CS233, CME251: Geometric and Topological Data Analysis

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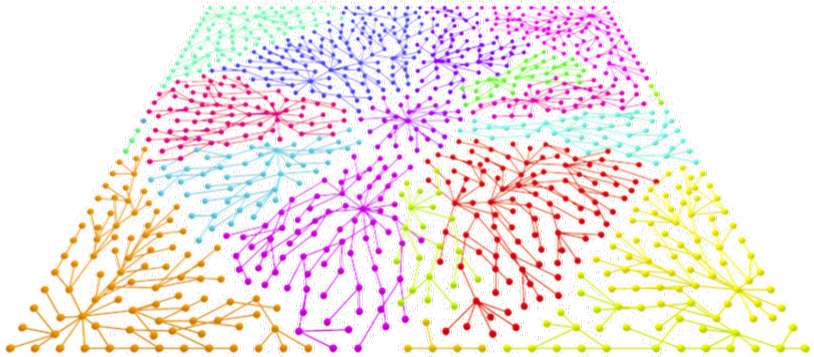
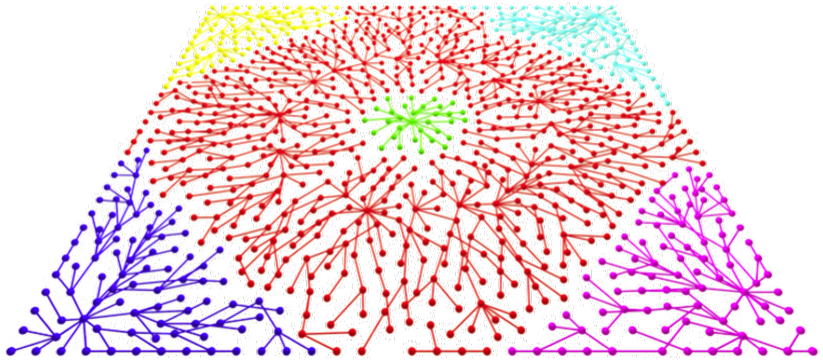
Lecture 8
20 April 2022





Class Logistics

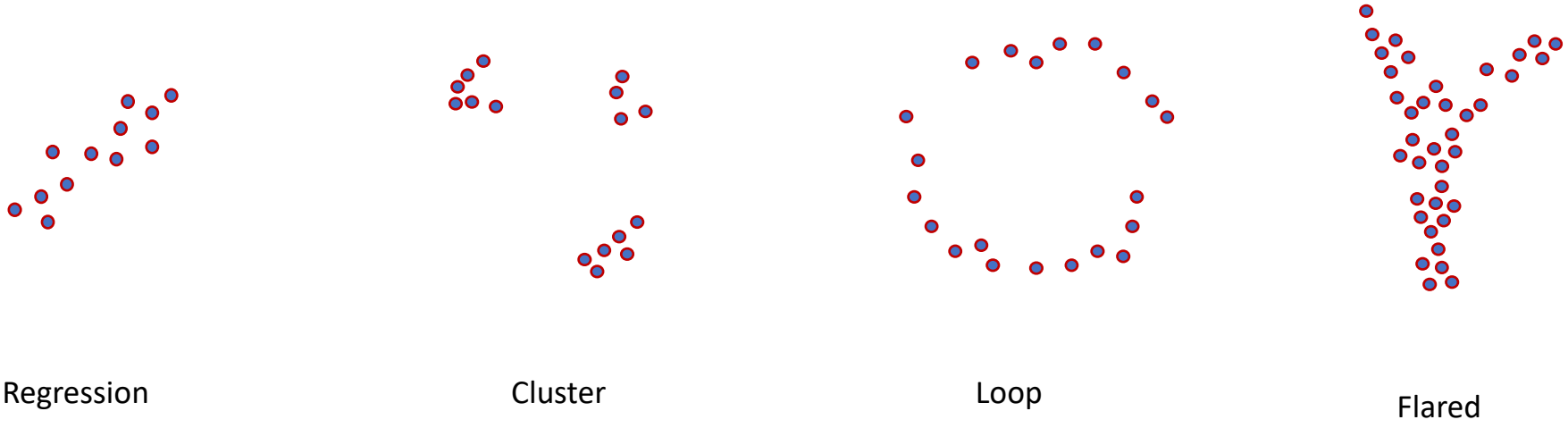
- Homework 1 is due today.
- Homework 2 (on TDA) is out and due Wed, May 4.

Last Time: Introduction to Computational Topology

Topological Data Analysis (TDA)

The “Shape of Data”

- TDA Studies Sampled Spaces

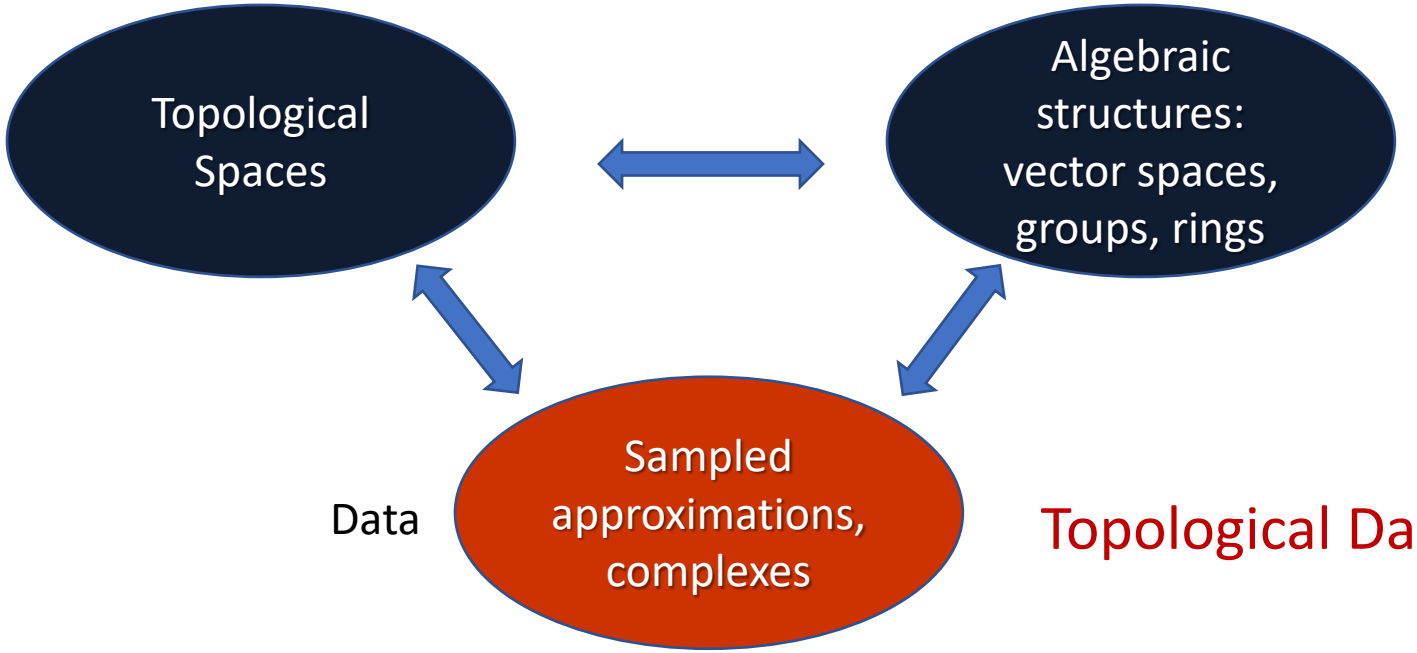


Regression Cluster Loop Flared

Topology “measures” connectivity, graded by dimension

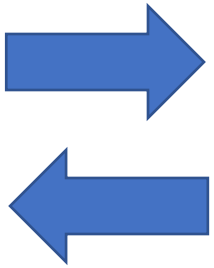
Algebraic Topology and Topology Inference

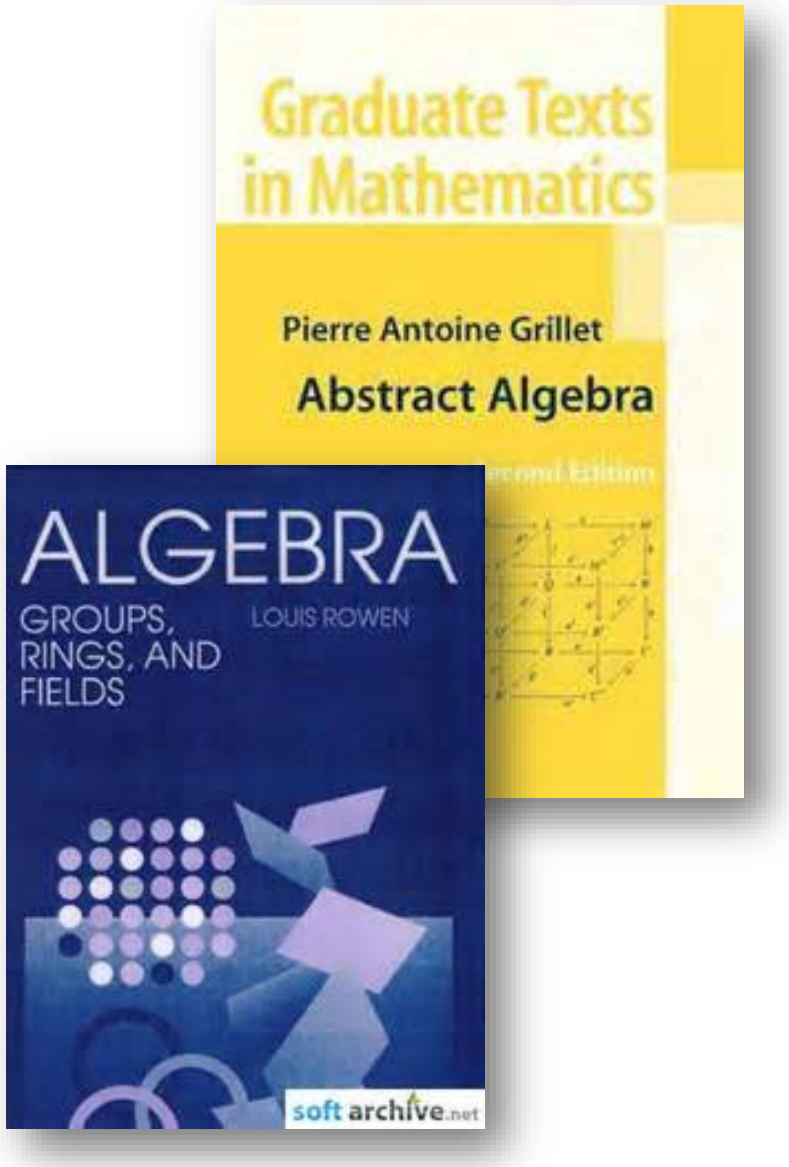
- Unlike geometry, topology studies the global structure of spaces
- Getting to this structure via algebra **algebraic topology**



Topological Data Analysis (TDA)

From Data to Algebraic Objects

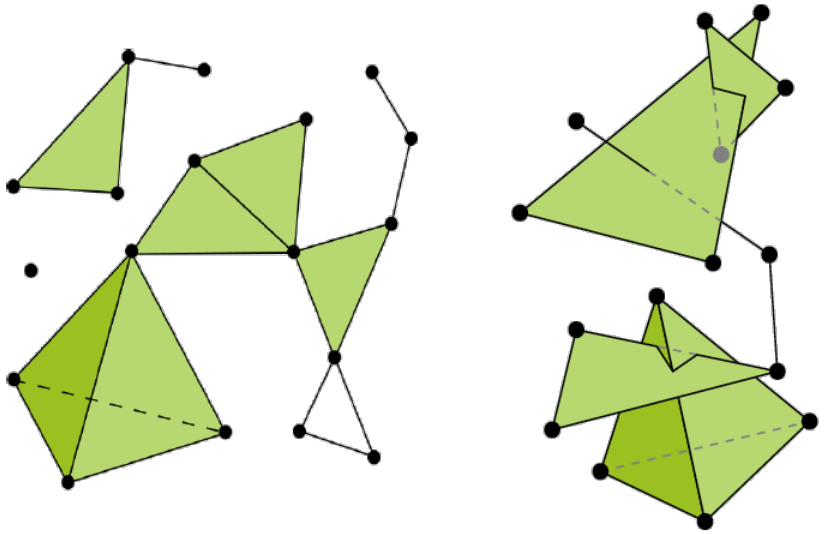




Algebraic entities as data descriptors

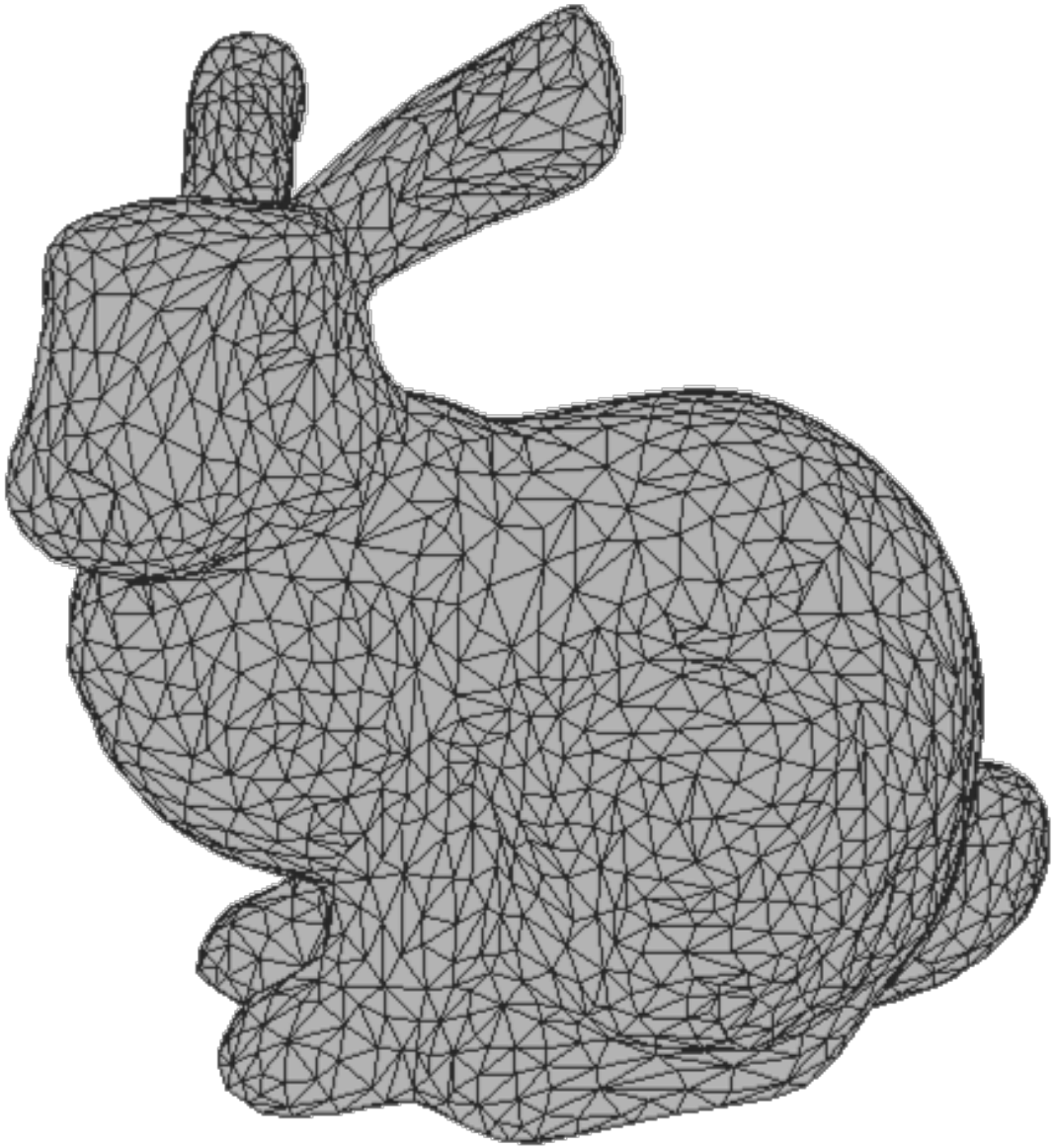
Simplicial Complexes

- A simplicial complex K is a finite set of simplices such that
  1. $\sigma \in K, \tau \leq \sigma \Rightarrow \tau \in K$,
  2. $\sigma, \sigma' \in K \Rightarrow \sigma \cap \sigma' \leq \sigma, \sigma'$ or $\sigma \cap \sigma' = \emptyset$.
- The dimension of K is $\dim K = \max\{\dim \sigma \mid \sigma \in K\}$.
- The vertices of K are the zero-simplices in K.
- A simplex is principal if it has no proper coface in K.

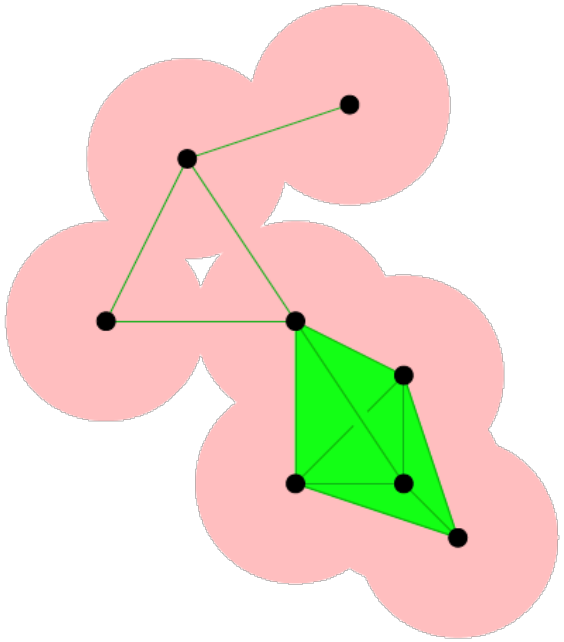


(left) an example (right) a non example

Meshes are 2-D Complexes

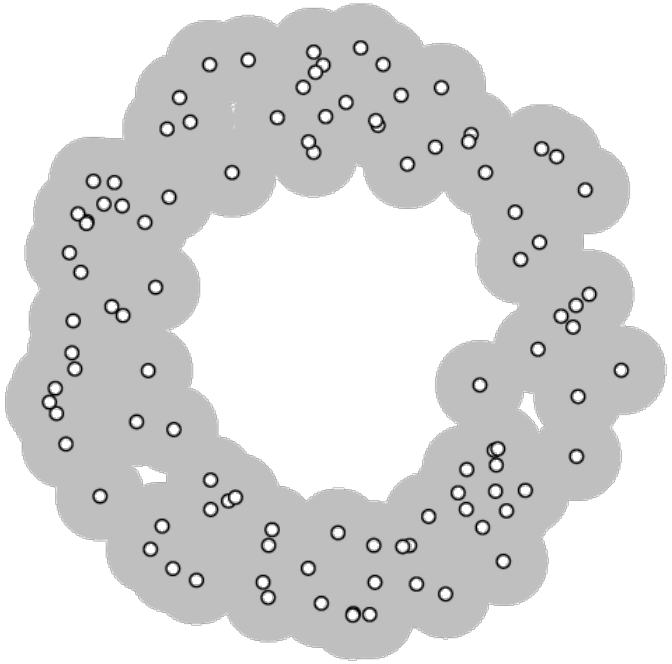


Čech Complex



- $C_\epsilon(M) = \left\{\operatorname{conv} T \mid T \subseteq M, \bigcap_{m_i \in T} B_\epsilon(m_i) \neq \emptyset\right\}.$
- $\sum_{k=0}^{m} \binom{m}{k} = 2^{m+1} - 1$
- $C_\epsilon(M) \simeq \tilde{\mathbb{M}}$

Čech Complex

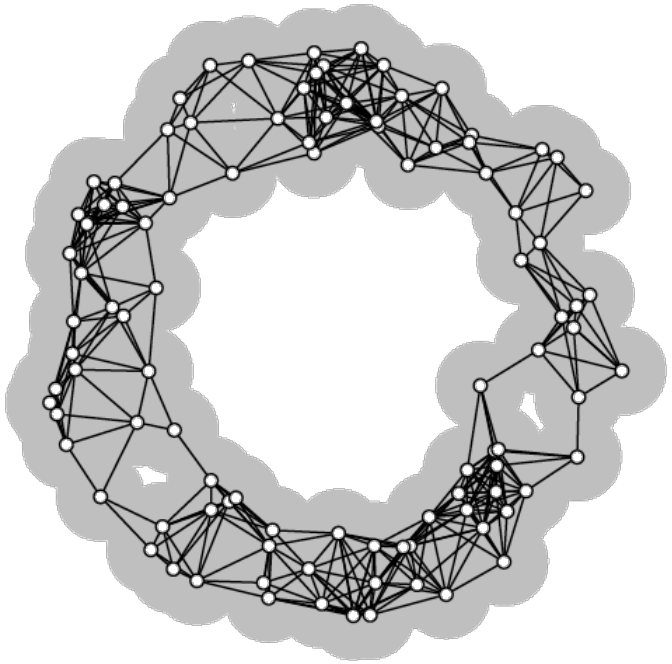


$\check{C}_{.6}$

The Čech complex $\check{C}_\epsilon$ encodes the intersection pattern of M_ϵ: Encode:

Points as *vertices* (0-cells)

Čech Complex



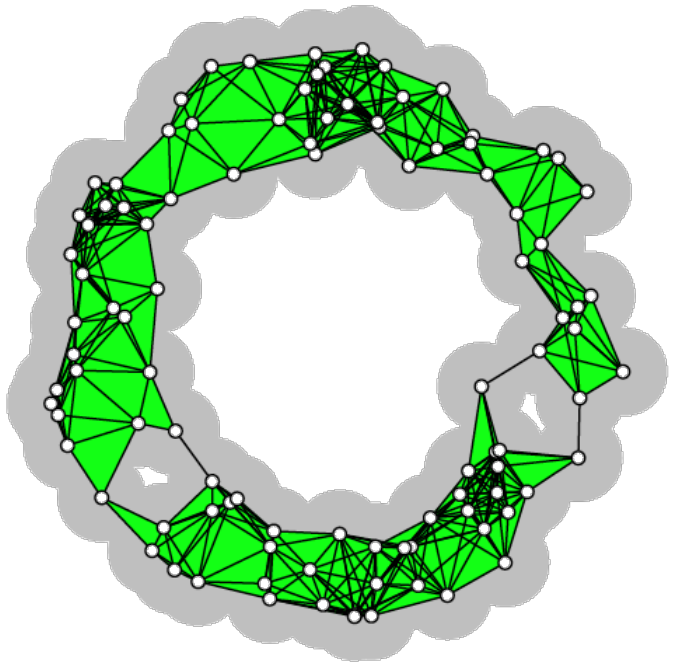
$\check{C}_{.6}$

The Čech complex $\check{C}_\epsilon$ encodes the intersection pattern of M_ϵ: Encode:

Points as *vertices* (0-cells)

Pairwise intersections as *edges* (1-cells)

Čech Complex



$\check{C}_{.6}$

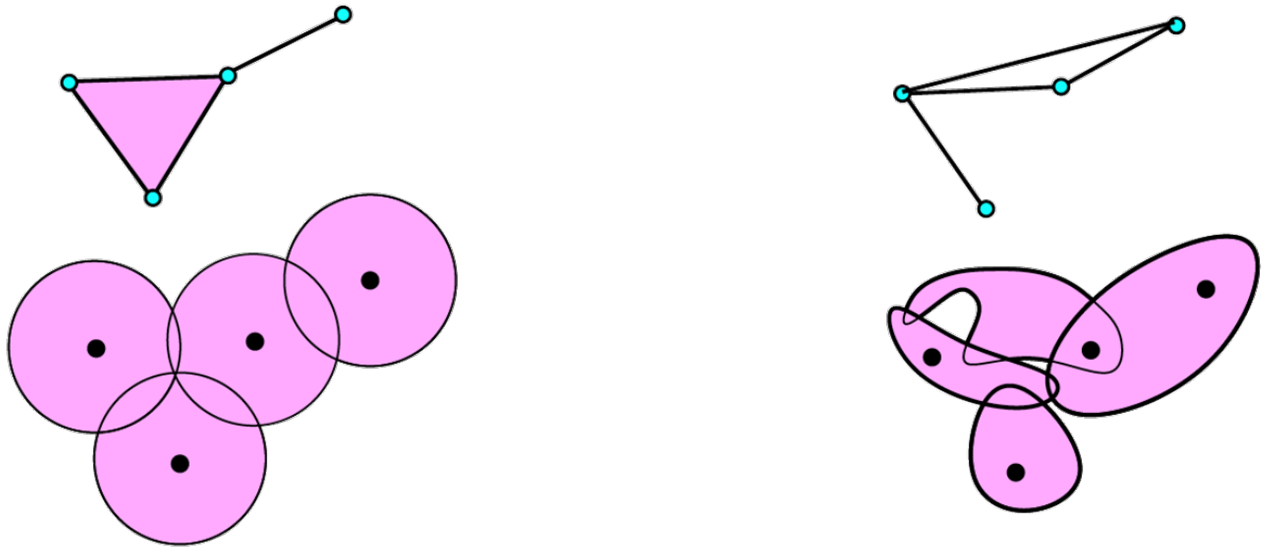
The Čech complex $\check{C}_\epsilon$ encodes the intersection pattern of M_ϵ: Encode:

- Points as *vertices* (0-cells)
- Pairwise intersections as *edges* (1-cells)
- Threeway intersections as *triangles* (2-cells)
- k-way intersections as *(k+1)-cells*

Can be hard to compute …

General Čech Complex

Lemma (Nerve Lemma, Leray '45)
$\check{C}_\epsilon$ is topologically equivalent to M_ϵ.



Nerve theorem (Leray): If all the intersections between opens in $\mathcal{U}$ are either empty or contractible then $C(\mathcal{U})$ and $X = \cup_{i \in I} U_i$ are homotopy equivalent.

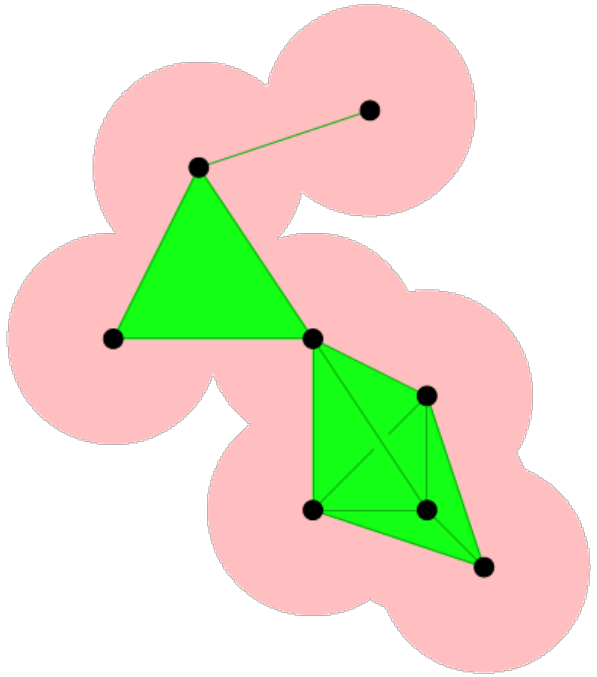
$\Rightarrow$ The combinatorics of the covering (a simplicial complex) carries the topology of the space.

Warning: even when the open sets are euclidean balls, the computation of the Čech complex is a very difficult task!

Rips-Vietoris Complex

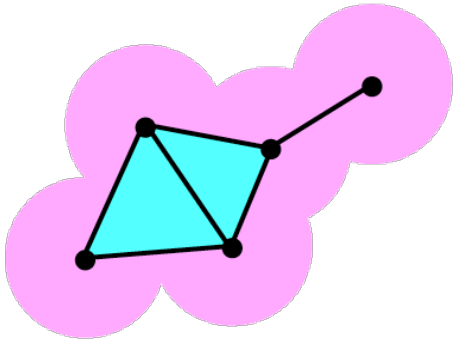
The “poor man’s” alternative to the Čech

This is a common complex For computations

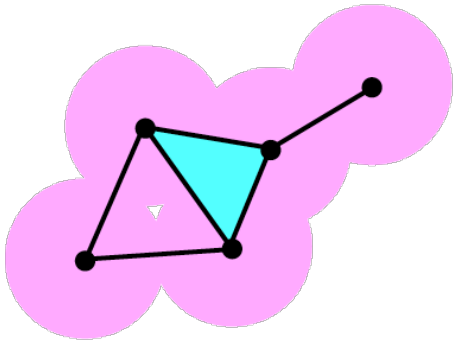


- $R_\epsilon(M) = \{\text{conv}\, T \mid T \subseteq M,\, d(m_i, m_j) < \epsilon, m_i, m_j \in T\}\,.$
- Still $O\left(\binom{m}{k}\right)$ for the kth skeleton
- Need $(k+1)$st skeleton for computing H_k

Rips vs. Čech



Rips vs Čech



Let $L = \{p_0, \cdots p_n\}$ be a (finite) point cloud (in a metric space).

The Rips complex $\mathcal{R}^\alpha(L)$: for $p_0, \cdots p_k \in L$,

$$\sigma = [p_0 p_1 \cdots p_k] \in \mathcal{R}^\alpha(L) \text{ iff } \forall i, j \in \{0, \cdots k\},\ d(p_i, p_j) \leq \alpha$$

- Easy to compute and fully determined by its 1-skeleton
- Rips-Čech interleaving: for any $\alpha > 0$,

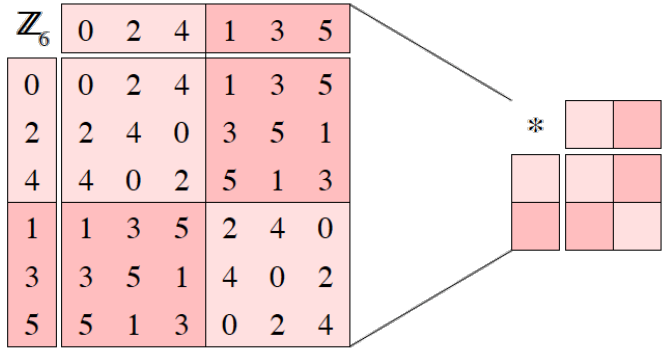
$$\mathcal{C}^{\frac{\alpha}{2}}(L) \subseteq \mathcal{R}^\alpha(L) \subseteq \mathcal{C}^\alpha(L) \subseteq \mathcal{R}^{2\alpha}(L) \subseteq \cdots$$

Groups

- A group $\langle G, * \rangle$ is a set G, together with a binary operation $*$ on G, such that the following axioms are satisfied:
  (a) $*$ is associative.
  (b) G has an identity e element for $*$ such that $e * x = x * e = x$ for all $x \in G$.
  (c) any element a has an inverse a' with respect to the operation $*$, i.e. $\forall a \in G, \exists a' \in G$ such that $a' * a = a * a' = e$.
- If G is finite, the order of G is $|G|$.
- We often omit the operation and refer to G as the group.
- $\langle \mathbb{Z}, + \rangle$, $\langle \mathbb{R}, \cdot \rangle$, $\langle \mathbb{R}, + \rangle$, are all groups.
- A group G is abelian if its binary operation $*$ is commutative.

Factor / Quotient Groups

- Let H be a normal subgroup of group G.
- Left coset multiplication is well-defined by the equation $(aH)(bH) = (ab)H$
- The cosets of H form a group G/H under left multiplication
- G/H is the factor group (or quotient group) of G modulo H.
- The elements in the same coset of H are congruent modulo H.

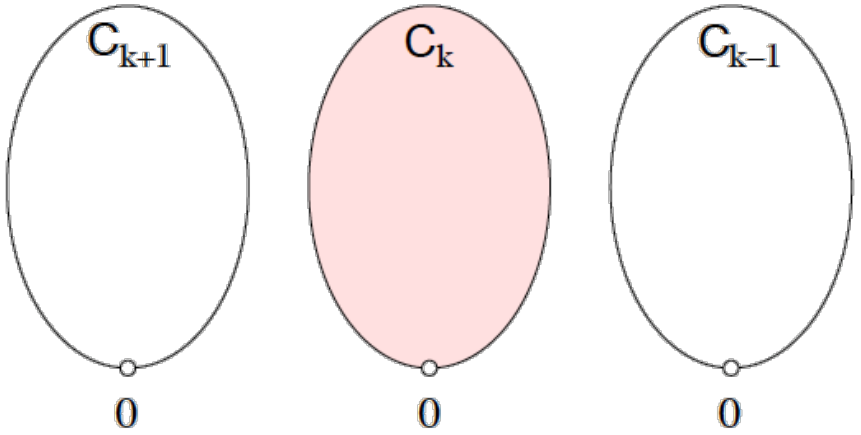


- $\{0, 2, 4\}$ is a normal subgroup
- Cosets $\{0, 2, 4\}, \{1, 3, 5\}$
- $\mathbb{Z}_6/\{0, 2, 4\} \cong \mathbb{Z}_2$

Chain Groups

Other coefficient fields/rings also OK

- Simplicial complex K
- k-chain: $c = \sum_i n_i[\sigma_i], n_i \in \mathbb{Z}, \sigma_i \in K$ (like a path)
- $[\sigma] = -[\tau]$ if $\sigma = \tau$ and σ and τ have different orientations.
- The kth chain group $\mathbf{C}_k$ of K is the free abelian group on its set of oriented k-simplices
- rank $\mathbf{C}_k$ =?



We take linear combinations of simplices of a given dimension *k*

Boundary Operator

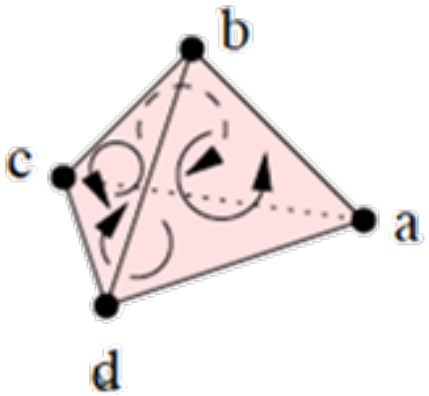
- The boundary operator $\partial_k : \mathsf{C}_k \to \mathsf{C}_{k-1}$ is a homomorphism defined linearly on a chain c by its action on any simplex $\sigma = [v_0, v_1, \ldots, v_k] \in c$,

$$\partial_k \sigma = \sum_i (-1)^i [v_0, v_1, \ldots, \hat{v}_i, \ldots, v_k],$$

  where $\hat{v}_i$ indicates that v_i is deleted from the sequence.

- $\partial_1 [a, b] = b - a.$
- $\partial_2 [a, b, c] = [b, c] - [a, c] + [a, b] = [b, c] + [c, a] + [a, b].$
- $\partial_3 [a, b, c, d] = [b, c, d] - [a, c, d] + [a, b, d] - [a, b, c].$

Boundary Theorem



- (Theorem) $\partial_{k-1}\partial_k = 0$, for all k.
- Proof:

$$\partial_{k-1}\partial_k[v_0, v_1, \ldots, v_k] =$$

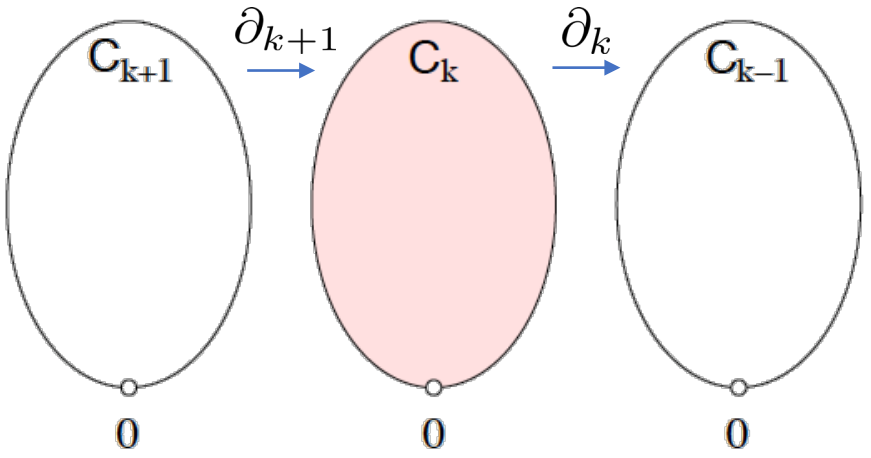
$$\begin{aligned}
&= \partial_{k-1} \sum_i (-1)^i [v_0, v_1, \ldots, \hat{v_i}, \ldots, v_k] \\
&= \sum_{j<i} (-1)^i (-1)^j [v_0, \ldots, \hat{v_j}, \ldots, \hat{v_i}, \ldots, v_k] \\
&\quad + \sum_{j>i} (-1)^i (-1)^{j-1} [v_0, \ldots, \hat{v_i}, \ldots, \hat{v_j}, \ldots, v_k] \\
&= 0,
\end{aligned}$$

as switching i and j in the second sum negates the first sum.

Chain Complex

- The boundary operator connects the chain groups into a chain complex C_*:

$$\ldots \to C_{k+1} \xrightarrow{\partial_{k+1}} C_k \xrightarrow{\partial_k} C_{k-1} \to \ldots.$$

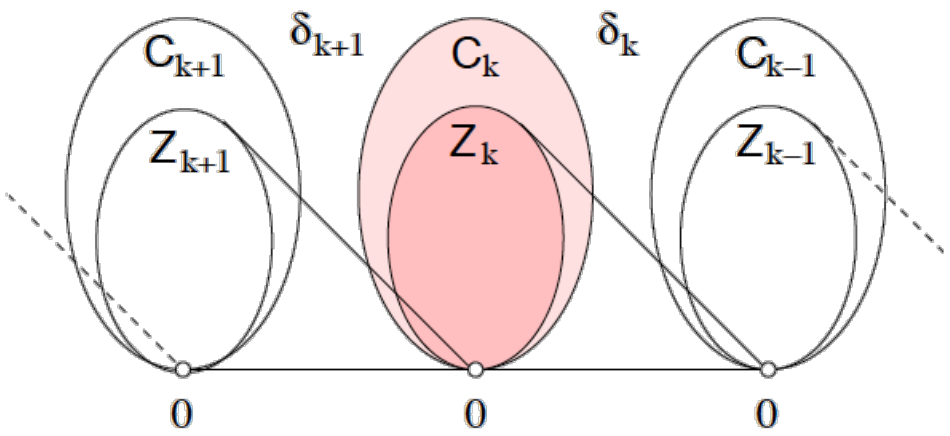


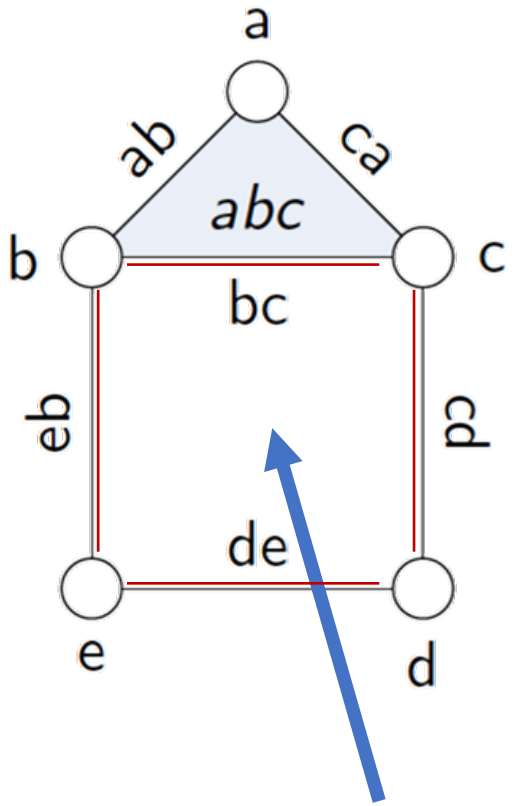
Cycle Group

- Let c be a k-chain
- If it has no boundary, it is a k-cycle (zycle?)
- $\partial_k c = \emptyset$, so $c \in \ker \partial_k$
- The kth cycle group is

$$\mathsf{Z}_k = \ker \partial_k = \{c \in \mathsf{C}_k \mid \partial_k c = \emptyset\}.$$

$$\partial = \delta$$





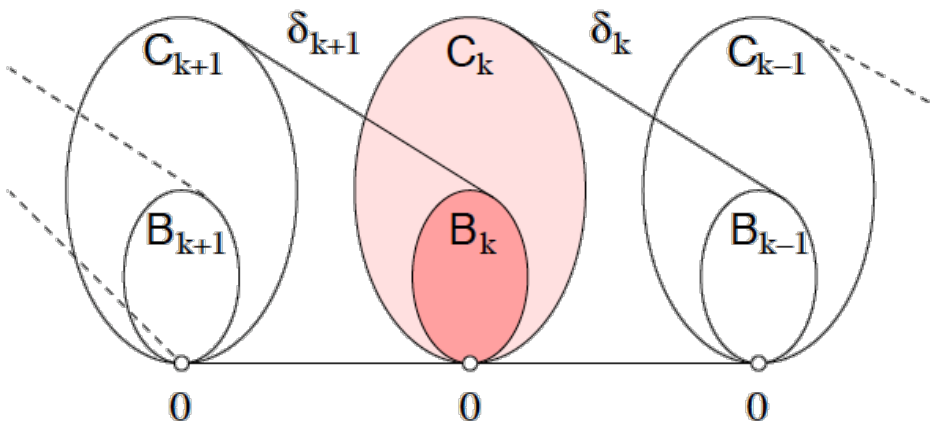
$$\partial(bc + cd + de + eb)$$
$$= c - b + d - c + e - d + b - e = 0.$$

Boundary Group

- Let b be a k-chain
- If b is a boundary of something, it is a k-boundary.
- The kth boundary group is

$$\mathsf{B}_k = \operatorname{im} \partial_{k+1} = \{c \in \mathsf{C}_k \mid \exists d \in \mathsf{C}_{k+1} : c = \partial_{k+1} d\}.$$

$$\partial = \delta$$



Boundaries are Cycles!

