CS233, CME251: Geometric and Topological Data Analysis

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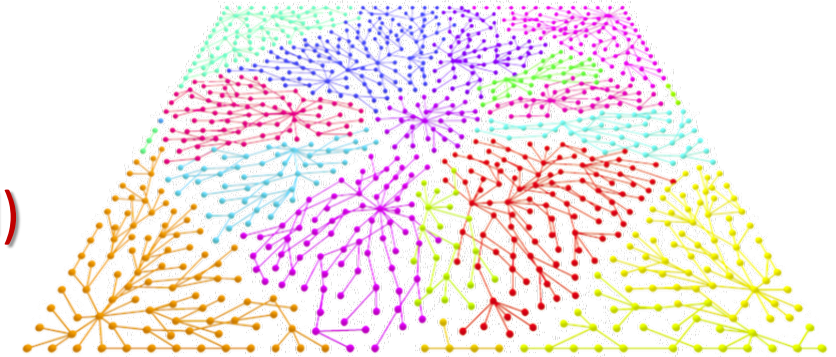
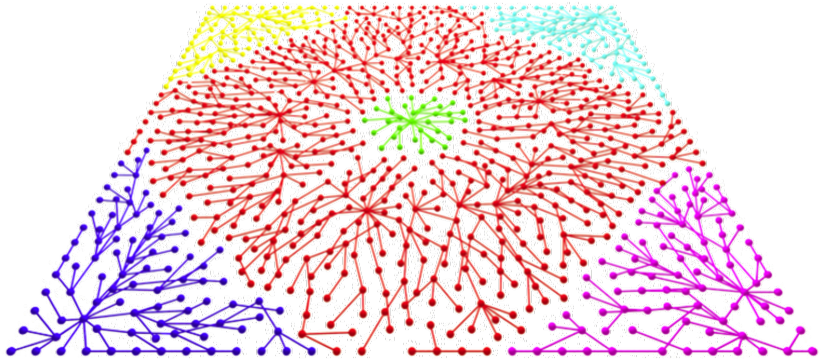
Guest lecture: Samir Chowdhury (Stanford)

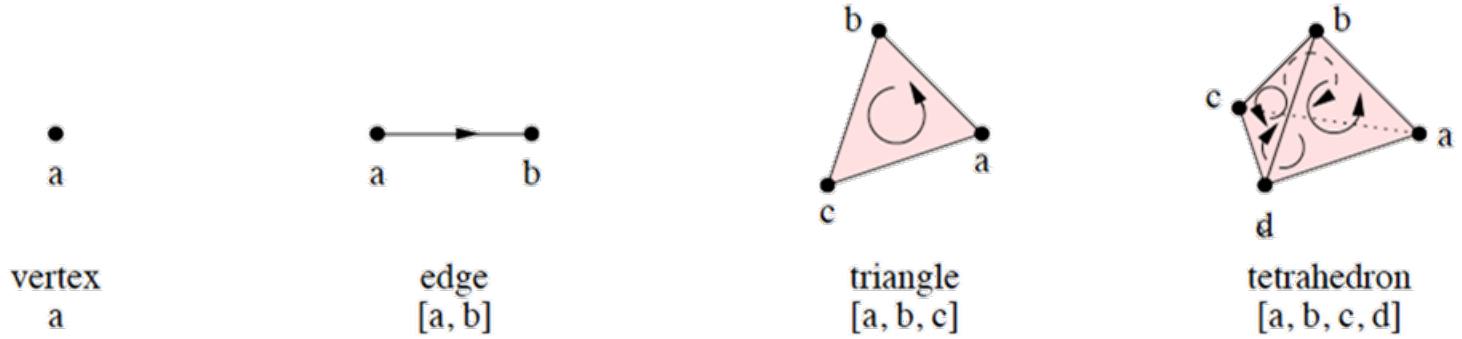




Lecture 8
29 April 2020

Last Time: From topology to (linear) algebra

Recall: simplicial complexes



- An (abstract) simplicial complex Σ on a vertex set K is a collection of nonempty, finite subsets of K (called simplices) that is closed under inclusion. In other words, whenever $\emptyset \neq \tau \subseteq \sigma \in \Sigma$, we also have $\tau \in \Sigma$. In this case, τ is called a face of σ.
- Notation: we'll reduce notation and write simplices as *a*, *ab*, *abc*, and *abcd*.

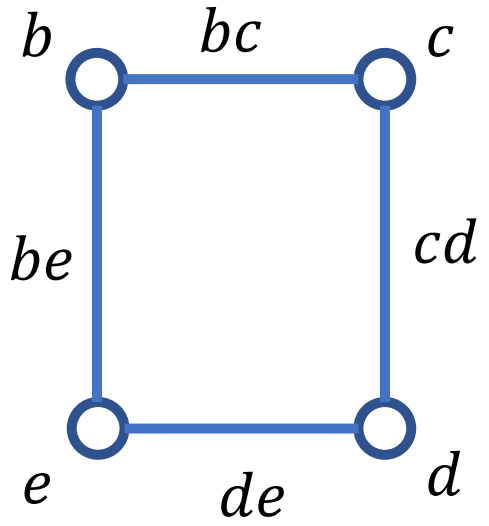
Recall: simplicial complexes → vector spaces

- $\mathbb{F}$ a field, typically $\mathbb{Z}/2\mathbb{Z} = \{0,1\}$
- Σ a simplicial complex, Σ_0 the 0-simplices (vertices), Σ_1 the 1-simplices (edges), Σ_2 the 2-simplices (triangles), …
- Algebraic gadget: the free vector spaces $\mathbb{F}[\Sigma_0], \mathbb{F}[\Sigma_1], \mathbb{F}[\Sigma_2], \ldots$
  - Intuitively, just allow addition and scalar multiplication of simplices!
  - Linear combinations of p-simplices will be called p-chains
- Standard notation: $C_p(\Sigma)$, the vector space of p-chains

Recall: simplicial complexes → vector spaces

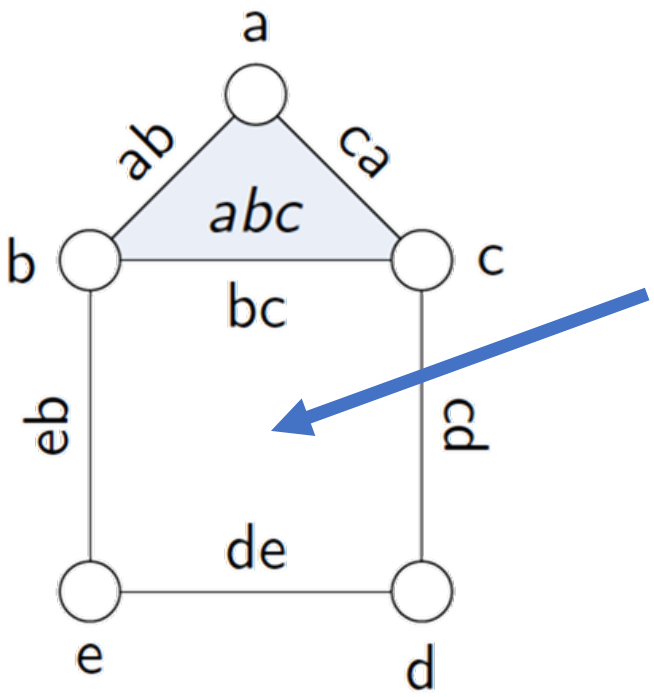
- Σ a simplicial complex, Σ_0 the 0-simplices (vertices), Σ_1 the 1-simplices (edges), Σ_2 the 2-simplices (triangles), …

