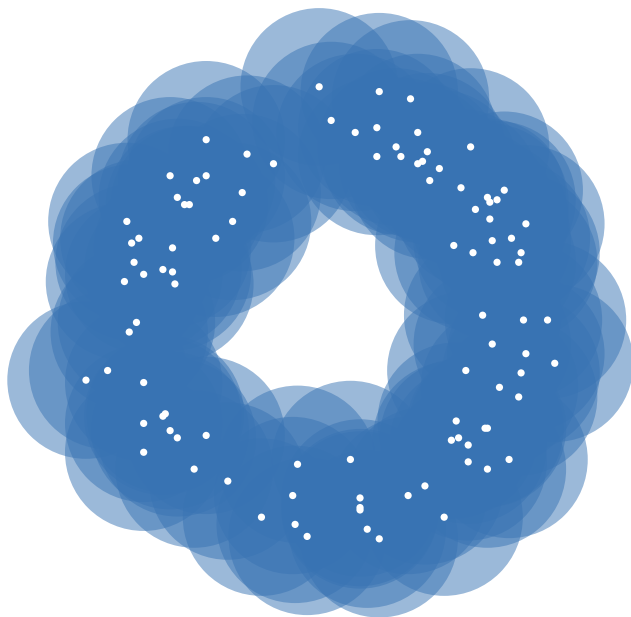
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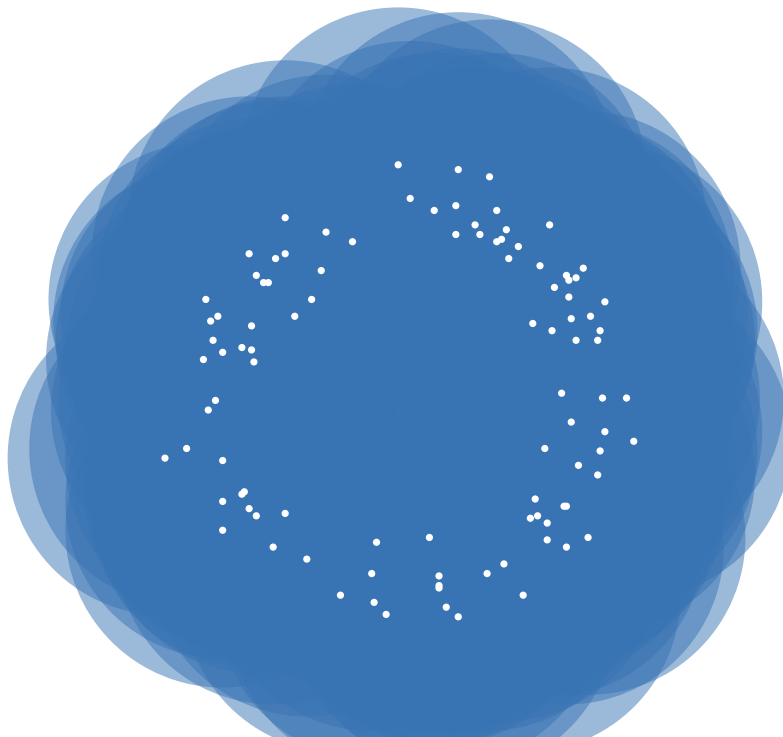
Manifold recovery I



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Manifold recovery I



Manifold recovery II

Theorem (Niyogi, Smale, Weinberger)

Let $M \subseteq \mathbb{R}^k$ be a manifold and $P \subseteq M$. There exists $c(M) > 0$ such that for every $c(M) > \delta > 0$ with $M \subseteq \bigcup_{x \in P} B_\delta(x)$ we have