- Let b be a k-boundary.
- Then, $\exists c \in \mathsf{C}_{k+1}$, such that $b = \partial_{k+1} c$.
- What is the boundary of b?

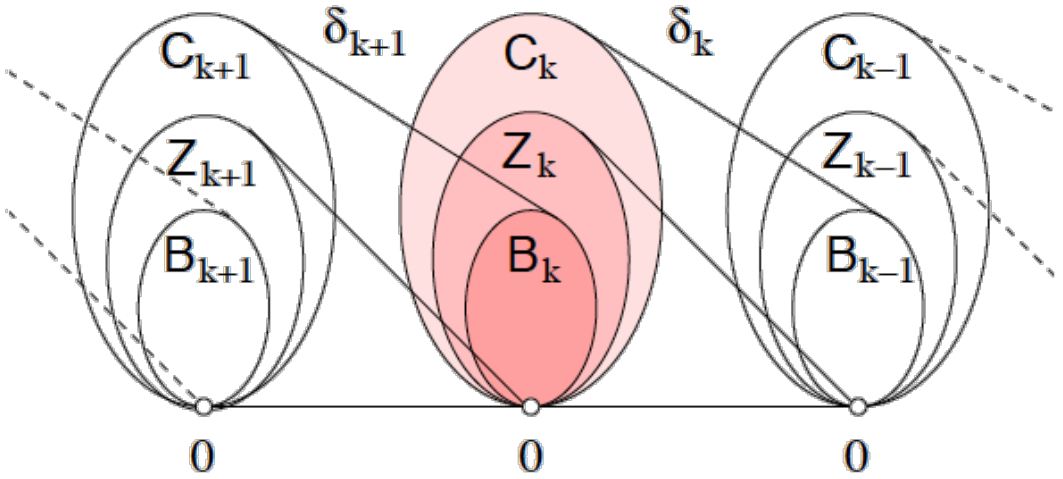
$$\partial_k b = \partial_k \partial_{k+1} c = \emptyset,$$

by the boundary theorem.

- That is, every boundary is a cycle!

- $\mathsf{B}_k \subseteq \mathsf{Z}_k \subseteq \mathsf{C}_k$

$\partial = \delta$

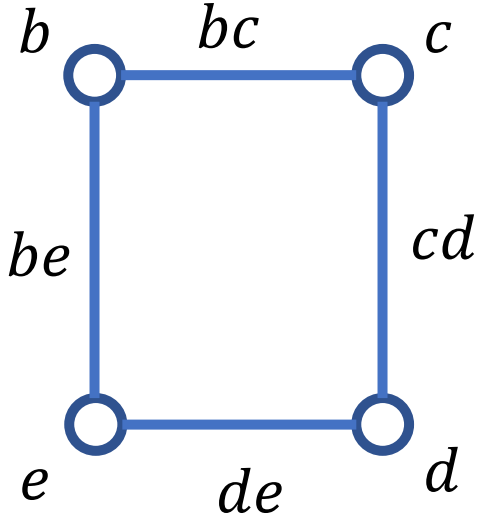


Nesting behavior!

Simplicial Complexes → Vector Spaces

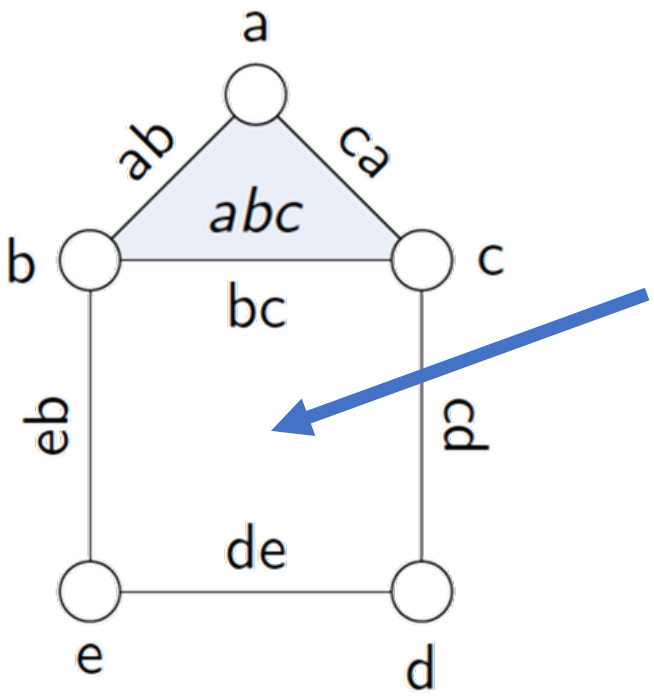
- Σ a simplicial complex, Σ_0 the 0-simplices (vertices), Σ_1 the 1-simplices (edges), Σ_2 the 2-simplices (triangles), …
- Linear combinations with coefficients from $\mathbb{F}$, a field or ring, in the sequel typically $\mathbb{Z}/2\mathbb{Z} = \{0,1\}$

- $C_p(\Sigma)$, the vector space of p-chains
  - Intuitively, just allow addition and scalar multiplication (using $\mathbb{F}$) of simplices!
  - Linear combinations of p-simplices will be called p-chains



- Intuitively, $bc + cd + de + be$ traces out a loop bounding a box.

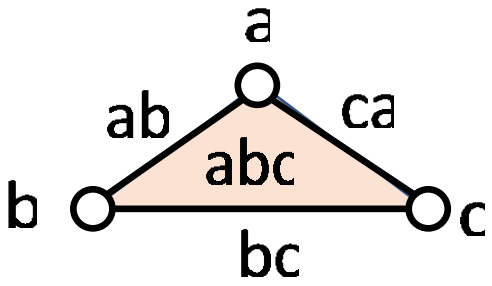
Main Actor: The Boundary Map ∂



- Alternating sum (hat denotes omission):

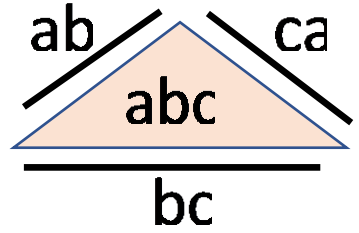
$$\partial[x_0, \dots x_n] = \sum_{i=0}^{n} (-1)^i \, [x_0, \dots, \hat{x}_i, \dots x_n]$$

$$\partial(bc + cd + de + eb)$$
$$= c - b + d - c + e - d + b - e = 0.$$



- Key identity: $\partial^2 = 0$.

$$\partial^2(abc) = \partial(bc - ac + ab)$$
$$= c - b - c + a + b - a = 0.$$



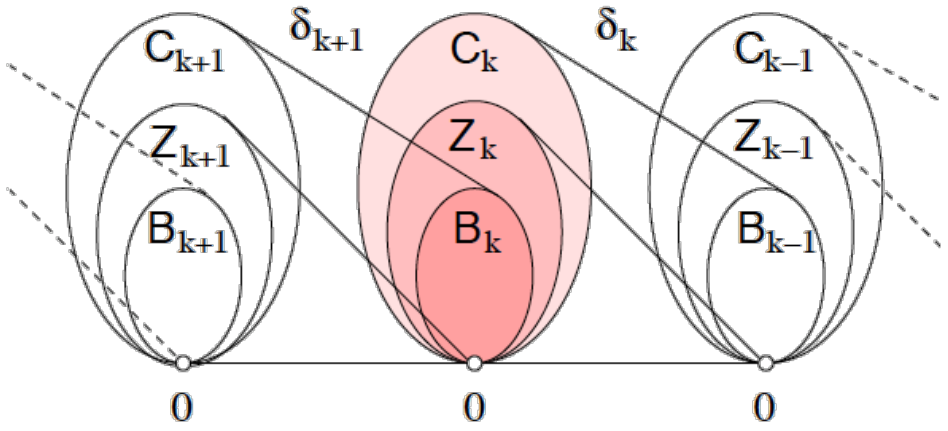
- $\partial = 0$ on linear combinations that are boundaries. Intuitively, $\partial^2 = 0$ says that the boundary of a simplex really is a boundary!

Simplicial Homology

- The kth homology group is

$$\mathsf{H}_k = \mathsf{Z}_k/\mathsf{B}_k = \ker \partial_k / \operatorname{im} \partial_{k+1}.$$

- If $z_1 = z_2 + \mathsf{B}_k, z_1, z_2 \in \mathsf{Z}_k$, we say z_1 and z_2 are homologous
- $z_1 \sim z_2$.



Homology Groups

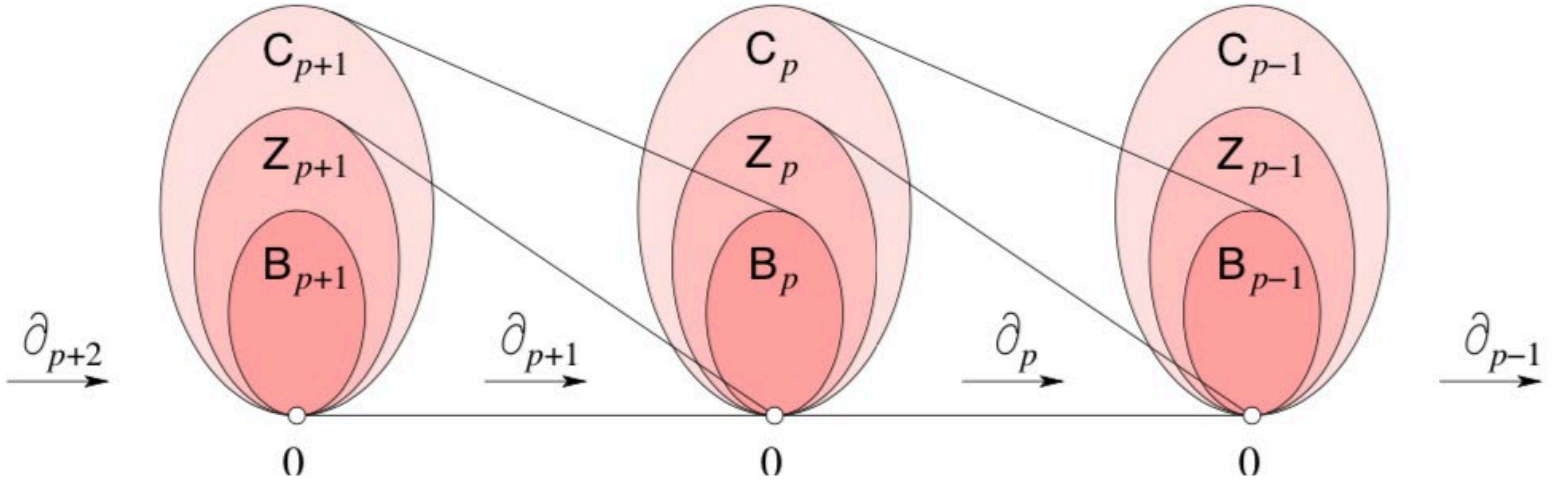
2-manifold	H_0	H_1	H_2
sphere	$\mathbb{Z}$	$\{0\}$	$\mathbb{Z}$
torus	$\mathbb{Z}$	$\mathbb{Z} \times \mathbb{Z}$	$\mathbb{Z}$
projective plane	$\mathbb{Z}$	$\mathbb{Z}_2$	$\{0\}$
Klein bottle	$\mathbb{Z}$	$\mathbb{Z} \times \mathbb{Z}_2$	$\{0\}$

The Chain Complex, Cycles and Boundaries

- We now have a sequence of vector spaces and linear maps:

$$\dots \xrightarrow{\partial_{p+2}} C_{p+1} \xrightarrow{\partial_{p+1}} C_p \xrightarrow{\partial_p} C_{p-1} \xrightarrow{\partial_{p-1}} \dots$$

- Notation: $Z_p := \ker \partial_p = \{v \in C_p : \partial_p(v) = 0\}$ the p-cycles, $B_p := im\ \partial_{p+1} \subseteq C_p$ the p-boundaries.



pth homology vector space:

$$H_p := \frac{\ker \partial_p}{im\ \partial_{p+1}}$$

Intuition: p-dimensional connectivity

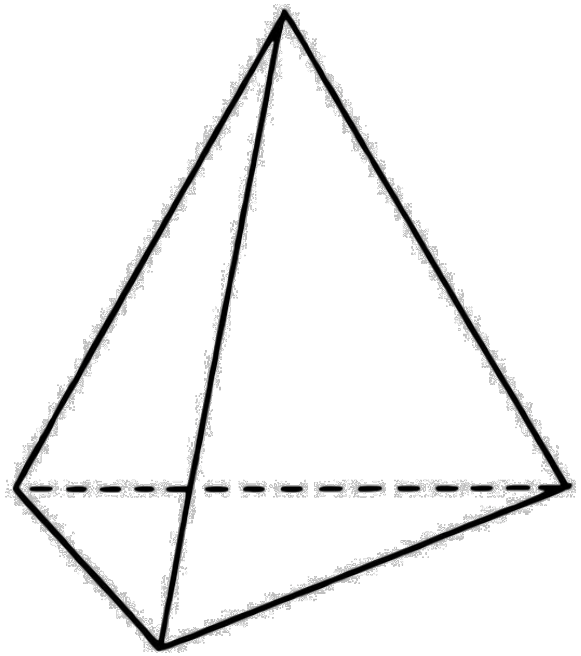
Focus on Betti Numbers β_i

- Ranks (dimensions) β_i of the free part of homology groups H_i

$$\beta_i = z_i - b_i$$

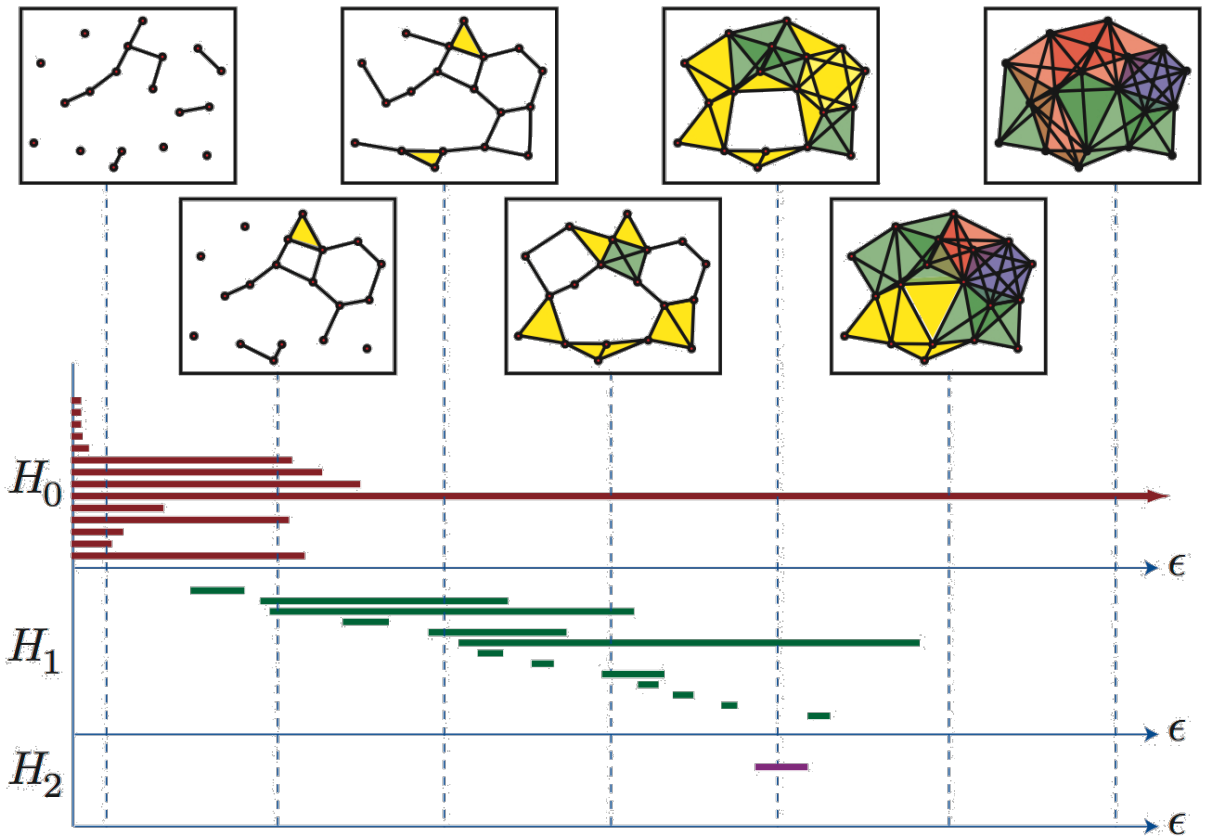
- β_0 counts the number of connected components
- β_1 counts the number of independent loops
- β_2 counts the number of independent voids
- …

rank = # of independent generators

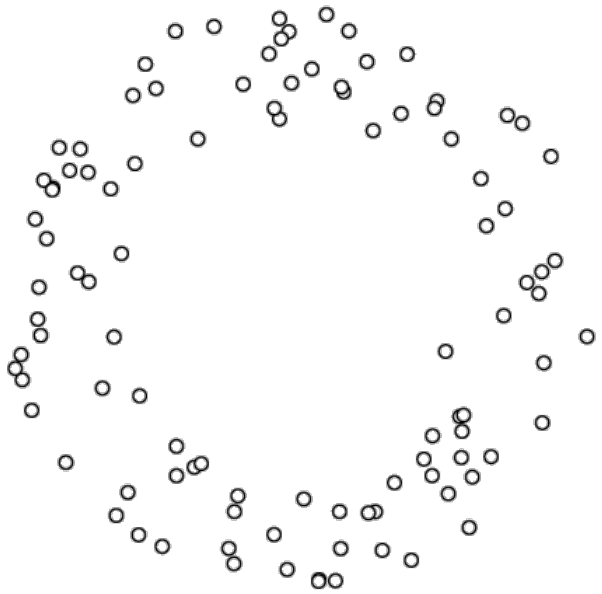


Topology is fundamentally a tool for classification

Today: Persistent Homology



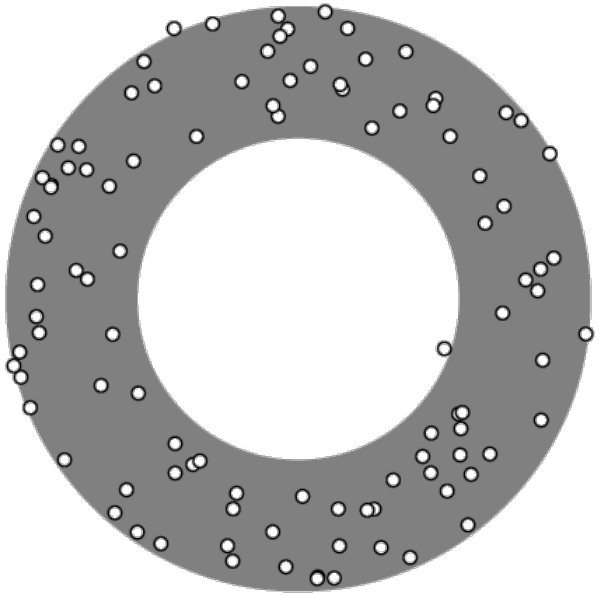
Sampled Data Has “Shape”



2-dimensional

Approximates annulus

Sampled Data Has “Shape”



2-dimensional

Approximates annulus

Topological features of annulus:

1 component ($\beta_0 = 1$)

1 loop ($\beta_1 = 1$)

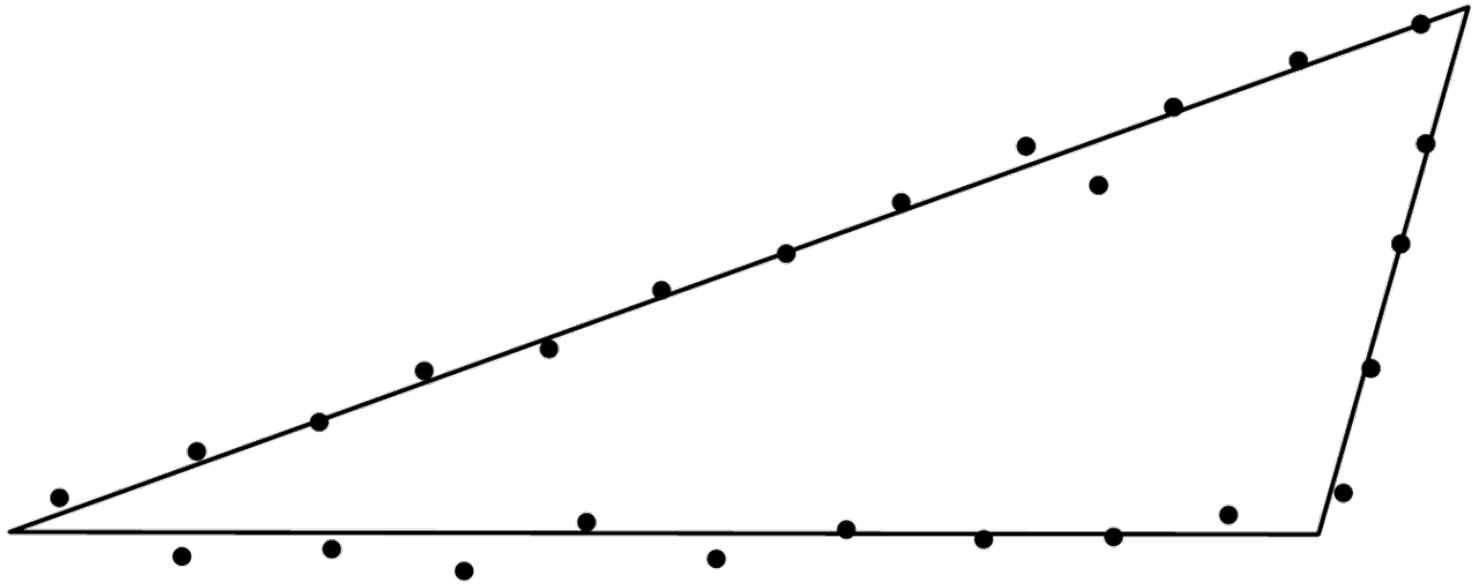
Goal: Recover *topology* of annulus from point cloud

We do so by building various complexes on the point cloud

Filtrations

How to Choose ϵ?

- How to determine the topology of the underlying space from a point cloud approximation?



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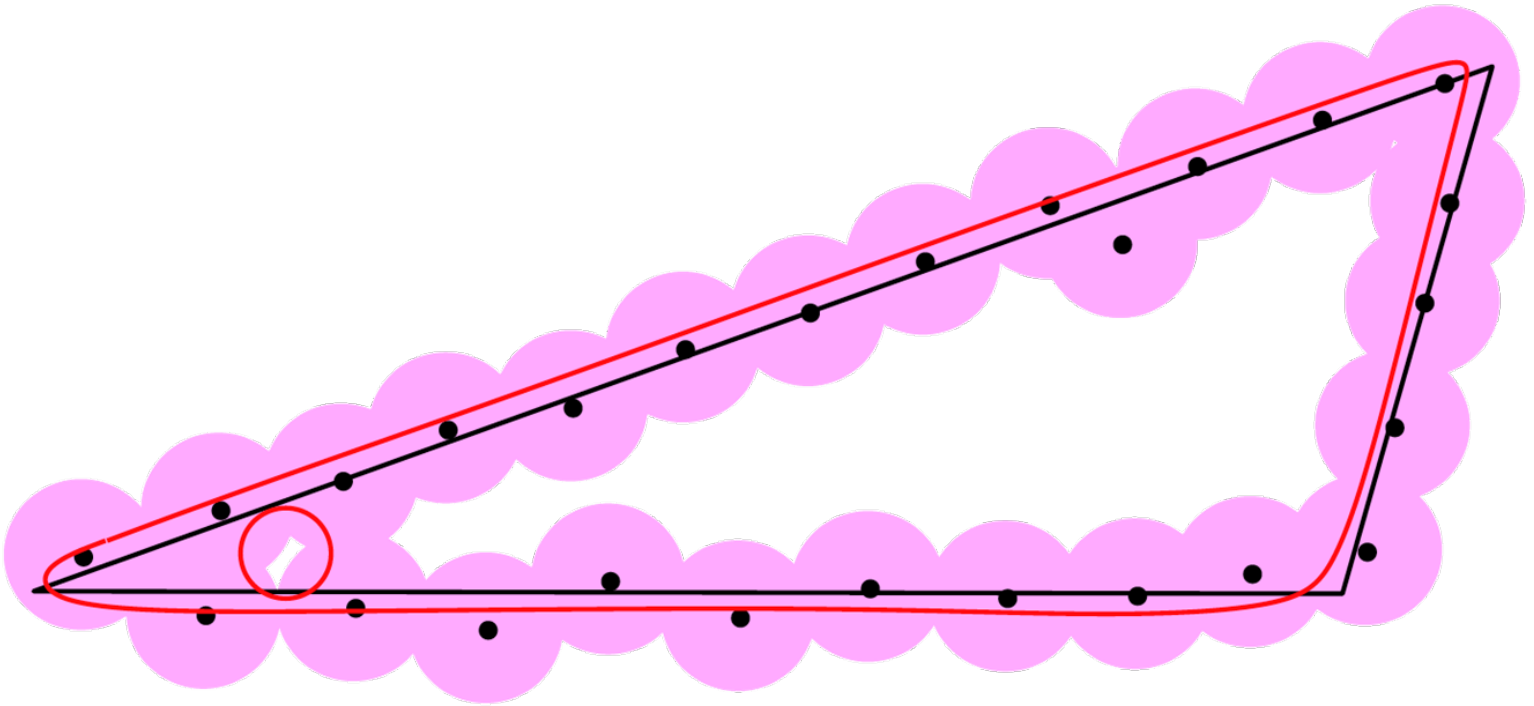

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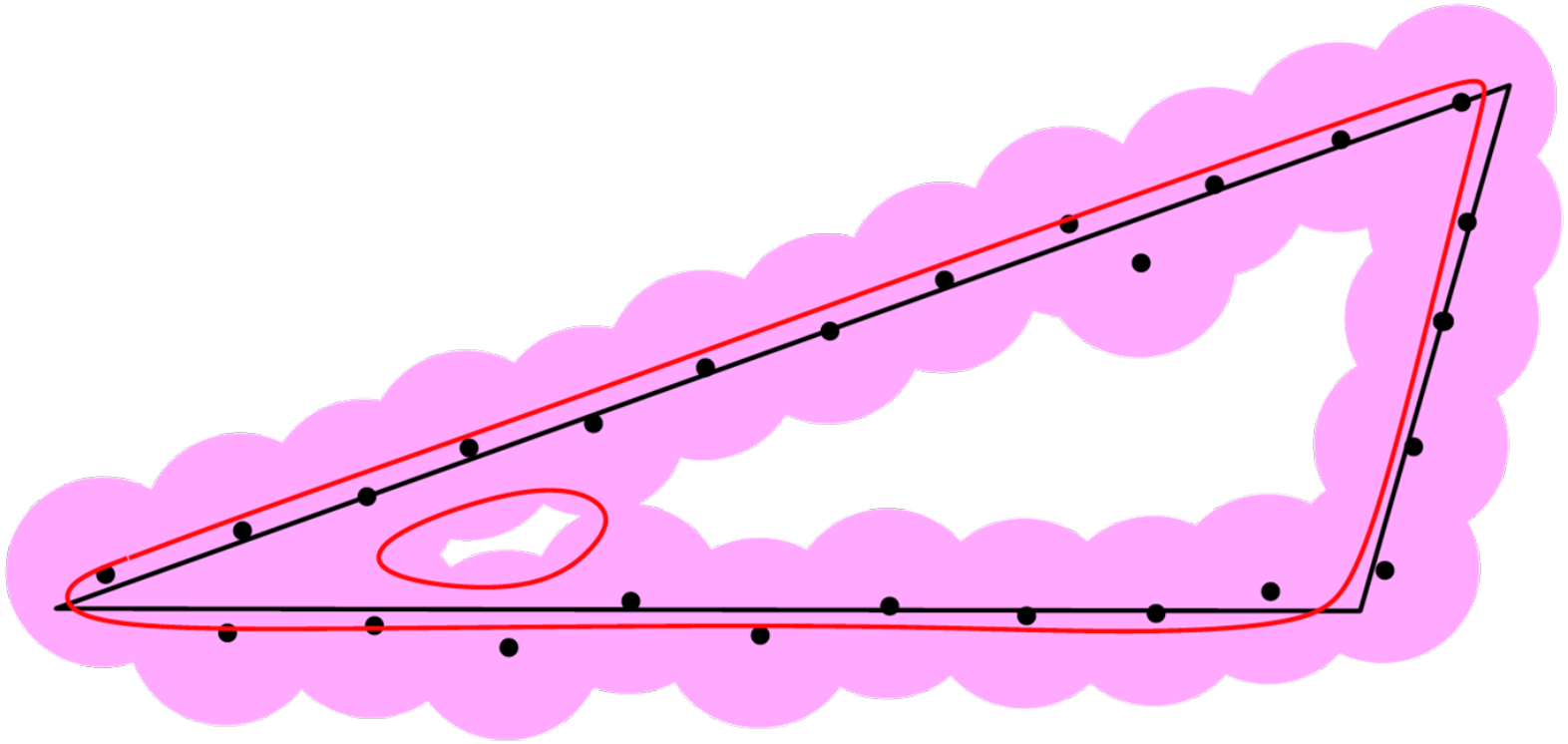

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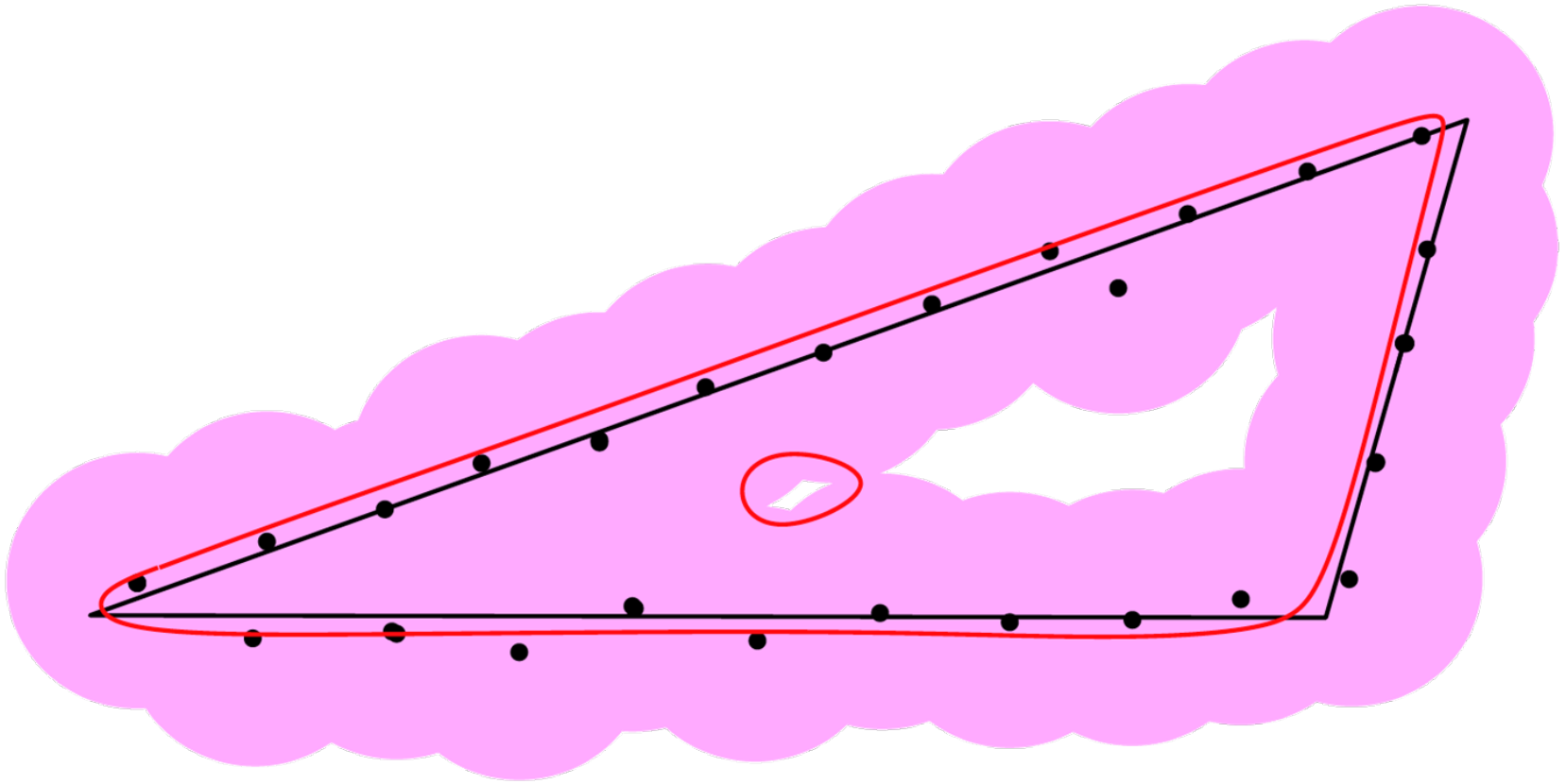
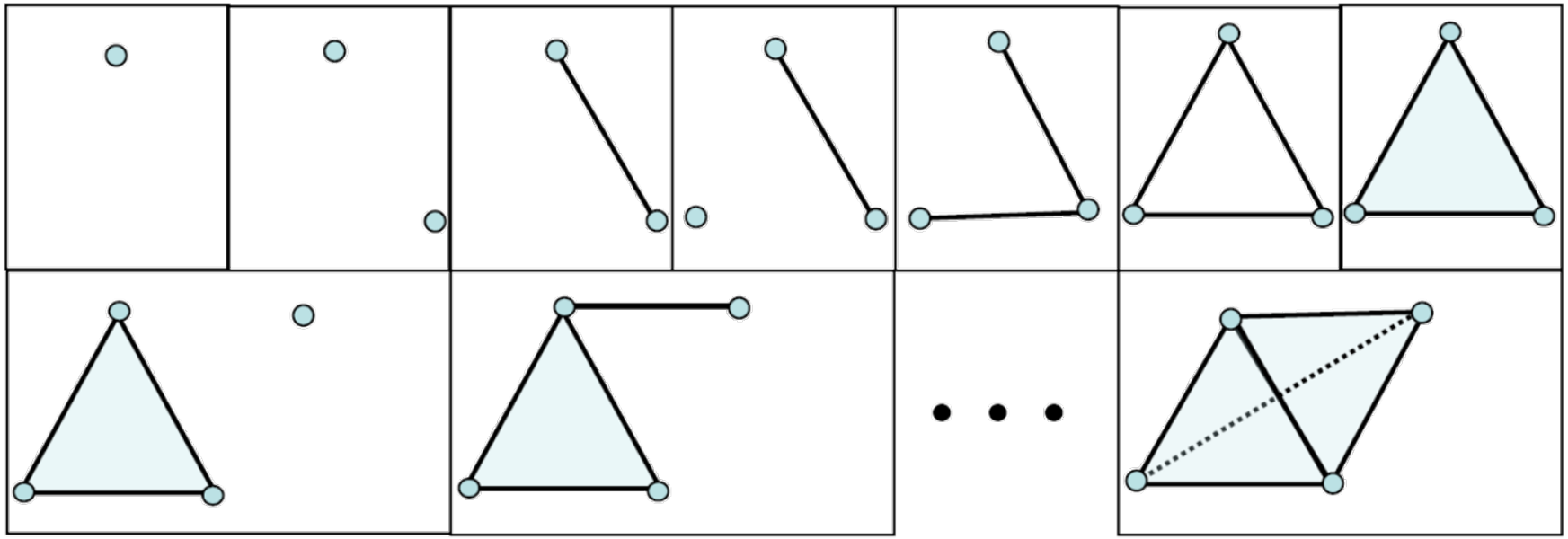


Filtrations



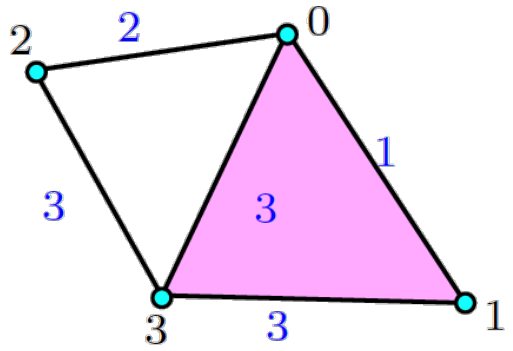
A filtration of a (finite) simplicial complex K is a sequence of subcomplexes such that

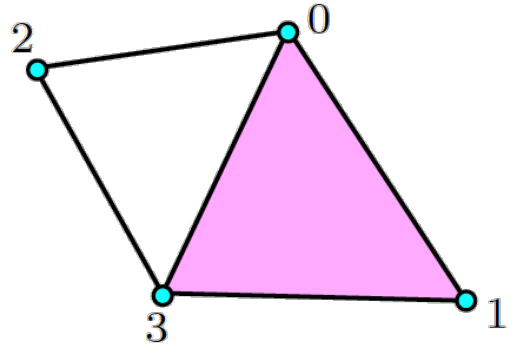
i) $\emptyset = K^0 \subset K^1 \subset \cdots \subset K^m = K$,

ii) $K^{i+1} = K^i \cup \sigma^{i+1}$ where σ^{i+1} is a simplex of K.

Sub-simplices of a simplex must be added before the simplex!