- $C_p(\Sigma)$, the vector space of p-chains



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

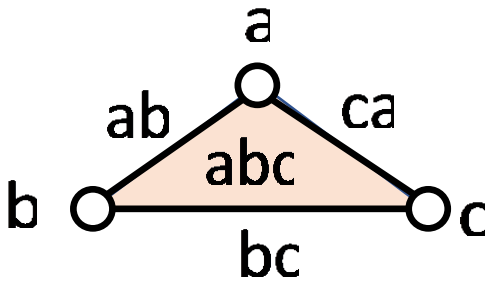
Recall: the boundary map ∂



- Alternating sum (hat denotes omission):

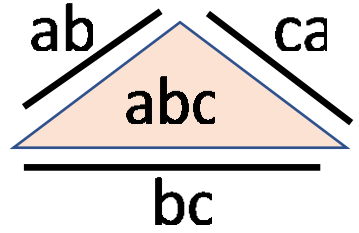
$$\partial[x_0, \dots x_n] = \sum_{i=0}^{n} (-1)^i \, [x_0, \dots, \hat{x}_i, \dots x_n]$$

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



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

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



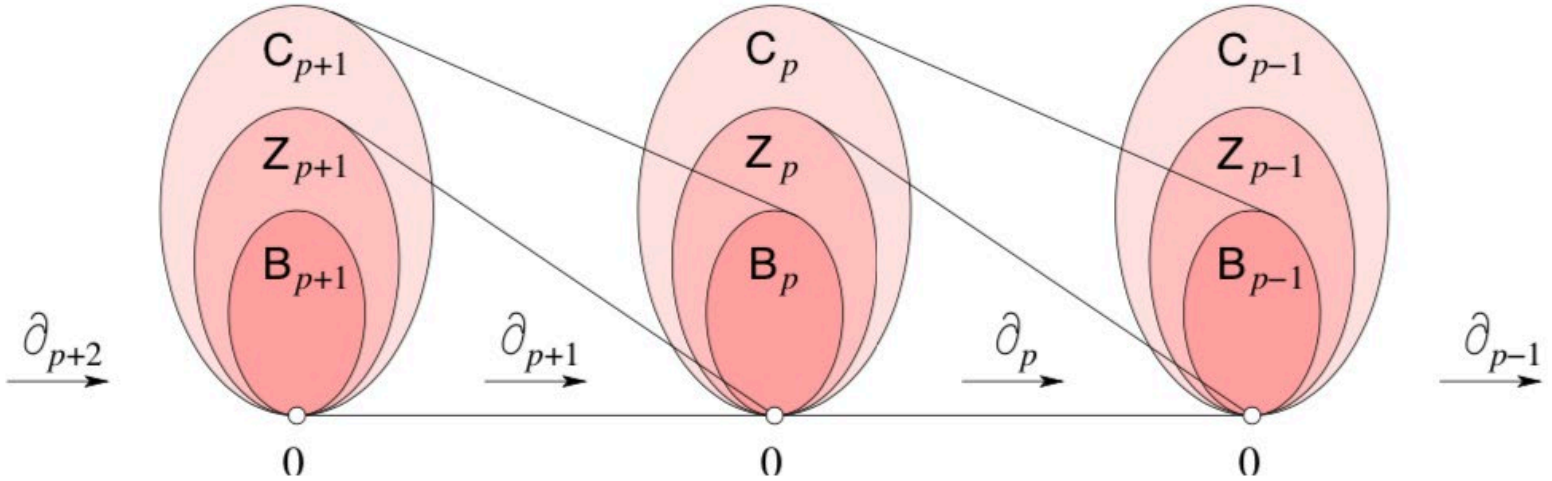
- $\partial = 0$ on linear combinations that are boundaries. Intuitively, $\partial^2 = 0$ says that the boundary of a simplex really is a boundary!

Recall: the chain complex

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



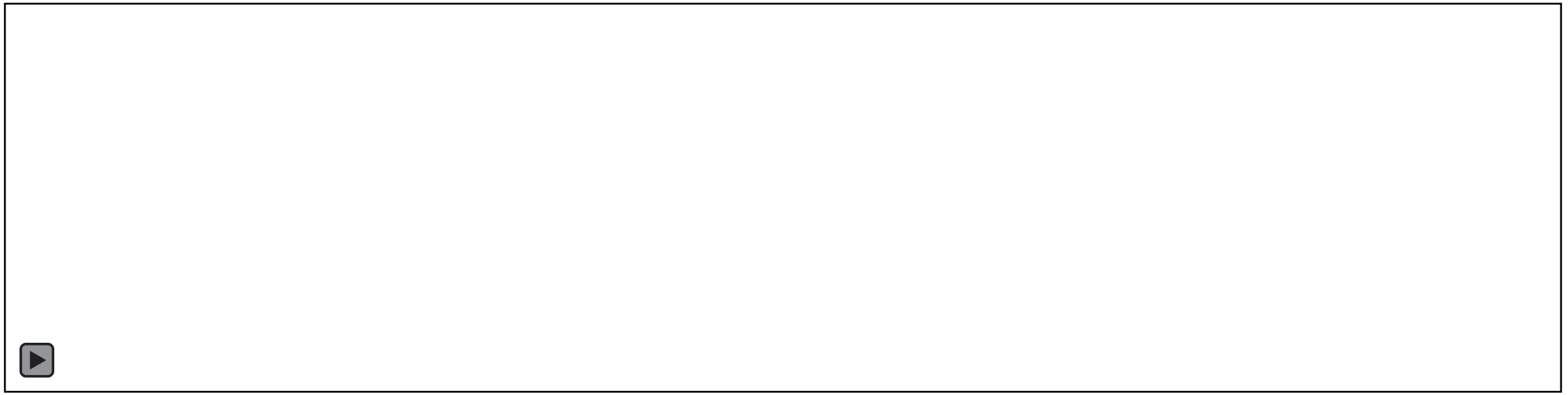
pth homology vector space:

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

Intuition: p-dimensional connectivity

Today: persistent homology

Youtube “**Persistent Homology on a noisy torus**”