$$H_*(M) \cong H_* \left(\bigcup_{x \in P} B_\delta(x) \right)$$

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Manifold recovery II

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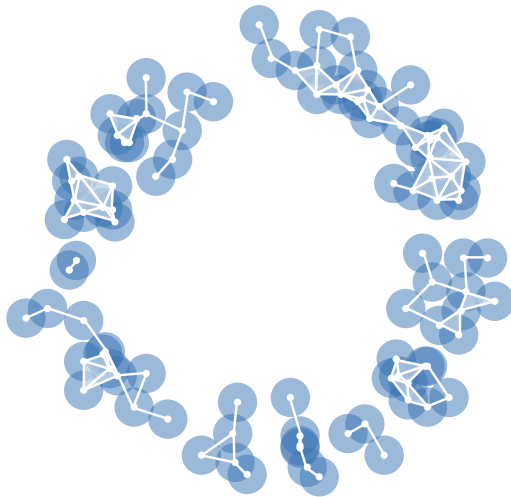
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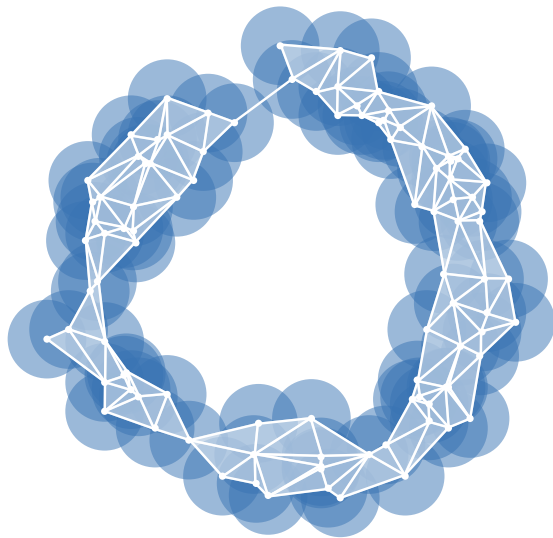
How do we choose δ ?

We don't!