The Sub-Level Set Filtration

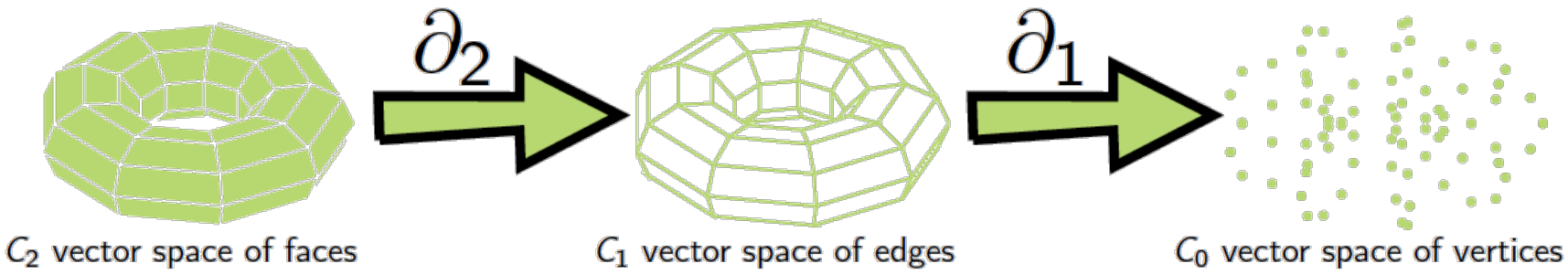




- f a real valued function defined on the vertices of K
- For $\sigma = [v_0, \cdots, v_k] \in K$, $f(\sigma) = \max_{i=0,\cdots,k} f(v_i)$
- The simplices of K are ordered according increasing f values (and dimension in case of equal values on different simplices).

Persistent Homology: Do not choose an ϵ!

Standard Homology



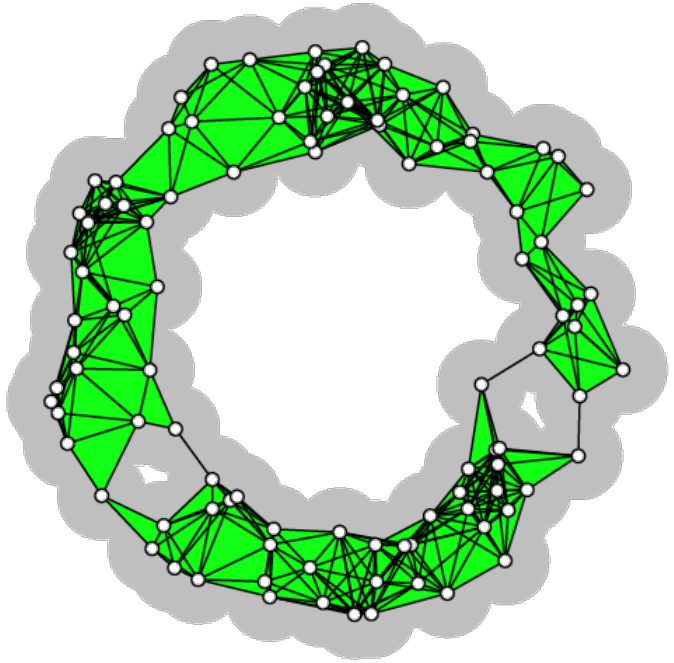
Take the linear extension of the boundary operator:

$$\partial_d([v_0, \dots v_d]) = \sum_{i=0}^{d} (-1)^i [v_0 \dots, \hat{v}_i, \dots v_d]$$

Fact: $\partial_{d-1} \circ \partial_d \equiv 0 \Rightarrow \operatorname{Im} \partial_d \subseteq \ker \partial_{d-1}$

Definition: $H_d(K) = \ker \partial_d / \operatorname{Im} \partial_{d+1}$

Čech Complex



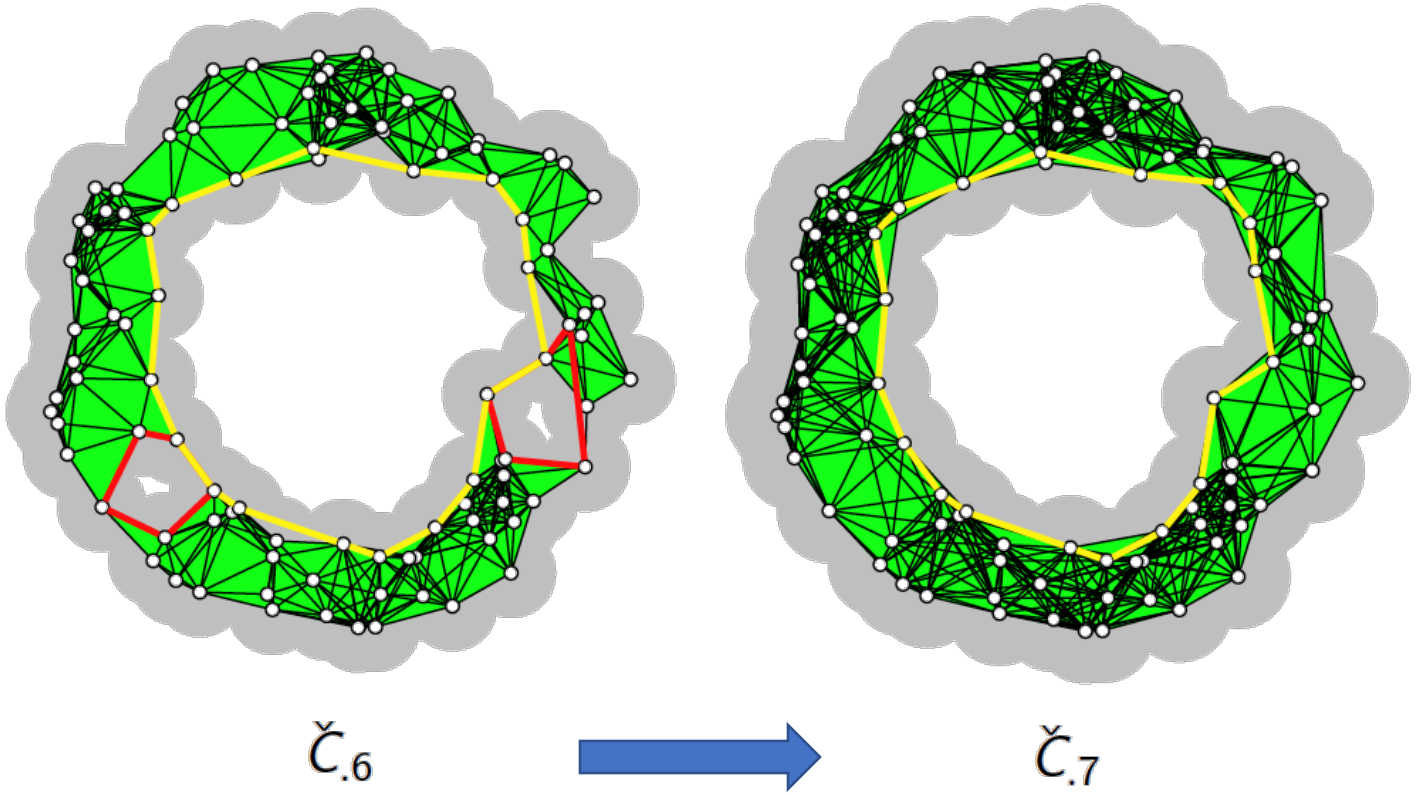
$\check{C}_{.6}$

The Čech complex $\check{C}_\epsilon$ encodes the intersection pattern of M_ϵ: Encode:

- Points as *vertices* (0-cells)
- Pairwise intersections as *edges* (1-cells)
- Threeway intersections as *triangles* (2-cells)
- k-way intersections as *(k+1)-cells*

Can be hard to compute …

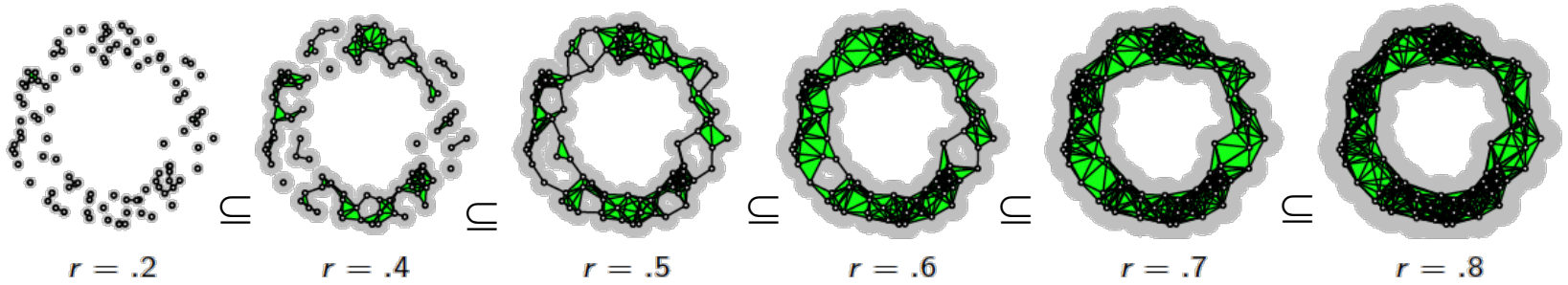
We Can Track Topological Features in a Filtration



Functorality allows us to systematically track holes over time!

The inclusion map among the complexes translates to a homomorphism between the homology groups

Persistent Homology is Functorial Homology

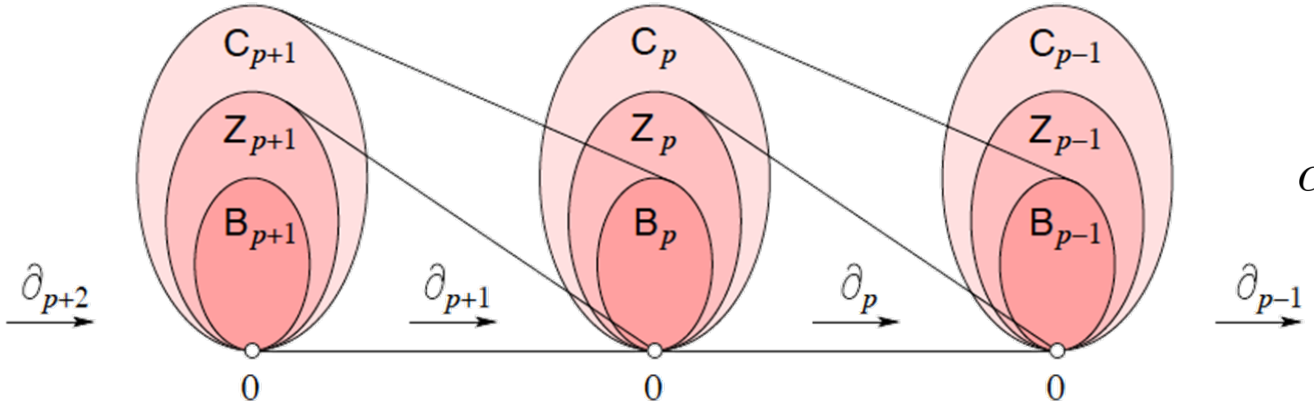


$$H_d(\check{C}_*) = \bigoplus_{\epsilon} H_d(\check{C}_\epsilon)$$

Homology of the entire filtration

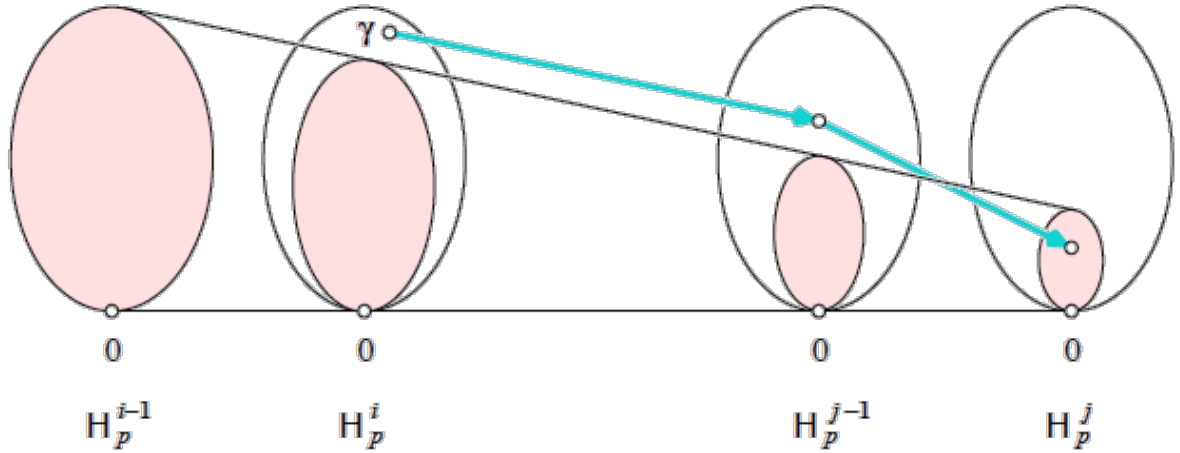
Homomorphisms at the homology level allow us
to track homology classes – i.e., topological features

Persistence of Homology Classes



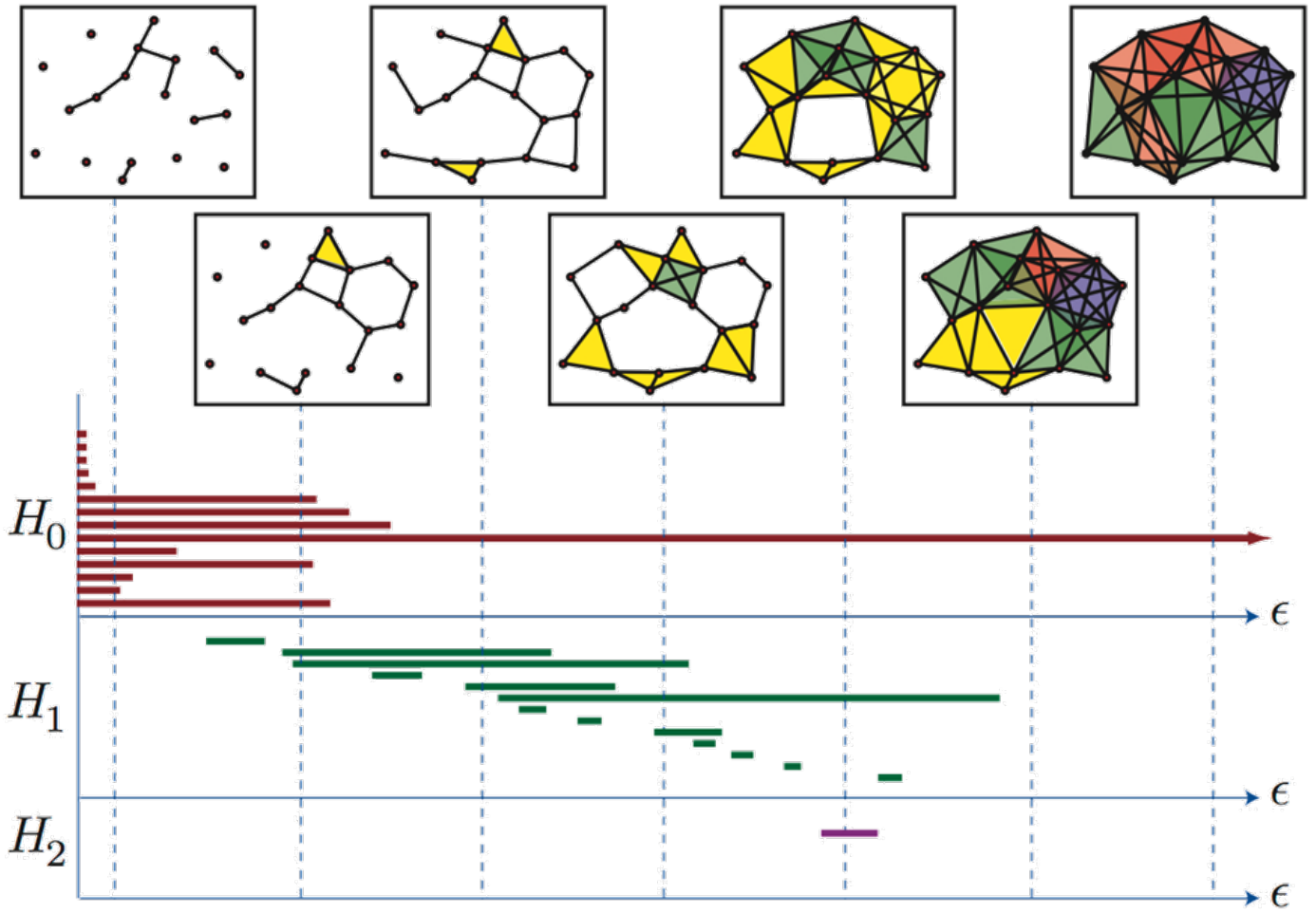
$$c_p = z_p + b_{p-1}$$

$$G/\ker(f) \equiv \mathrm{im}(f)$$



Lifetime of topological feature γ

Barcodes are the Lifetimes of Topological Features



Barcodes are the output of persistent homology

Persistent Homology

(3) Visualization/input to ML pipeline

Youtube "**Persistent homology on a noisy torus**"

$$\emptyset \subseteq \Sigma^{(1)} \subseteq \Sigma^{(2)} \subseteq \ \ldots \subseteq \Sigma^{(n-1)} \subseteq \Sigma^{(n)}$$

(1) Topology

Functoriality of homology

$$0 \ \rightarrow H_p\left(\Sigma^{(1)}\right) \ \rightarrow \ H_p(\Sigma^{(2)}) \ \rightarrow \ \ldots \rightarrow \ H_p(\Sigma^{(n-1)}) \ \rightarrow \ H_p(\Sigma^{(n)})$$

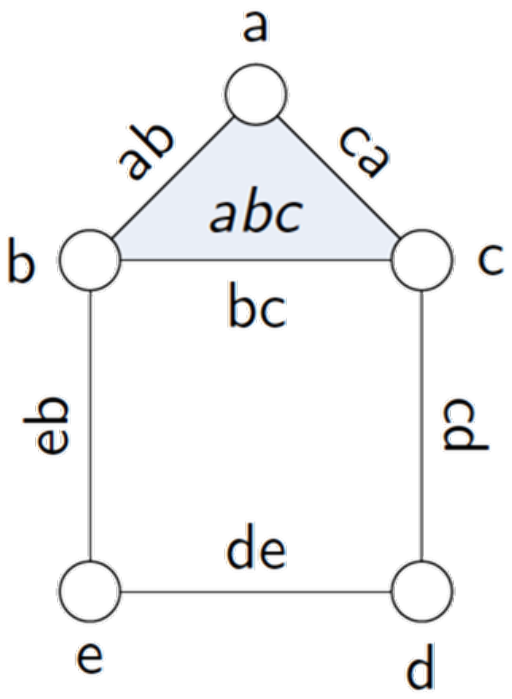
(2) Algebra

Computing Homology: Linear Algebra

We'll use algebra over $\mathbb{Z}_2 = \mathbb{Z}/2\mathbb{Z}$

Setting up the Linear Algebra

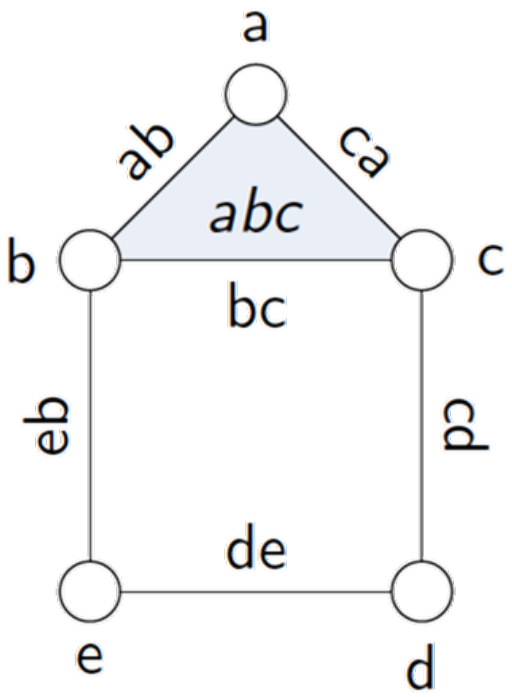
- $\partial_p : C_p \to C_{p-1}$ is a linear map between vector spaces, so we'll use matrices



$$\partial_1 = \begin{array}{c} \\ a \\ b \\ c \\ d \\ e \end{array} \begin{array}{c} \begin{array}{cccccc} ab & ca & bc & cd & de & eb \end{array} \\ \begin{bmatrix} 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 \\ 0 & 1 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 \end{bmatrix} \end{array}$$

$$\partial_2 = \begin{array}{c} \\ ab \\ ca \\ bc \\ cd \\ de \\ eb \end{array} \begin{array}{c} \begin{array}{c} abc \end{array} \\ \begin{bmatrix} 1 \\ 1 \\ 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \end{array}$$

Setting up the Linear Algebra



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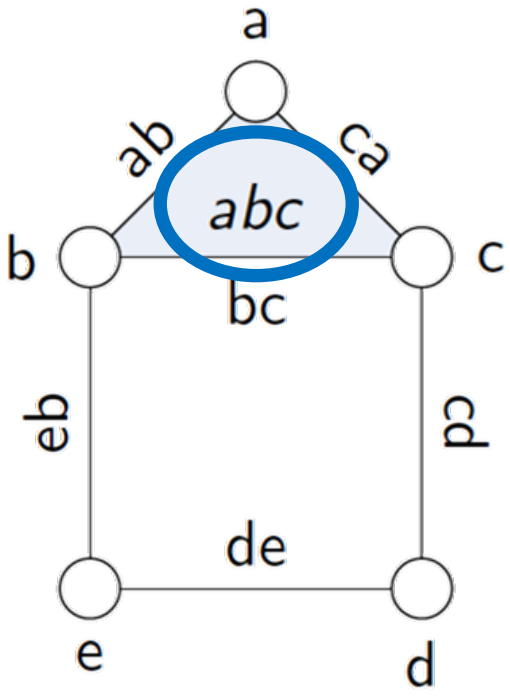
- E. g. $H_1 = \frac{\ker \partial_1}{im\ \partial_2}$, so we need to extract bases for these vector spaces

Setting up the Linear Algebra



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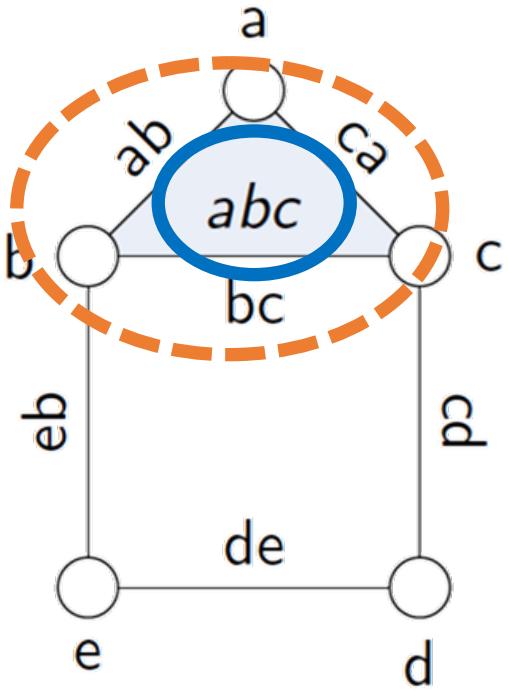
$$\partial_2 = \begin{array}{c} abc \\ \begin{array}{c} ab \\ ca \\ bc \\ cd \\ de \\ eb \end{array} \begin{bmatrix} 1 \\ 1 \\ 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \end{array}$$

Setting up the Linear Algebra



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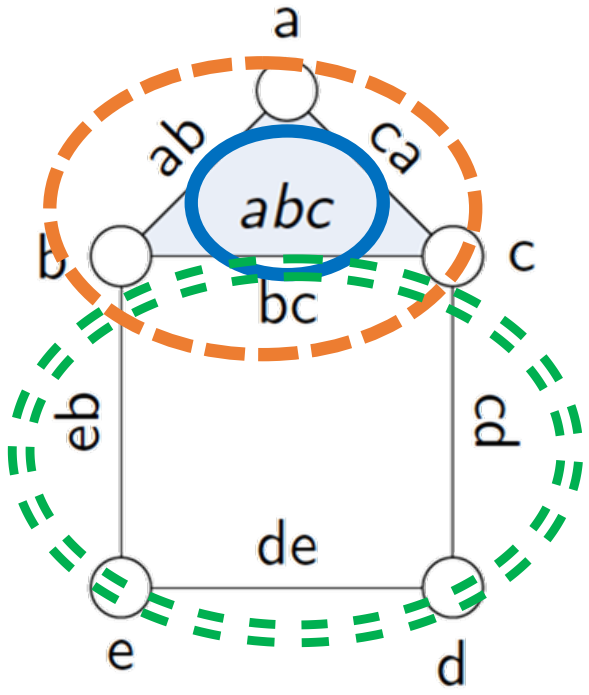
Setting up the Linear Algebra



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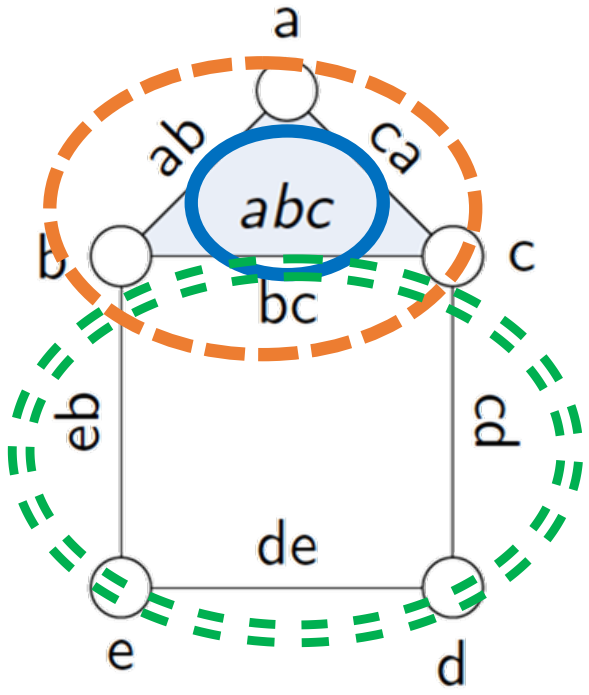

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$$\partial_2 = \begin{array}{c} \begin{array}{c} abc \end{array} \\ \begin{bmatrix} 1 \\ 1 \\ 1 \\ 0 \\ 0 \\ 0 \end{bmatrix} \end{array} \begin{array}{l} ab \\ ca \\ bc \\ cd \\ de \\ eb \end{array}$$

- Will work with $\mathbb{Z}/2\mathbb{Z}$ arithmetic
- Column operations

Column operations in $\mathbb{Z}/2\mathbb{Z}$

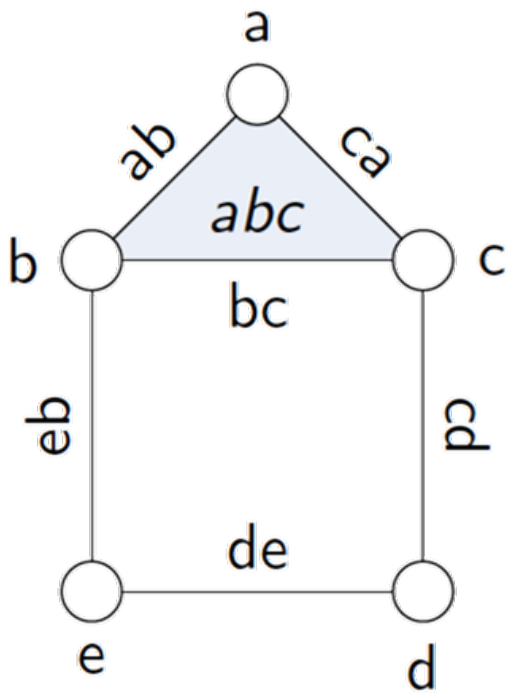
Arithmetic in $\mathbb{Z}/2\mathbb{Z}$ is very easy:

$$\begin{bmatrix}1\\0\end{bmatrix} + \begin{bmatrix}0\\1\end{bmatrix} = \begin{bmatrix}1\\1\end{bmatrix}$$

$$\begin{bmatrix}1\\1\end{bmatrix} + \begin{bmatrix}0\\1\end{bmatrix} = \begin{bmatrix}1\\0\end{bmatrix}$$

$$\begin{bmatrix}1\\1\end{bmatrix} + \begin{bmatrix}1\\1\end{bmatrix} = \begin{bmatrix}0\\0\end{bmatrix}$$

Summary So Far



$$\ldots \to C_2 \xrightarrow{\partial_2} C_1 \xrightarrow{\partial_1} C_0 \to 0$$

{abc} $\xrightarrow{\partial_2}$ {ab,ca,bc,cd,de,eb} $\xrightarrow{\partial_1}$ {a,b,c,d,e}

∂_2

	abc
ab	1
ca	1
bc	1
cd	0
eb	0
de	0

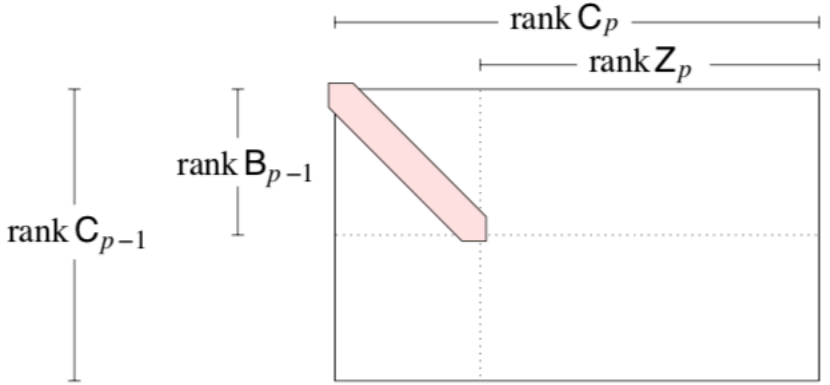
∂_1

	ab	ca	bc	cd	eb	de
a	1	1	0	0	0	0
b	1	0	1	0	1	0
c	0	1	1	1	0	0
d	0	0	0	1	0	1
e	0	0	0	0	1	1

Traditional Approach: Smith Normal Form

Standard algorithm for homology:

- Use row/column operations (Gaussian elimination) on boundary matrices to get form where initial segment of diagonal is 1, everything else 0



- Read off basis for $\ker \partial_p$ (nullspace) and $im\ \partial_{p+1}$(range)

- Diagonal form means we have 1-1 correspondence, know which cycles are boundaries

- We'll see a slightly different method that only uses column operations and goes through unchanged for *persistent* homology

Reduction Algorithm for Homology*

*Cohen-Steiner, Edelsbrunner, Morozov - **Vines and Vineyards by Updating Persistence in Linear Time**

To get H_p, we need: (1) a basis for $\ker \partial_p$, and (2) a sub-basis for $im\ \partial_{p+1}$.

	ab	ca	bc	cd	de	eb	abc
a	1	1	0	0	0	0	0
b	1	0	1	0	0	1	0
c	0	1	1	1	0	0	0
d	0	0	0	1	1	0	0
e	0	0	0	0	1	1	0
ab	0	0	0	0	0	0	1
ca	0	0	0	0	0	0	1
bc	0	0	0	0	0	0	1
cd	0	0	0	0	0	0	0
de	0	0	0	0	0	0	0
eb	0	0	0	0	0	0	0

R

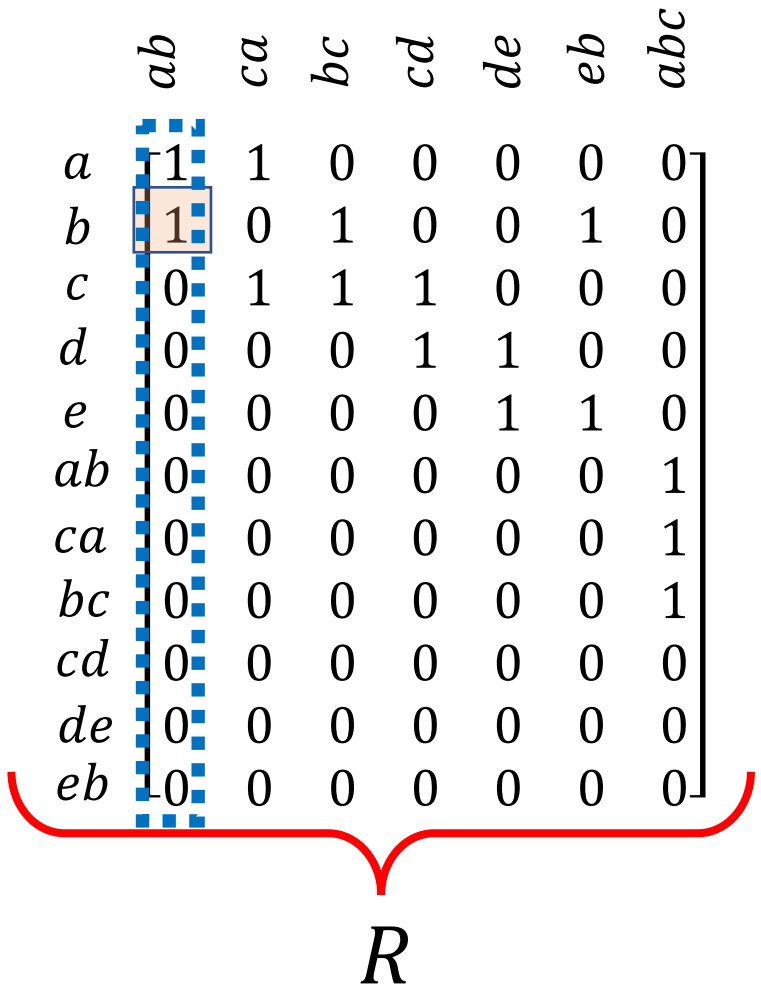
Notation: $low_R(j)$= row index of bottom 1 in column j of matrix R

Algorithm:

Initialize boundary information in incidence matrix D
Initialize $R \coloneqq D$

For column $j = 1, 2, \ldots, n$
  while $\exists j' < j, low_R(j') = low_R(j)$ do
    add column j' to column j

Reduction Algorithm for Homology



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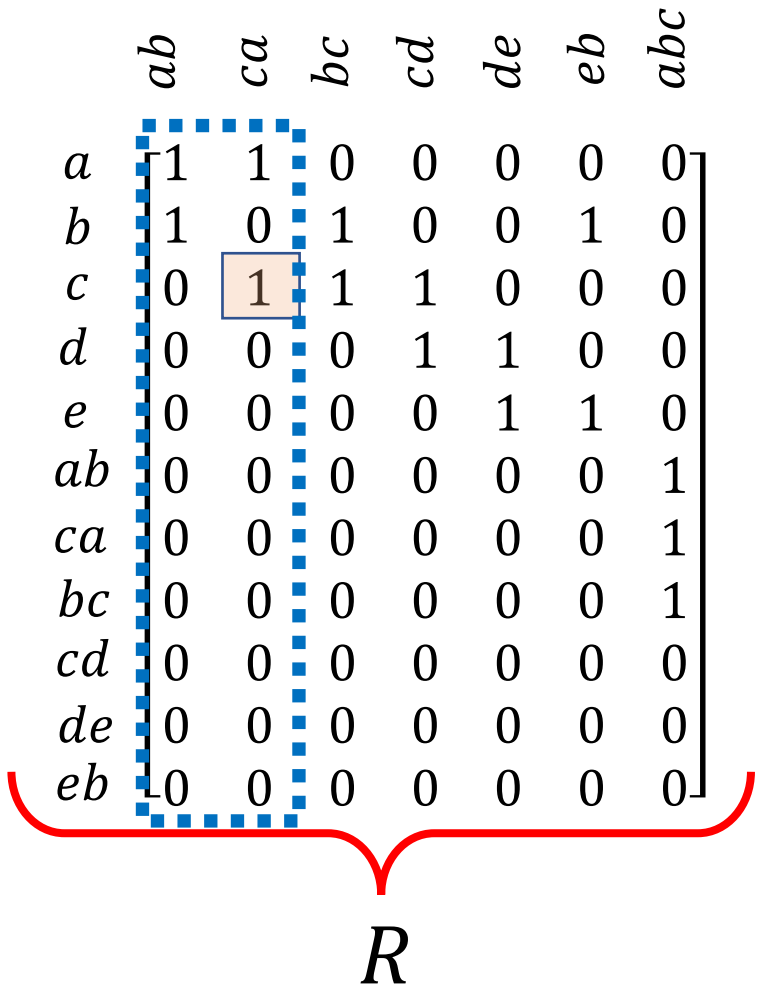

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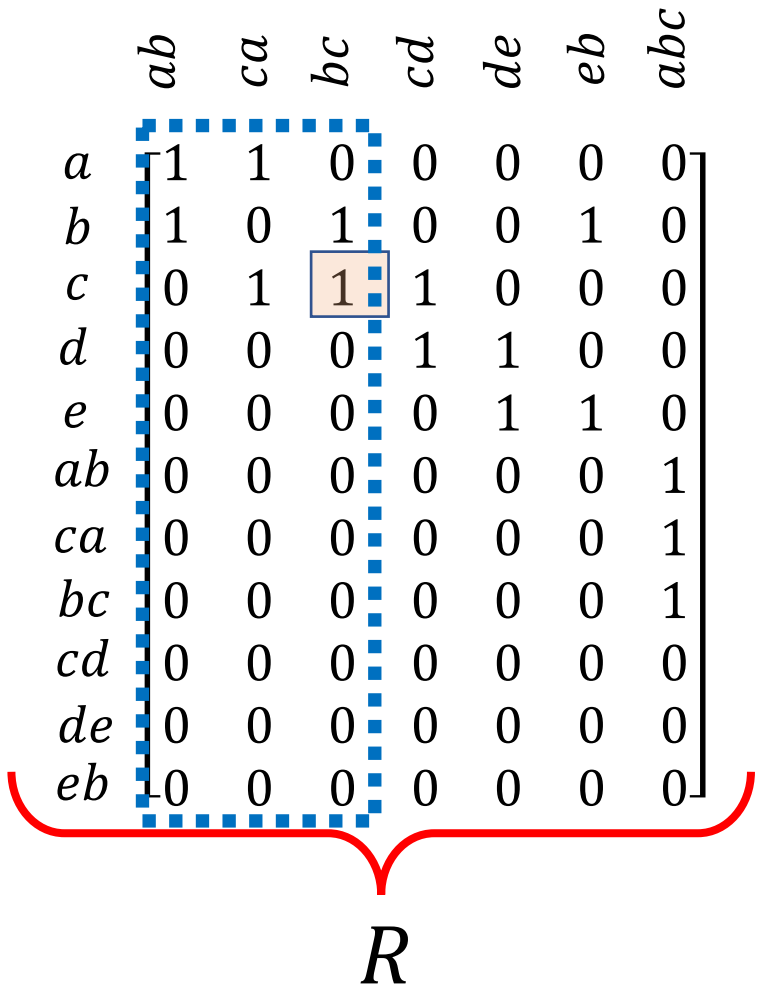

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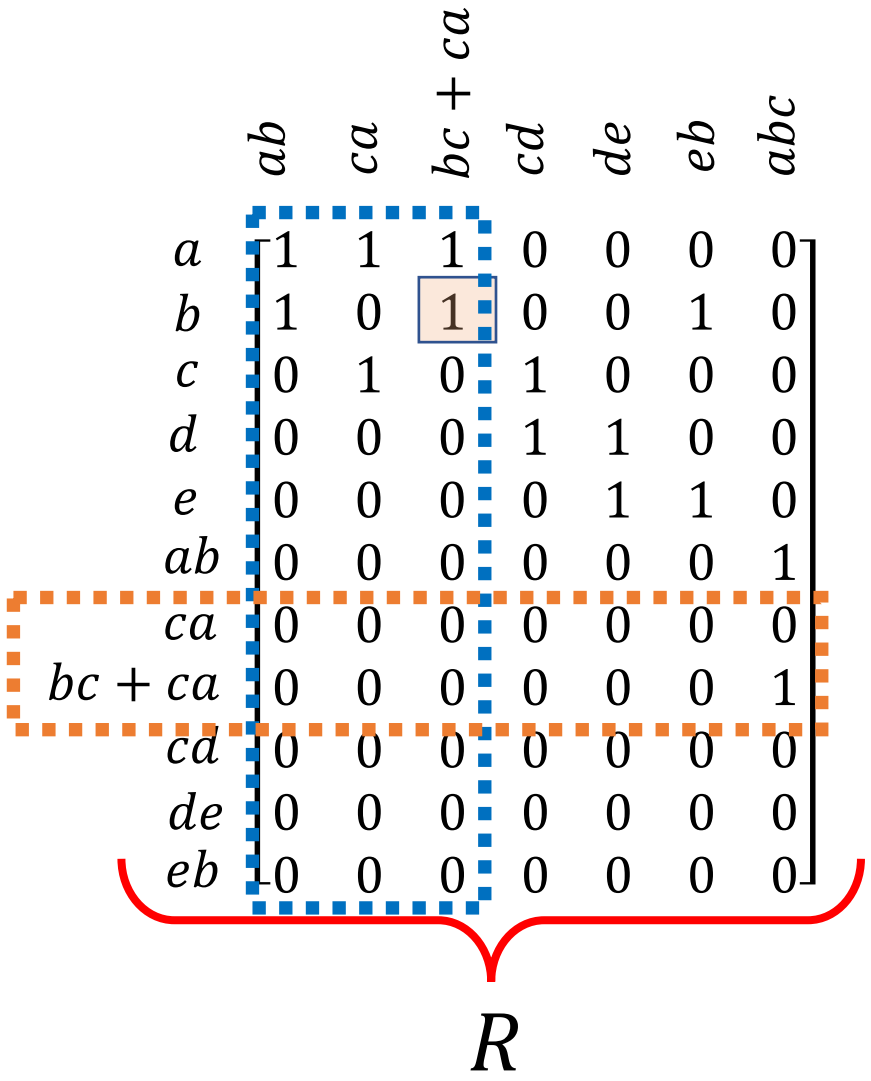


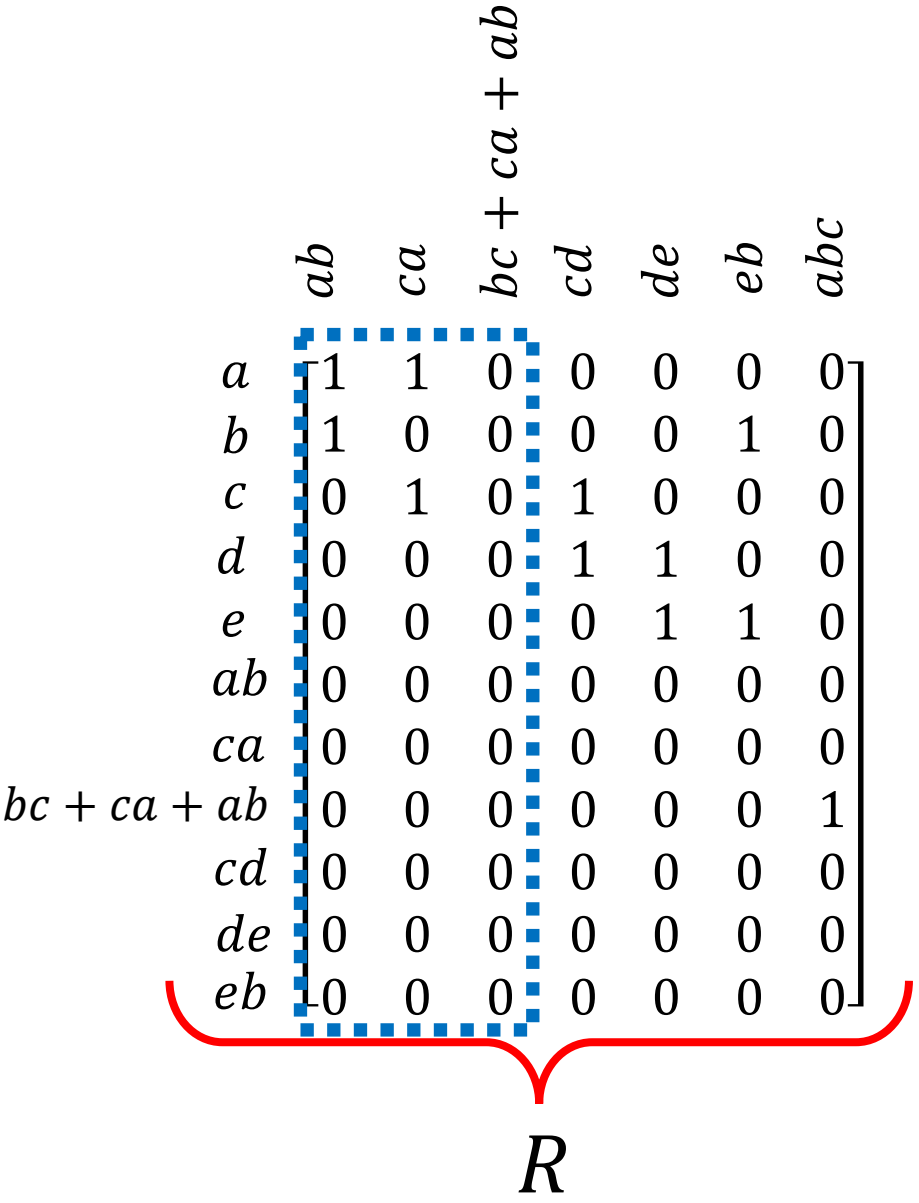
Reminder: to keep bases compatible, column operations require corresponding row operation!