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

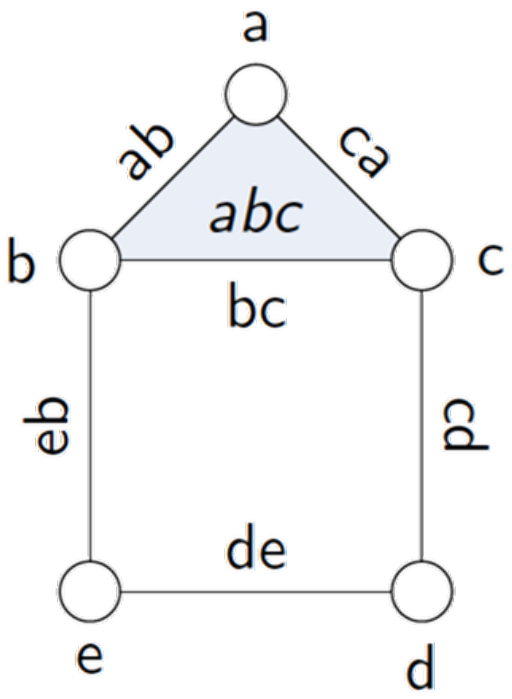
Functoriality of homology

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

Background: Computing homology

Setting up the linear algebra

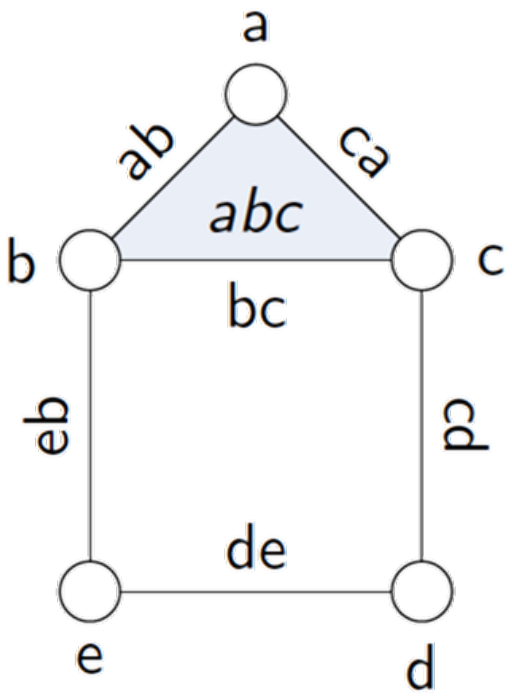
- $\partial_p : C_p \to C_{p-1}$ is a linear map between vector spaces, so we'll use matrices



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

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

Setting up the linear algebra



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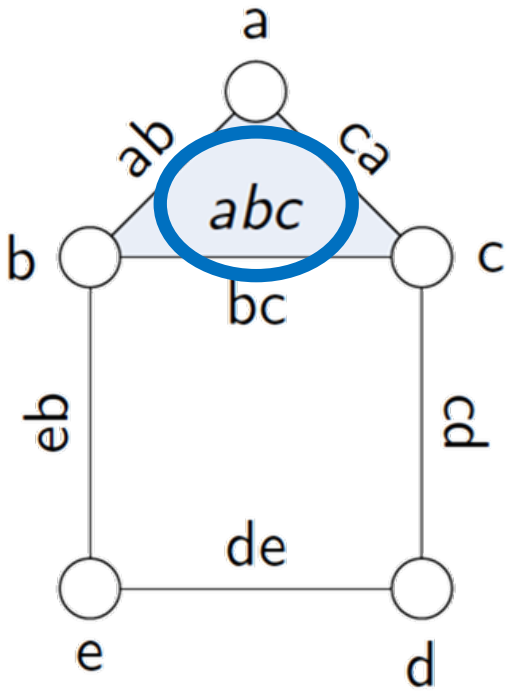
- E. g. $H_1 = \frac{\ker \partial_1}{im\ \partial_2}$, so we need to extract bases for these vector spaces

Setting up the linear algebra



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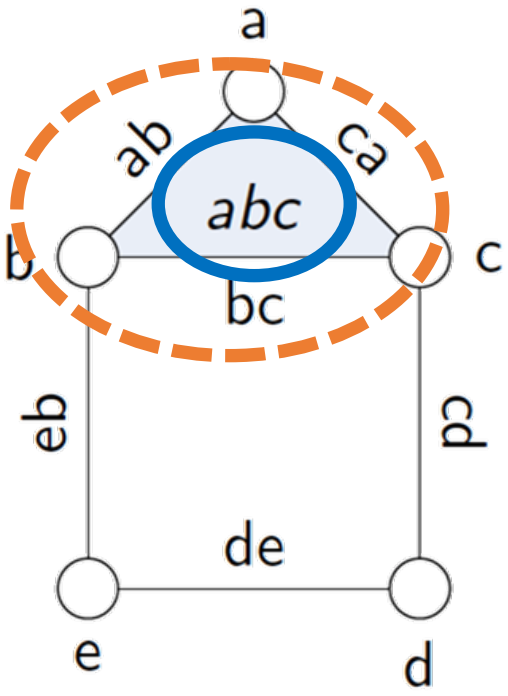

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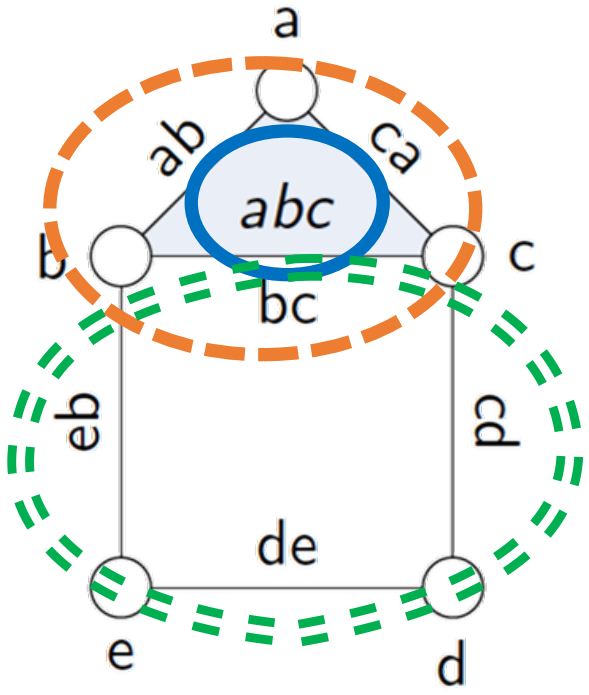

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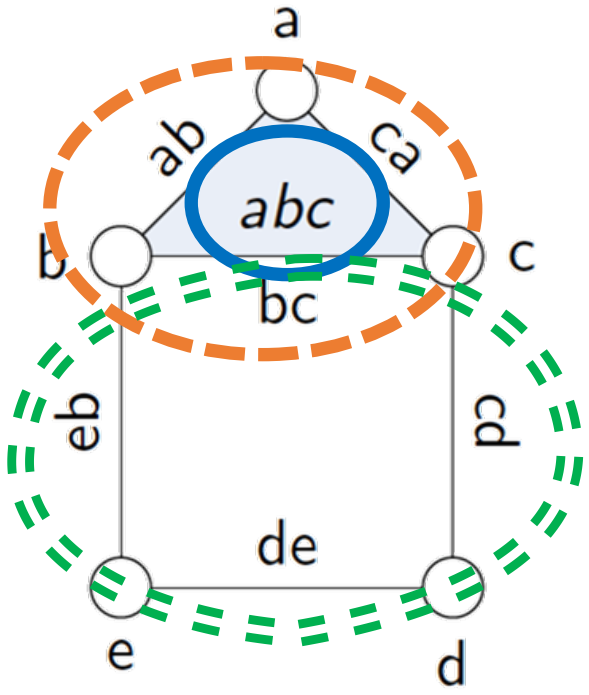

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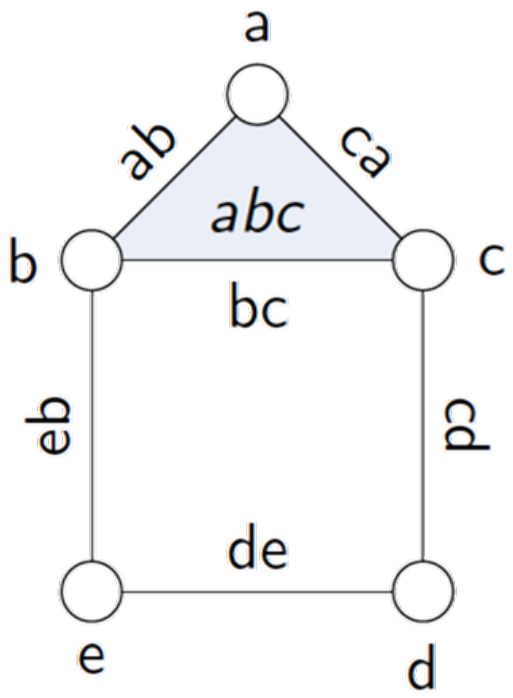
- Need $\mathbb{Z}/2\mathbb{Z}$ arithmetic
- Column operations