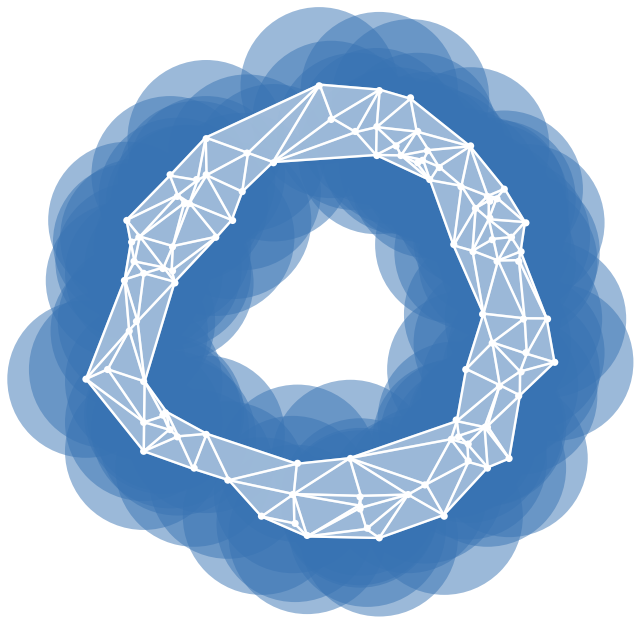
Complexes from balls I



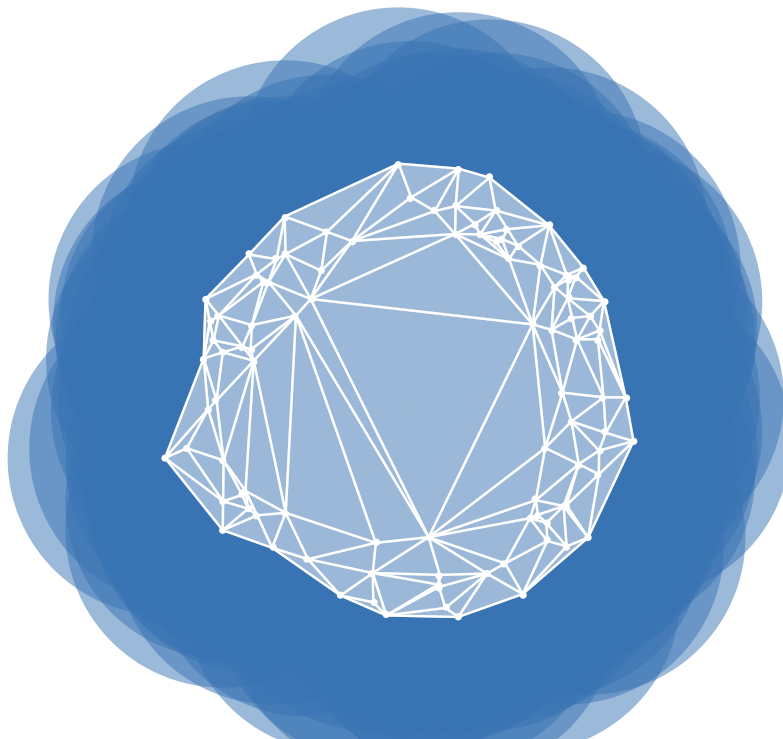
Complexes from balls I



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Complexes from balls I



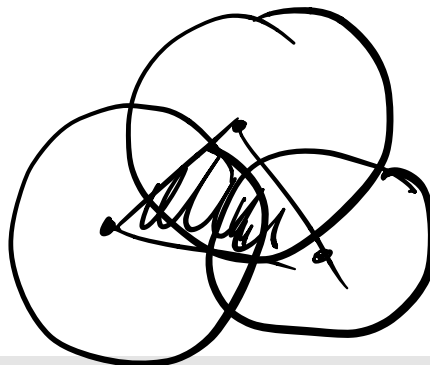
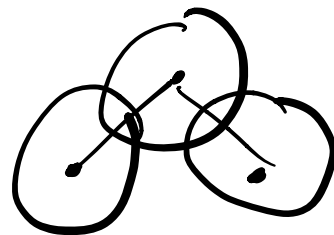
Complexes from Balls II

Definition

Let $P \subseteq \mathbb{R}^k$ be a finite set. For $t > 0$ define the Čech complex

$$\check{\text{Cech}}_t(P) = \{Q \subseteq P \mid \bigcap_{x \in Q} B_t(x) \neq \emptyset\}.$$

Note: $\check{\text{Cech}}_t(P) \subseteq \check{\text{Cech}}_u(P)$ whenever $t \leq u$.



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Theorem (Nerve Theorem)

Let $P \subseteq \mathbb{R}^k$ be a finite set and $t \geq 0$. If $\bigcap_{x \in Q} B_t(x)$ can be deformed to a point for all $Q \subseteq P$, then

$$H_*\left(\bigcup_{x \in P} B_t(x)\right) \cong H_*(\check{\text{Cech}}_t(P))$$

Rips complexes

Definition

Let $P \subseteq \mathbb{R}^k$ be a finite set. For $t \geq 0$ we define the *Rips complex*

$$\text{Rips}_t(P) = \{Q \subseteq P \mid \sup_{x,y \in Q} d(x,y) \leq t\}.$$

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Theorem

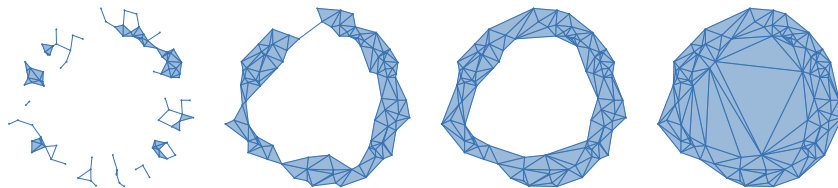
There exists $\theta > 0$ such that for all finite sets $P \subseteq \mathbb{R}^k$ and $t > 0$ we have