E.g. $T: V \to W$ linear map, $\{v_1, v_2\}, \{w_1, w_2\}$ bases, $T(v_1) = a_{11}w_1 + a_{21}w_2$. Changing codomain basis by setting $w_1 \leftarrow w_1, w_2 \leftarrow w_2 + w_1$ means we have:

$$T(v_1) = a_{11}w_1 + a_{21}(w_2 + w_1) - a_{21}w_1$$
$$= (a_{11} - a_{21})w_1 + a_{21}(w_2 + w_1).$$

I.e. subtract row 2 from row 1 (notice the "reflected" operation). In $\mathbb{Z}/2\mathbb{Z}$, this is just addition!

Reduction Algorithm for Homology



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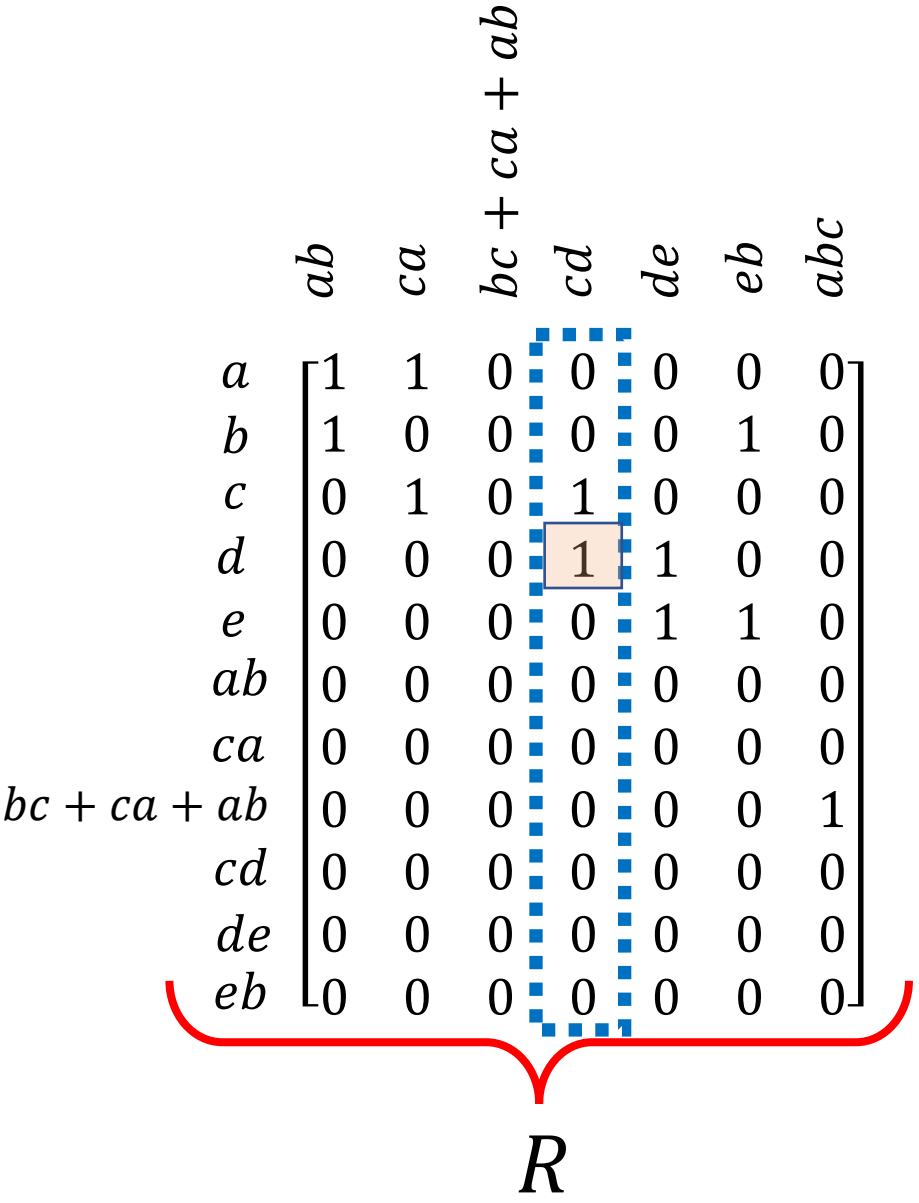

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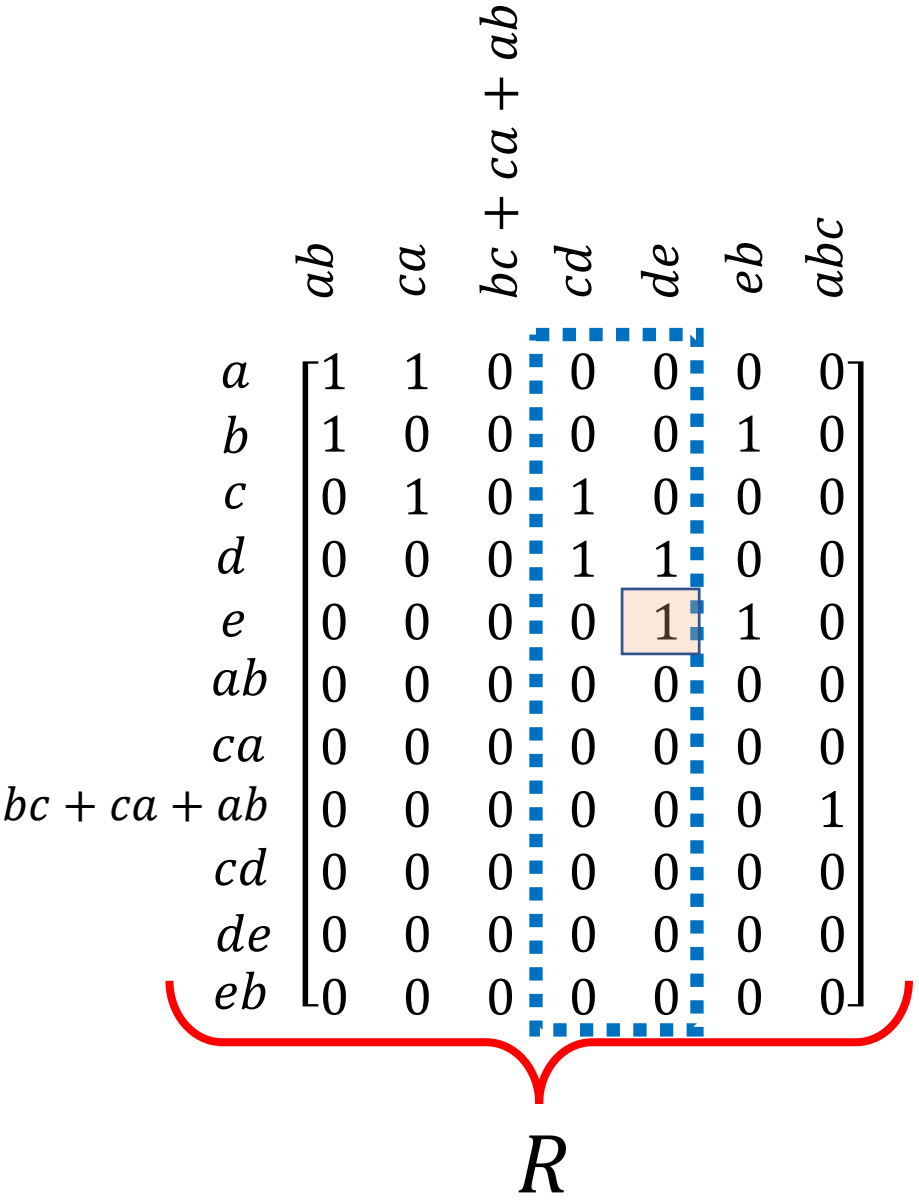

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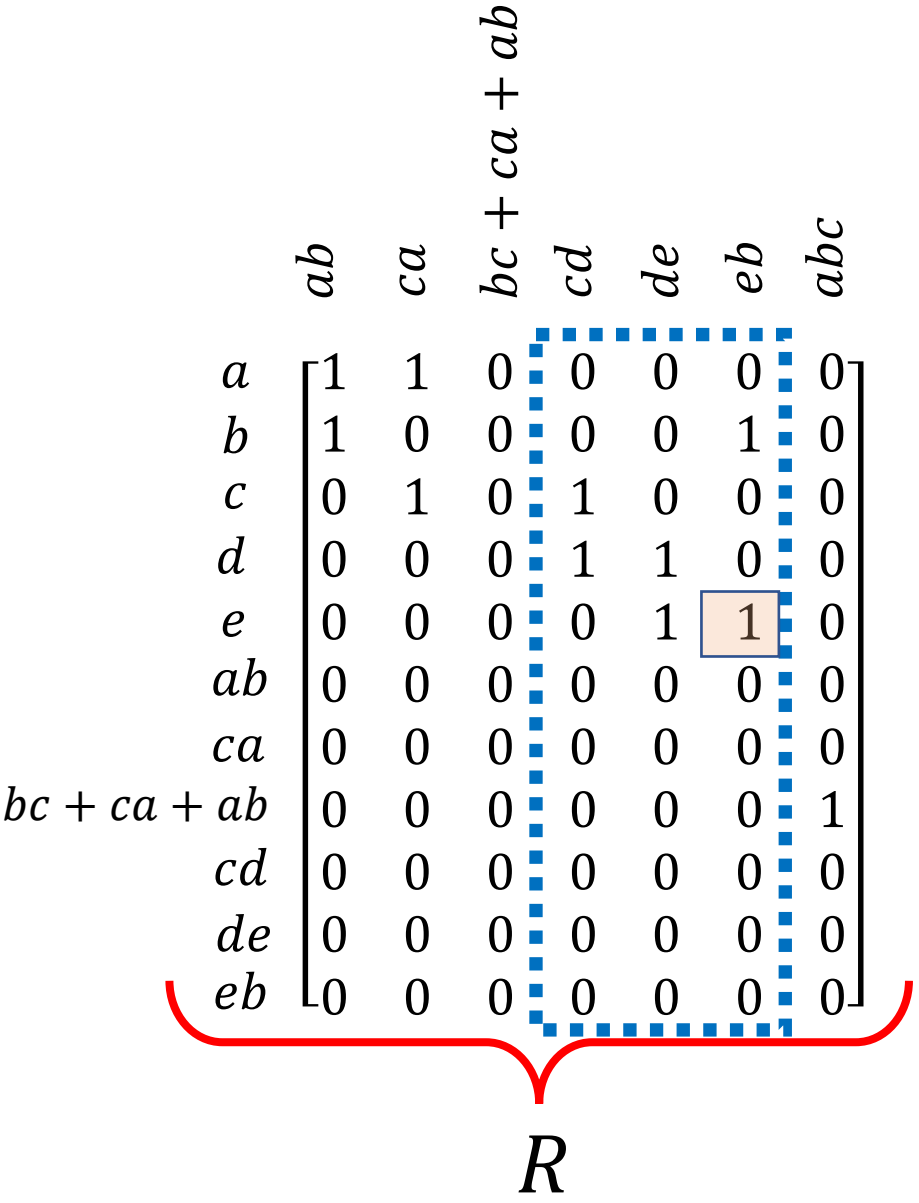

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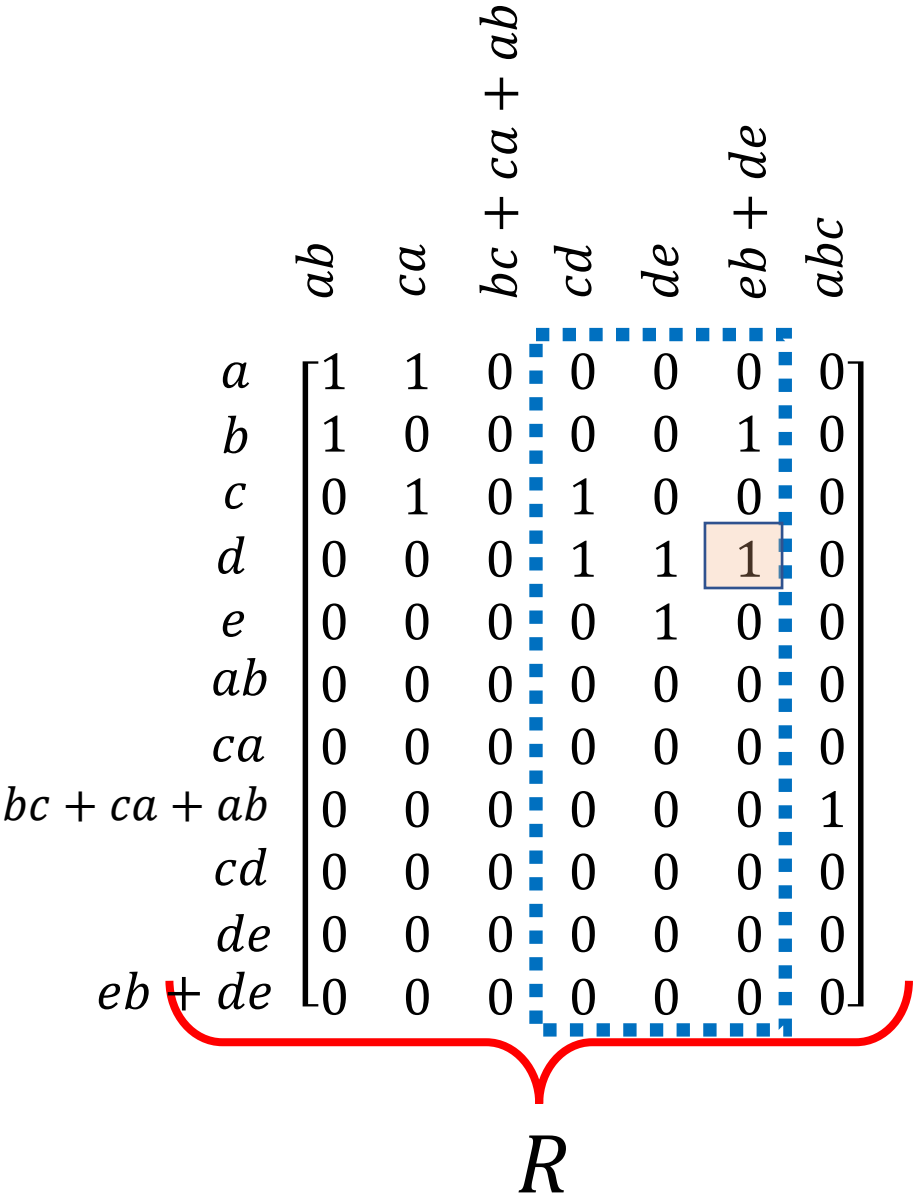
Reduction Algorithm for Homology



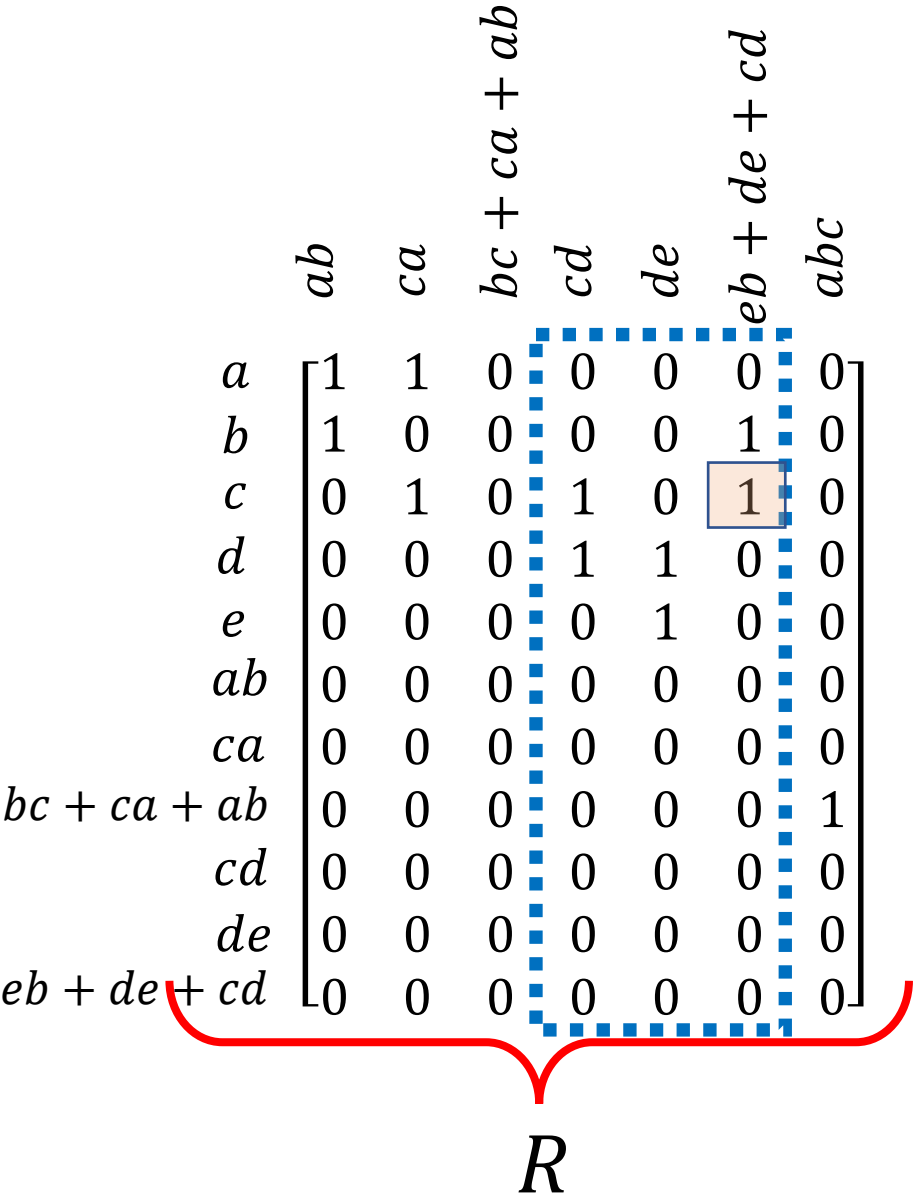
Notation: $low_R(j)$= row index of bottom 1 in column j of matrix R

Algorithm:

Initialize boundary information in incidence matrix D
Initialize $R \coloneqq D$

For column $j = 1, 2, \ldots, n$
  while $\exists j' < j, low_R(j') = low_R(j)$ do
    add column j' to column j

Reduction Algorithm for Homology



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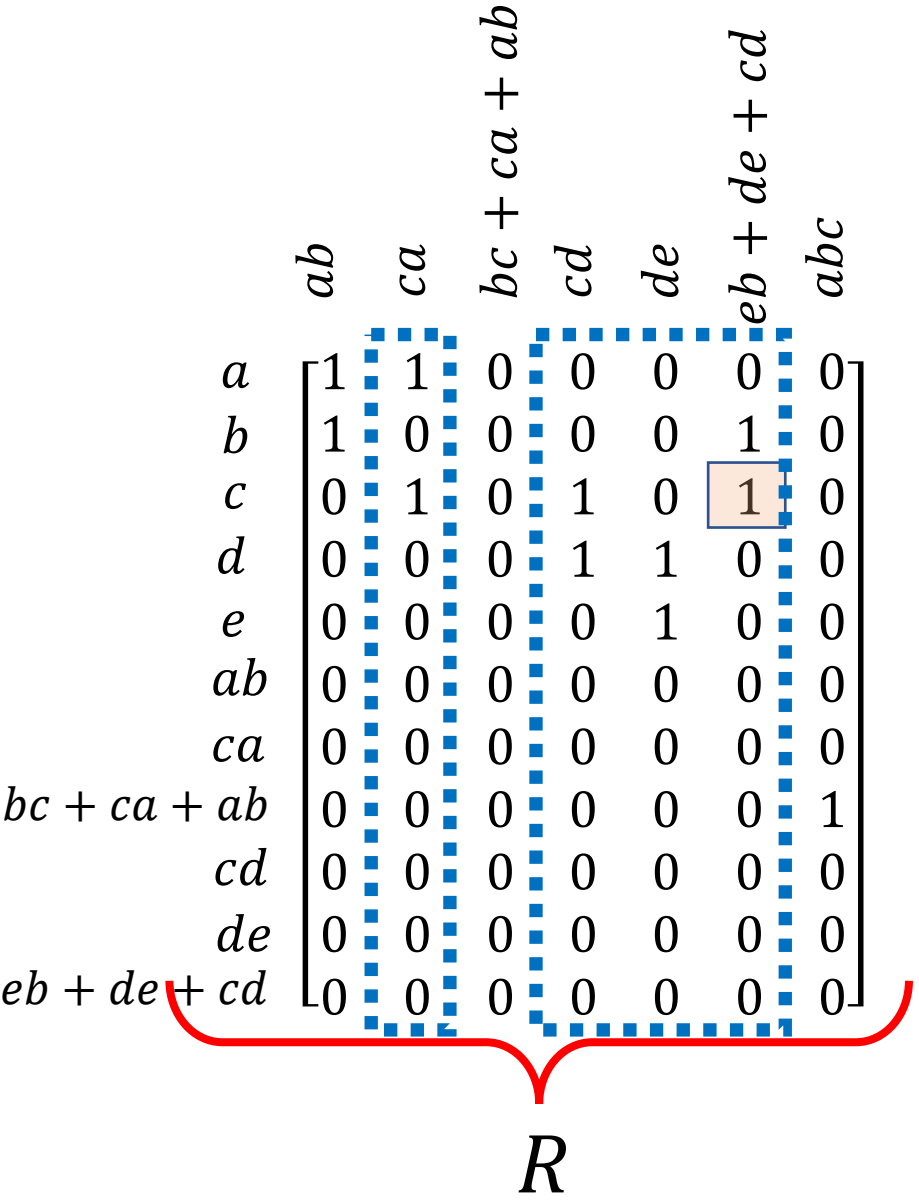

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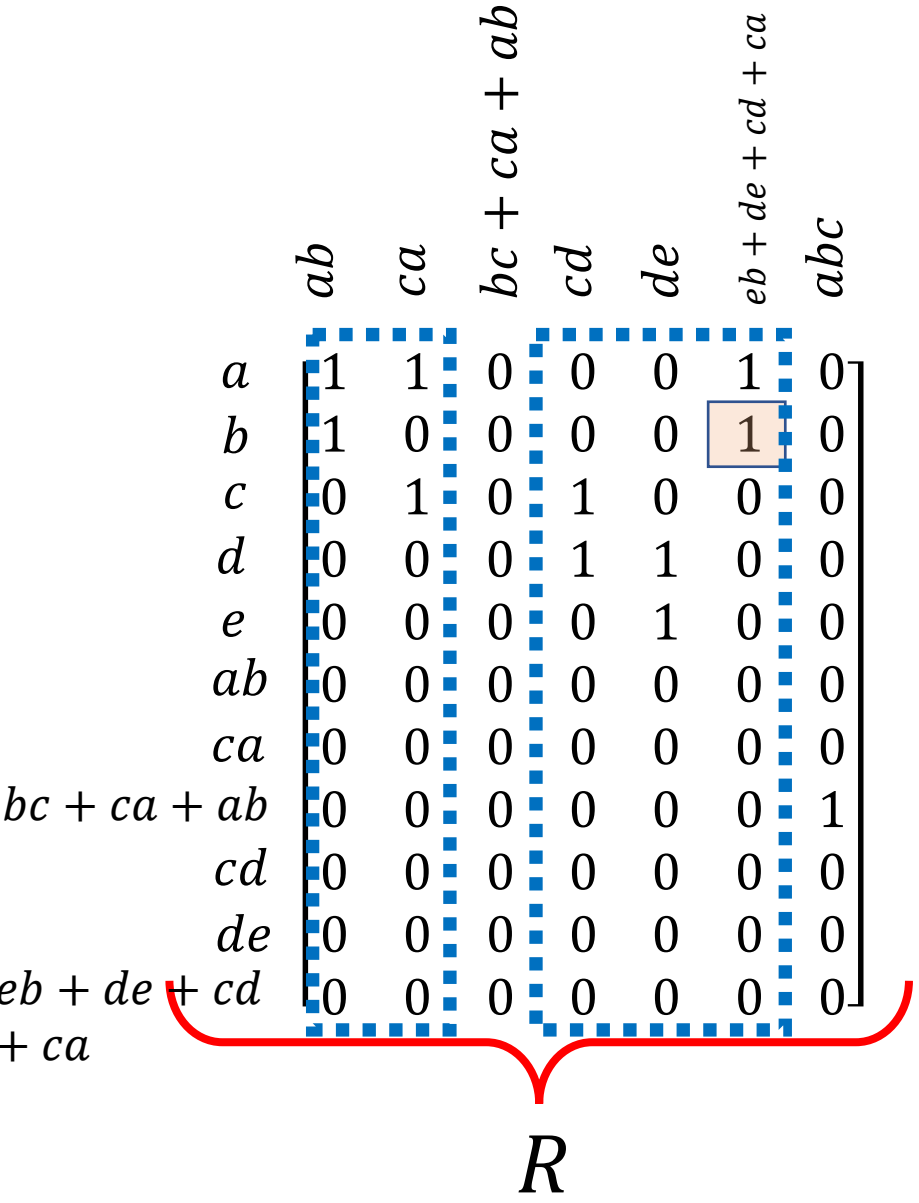

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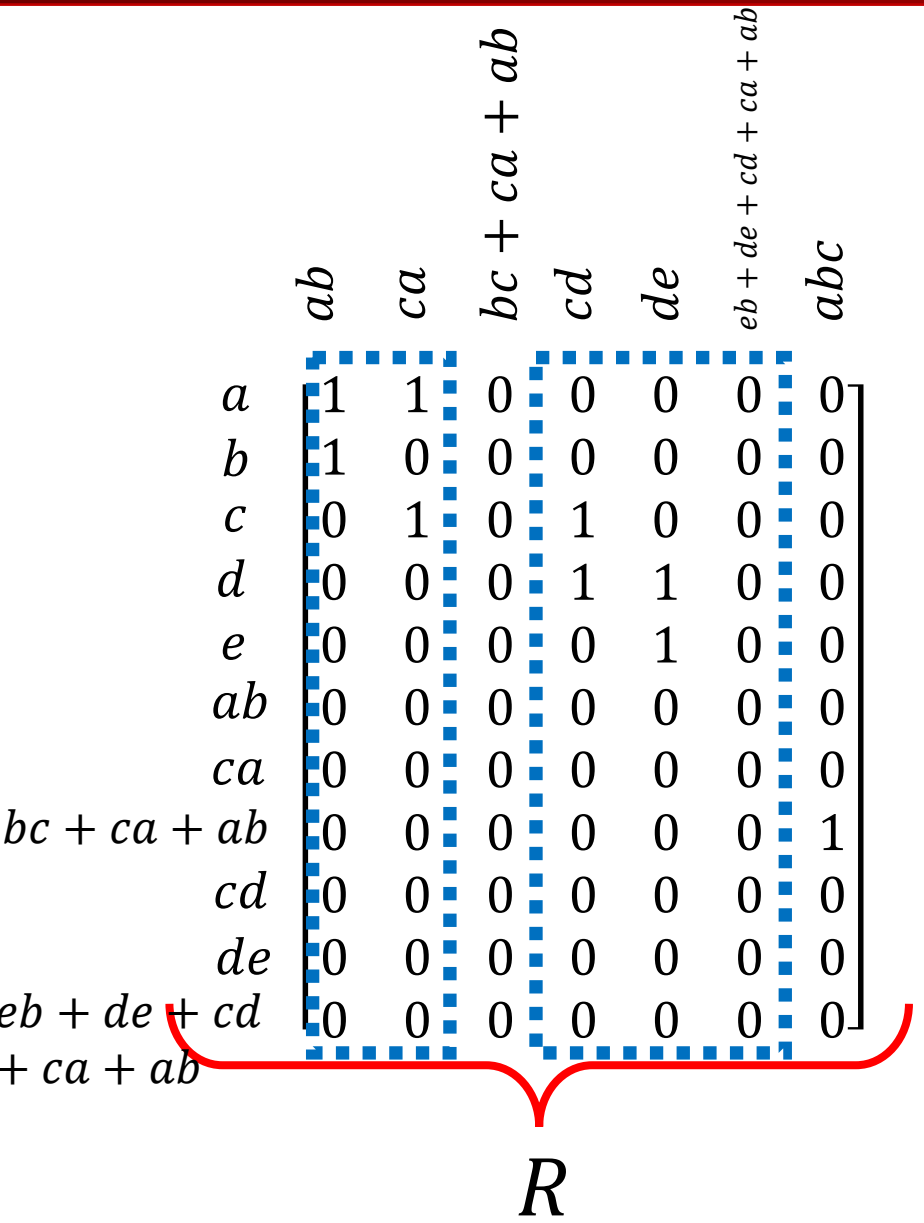

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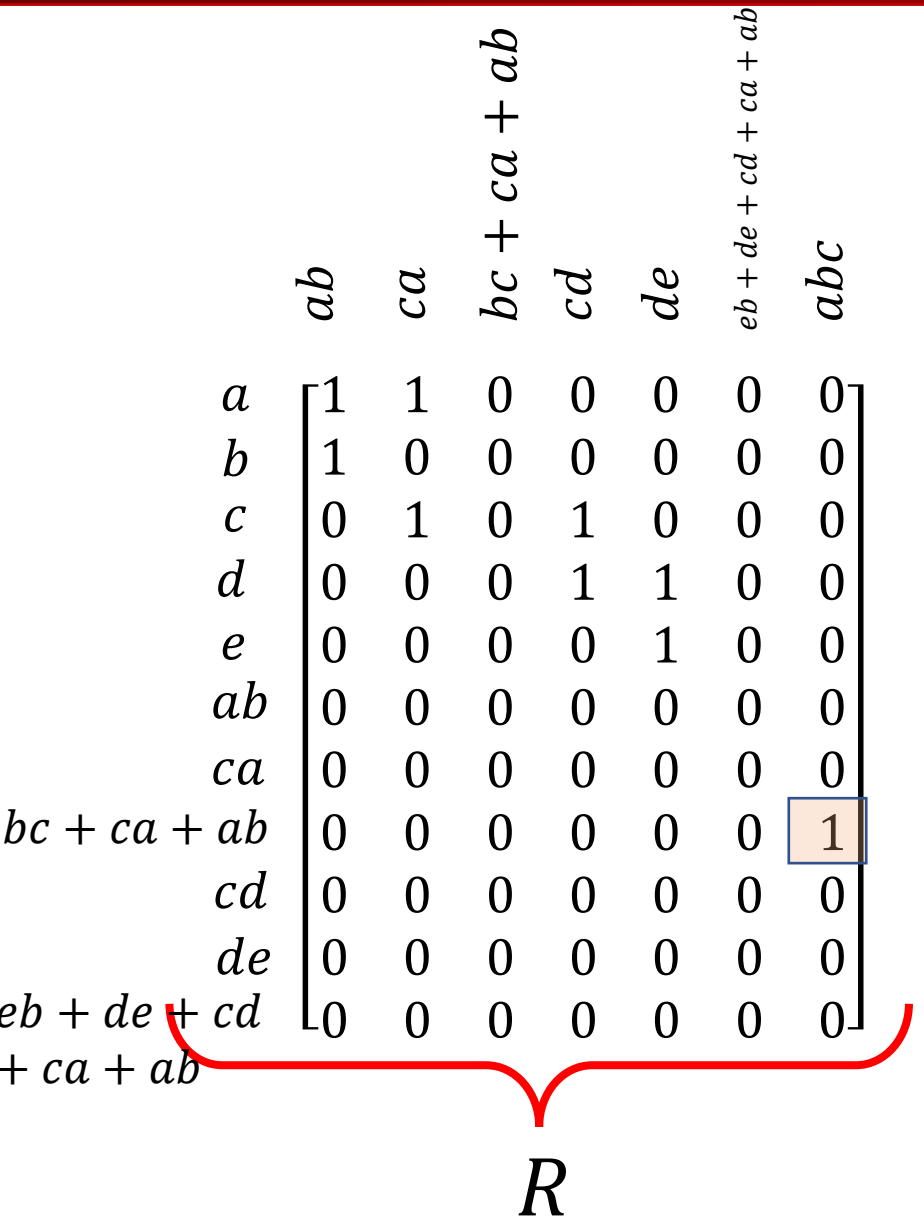


Reduction Algorithm for Homology

	a	b	c	d	e	ab	ca	$bc+ca+ab$	cd	de	$eb+de+cd+ca+ab$	abc
a	0	0	0	0	0	1	1	0	0	0	0	0
b	0	0	0	0	0	1	0	0	0	0	0	0
c	0	0	0	0	0	0	1	0	1	0	0	0
d	0	0	0	0	0	0	0	0	1	1	0	0
e	0	0	0	0	0	0	0	0	0	1	0	0
ab	0	0	0	0	0	0	0	0	0	0	0	0
ca	0	0	0	0	0	0	0	0	0	0	0	0
$bc+ca+ab$	0	0	0	0	0	0	0	0	0	0	0	1
cd	0	0	0	0	0	0	0	0	0	0	0	0
de	0	0	0	0	0	0	0	0	0	0	0	0
$eb+de+cd+ca+ab$	0	0	0	0	0	0	0	0	0	0	0	0
abc	0	0	0	0	0	0	0	0	0	0	0	0

Full matrix at termination. Observe:

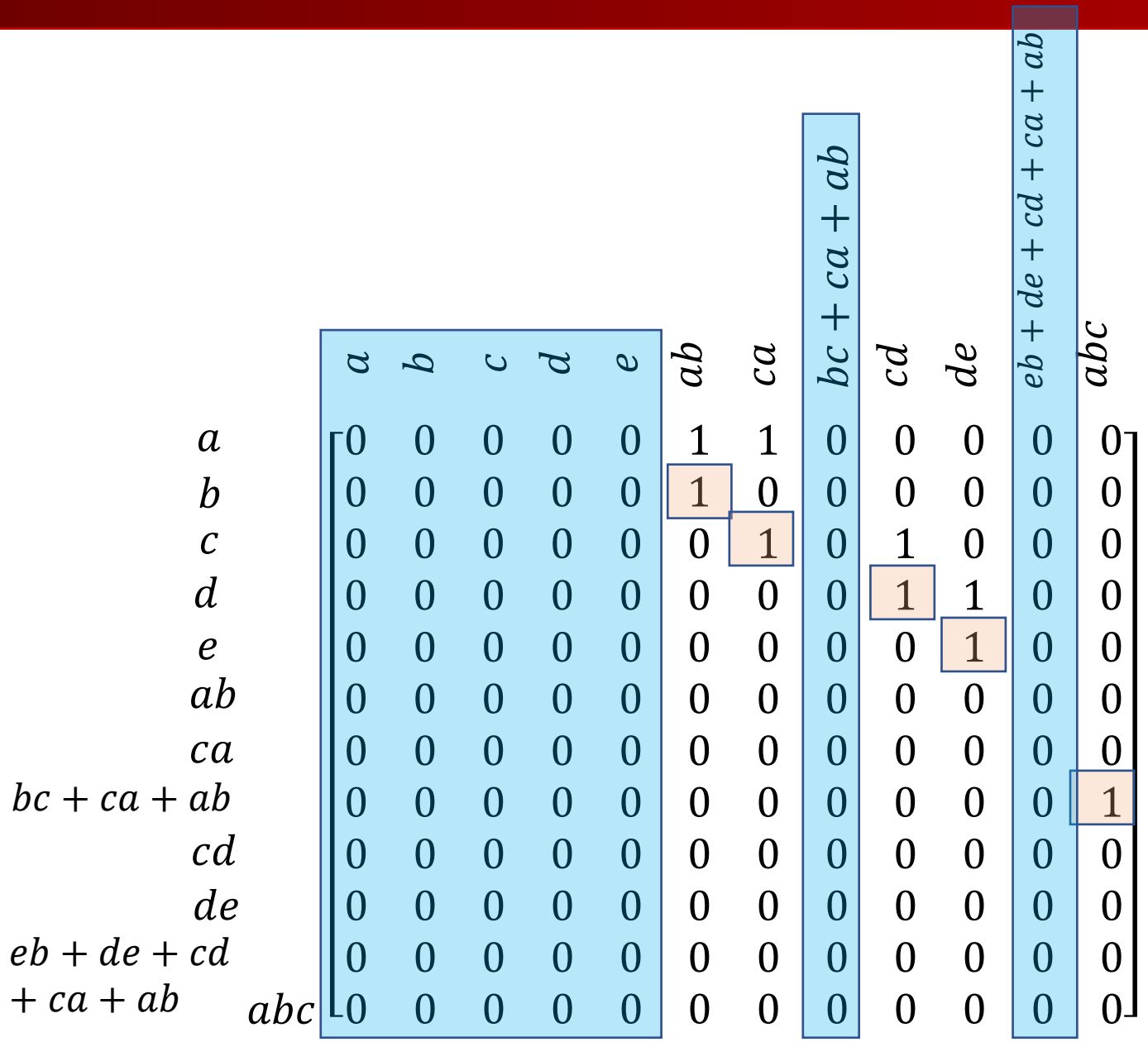
Reduction Algorithm for Homology

	a	b	c	d	e	ab	ca	$bc+ca+ab$	cd	de	$eb+de+cd+ca+ab$	abc
a	0	0	0	0	0	1	1	0	0	0	0	0
b	0	0	0	0	0	1	0	0	0	0	0	0
c	0	0	0	0	0	0	1	0	1	0	0	0
d	0	0	0	0	0	0	0	0	1	1	0	0
e	0	0	0	0	0	0	0	0	0	1	0	0
ab	0	0	0	0	0	0	0	0	0	0	0	0
ca	0	0	0	0	0	0	0	0	0	0	0	0
$bc+ca+ab$	0	0	0	0	0	0	0	0	0	0	0	1
cd	0	0	0	0	0	0	0	0	0	0	0	0
de	0	0	0	0	0	0	0	0	0	0	0	0
$eb+de+cd+ca+ab$	0	0	0	0	0	0	0	0	0	0	0	0
abc	0	0	0	0	0	0	0	0	0	0	0	0

Full matrix at termination. Observe:

- (Proposition) No two columns with the same low_R value

Reduction Algorithm for Homology



Full matrix at termination. Observe:

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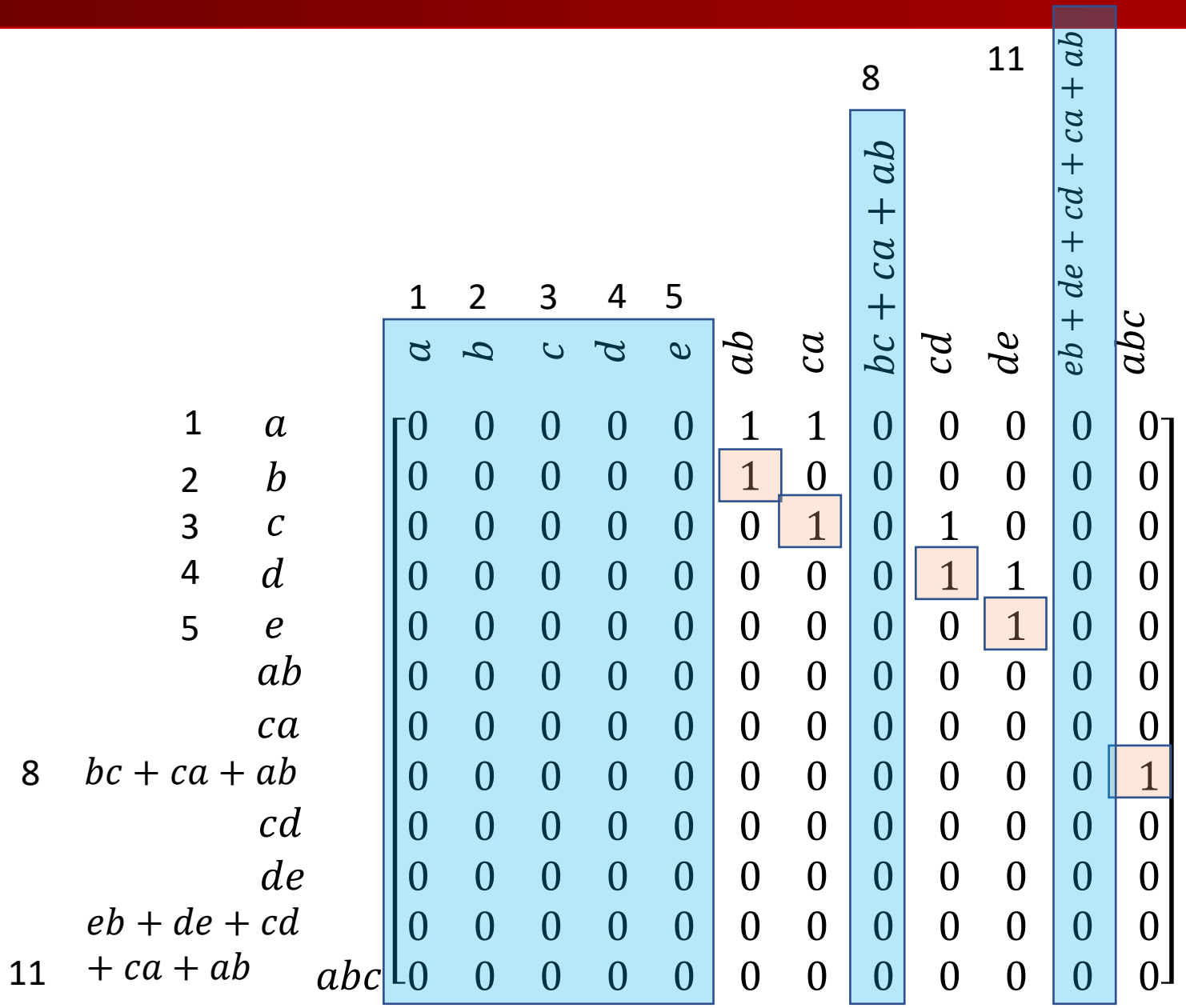
- Zero columns can be read off immediately to get $\ker \partial_p$

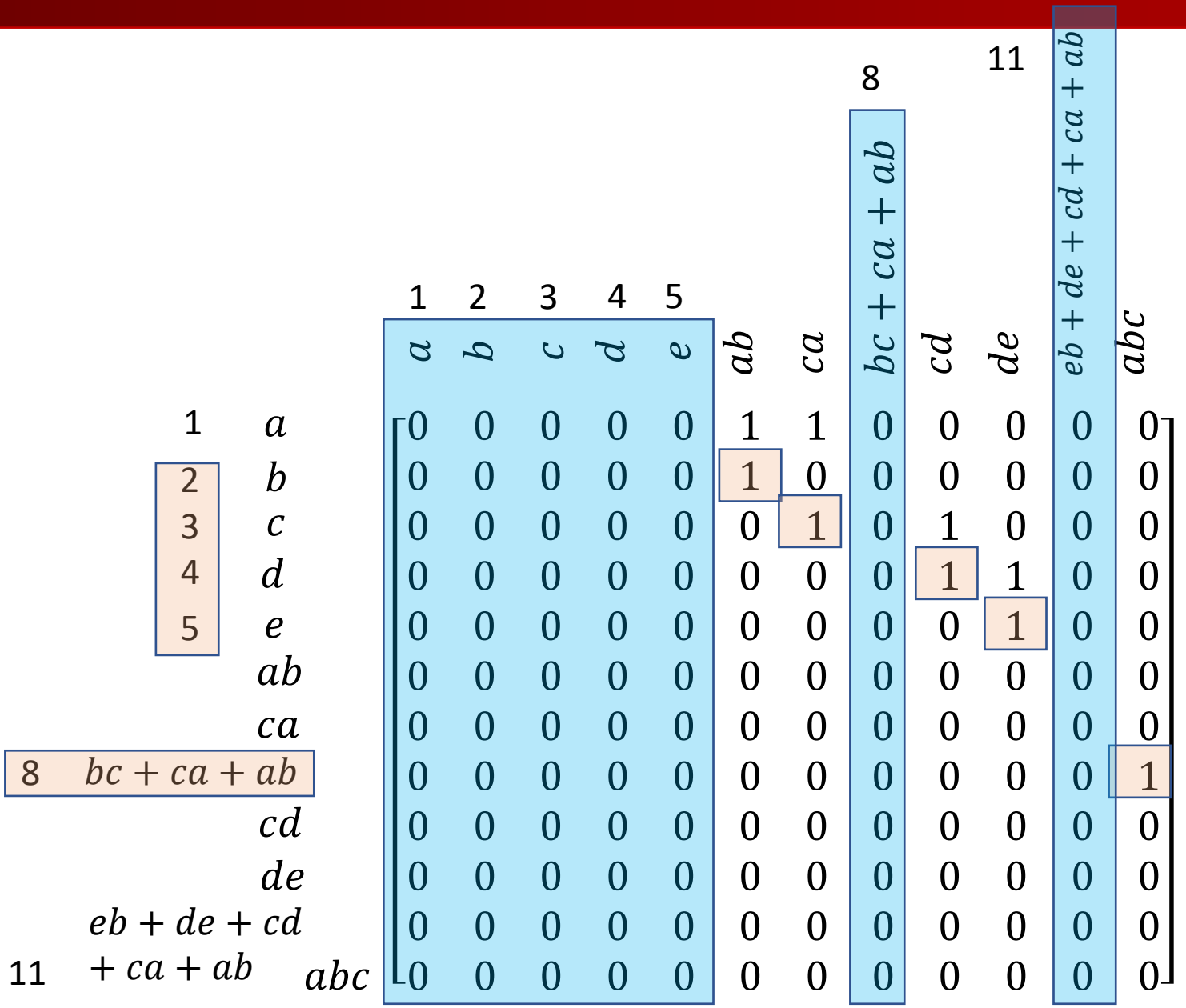
Reduction Algorithm for Homology



Full matrix at termination. Observe:

- (Proposition) No two columns with the same low_R value
- Zero columns can be read off immediately to get $\ker \partial_p$
- (Proposition) Indices i such that column i is zero but $i \neq low_R(j)$ for any j correspond exactly to the cycles that are not boundaries!
- Thus we get a basis for homology in each dimension.

Reduction Algorithm for Homology



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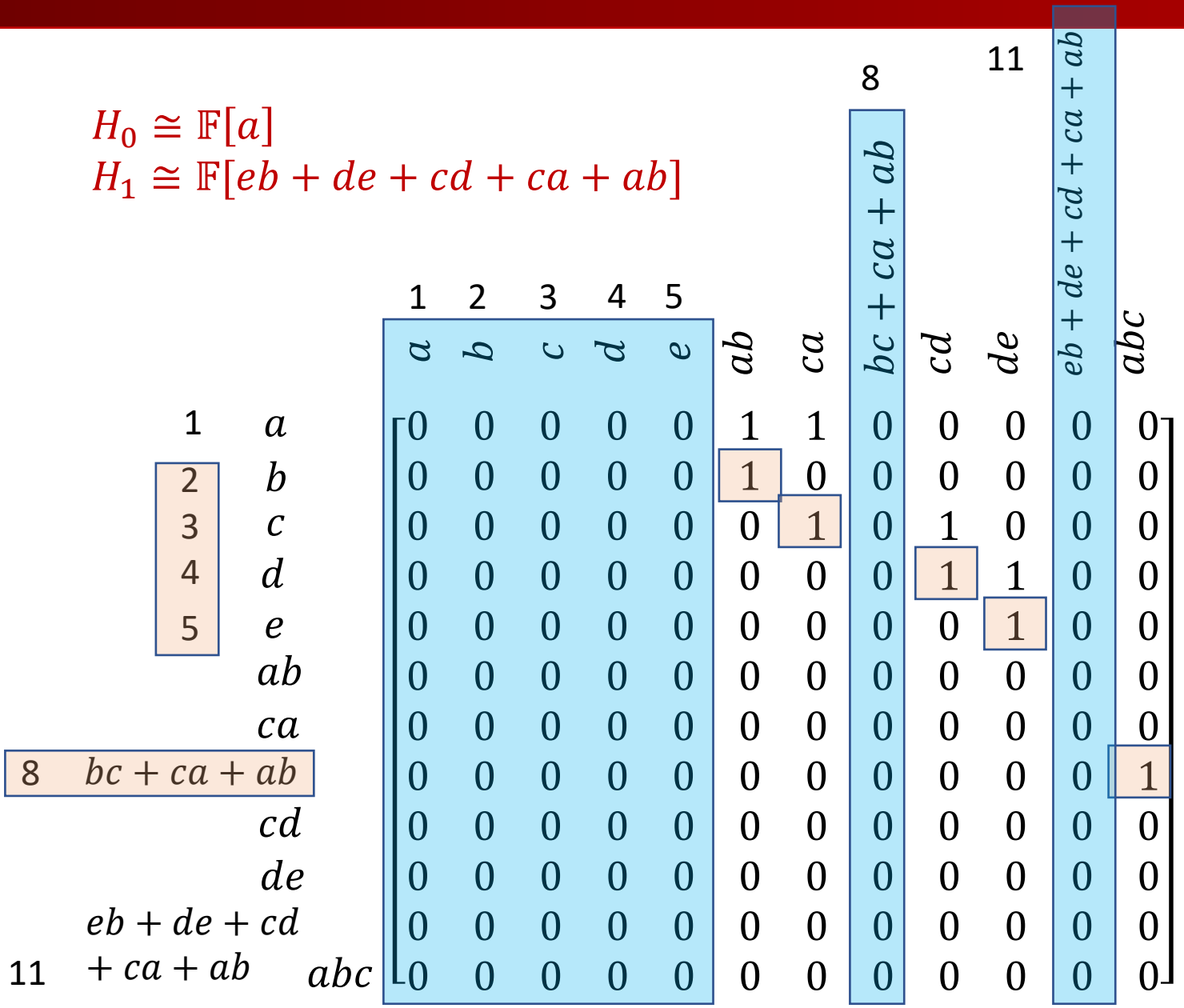
Reduction Algorithm for Homology

$H_0 \cong \mathbb{F}[a]$

$H_1 \cong \mathbb{F}[eb + de + cd + ca + ab]$



Full matrix at termination. Observe:

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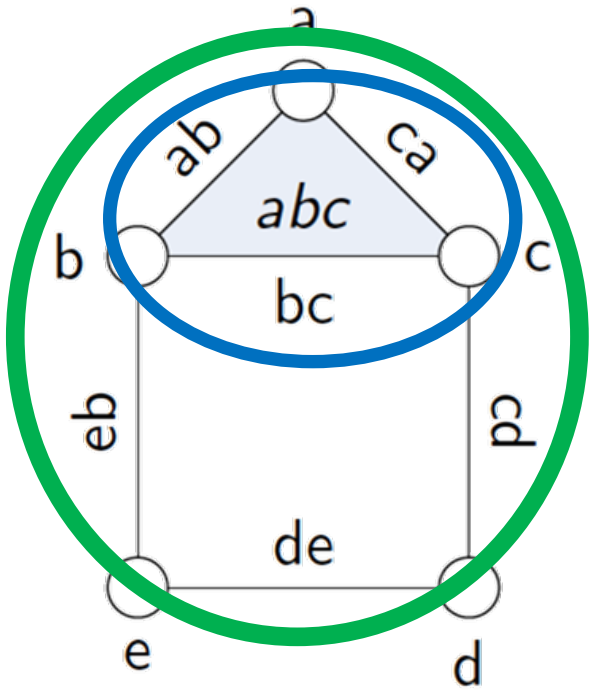
- Thus we get a basis for homology in each dimension.

Reduction Algorithm for Homology

$H_0 \cong \mathbb{F}[a]$

$H_1 \cong \mathbb{F}[eb + de + cd + ca + ab]$

		1	2	3	4	5	1	1	8	1	1	11	1
		a	b	c	d	e	ab	ca	$bc+ca+ab$	cd	de	$eb+de+cd+ca+ab$	abc
1	a	0	0	0	0	0	1	1	0	0	0	0	0
2	b	0	0	0	0	0	1	0	0	0	0	0	0
3	c	0	0	0	0	0	0	1	0	1	0	0	0
4	d	0	0	0	0	0	0	0	0	1	1	0	0
5	e	0	0	0	0	0	0	0	0	0	1	0	0
	ab	0	0	0	0	0	0	0	0	0	0	0	0
	ca	0	0	0	0	0	0	0	0	0	0	0	0
8	$bc+ca+ab$	0	0	0	0	0	0	0	0	0	0	0	1
	cd	0	0	0	0	0	0	0	0	0	0	0	0
	de	0	0	0	0	0	0	0	0	0	0	0	0
	$eb+de+cd$	0	0	0	0	0	0	0	0	0	0	0	0
11	$+ca+ab$	0	0	0	0	0	0	0	0	0	0	0	0
	abc	0	0	0	0	0	0	0	0	0	0	0	0

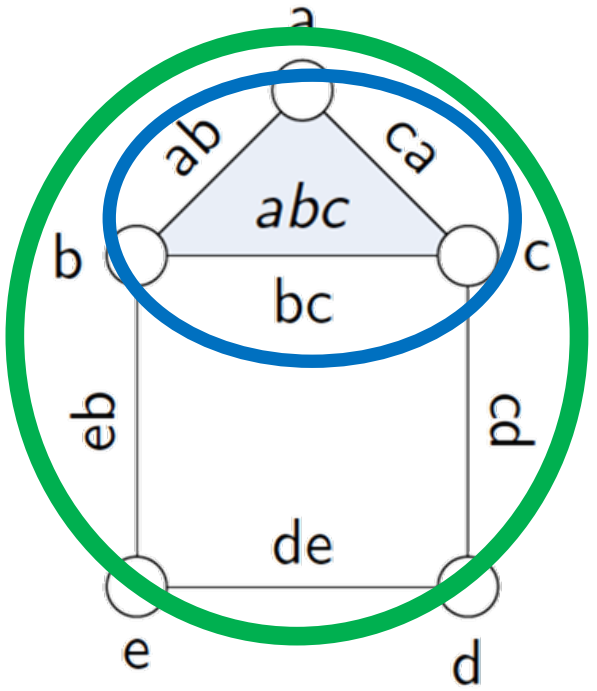


Basis Selection

$H_0 \cong \mathbb{F}[a]$

$H_1 \cong \mathbb{F}[eb + de + cd + ca + ab]$

		1	2	3	4	5	ab	ca	8 $bc + ca + ab$	cd	de	11 $eb + de + cd + ca + ab$	abc
		a	b	c	d	e							
1	a	0	0	0	0	0	1	1	0	0	0	0	0
2	b	0	0	0	0	0	1	0	0	0	0	0	0
3	c	0	0	0	0	0	0	1	0	1	0	0	0
4	d	0	0	0	0	0	0	0	0	1	1	0	0
5	e	0	0	0	0	0	0	0	0	0	1	0	0
	ab	0	0	0	0	0	0	0	0	0	0	0	0
	ca	0	0	0	0	0	0	0	0	0	0	0	0
8	$bc + ca + ab$	0	0	0	0	0	0	0	0	0	0	0	1
	cd	0	0	0	0	0	0	0	0	0	0	0	0
	de	0	0	0	0	0	0	0	0	0	0	0	0
11	$eb + de + cd + ca + ab$	0	0	0	0	0	0	0	0	0	0	0	0
	abc	0	0	0	0	0	0	0	0	0	0	0	0



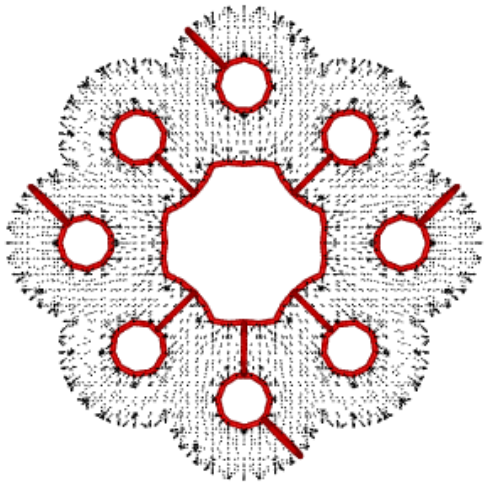
Caveat: homology involves an equivalence class, so we get "representative cycles". E.g. we got $eb + de + cd + ca + ab$ instead of $eb + de + cd + bc$.

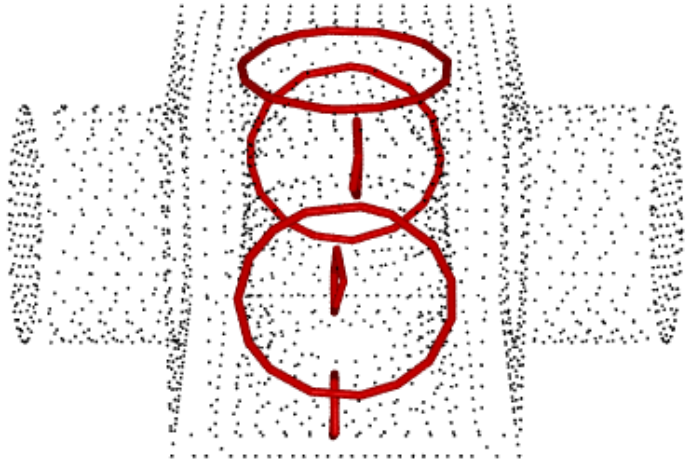
Operating at the algebraic level gives up some control over geometric correspondence.

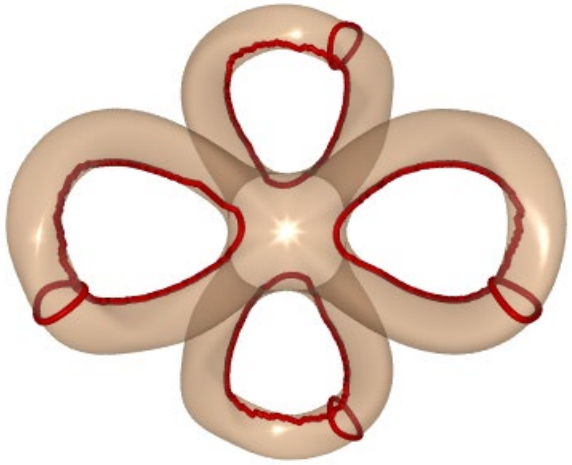
ShortLoop

Oleksiy Busaryev, Tamal Dey, Jian Sun, Yusu Wang

Figures from http://web.cse.ohio-state.edu/~dey.8/shortloop-pictures.html







Computing Persistent Homology

Reduction Algorithm for Persistent Homology

Ulrich Bauer, *Ripser: efficient computation of Vietoris–Rips persistence barcodes*

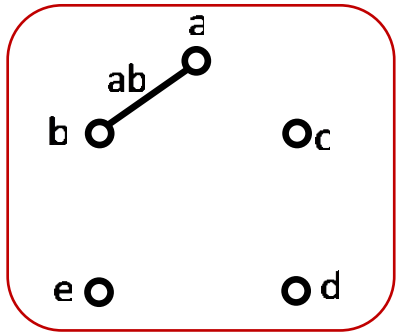
Persistence algorithm:

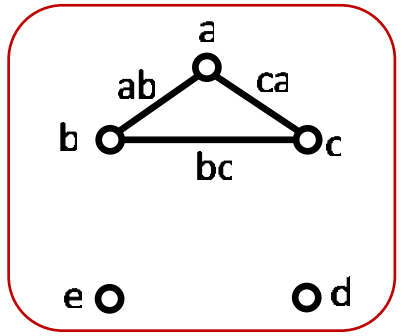
- When setting up boundary matrices/overall incidence matrix, order basis vectors according to order of appearance of simplices
- Apply reduction algorithm from before
- Read off persistence pairs $\{(i,j) \mid i = low_R(j) \neq 0\}$ and essential indices $\{i \mid R[:,i] = 0,\ i \neq low_R(j) \text{ for any } j\}$
- Persistence pairs track representative cycles that are born at index i and die at index j
- Essential indices track cycles that are born at index i and live forever
- Complexity: Gaussian elimination, so essentially cubic in the number of simplices (state-of-the-art: matrix multiplication time)

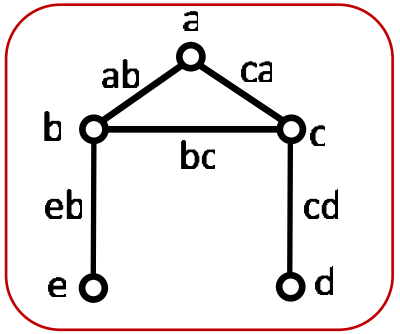
Back to the House Example

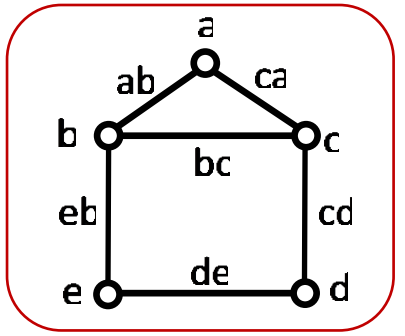
Entry time:	1	1	1	1	1	1	2	2	3	3	4	5
Index:	1	2	3	4	5	6	7	8	9	10	11	12
	a	b	c	d	e	ab	ca	bc	cd	eb	de	abc

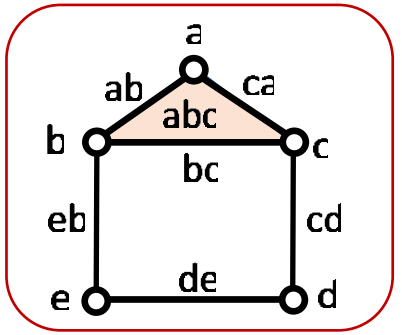
$$
\begin{array}{c}
a \\ b \\ c \\ d \\ e \\ ab \\ ca \\ bc \\ cd \\ eb \\ de \\ abc
\end{array}
\begin{bmatrix}
0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{bmatrix}
$$





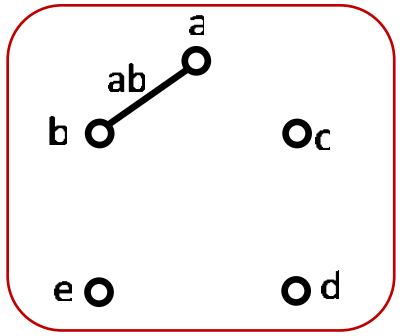


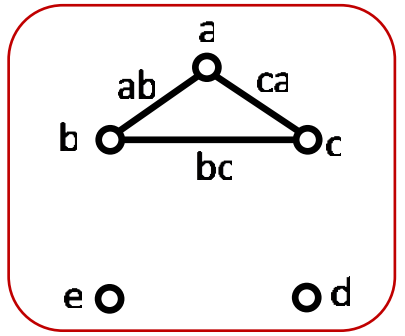


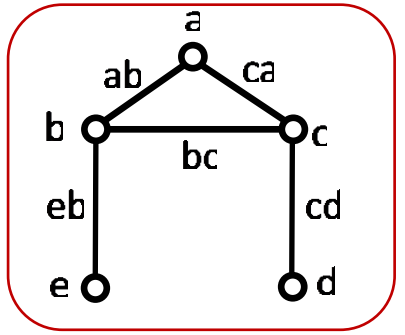


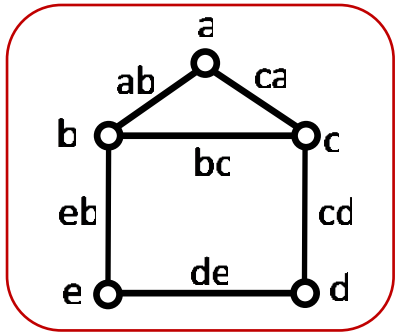
Back to the House Example

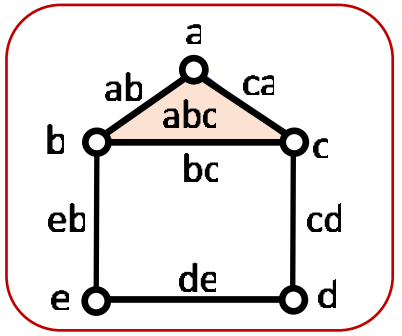
		1	2	3	4	5	ab	ca	8	cd	eb	11	abc
		a	b	c	d	e			bc + ca + ab			de + eb + cd + ca + ab	
1	a	0	0	0	0	0	1	1	0	0	0	0	0
2	b	0	0	0	0	0	1	0	0	0	1	0	0
3	c	0	0	0	0	0	0	1	0	1	0	0	0
4	d	0	0	0	0	0	0	0	0	1	0	0	0
5	e	0	0	0	0	0	0	0	0	0	1	0	0
	ab	0	0	0	0	0	0	0	0	0	0	0	0
	ca	0	0	0	0	0	0	0	0	0	0	0	0
8	bc + ca + ab	0	0	0	0	0	0	0	0	0	0	0	1
	cd	0	0	0	0	0	0	0	0	0	0	0	0
	eb	0	0	0	0	0	0	0	0	0	0	0	0
11	de + eb + cd + ca + ab	0	0	0	0	0	0	0	0	0	0	0	0
	abc	0	0	0	0	0	0	0	0	0	0	0	0











Back to the House Example

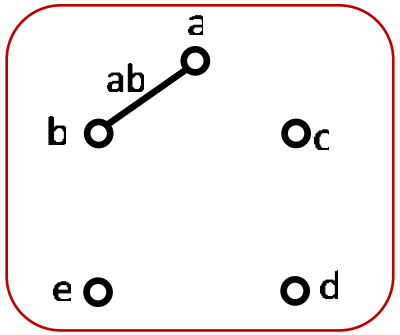
Persistence pairs: $\{(2,6),(3,7),(4,9),(5,10),(8,12)\}$
(column indices)

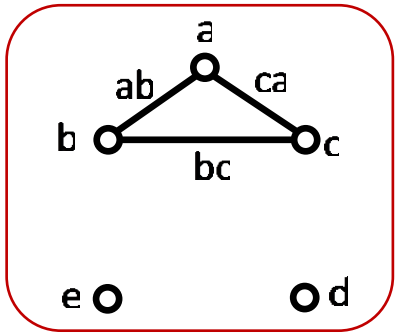
Lifetimes (dim 0): $\{[1,1),[1,2),[1,3),[1,3)\}$
(time indices)

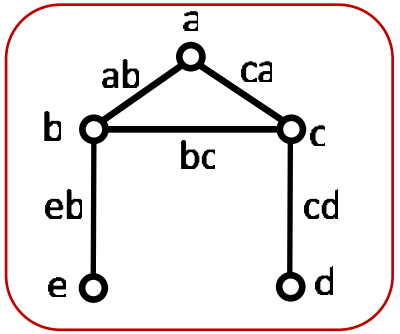
Lifetimes (dim 1): $\{[2,5)\}$
(time indices)

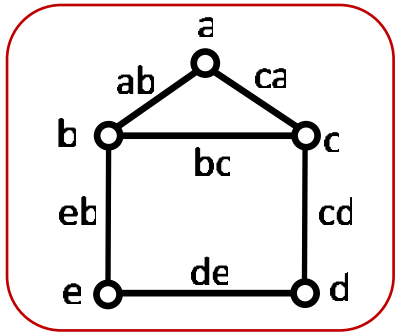
Essential indices: $\{1,11\}$
(column indices)

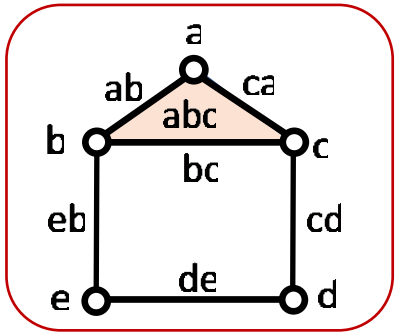
Lifetimes: $\{[1,\infty)$ (connected component), $[4,\infty)$ (loop)$\}$
(time indices)











Simplices are “Creators” or “Destroyers”

- Every simplex either creates a homology class or destroys one
- Specifically, a k-simplex either creates a k-dimensional feature or destroys a $(k-1)$-dimensional feature

Simplices are Creators or Destroyers

- A k-simplex either creates a k-dimensional feature or destroys a $(k-1)$-dimensional feature
- Persistence pairs a creator simplex σ with a destroyer simplex τ, and records the birth-death times (b, d) as the appearance times of (σ, τ).

Proof: Suppose we add a p-simplex σ. Assume simplices are added incrementally, so we have not yet added a $(p+1)$-simplex with σ as a face.

- Case 1: $\partial_p(\sigma) \in im(\partial_p)$, i.e. $\partial_p(\sigma) = \partial_p(\tau)$ for some τ. Then $\partial_p(\sigma - \tau) = 0$, so $\ker(\partial_p)$ grows by one dimension. Because we don't yet have a $(p+1)$-simplex with σ as a face, $im(\partial_{p+1})$ is unchanged. Therefore H_p grows by one dimension, i.e. we created a p-dimensional feature.
- Case 2: $\partial_p(\sigma) \notin im(\partial_p)$, i.e. $im(\partial_p)$ grows by one dimension. But $\partial_{p-1}\partial_p(\sigma) = 0$, and the elements in $\partial_p(\sigma)$ had already been added by the incremental addition assumption, so $\ker(\partial_{p-1})$ remains unchanged. Thus H_{p-1} loses one dimension, i.e. we destroyed a $(p-1)$-dimensional feature.

A Deeper Look at the Persistence Algorithm

- Why the restriction on directions of column operations?
- Why is persistent homology different from computing standard homology a bunch of times in parallel?

$$0 \rightarrow H_p\left(\Sigma^{(1)}\right) \rightarrow H_p(\Sigma^{(2)}) \rightarrow \ldots \rightarrow H_p(\Sigma^{(n-1)}) \rightarrow H_p(\Sigma^{(n)})$$

A Deeper Look at the Algorithm

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Obtaining bases for the individual vector spaces is not sufficient. To encode linear maps, we need compatible bases.