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}

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

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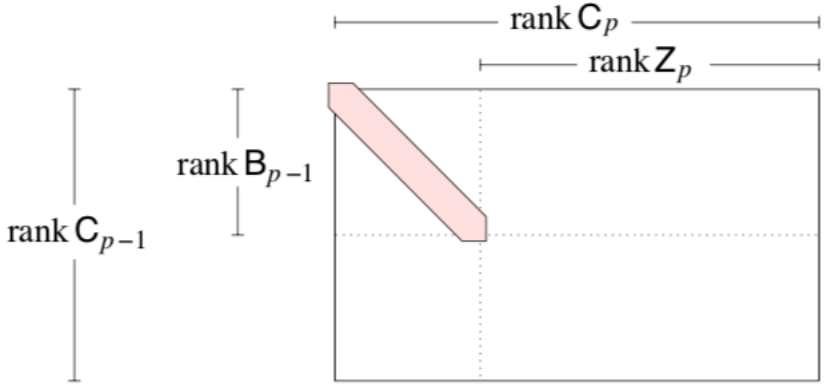
Smith Normal Form

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

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

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

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

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

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

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

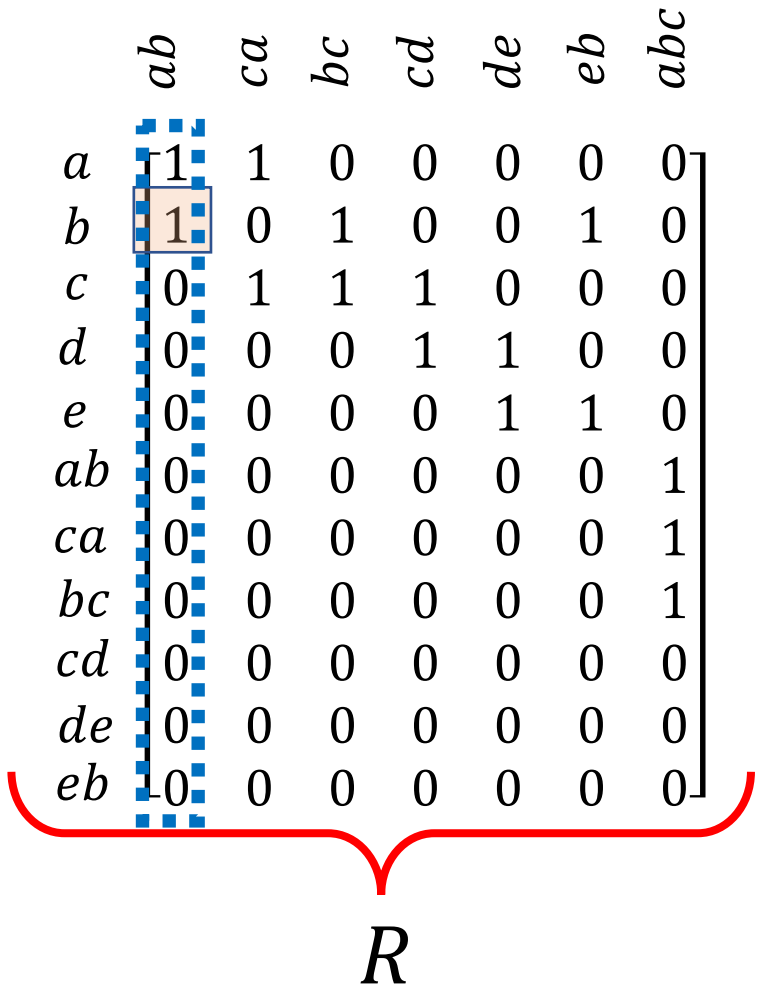
Notation: $low_R(j)$= row index of bottom 1 in column j of matrix R

Algorithm:

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

For column $j = 1, 2, \dots, n$
  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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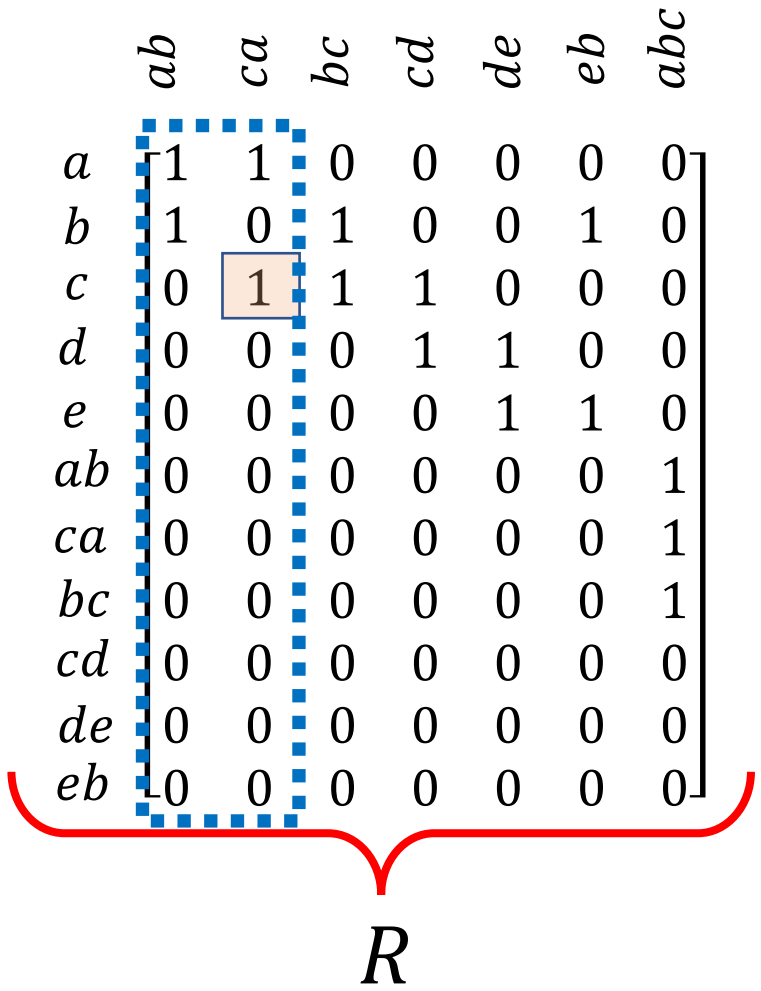