$$\text{Rips}_t \subseteq \check{\text{Cech}}_{\theta t}(P)$$

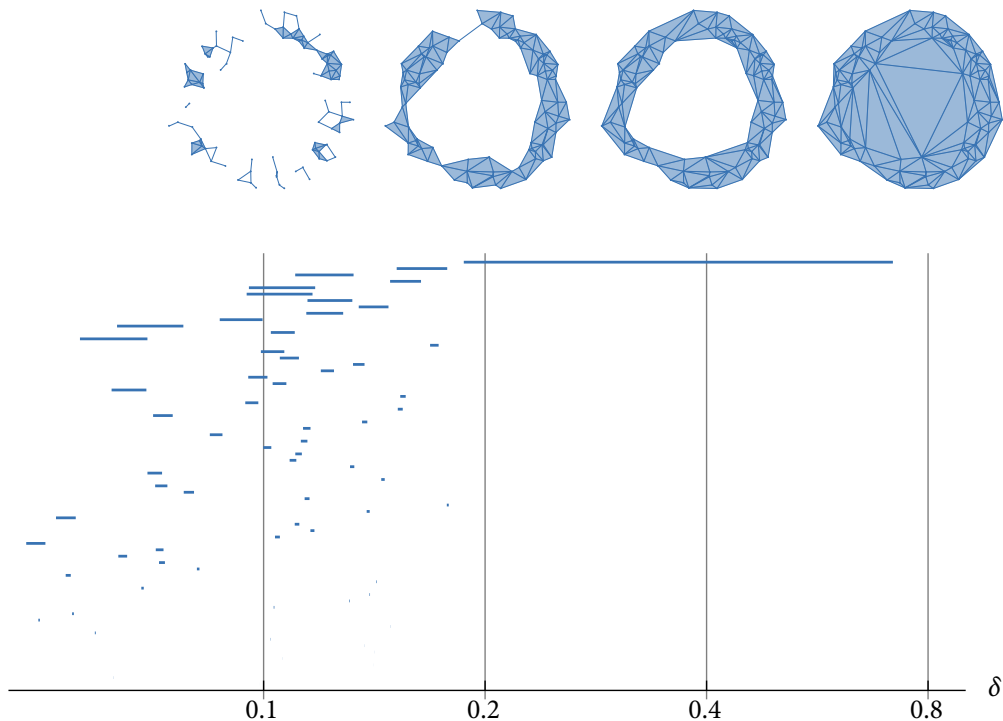
and

$$\check{\text{Cech}}_t \subseteq \text{Rips}_{\theta t}(P)$$

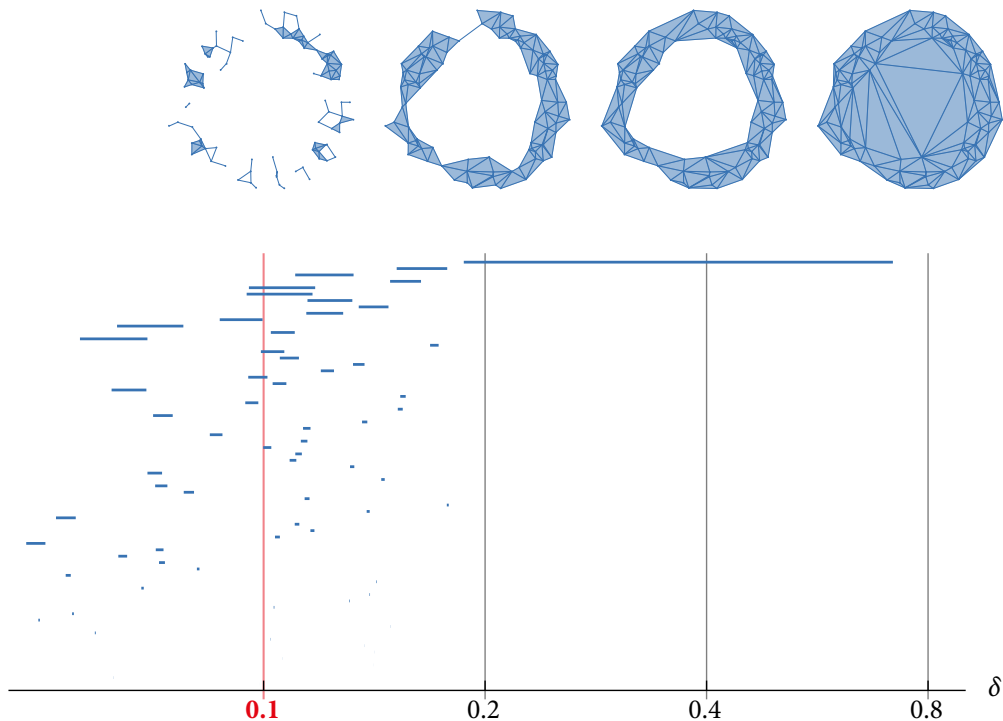