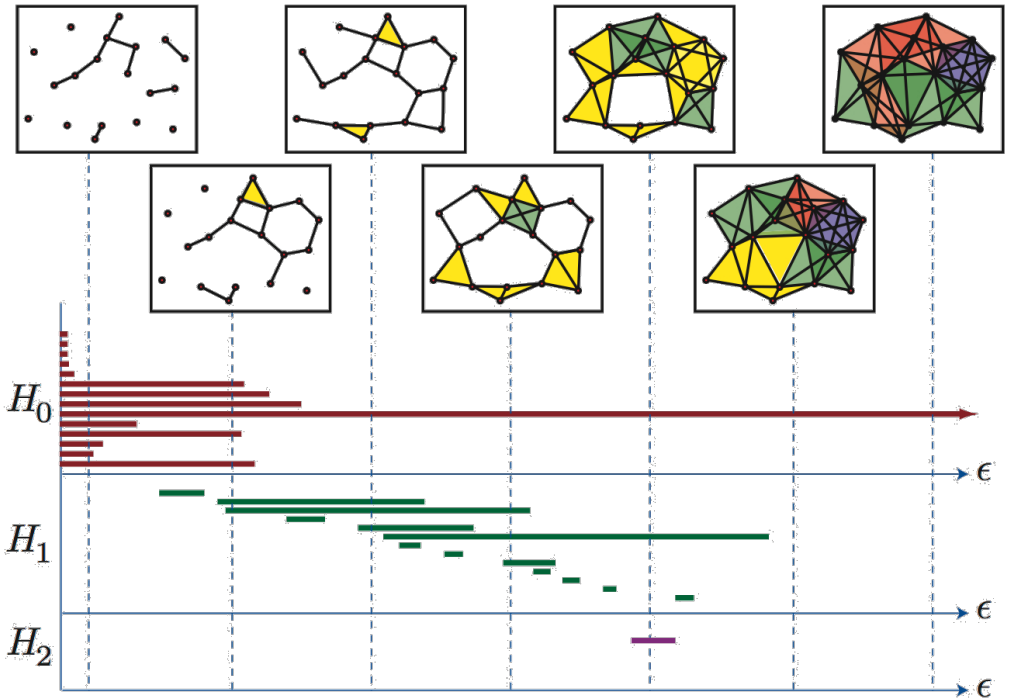
Pipeline

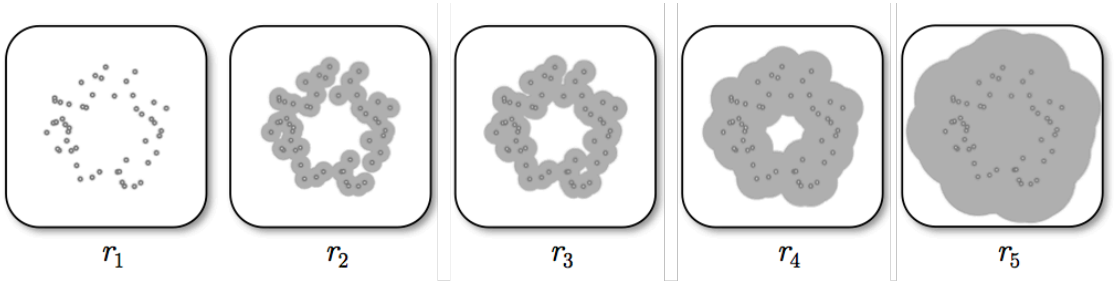
Dataset:
- **Euclidean point cloud data**
- **Metric spaces**
- **Triangulated shapes**
- Graphs, matrices…

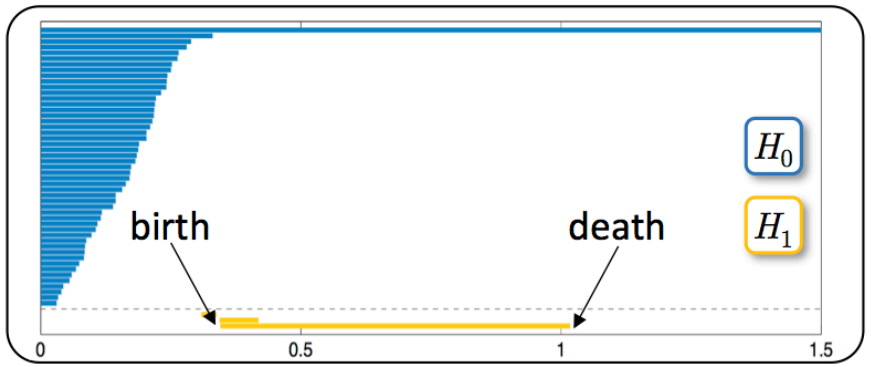
Filtered simplicial complex
- Possible to have both inclusions and deletions (dynamic data)

Vector spaces with linear maps: a **persistent vector space**

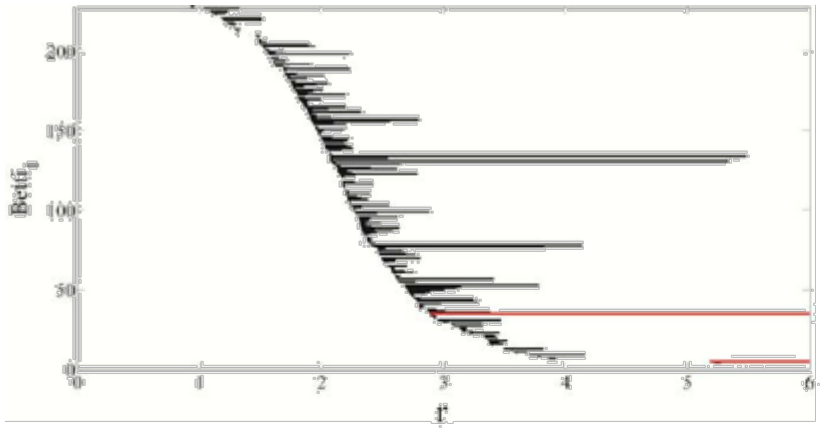
Visual summary: a **persistence diagram** or **persistence barcode**
- Postprocessing available for ML-friendly output

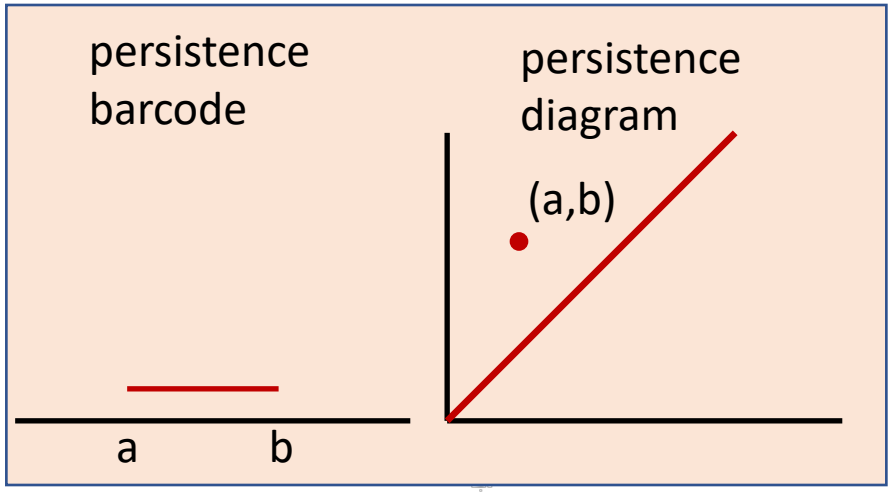




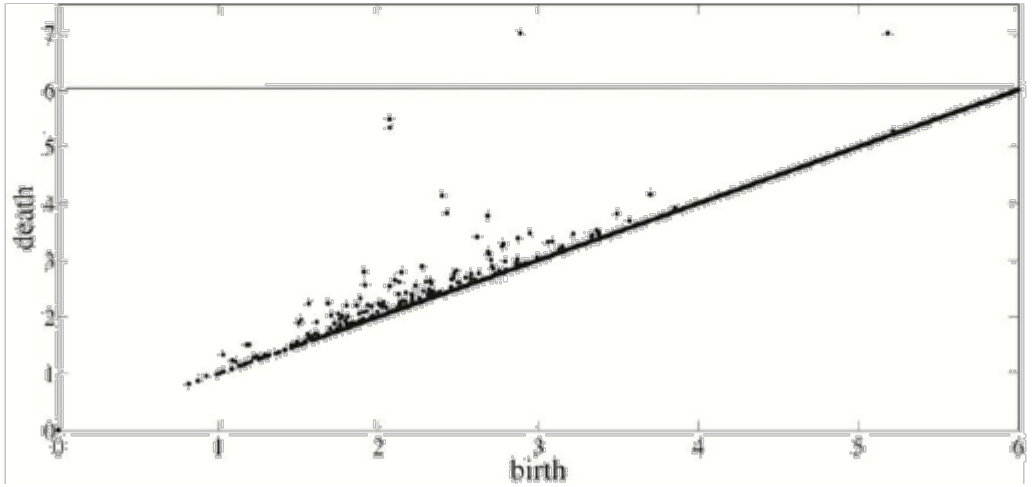


Another View: Persistence Diagrams





long barcodes = points away from the diagonal = robust features



Short barcodes = points near the diagonal = noise

Map 1-D intervals to points in 2-D

Illustration – Ripser

README.md

Ripser

Description

Ripser is a lean C++ code for the computation of Vietoris–Rips persistence barcodes. It can do just this one thing, but does it extremely well.

To see a live demo of Ripser's capabilities, go to live.ripser.org. The computation happens inside the browser (using Emscripten to compile Ripser to WebAssembly, supported on recent browsers).

The main features of Ripser:

- time- and memory-efficient
- only about 1000 lines of code in a single C++ file
- support for coefficients in prime finite fields
- no external dependencies (optional support for Google's [sparsehash])

localhost:8889/lab/tree/demo_ripser.ipynb

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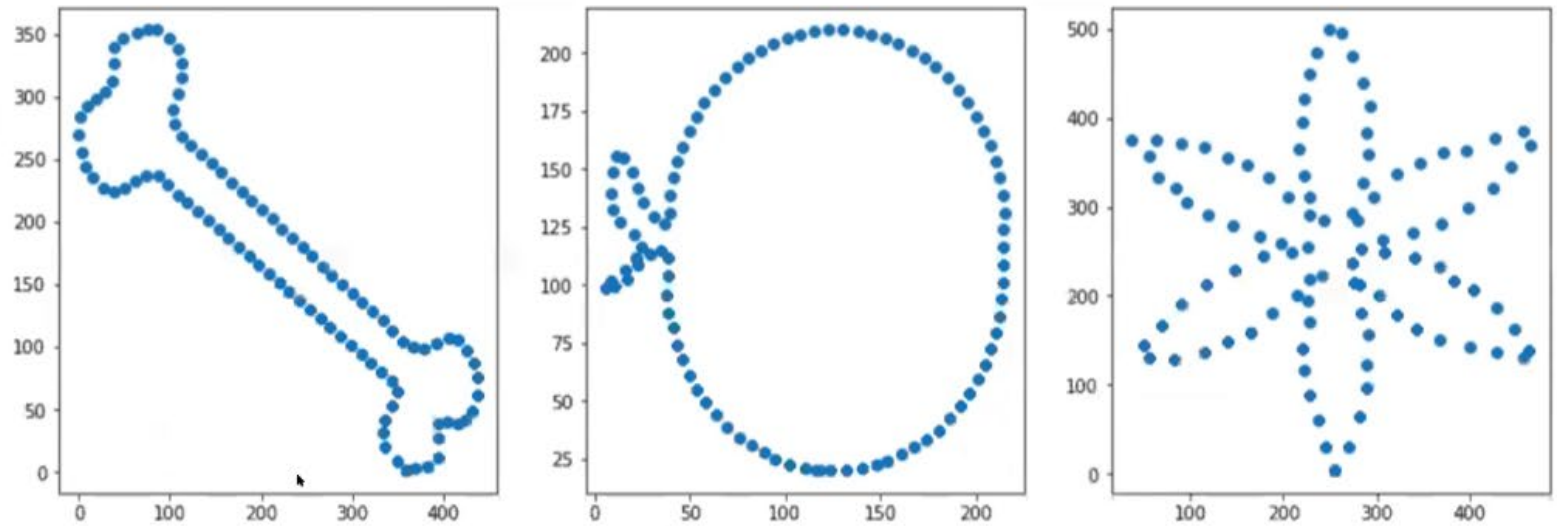
planarShapes.mat	a year ago
README.md	6 hours ago
requirements.txt	6 hours ago
utils.py	an hour ago
Vietoris-Rips barcod...	an hour ago

```
idx=500
axs[2].scatter(planarShapes[0,:,idx],planarShapes[1,:,idx])
```

[4]: <matplotlib.collections.PathCollection at 0x7fe6fb830ac8>



[5]:
```
idx = 0
data = planarShapes[:,:,idx].T
print(data.shape)
```

```
(100, 2)
```

Running persistence can be as simple as the following two lines:

[7]:
```
diagrams = ripser(data)['dgms']
plot_diagrams(diagrams, show=True)
```

Simple | 0 | 2 | Python 3 | Idle | Saving completed | Mode: Command | Ln 1, Col 1 | demo_ripser.ipynb

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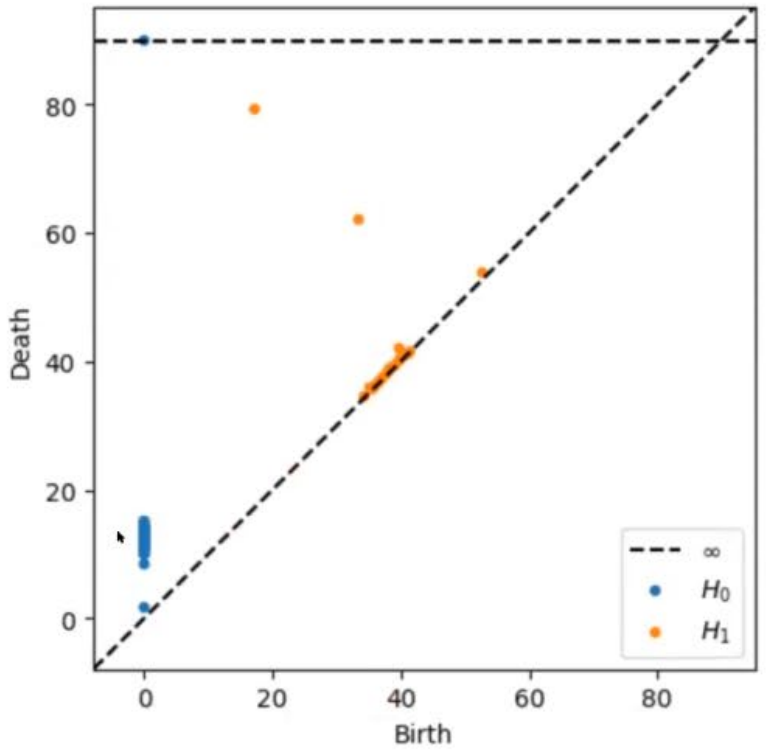

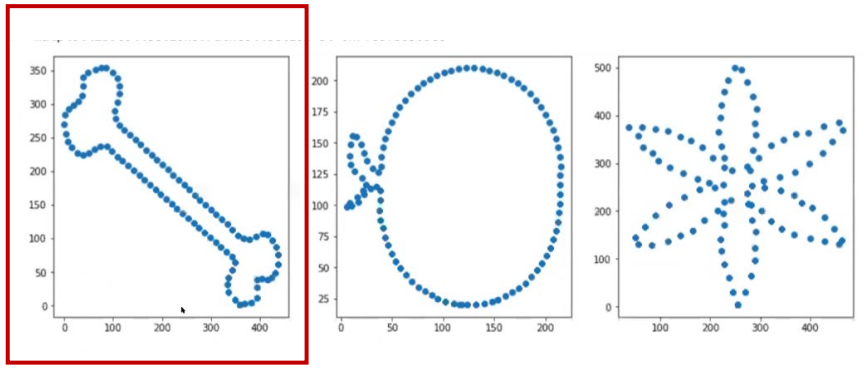

Interpretation: Here we plotted the persistence diagram coming from the `bone` data. There are two persistent 1-cycles, corrresponding to the two epiphysia at either end.

Next let's try the `apple` shape.

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requirements.txt	6 hours ago
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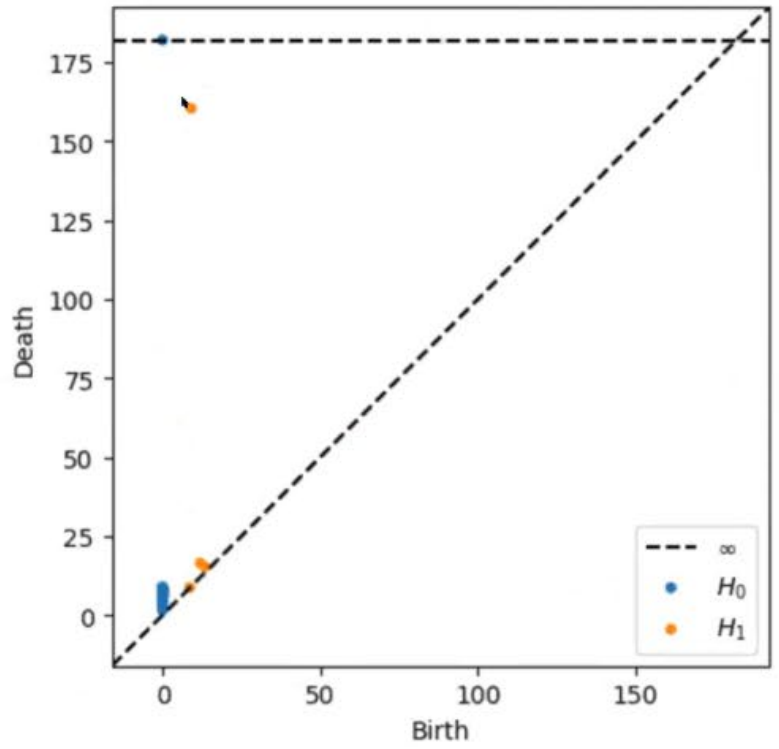
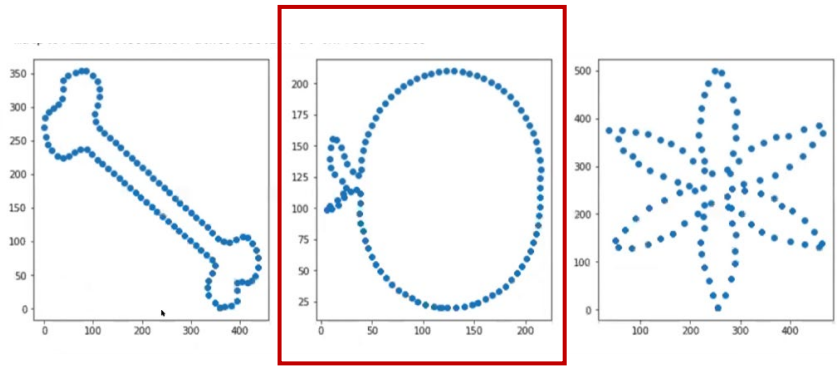
Next let's try the `apple` shape.

[8]:
```
idx = 100
data = planarShapes[:,:,idx].T
diagrams = ripser(data)['dgms']
plot_diagrams(diagrams, show=True)
```





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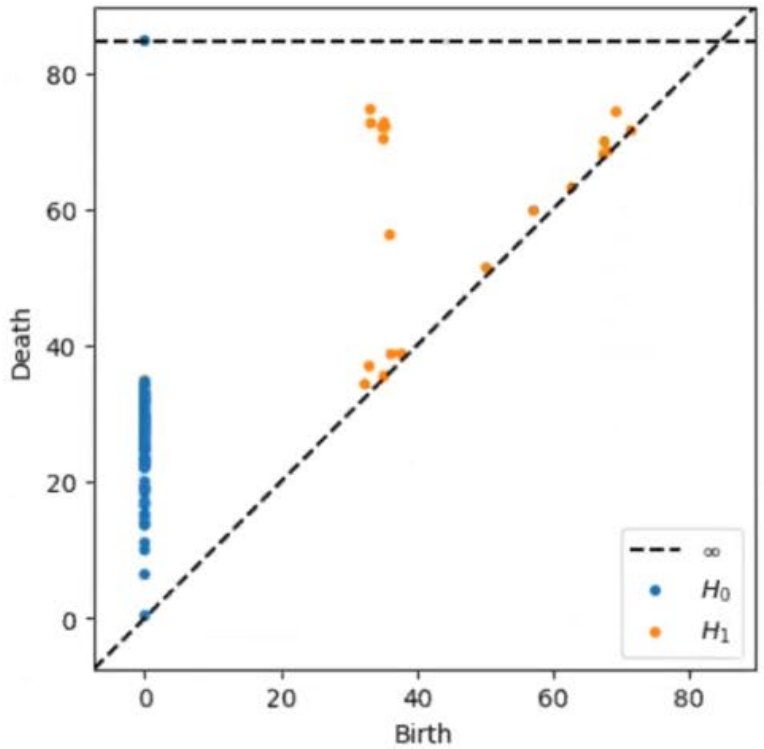
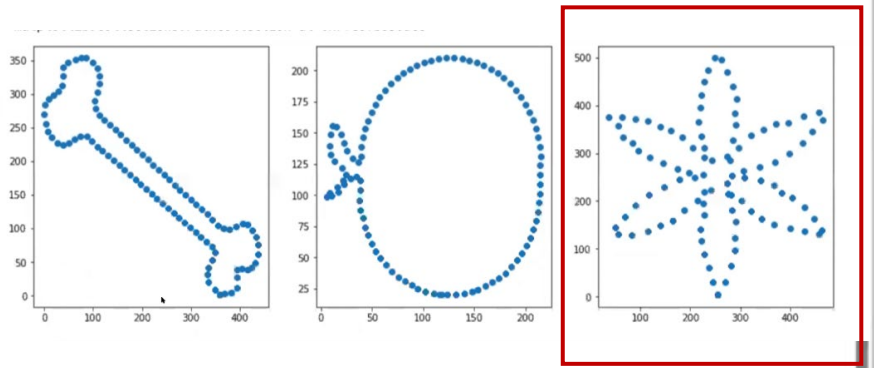
README.md	6 hours ago
requirements.txt	6 hours ago
utils.py	an hour ago
Vietoris-Rips barcod...	an hour ago

Now let's try the `flower` shape.

[9]:
```
idx = 500
data = planarShapes[:,:,idx].T
diagrams = ripser(data)['dgms']
plot_diagrams(diagrams, show=True)
```



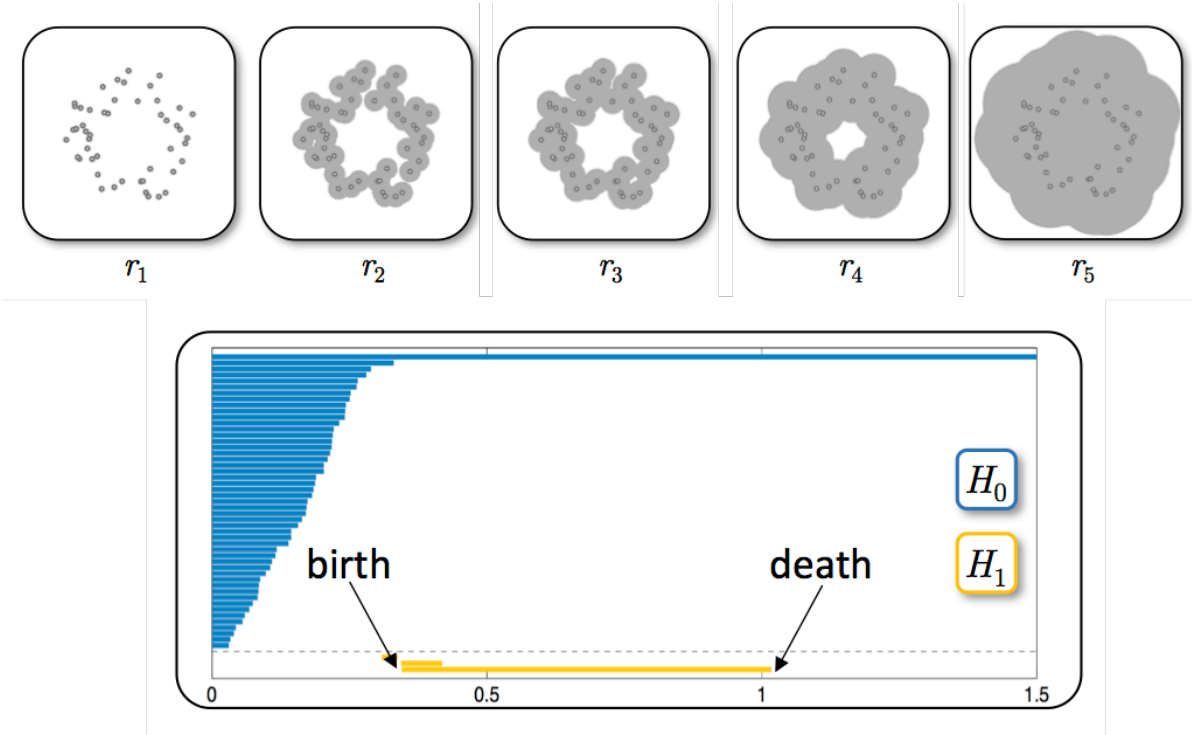


Simple 0 2 Python 3 | Idle Saving completed Mode: Command Ln 1, Col 1 demo_ripser.ipynb

Sublevel Set Persistence

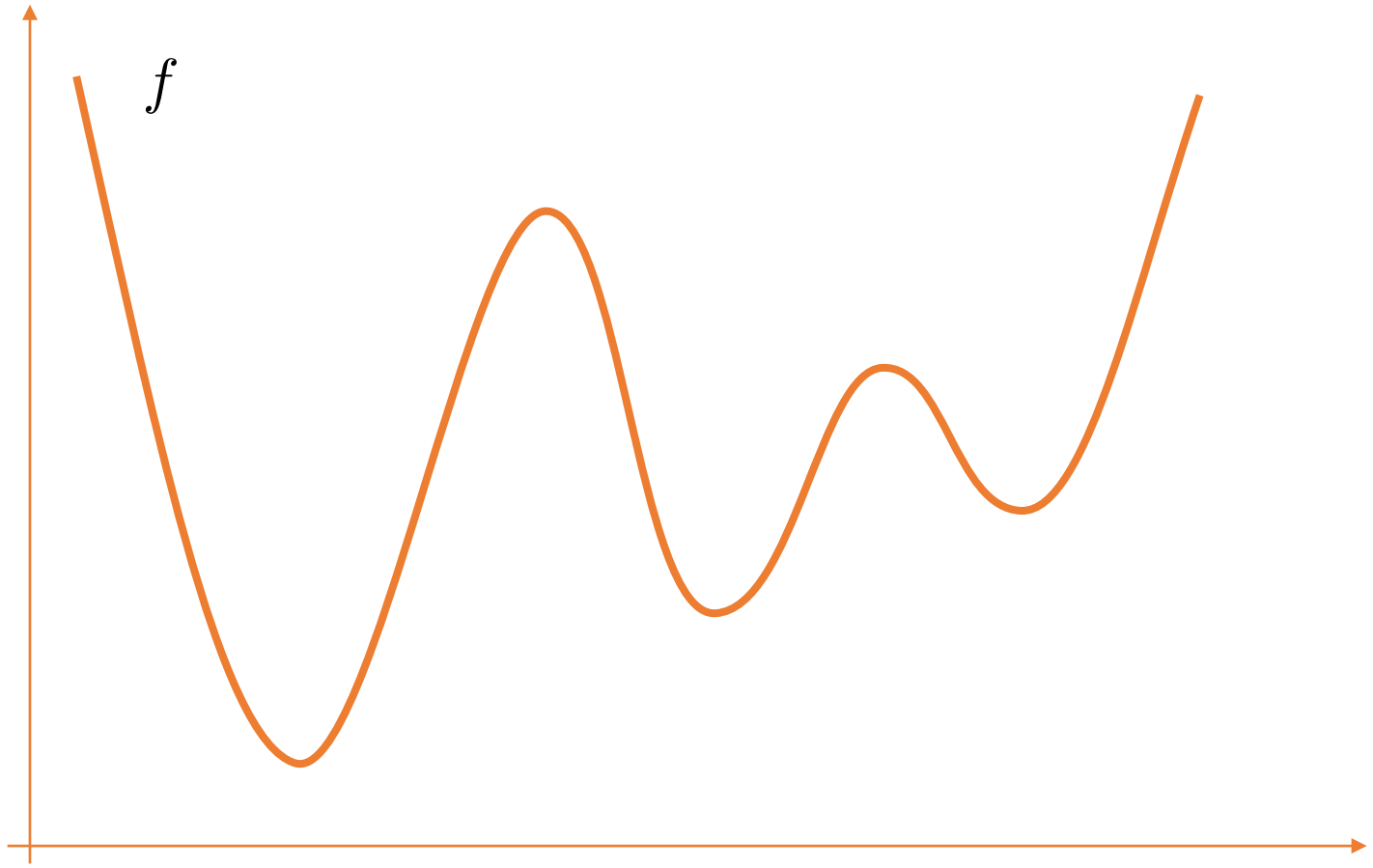
Sublevel Set Persistence

- For general point cloud or metric data, we build filtered simplicial complexes using the metric as a filter

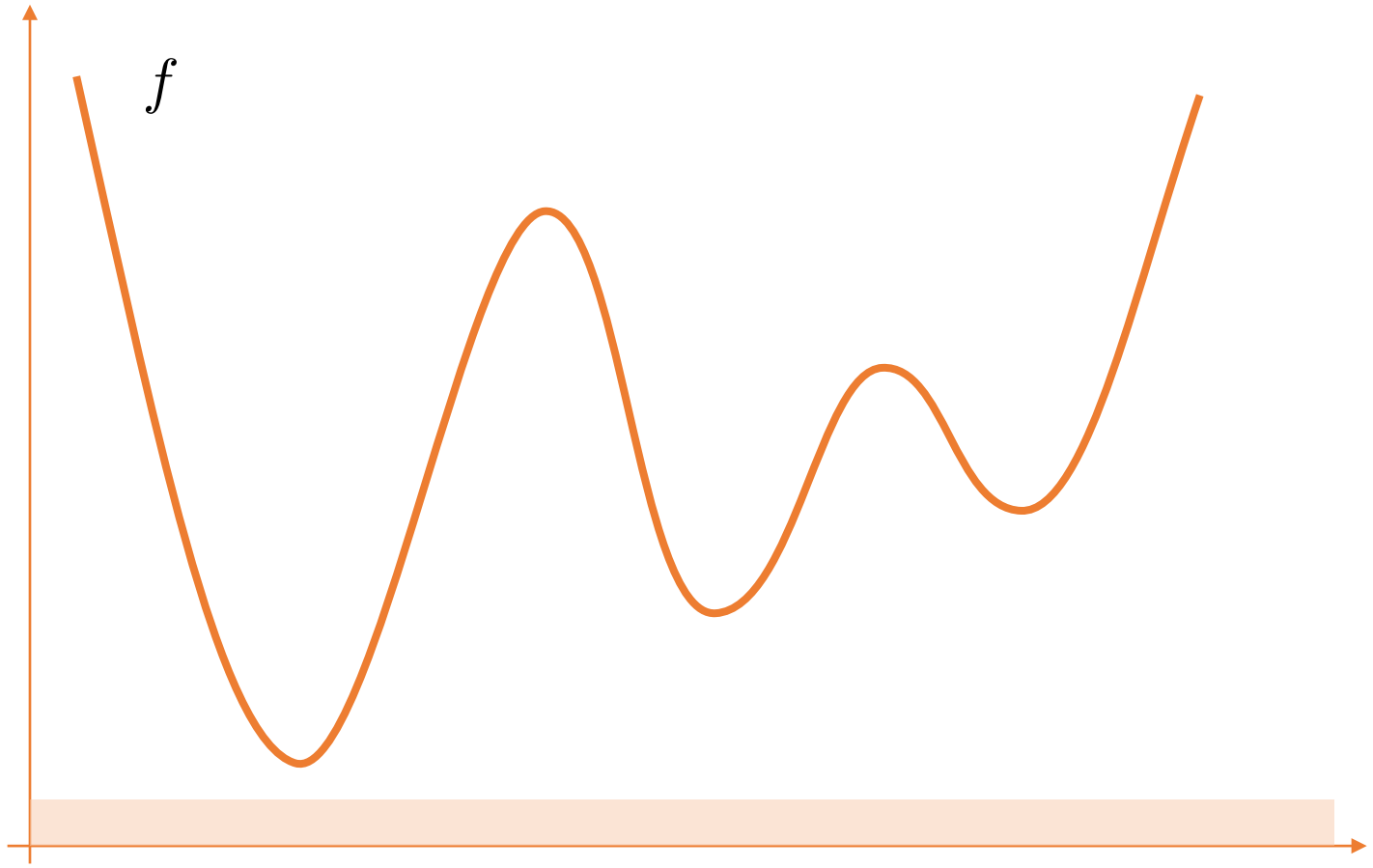


- When given a function $f: \mathcal{M} \to \mathbb{R}$ where $\mathcal{M}$ is a triangulated space (i.e. a simplicial complex at the outset), we can use f as a filter

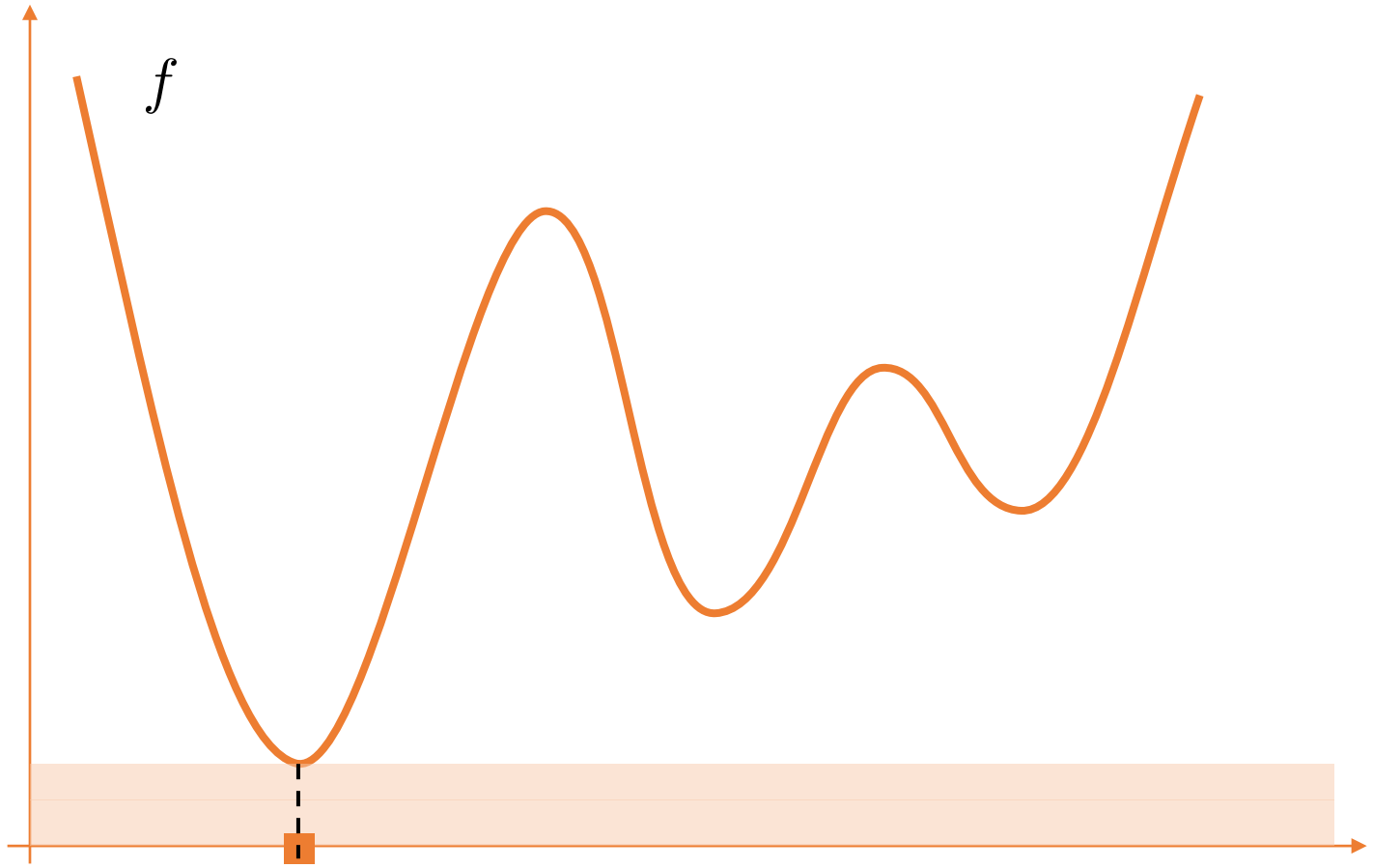
Sublevel Set Persistence



Sublevel Set Persistence



Sublevel Set Persistence



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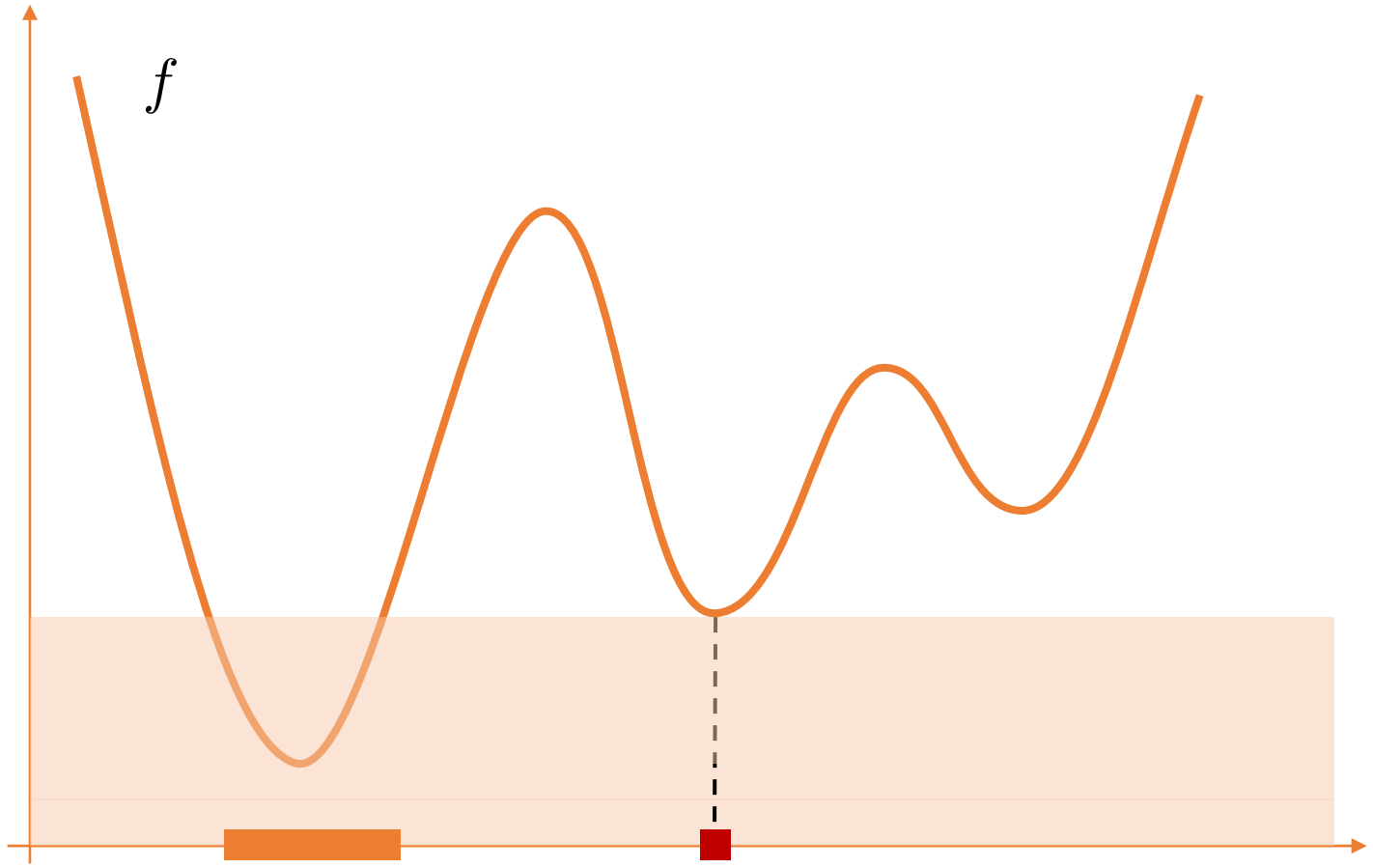

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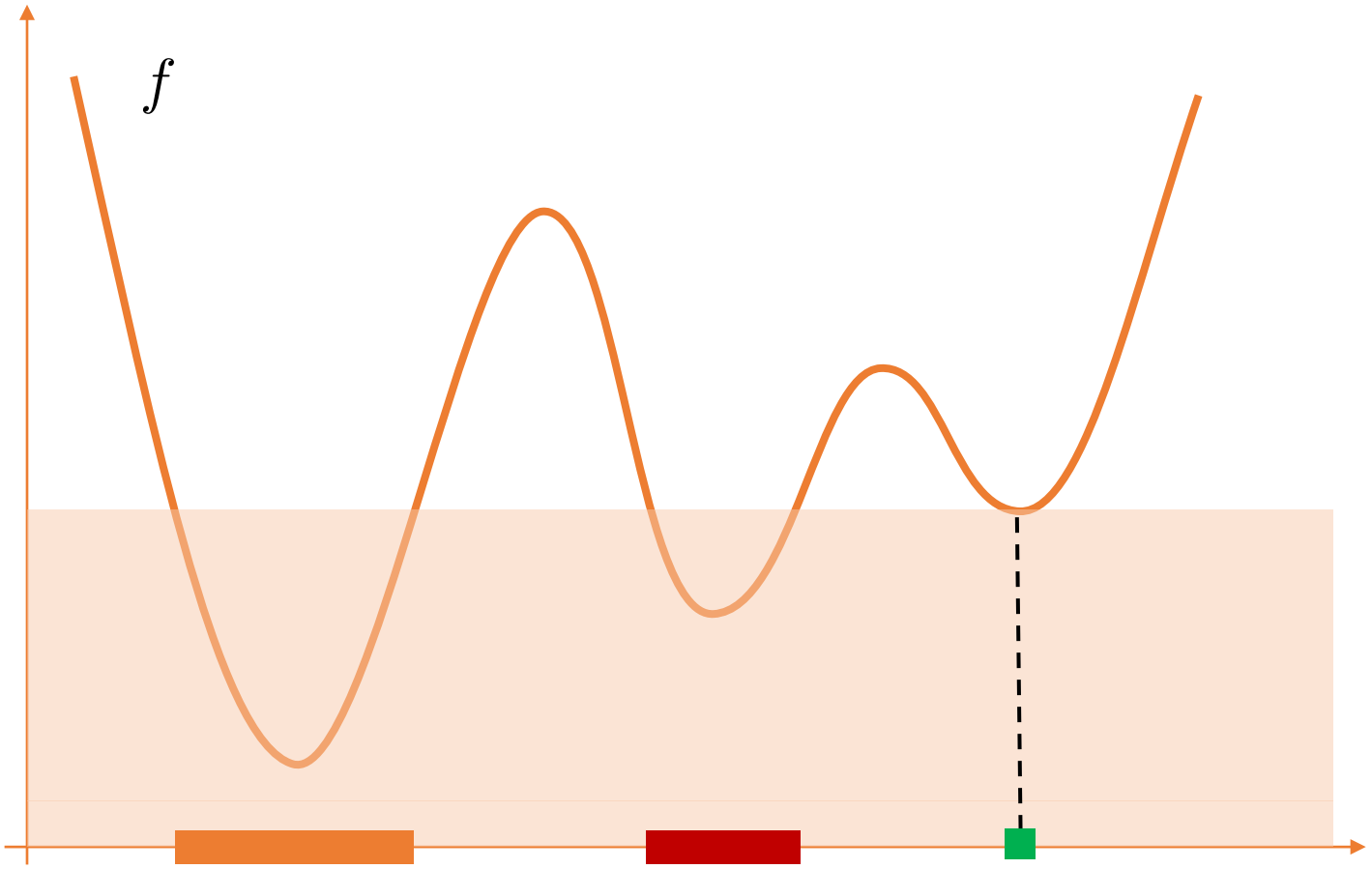