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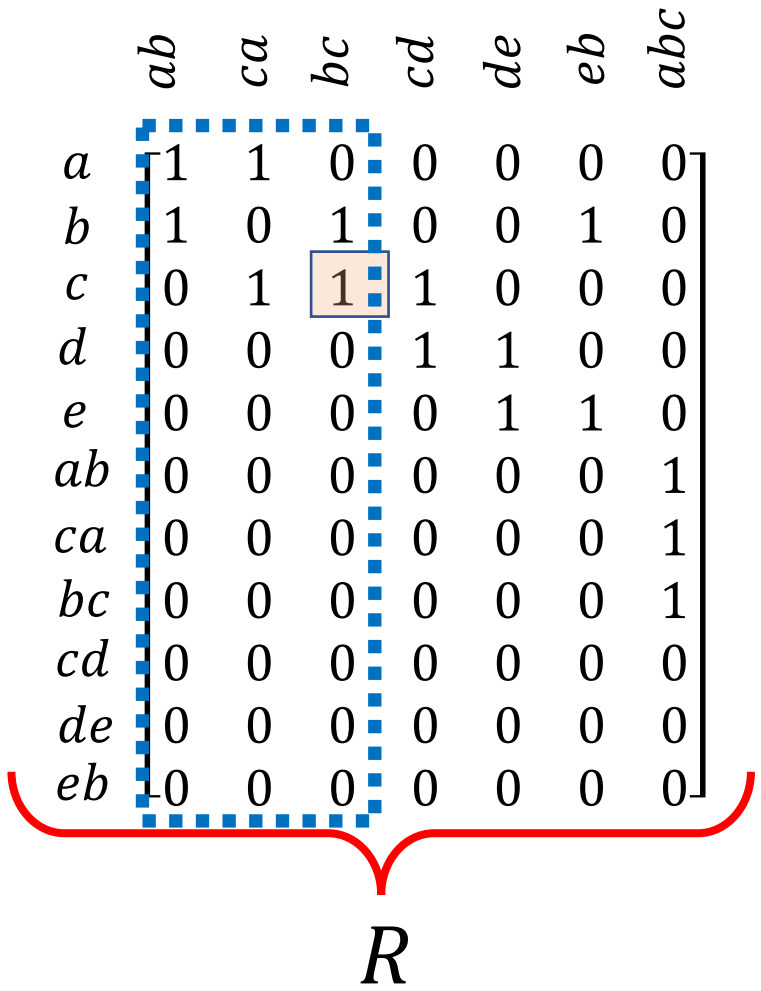

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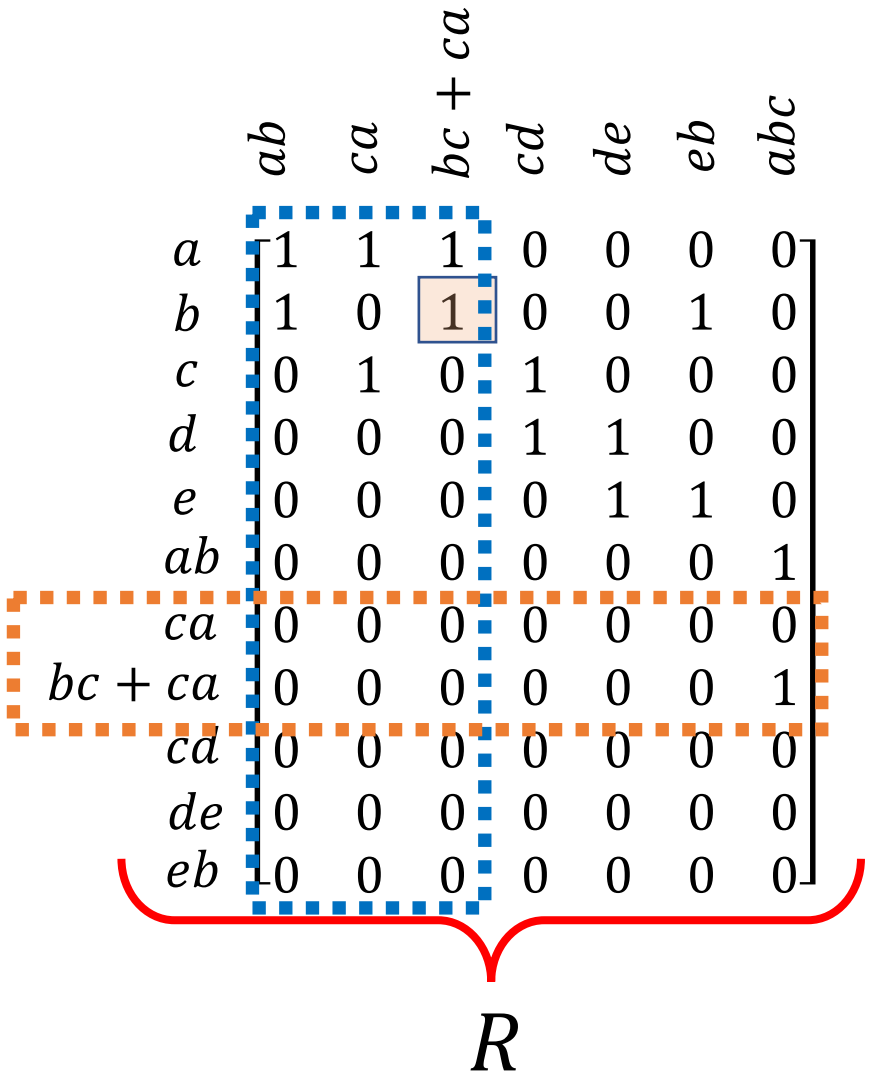


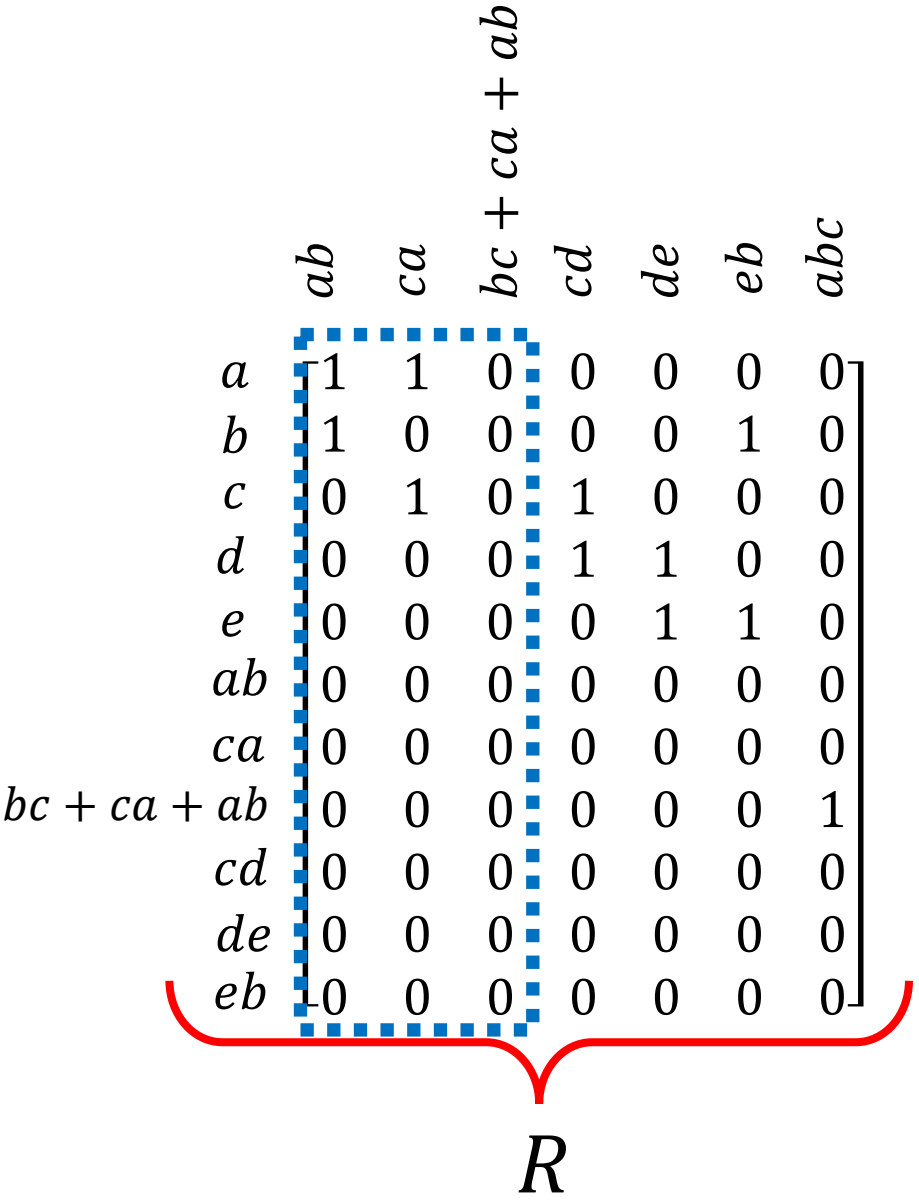
Reminder: to keep bases compatible, column operations require corresponding row operation!