Homology for Data



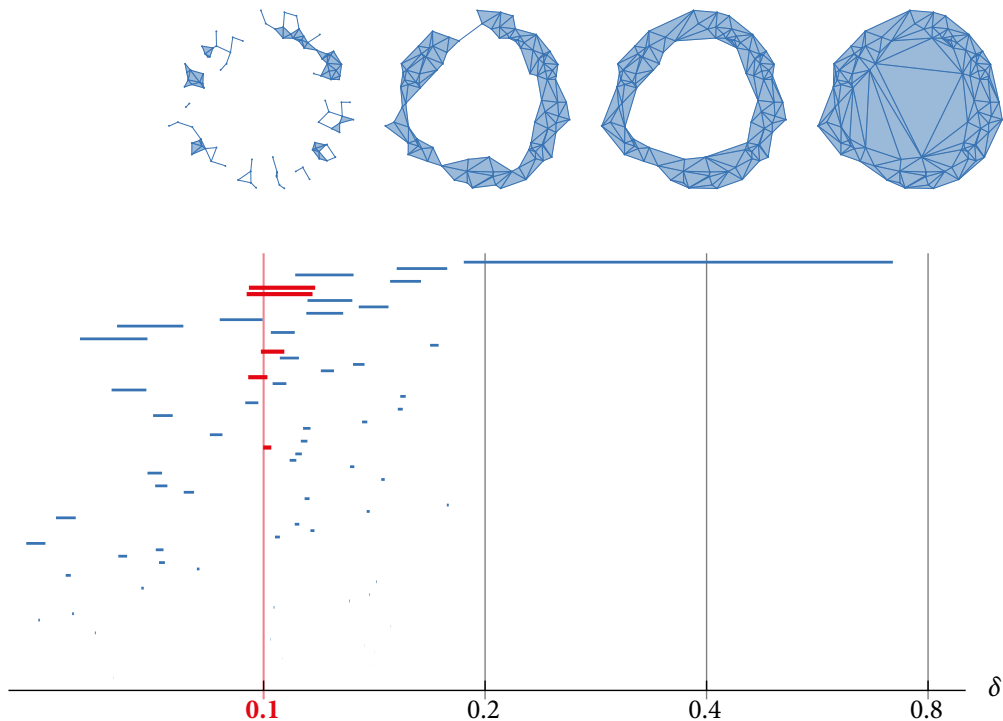
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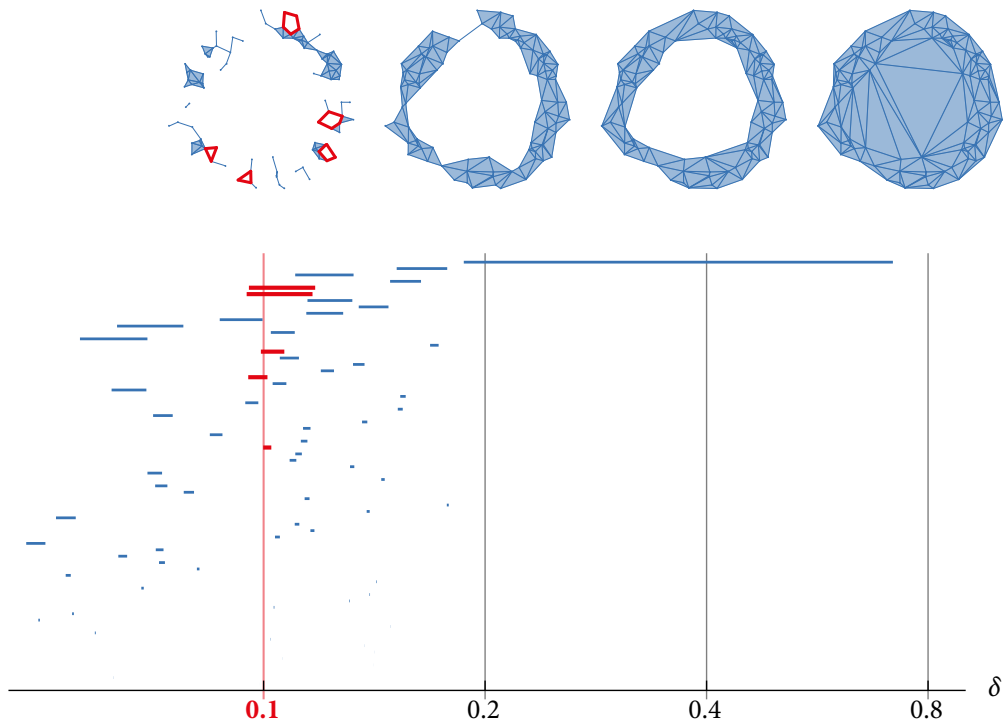