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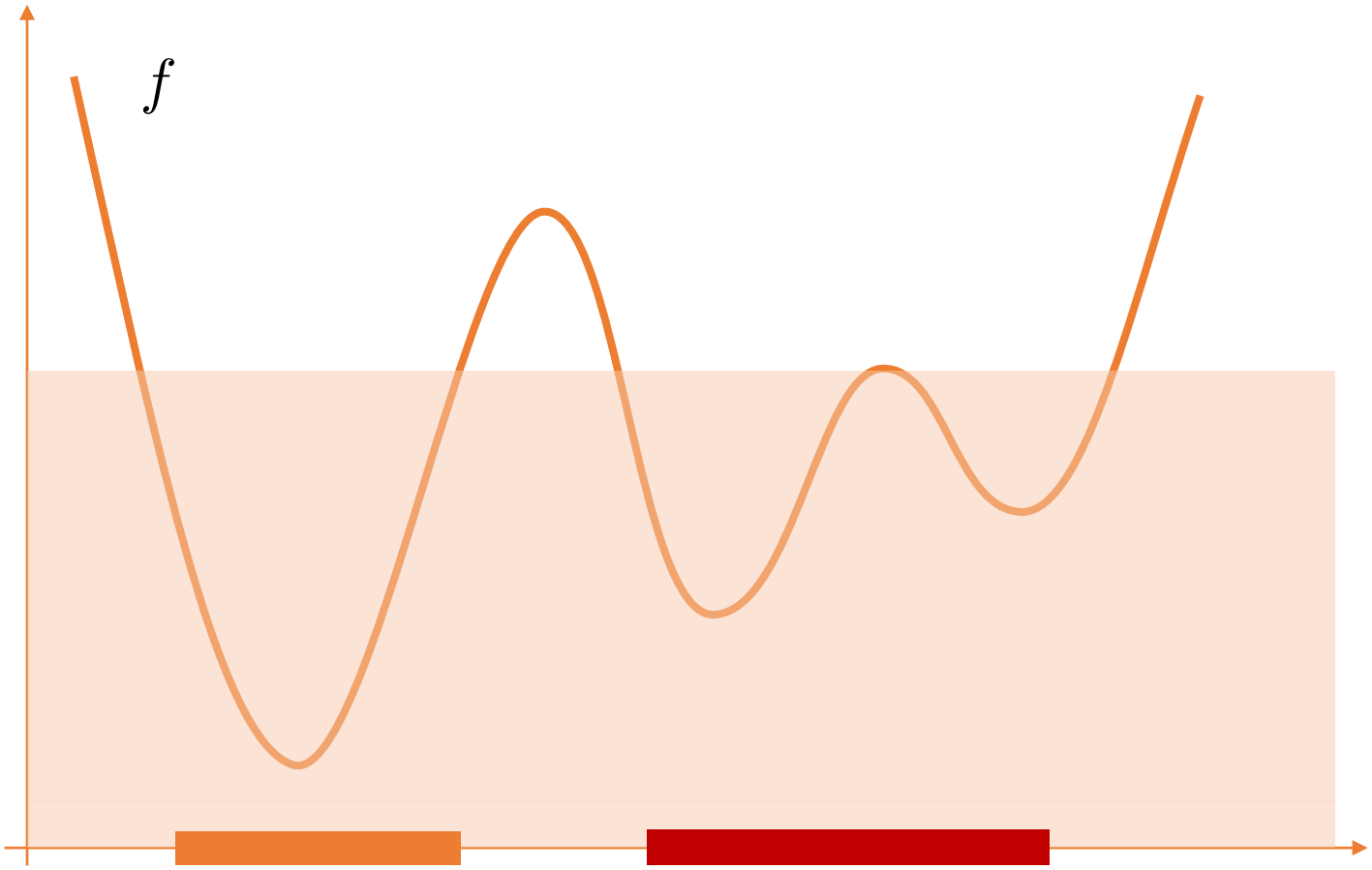
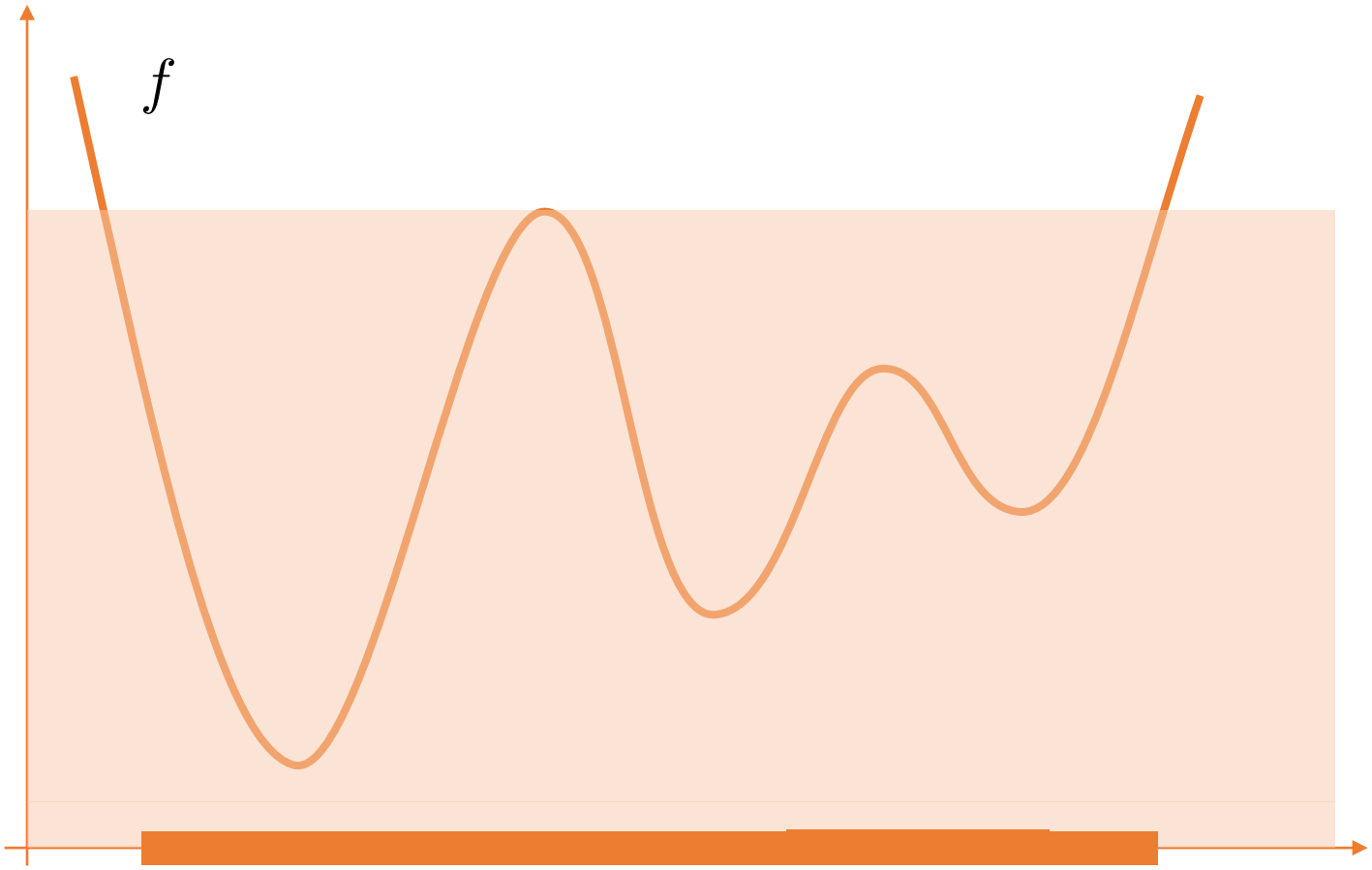


Sublevel Set Persistence



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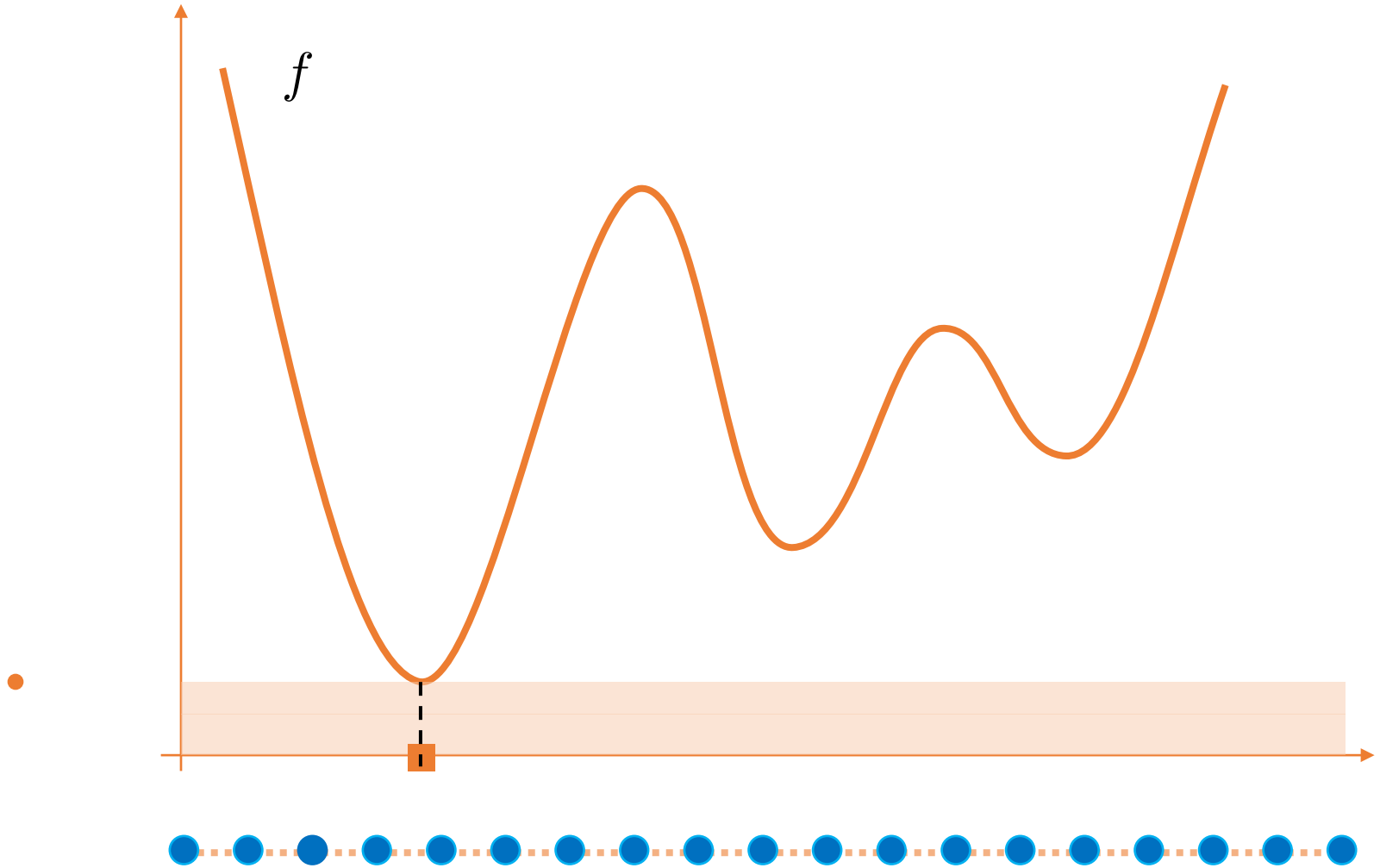

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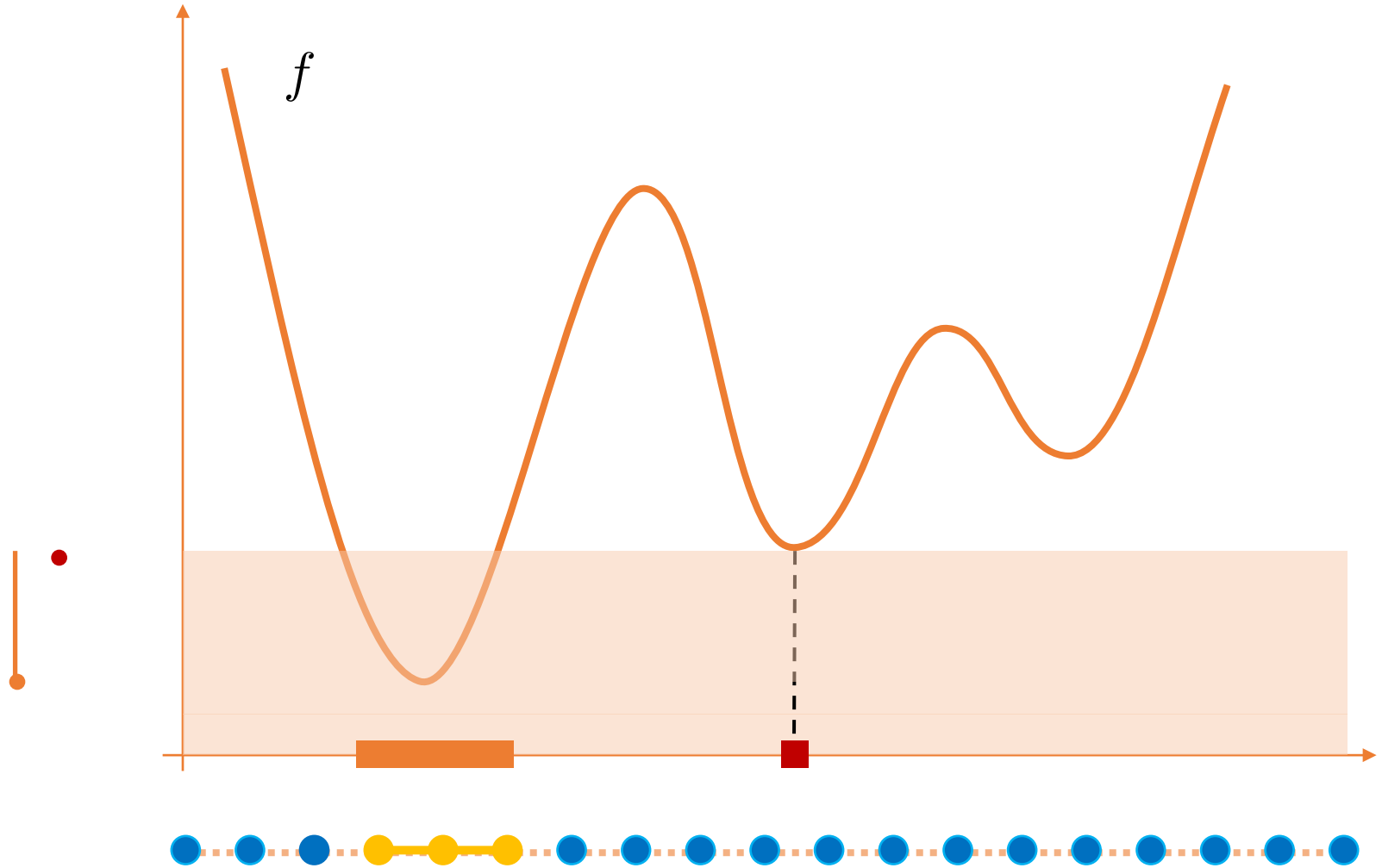

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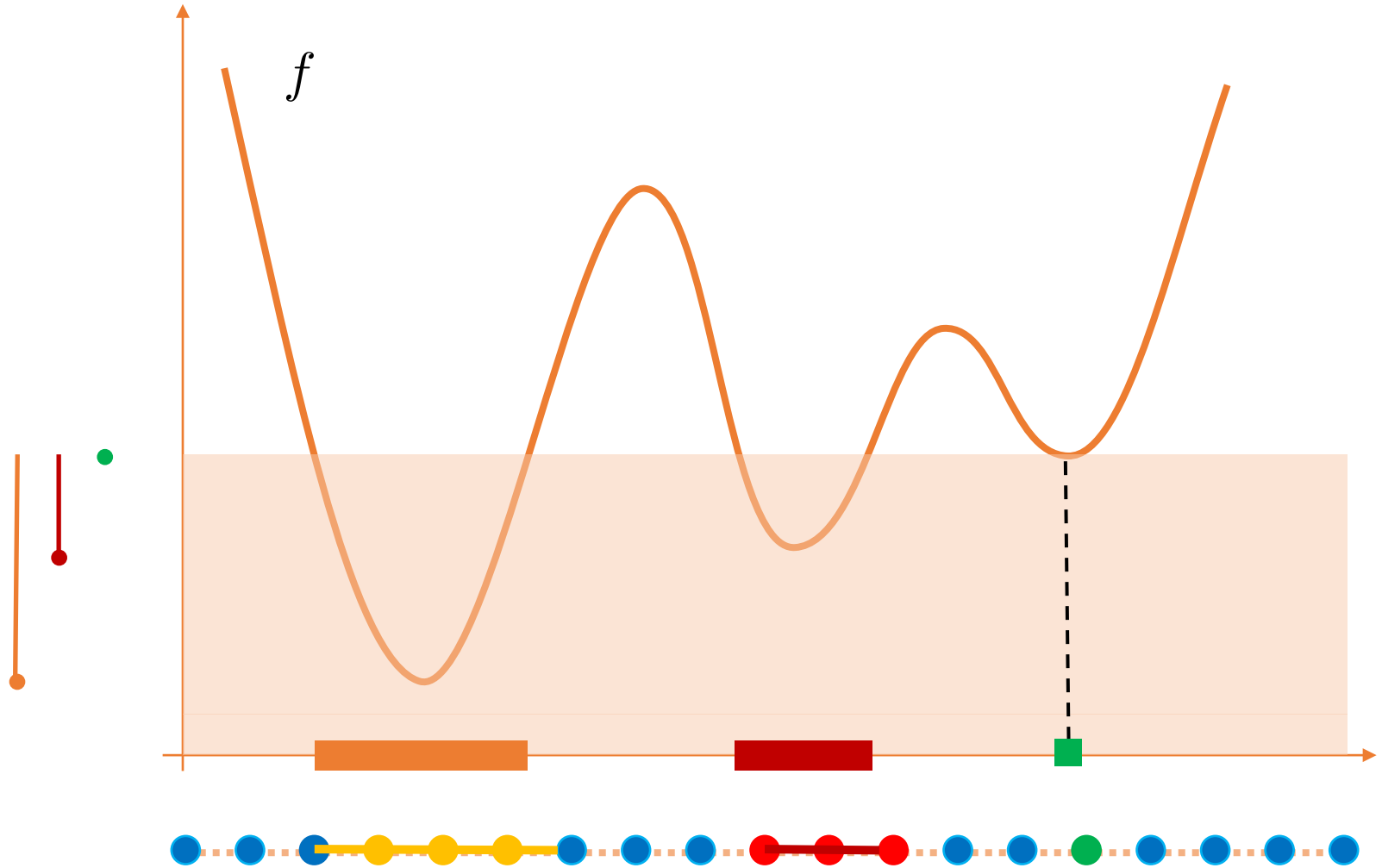

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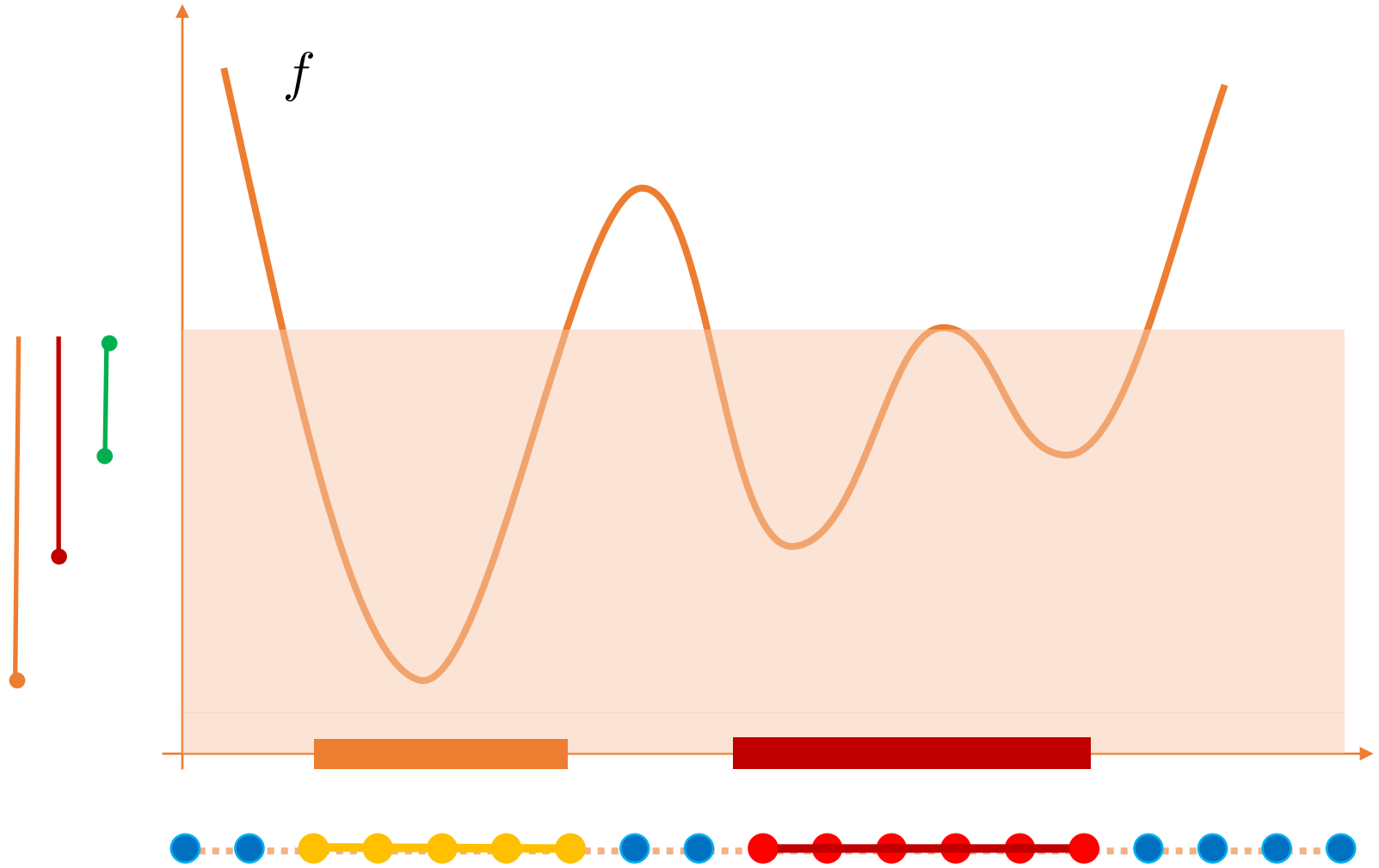

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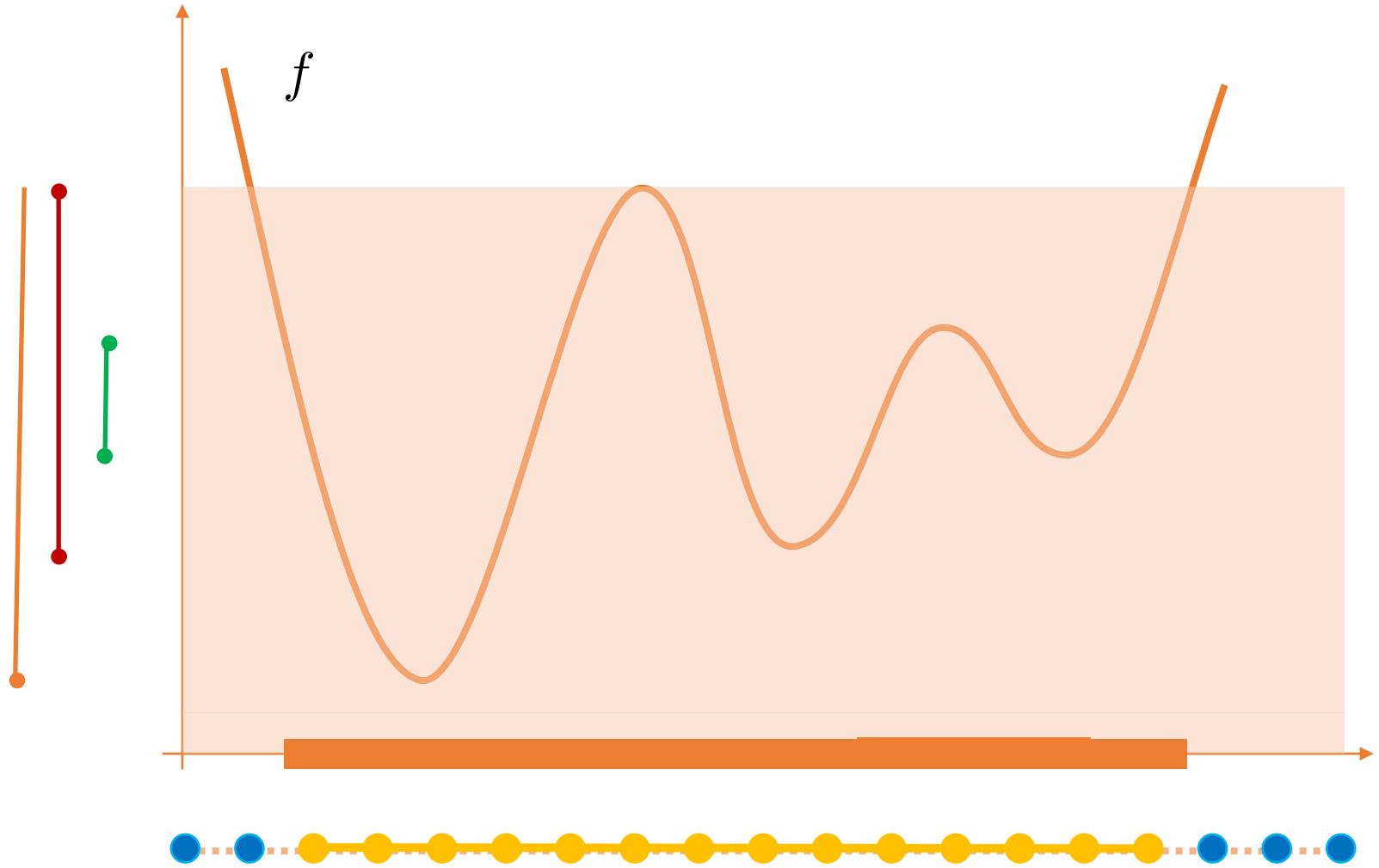

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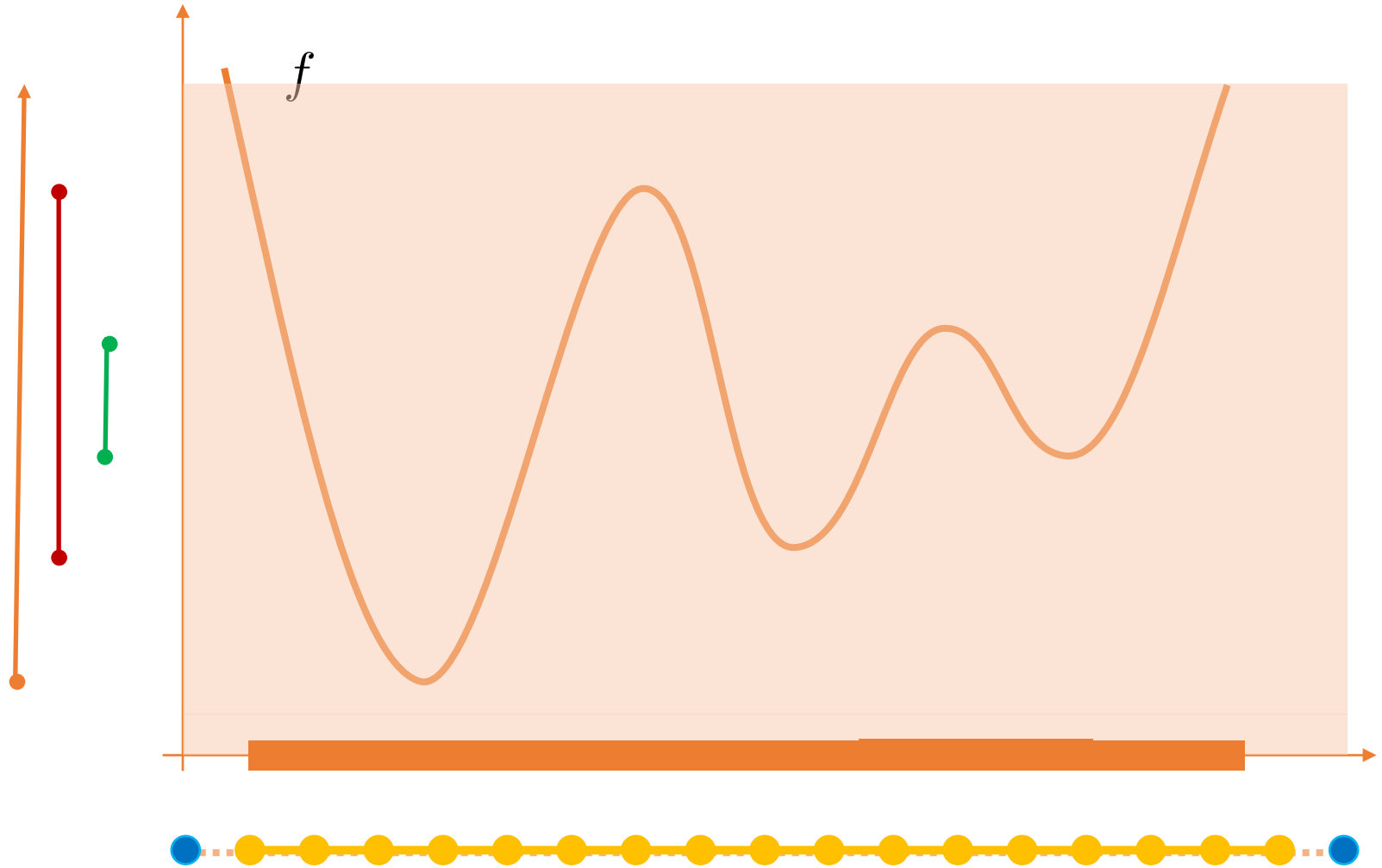
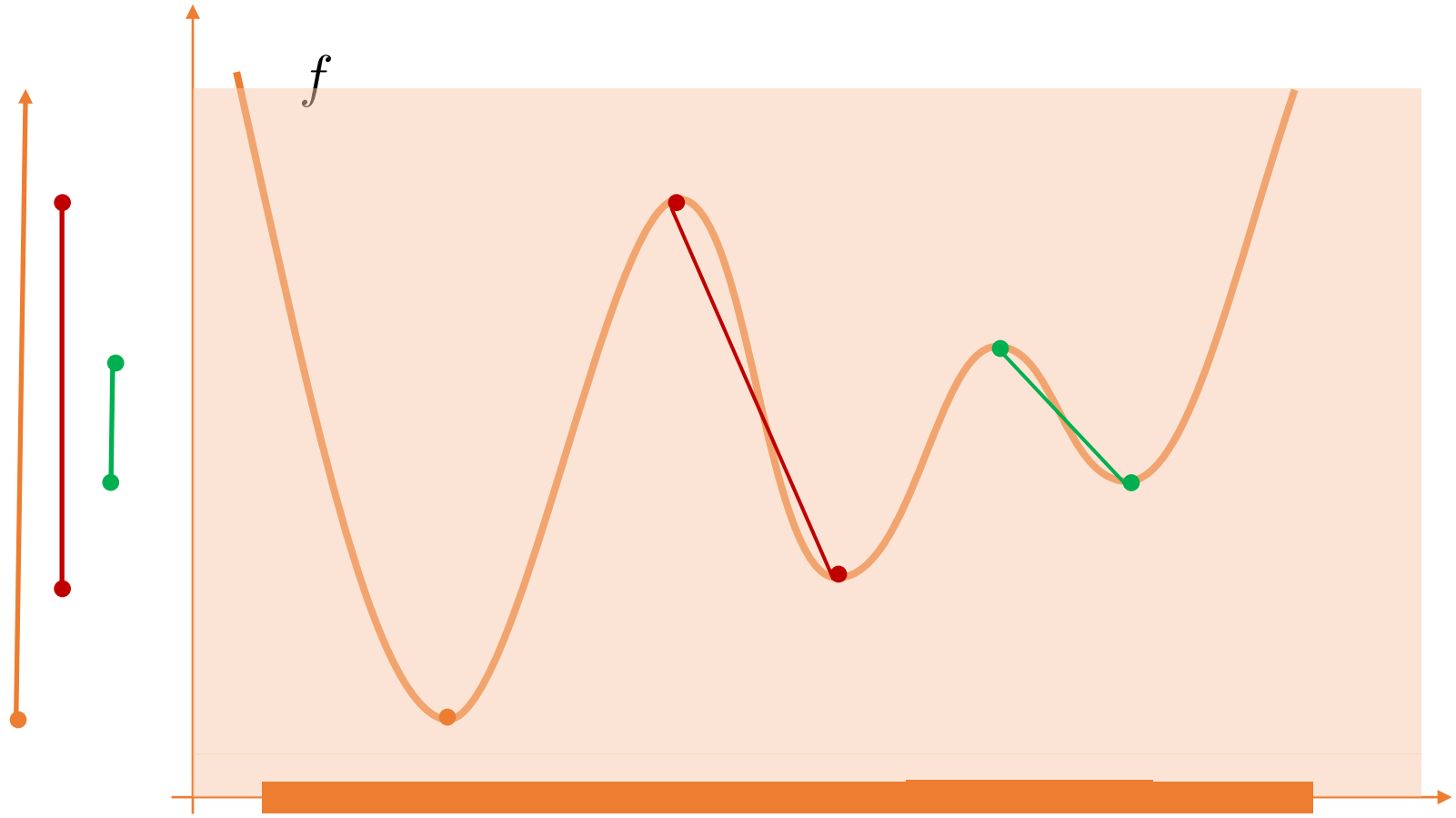


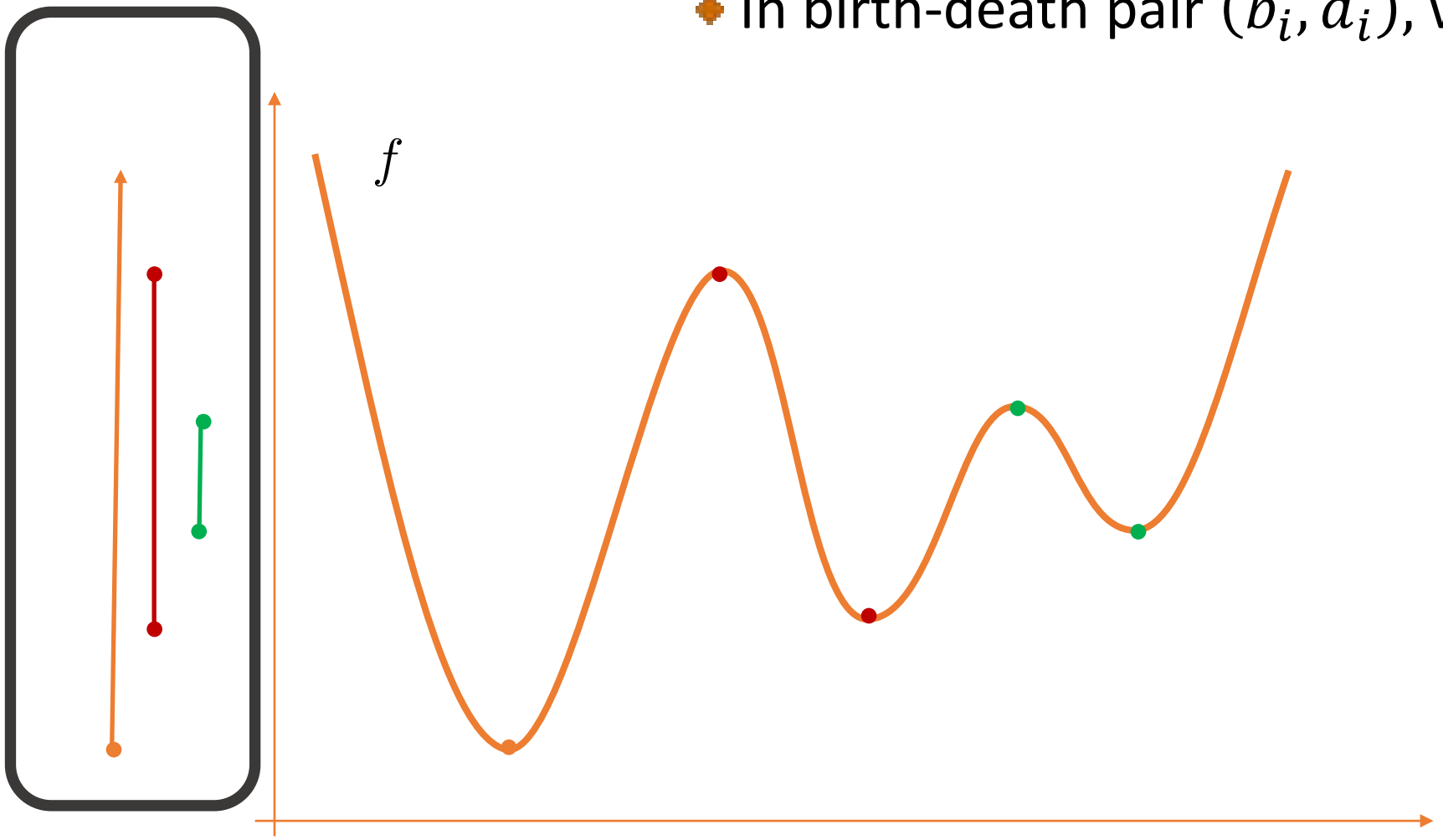
Elder Rule



Persistence Barcodes and Diagrams Stability

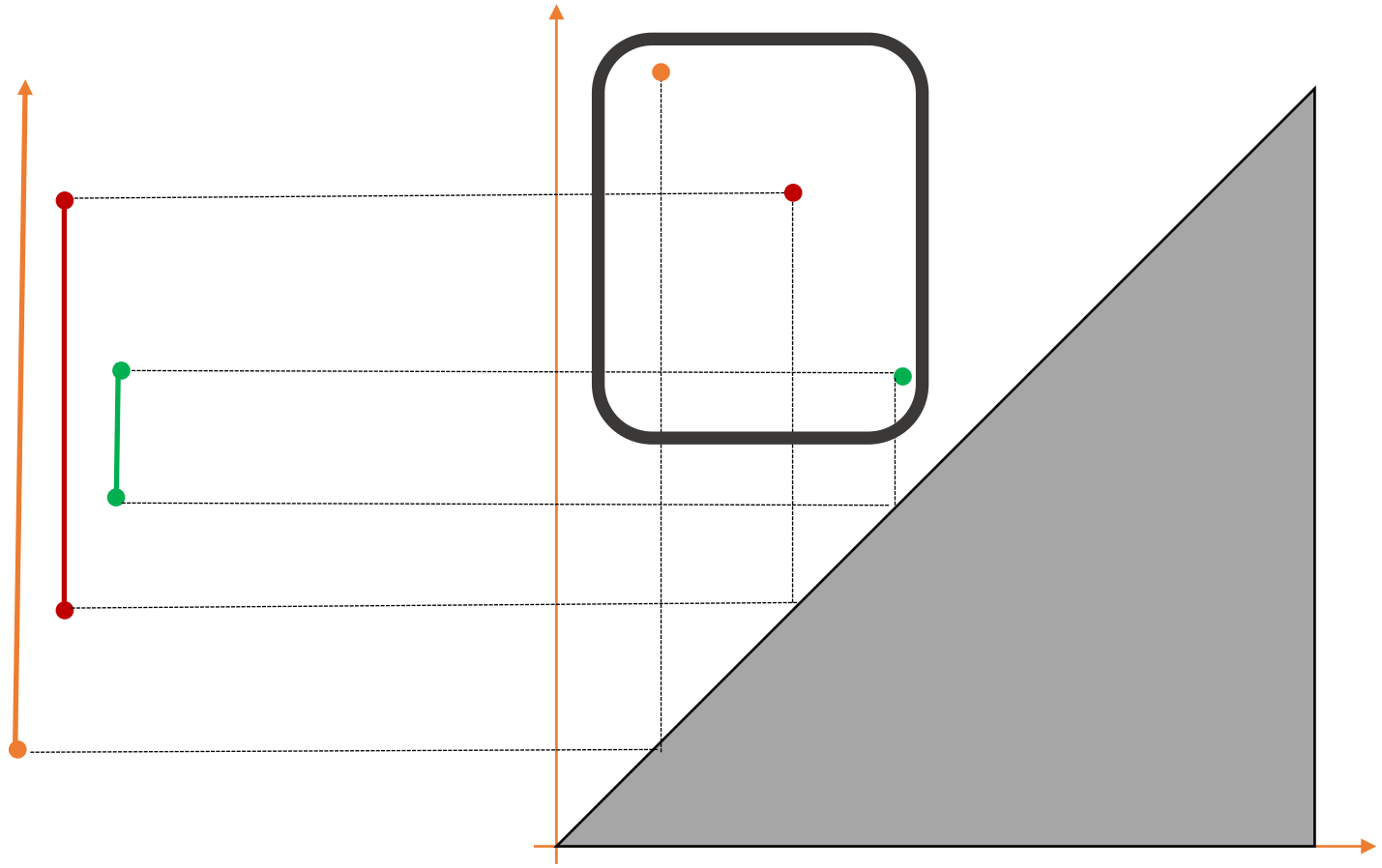
Persistence Pairing Yields a Barcode

- In birth-death pair (b_i, d_i), we have $d_i \geq b_i$



Equivalently, a Diagram

- Pairs (b_i, d_i) are represented as points on upper-half plane
- Often (but not always), short bars correspond to "topological noise"