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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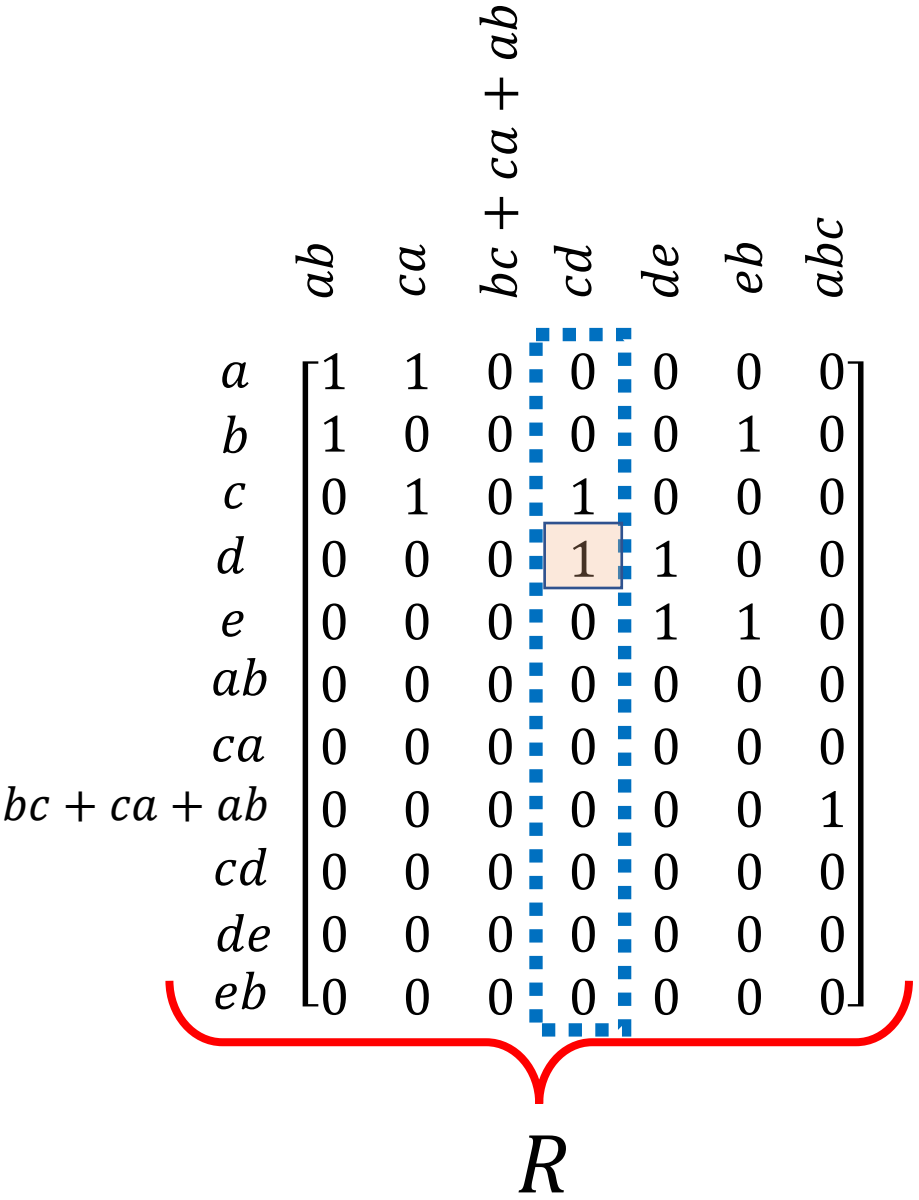

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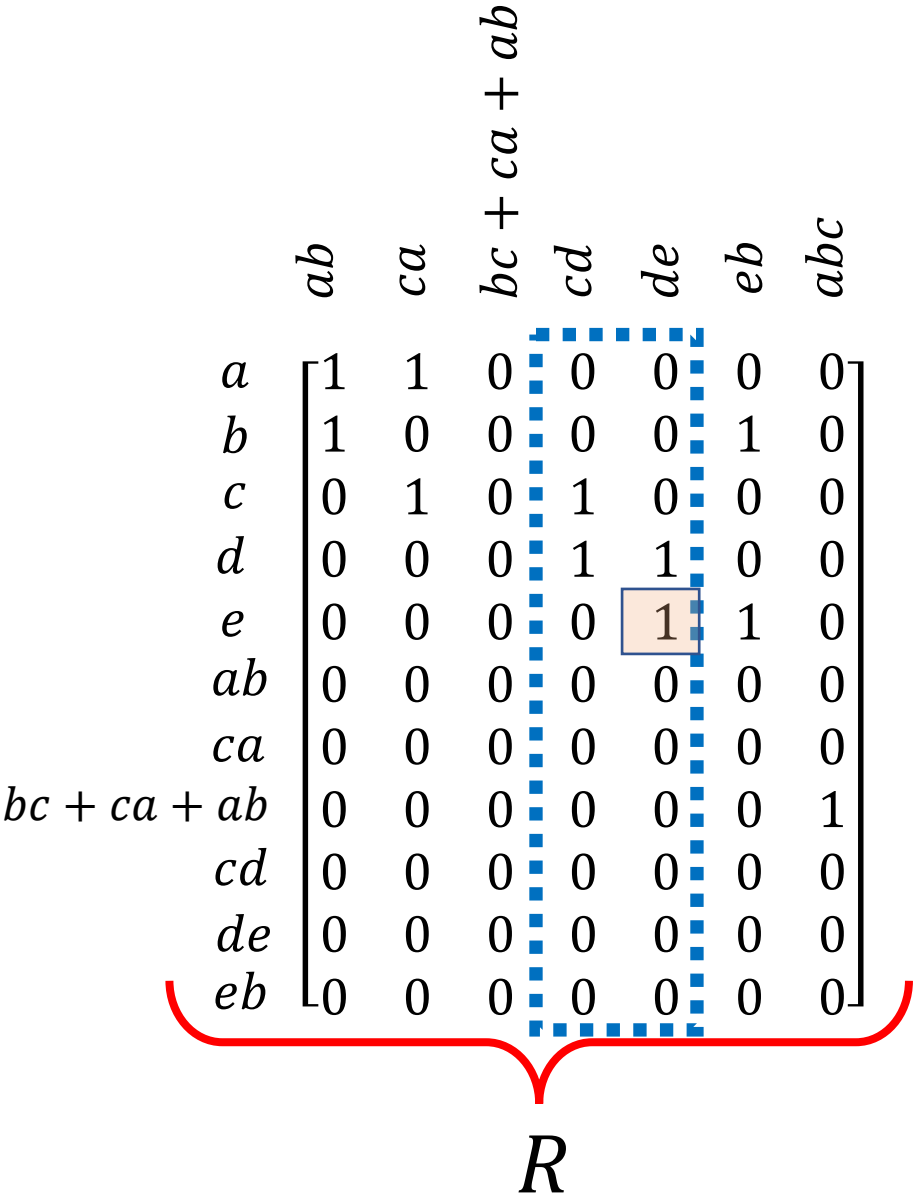