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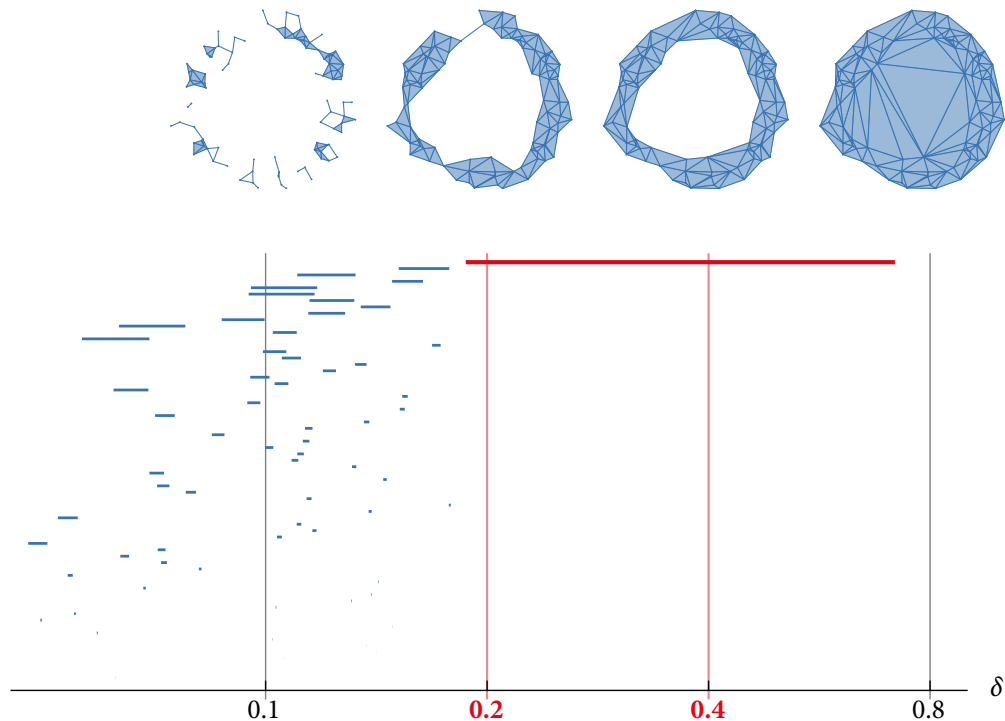
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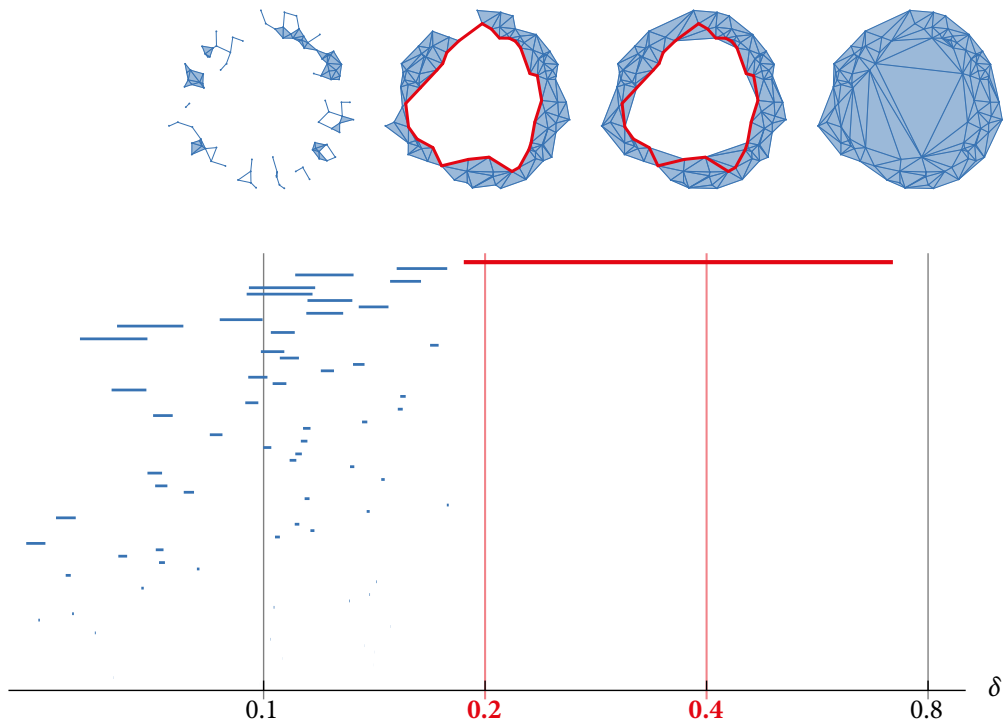
Homology for Data