Stability of Persistent Homology

- Persistent homology outputs are robust to small perturbations of data

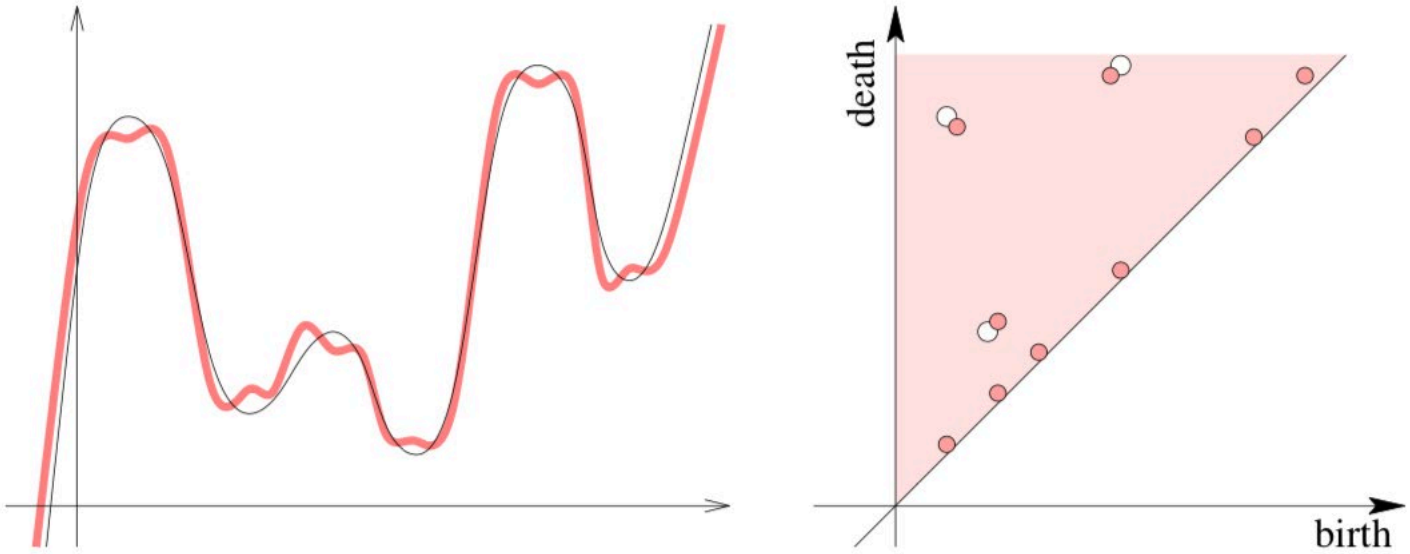
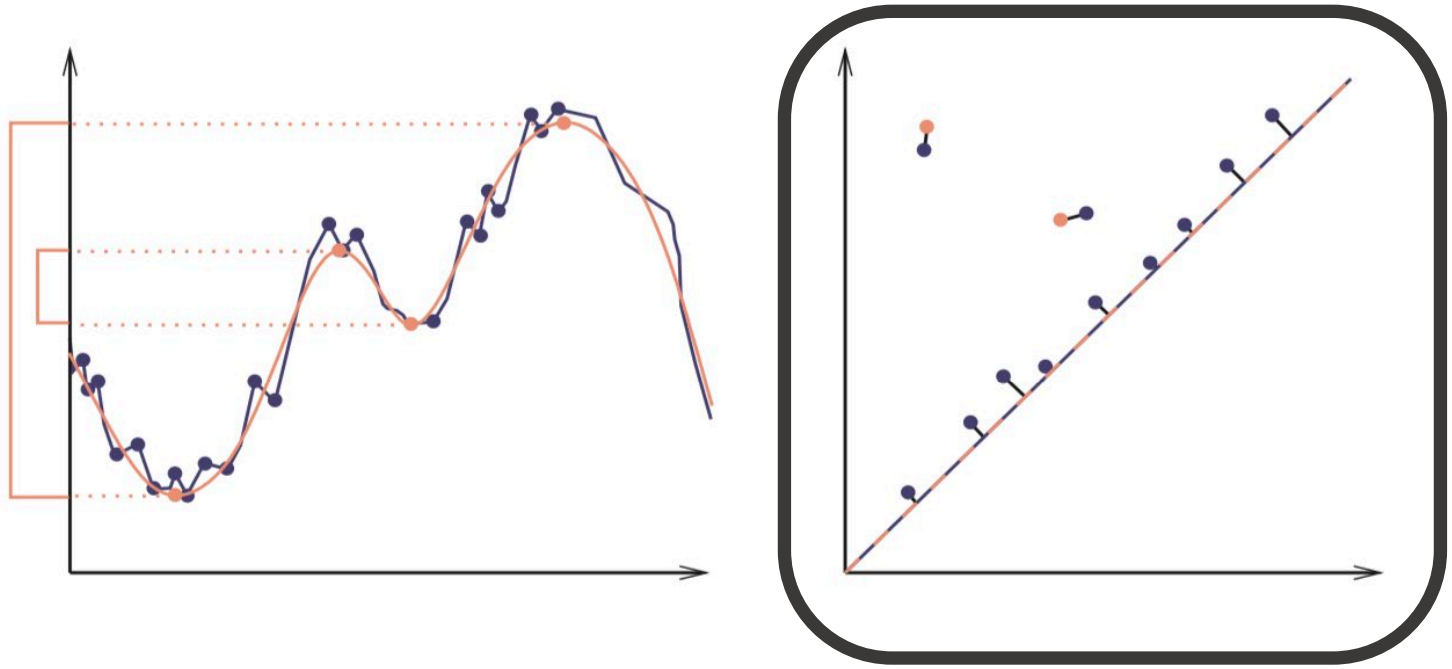


Figure from Edelsbrunner, Harer, *Computational Topology*

- Theorem (Cohen-Steiner, Edelsbrunner, Harer): $\mathcal{M}$ a triangulable space, $f, g: \mathcal{M} \to \mathbb{R}$ "nice". Then,
$$d_B\big(D_k(f), D_k(g)\big) \leq \|f - g\|_\infty.$$

Here D_k is the persistence diagram in dimension k, $\|\cdot\|_\infty$ is the max-norm, and d_B is the bottleneck distance (TBD)

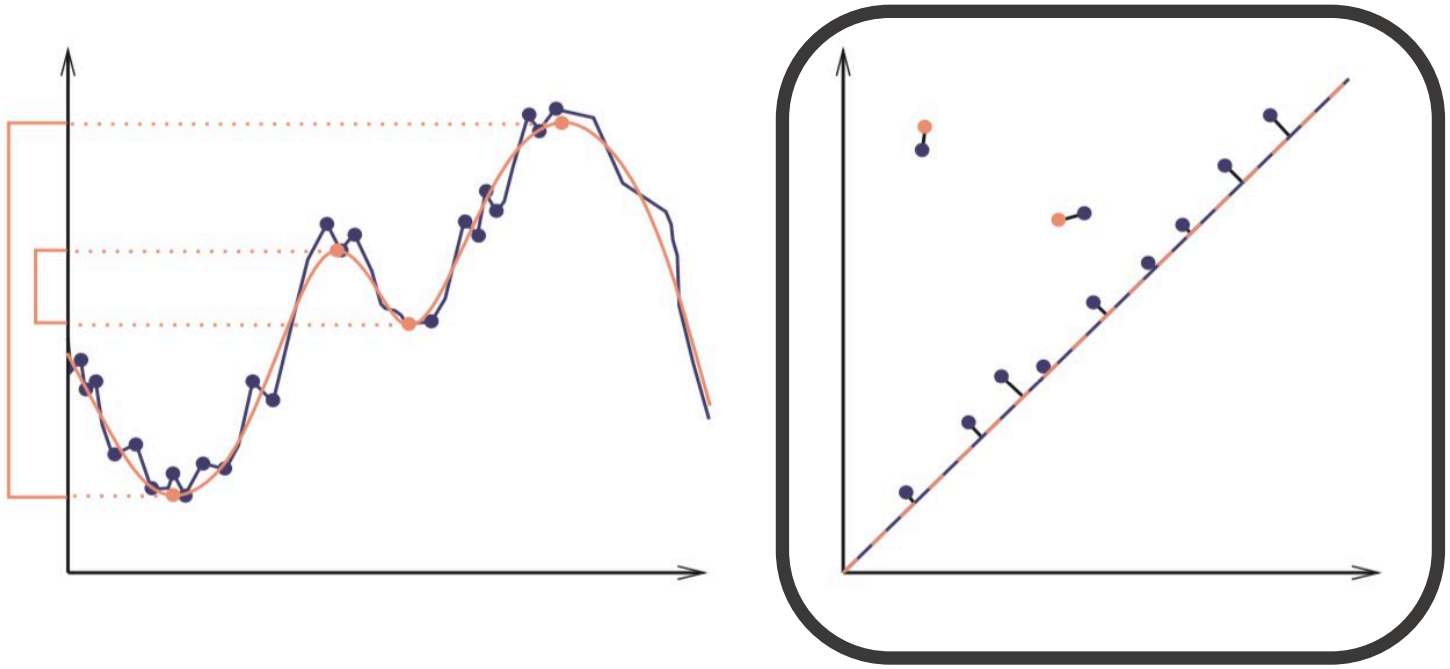
The Bottleneck Distance



Method for comparing persistence diagrams:

- Choose a bijection, matching points to the diagonal if needed
- Compute the l^{∞} distance between each pair of matched points (max-norm)
- Take worst case matching cost
- Optimize over all possible bijections

The Bottleneck Distance

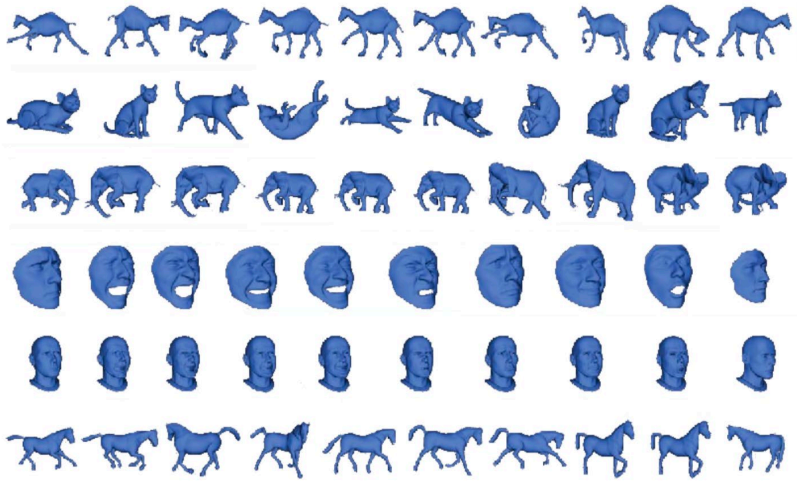


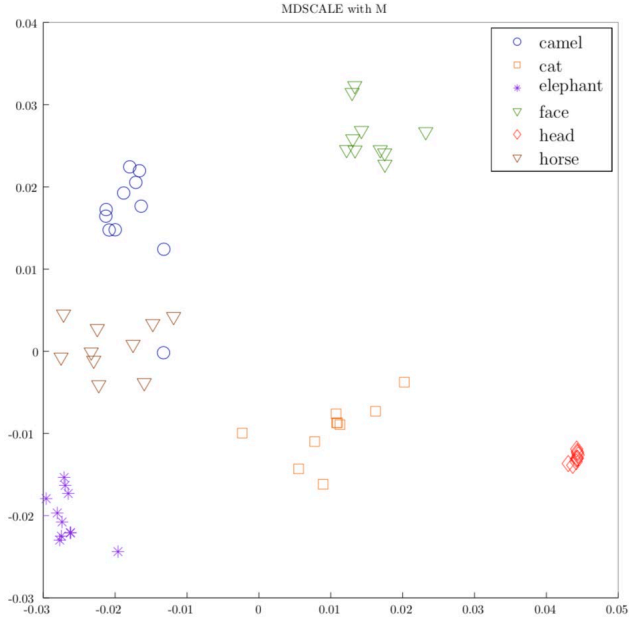
A, B two persistence diagrams.

$$d_B(A,B) := \inf\{ \sup_{x \in A \cup \Delta} \|x - \phi(x)\|_\infty : \phi : A \cup \Delta \to B \cup \Delta \text{ a bijection}\}$$

Stability of Persistent Homology

- We also have stability when building filtered complexes from metric data





- Theorem (Chazal, Cohen-Steiner, Guibas, Mémoli, Oudot): $(X, d_X), (Y, d_Y)$ finite metric spaces. Then,
$$d_B\big(D_k(VR(X)), D_k(VR(Y))\big) \leq 2d_{GH}(X, Y).$$

Here d_{GH} is the Gromov-Hausdorff distance between metric spaces (TBD)

Gromov-Hausdorff Stability

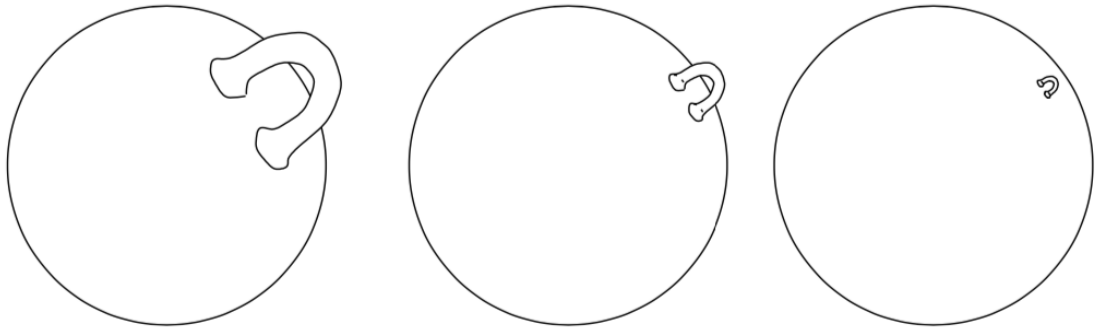


Figure from Burago, Burago, Ivanov, *A course in metric geometry*

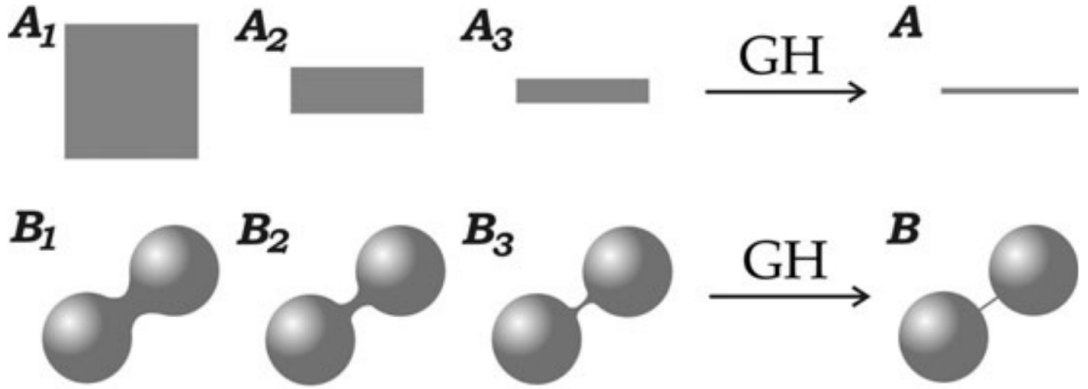


Figure from Sormani, *How Riemannian manifolds converge*

The space of metric spaces is a metric space under the Gromov-Hausdorff distance

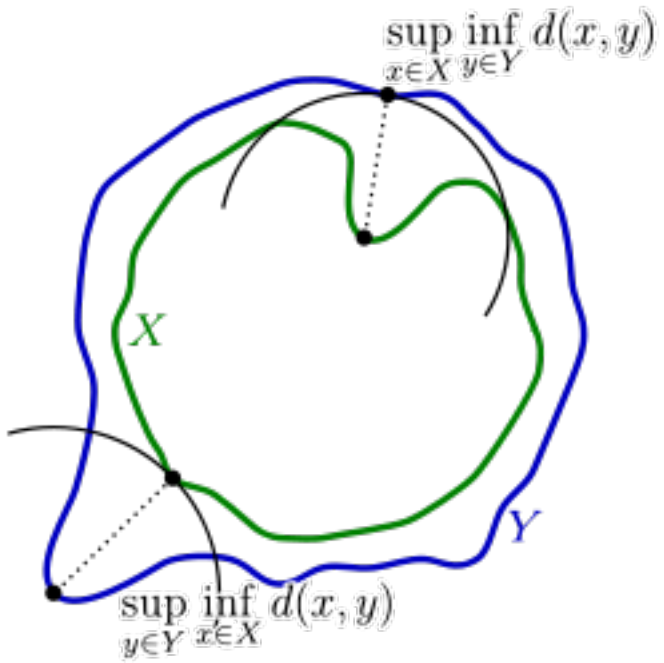
- Used to study convergence of spaces
- Popularized by Gromov in the context of geometric group theory

Gromov-Hausdorff stability

X, Y subsets of a finite metric space (Z, d)

Hausdorff distance:

$$d_H(X,Y) = \max(\max_{x\in X} \min_{y\in Y} d(x,y),\ \max_{y\in Y} \min_{x\in X} d(x,y))$$

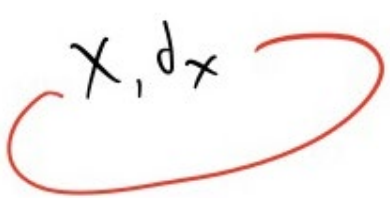


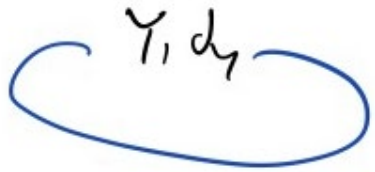
$(X, d_X), (Y, d_Y)$ finite metric spaces

Gromov-Hausdorff distance:

$d_{GH}(X,Y) = \inf_{Z,\phi_X,\phi_Y} d_H^Z(\phi_X(X), \phi_Y(Y))$, where

ϕ_X, ϕ_Y are isometric embeddings



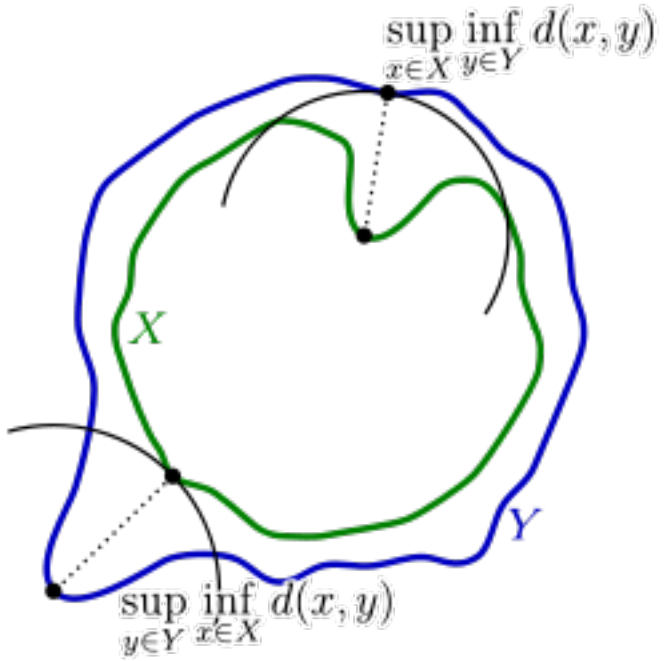


Gromov-Hausdorff Stability

X, Y subsets of a finite metric space (Z, d)

Hausdorff distance:

$$d_H(X,Y) = \max(\max_{x\in X} \min_{y\in Y} d(x,y),\ \max_{y\in Y} \min_{x\in X} d(x,y))$$



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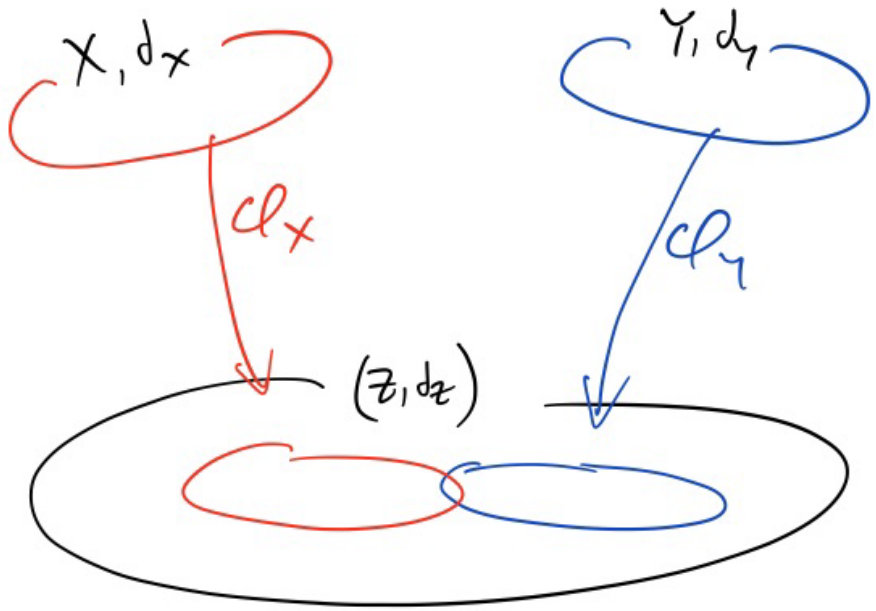
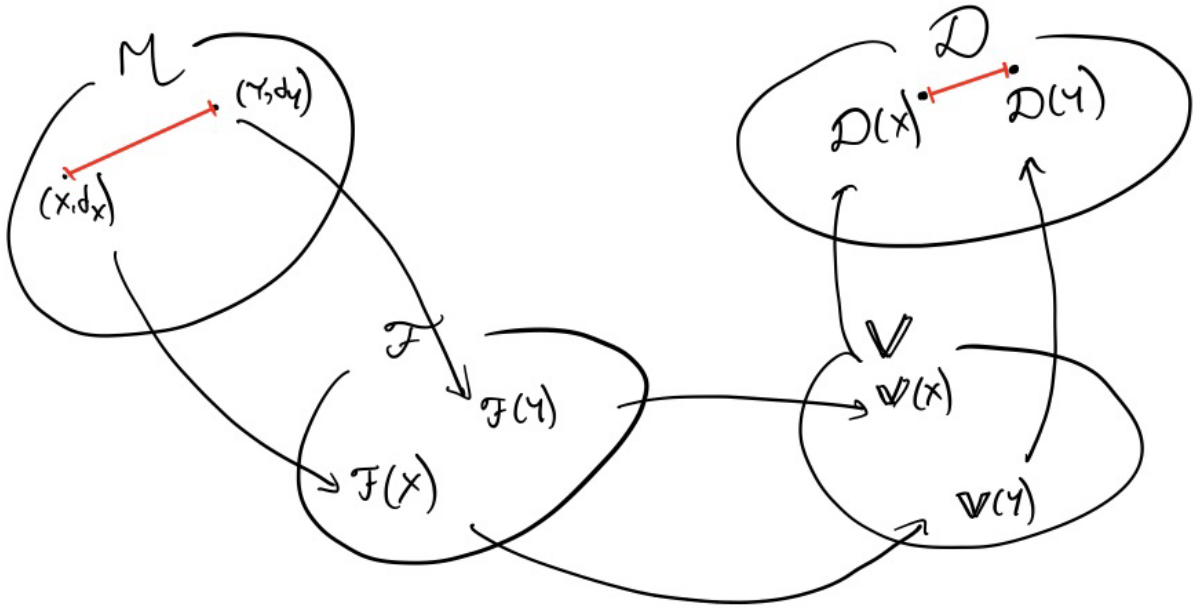


Gromov-Hausdorff Stability



$\mathcal{M}$ = finite metric spaces
$\mathcal{F}$ = filtered simplicial complexes
$\mathbb{V}$ = persistent vector spaces
$\mathbb{D}$ = persistence diagrams

- Theorem (Chazal, Cohen-Steiner, Guibas, Mémoli, Oudot): $(X, d_X), (Y, d_Y)$ finite metric spaces. Then,

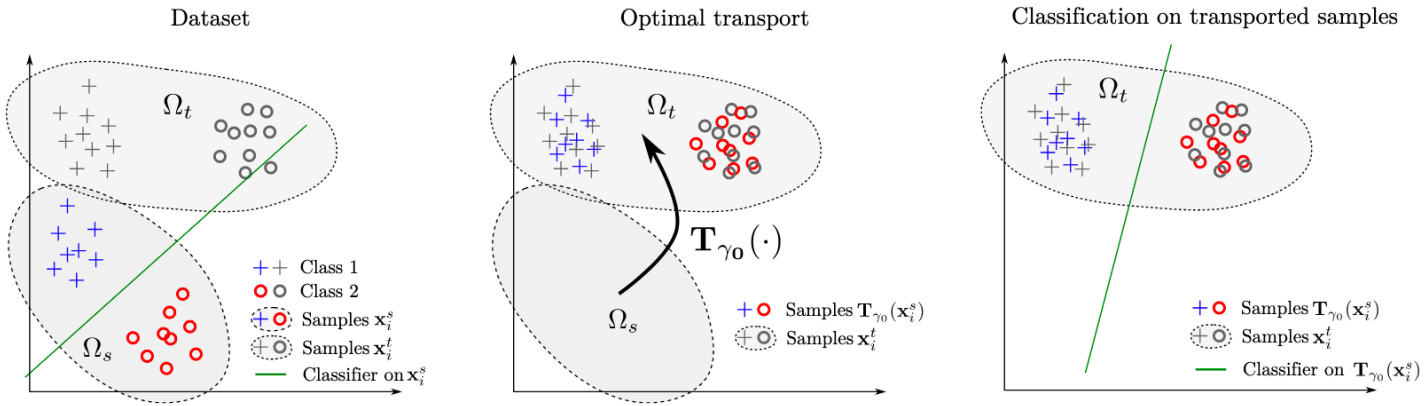
$$d_B\big(D_k(VR(X)), D_k(VR(Y))\big) \leq 2d_{GH}(X, Y).$$

$O(n^3)$ with Hungarian algorithm, $O\left(n^{3/2}\right)$ state-of-the-art (Kerber, Morozov, Nigmetov 2017)

NP-hard

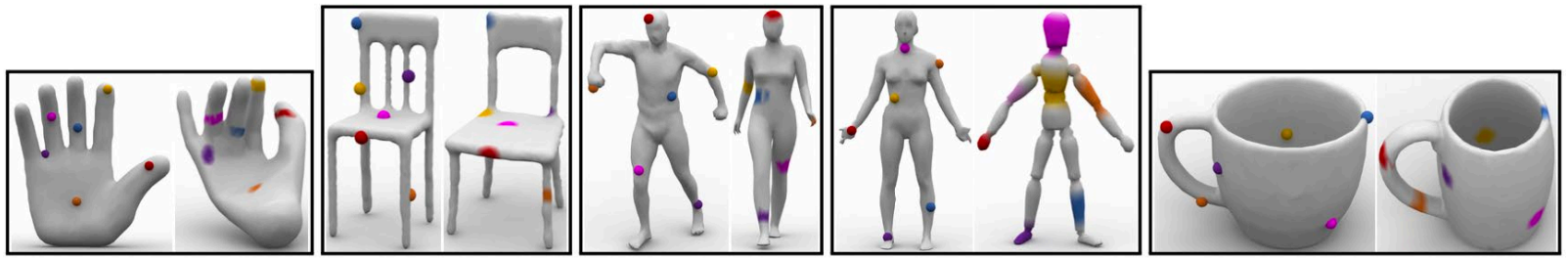
Connections

- Wasserstein distance: a probabilistic analog of Hausdorff distance
  - Popularized in the study of *optimal transport*
  - Used in Wasserstein-GANs, domain adaptation, transfer learning



Courty, Flamary, Tuia, Rakotomamonjy, *Optimal transport for domain adaptation*. PAMI'16

- Gromov-Wasserstein distance: probabilistic analog of Gromov-Hausdorff
  - Arises as convex relaxation (loss remains nonconvex, but optimization is over a convex set)
  - Useful for obtaining correspondences across shapes

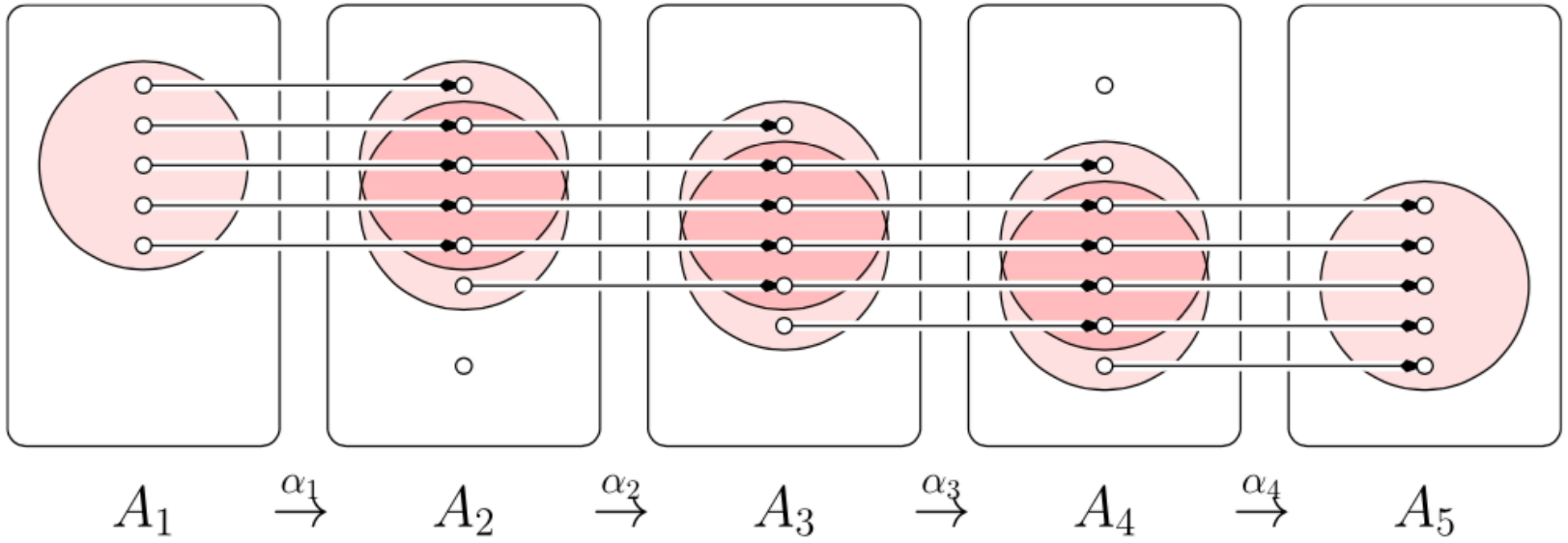


Solomon, Peyré, Kim, Sra, *Entropic metric alignment for correspondence problems. SIGGRAPH'16*

Mathematical Theory

A Deeper Look at the Algorithm

Figure from Edelsbrunner, Jablonski, Mrozek, *The persistent homology of a self-map*



- Left-to-right ordering of chain complex basis vectors + left-to-right column operations gets us to compatible bases for homology
- "Existence and uniqueness" comes from commutative algebra

PH as Applied Representation Theory

Carlsson, de Silva, *Zigzag Persistence*

- $\mathbb{V} := V_1 \xrightarrow{f_1} V_2 \xrightarrow{f_2} \ldots \to V_{n-1} \xrightarrow{f_{n-1}} V_n$ = $\cdot \to \cdot \to$ ... $\to \cdot \to \cdot$ ✚ choice of vector spaces and linear maps

- This is a quiver representation. Given equal-length quiver reps $\mathbb{W}, \mathbb{X}$, say $\mathbb{V} = \mathbb{W} \oplus \mathbb{X}$ if $V_i = W_i \oplus X_i$ and $f_i(W_i) \subseteq W_{i+1}$, $f_i(X_i) \subseteq X_{i+1}$ for each i

Theorem (Gabriel '72): Any $\mathbb{V}$ as above can be written $\mathbb{V} = \bigoplus_i \mathbb{I}(b_i, d_i)$, where

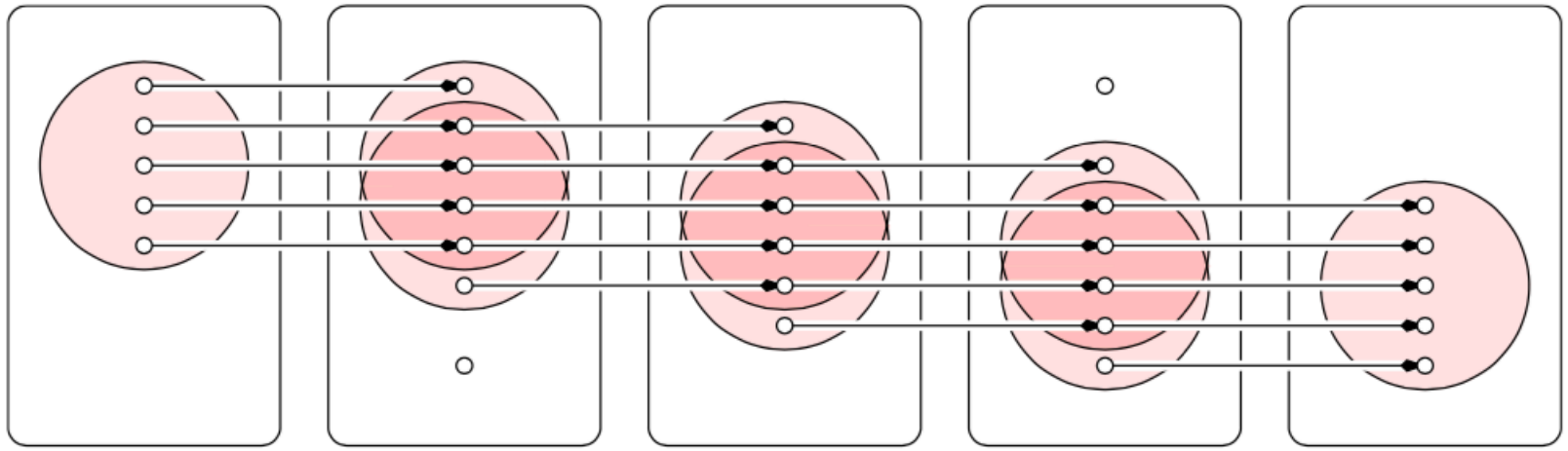
$$\mathbb{I}(b_i, d_i) = 0 \to 0 \to \cdots 0 \to \mathbb{F} \to \mathbb{F} \to \mathbb{F} \to \cdots \to \mathbb{F} \to 0 \to 0 \to 0$$

Index 1 | Index b_i | Index d_i | Index n

Theorem (Krull-Remak-Schmidt): Such a decomposition is unique up to relabeling.

PH as Applied Representation Theory

Carlsson, de Silva, *Zigzag Persistence*



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Index 1 | Index b_i | Index d_i | Index n

Theorem (Krull-Remak-Schmidt): Such a decomposition is unique up to relabeling.

Zigzag Persistence

Carlsson, de Silva, *Zigzag Persistence*

- Gabriel's theorem does not need all the arrows to point in the same direction!
  - Standard persistence:
    $$V_1 \to V_2 \to \cdots \to V_n$$
  - Zigzag persistence:
    $$V_1 \overset{p_1}{\longleftrightarrow} V_2 \overset{p_2}{\longleftrightarrow} \cdots \overset{p_{n-1}}{\longleftrightarrow} V_n.$$
  - Each p_i can be forward or backward

- Application: inclusion not needed, can compare/correlate features across incomparable spaces
  - E.g. Union sequence: $X_1 \to X_1 \cup X_2 \leftarrow X_2 \to \cdots \leftarrow X_n$

Software Packages

- Javaplex - http://appliedtopology.github.io/javaplex/
- Ripser - https://github.com/Ripser/ripser
  - Ripser.py - https://github.com/scikit-tda/ripser.py
  - Ripser live - https://live.ripser.org/
- Ripser++ - https://github.com/simonzhang00/ripser-plusplus
- Dionysus 2 - https://mrzv.org/software/dionysus2/
- Gudhi - https://gudhi.inria.fr/python/latest/
- DIPHA - https://github.com/DIPHA/dipha
- PHAT - https://bitbucket.org/phat-code/phat
- Eirene - https://github.com/Eetion/Eirene.jl
- BATS - https://bnels.github.io/BATS.py/#/

That’s All