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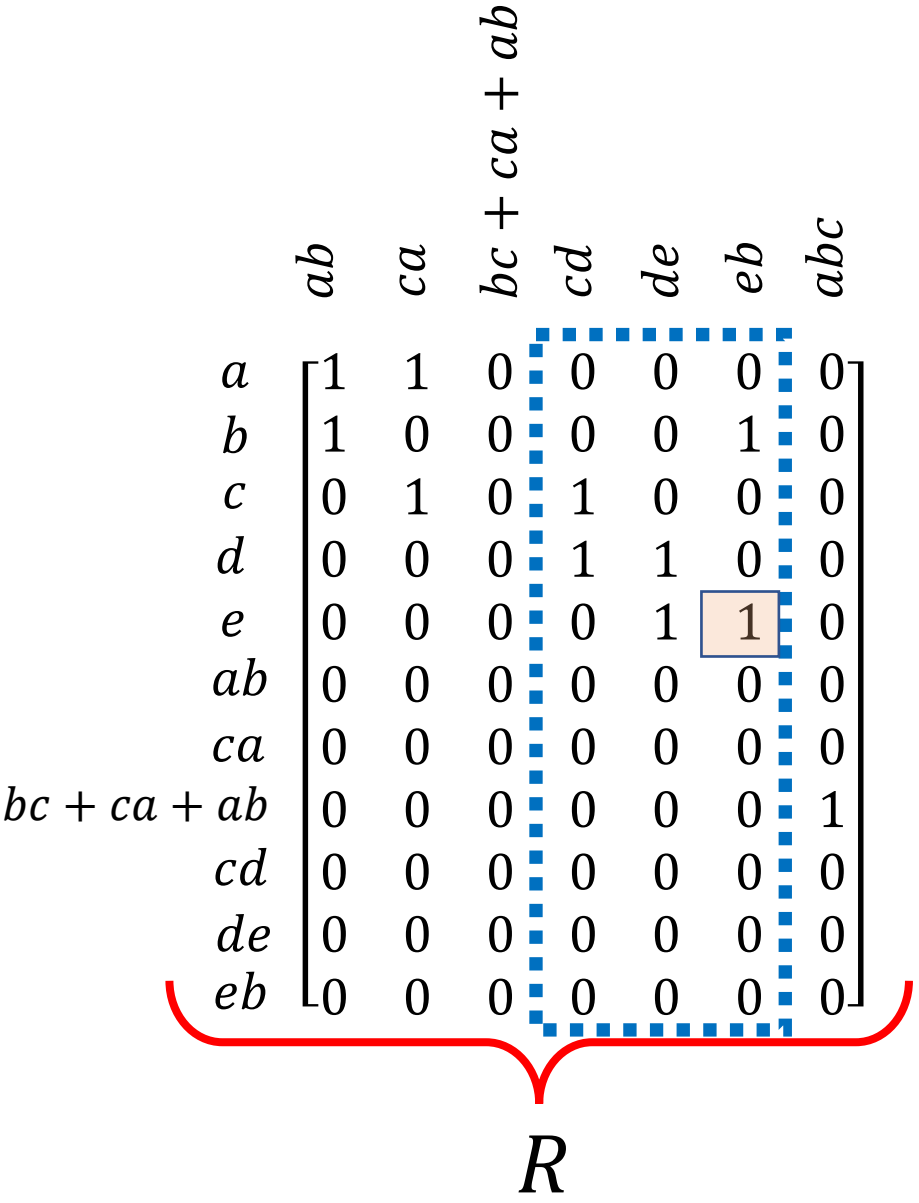

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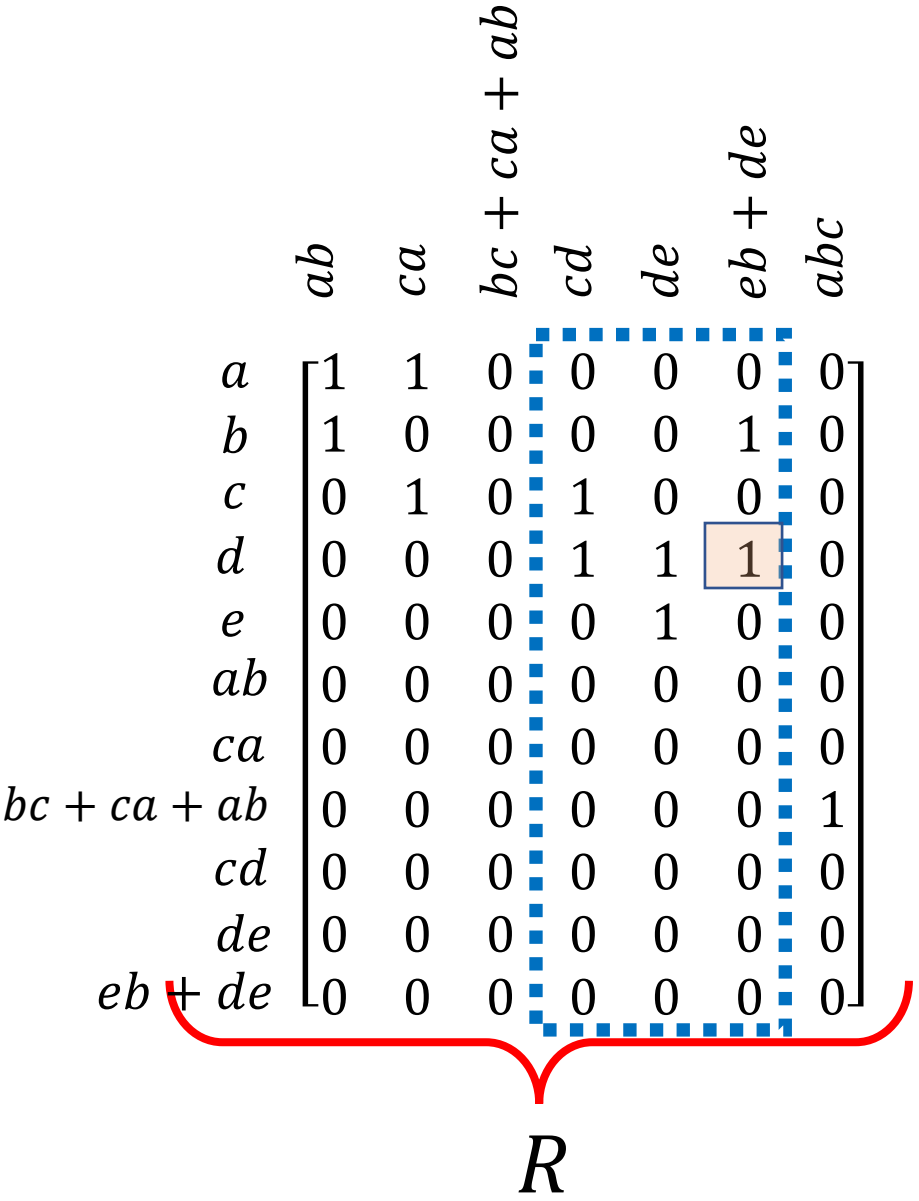