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Homology for Data



Definition

A family of finite-dimensional vector spaces V_i , $i = 1, \dots, n$ with linear maps $V_i \rightarrow V_{i+1}$ for each i is called a *persistence module*.

$$U_1 \subseteq U_2 \subseteq U_3 \subseteq \dots \subseteq U_n$$

Definition $H(U_1) \rightarrow H(U_2) \rightarrow \dots \rightarrow H(U_n)$

A family of finite-dimensional vector spaces V_i , $i = 1, \dots, n$ with linear maps $V_i \rightarrow V_{i+1}$ for each i is called a *persistence module*.

Theorem *Gabriel* $(V_t)_{t \in \mathbb{R}}$ $V_t \rightarrow V_s$ $s \leq t$
 Let

$$V_1 \longrightarrow V_2 \longrightarrow \dots \longrightarrow V_{n-1} \longrightarrow V_n$$

be a persistence module. Then there exists a unique family of intervals $(I_k)_{k \in K}$ with $I_k \subseteq \{1, \dots, n\}$ such that

$$\dim V_i = \#\{k \in K \mid i \in I_k\}$$

and

$$\text{rank}(V_i \rightarrow V_j) = \#\{k \in K \mid i, j \in I_k\}$$

Definition

Let K be a simplicial complex. A *filtration* of K is a family of simplicial complexes $K_1, \dots, K_n$ such that $K_n = K$ and $K_i \subseteq K_{i+1}$ for all n .

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We call

$$H_*(K_1) \longrightarrow H_*(K_2) \longrightarrow \dots \longrightarrow H_*(K_{n-1}) \longrightarrow H_*(K_n)$$

the *persistent homology* of the filtration.

Computing persistent homology

Theorem (Barannikov, Carlsson & Zomorodian, Edelsbrunner et al.)

Let $K = \{\sigma_1, \dots, \sigma_n\}$ be a simplicial complex such that $K_i = \{\sigma_1, \dots, \sigma_i\}$ is a subcomplex.



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Let D be the corresponding boundary matrix and (R, V) a reduction of D .

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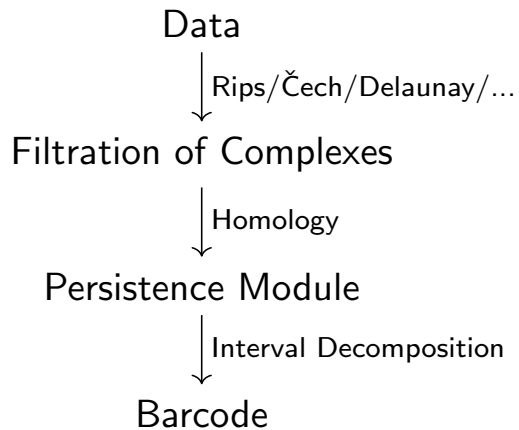
*Let D be the corresponding boundary matrix and (R, V) a reduction of D .
Then*

$$\{[i, \infty) \mid R_i = 0, i \notin \text{pivots } R\} \cup \{[i, j) \mid i = \text{pivot } R_j\}$$

is the barcode of

$$H_*(K_1) \longrightarrow H_*(K_2) \longrightarrow \dots \longrightarrow H_*(K_{n-1}) \longrightarrow H_*(K_n)$$

Persistent homology pipeline



Definition

Let $P, Q \subseteq \mathbb{R}^k$. We define their *Hausdorff distance* as

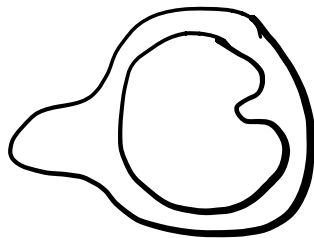
$$d_H(P, Q) = \max \left\{ \sup_{p \in P} \inf_{q \in Q} d(p, q), \sup_{q \in Q} \inf_{p \in P} d(p, q) \right\}$$

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Example



Stability II

Definition

Let $B = (I_\alpha)_{\alpha \in A}$ and $C = (J_\beta)_{\beta \in B}$ be barcodes.

A δ -*matching* between them consists of subsets $A' \subseteq A$, $B' \subseteq B$ and a bijection $f: A' \rightarrow B'$ such that:

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- ▶ If $\alpha \notin A'$, $\beta \notin B'$, then $\text{length}(I_\alpha), \text{length}(J_\beta) < \delta$.
- ▶ If $f(I_\alpha) = J_\beta$, then the endpoints of I_α and J_β are within δ of each other.

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- ▶ If $f(I_\alpha) = J_\beta$, then the endpoints of I_α and J_β are within δ of each other.

We define the *bottleneck distance* as

$$d_b(B, C) = \inf\{\delta > 0 \mid \text{there exists a } \delta\text{-matching between } B \text{ and } C\}.$$

Stability II

Definition

Let $B = (I_\alpha)_{\alpha \in A}$ and $C = (J_\beta)_{\beta \in B}$ be barcodes.

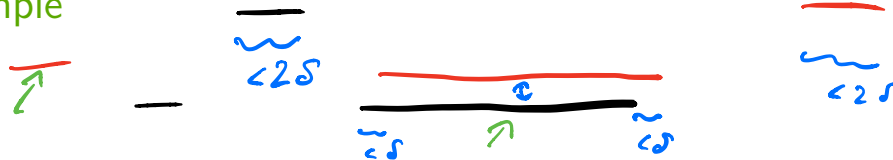
A δ -matching between them consists of subsets $A' \subseteq A$, $B' \subseteq B$ and a bijection $f: A' \rightarrow B'$ such that:

- ▶ If $\alpha \notin A'$, $\beta \notin B'$, then $\text{length}(I_\alpha), \text{length}(J_\beta) < 2\delta$.
- ▶ If $f(I_\alpha) = J_\beta$, then the endpoints of I_α and J_β are within δ of each other.

We define the *bottleneck distance* as

$$d_b(B, C) = \inf\{\delta > 0 \mid \text{there exists a } \delta\text{-matching between } B \text{ and } C\}.$$

Example



Theorem (Cohen-Steiner et al.)

Let $P, Q \subseteq \mathbb{R}^k$ be finite subsets and let $B(P)$ and $B(Q)$ be the barcodes of the persistent homology of their Rips filtrations. Then

$$d_b(B(P), B(Q)) \leq d_H(P, Q).$$

Persistence diagrams

Definition

If $B = (I_\alpha)_{\alpha \in A}$ is a barcode, we define its *persistence diagram* as

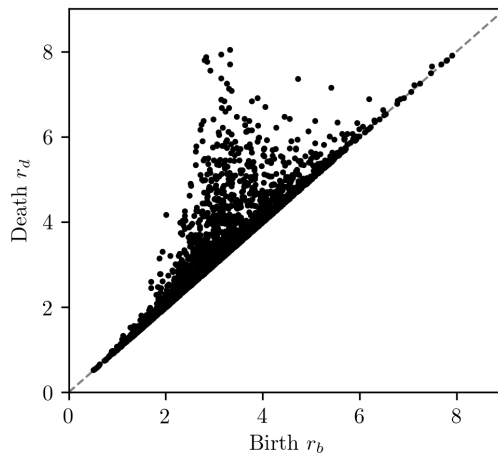
$$\text{dgm}(B) = ((\inf I_\alpha, \sup I_\alpha))_{\alpha \in A} \subseteq \mathbb{R}^2.$$

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Also implemented in scikit-tda:

```
from ripser import ripser
from persim import plot_diagrams

# Compute the persistence diagram of a Rips filtration
# data is numpy array of points in euclidean space or a distance matrix
dgm = ripser(data, maxdim = 1, thresh = inf, distance_matrix = False)

# Plot the persistence diagram
plot_diagrams(dgm, show = False)
```


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- ▶ Infer something about the shape of a data set (e.g. Cosmic Microwave Background, Edelsbrunner et al.)
- ▶ Infer something about the complexity of a data set (e.g. lung disease detection, Brodzki et al.)
- ▶ Use it as an additional layer in machine learning methods