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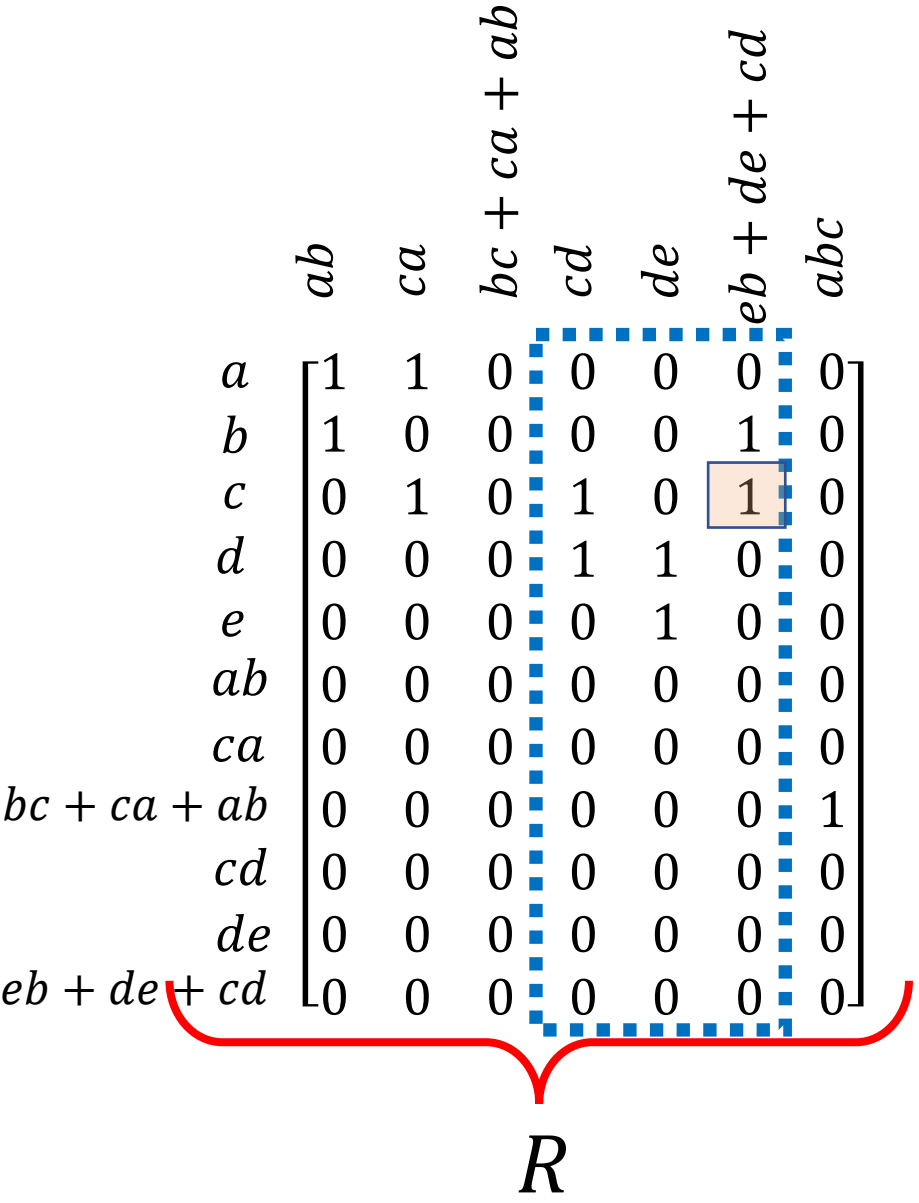

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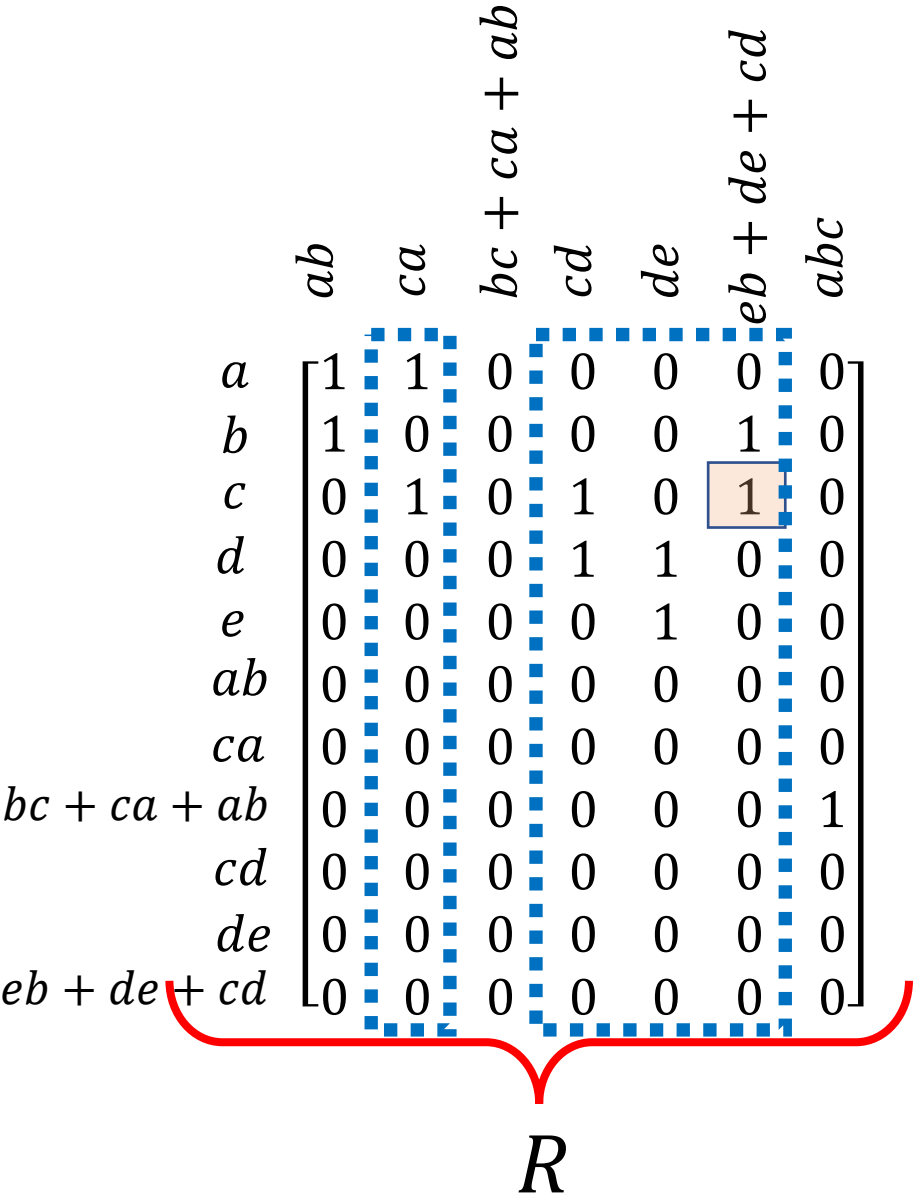
Reduction algorithm for homology



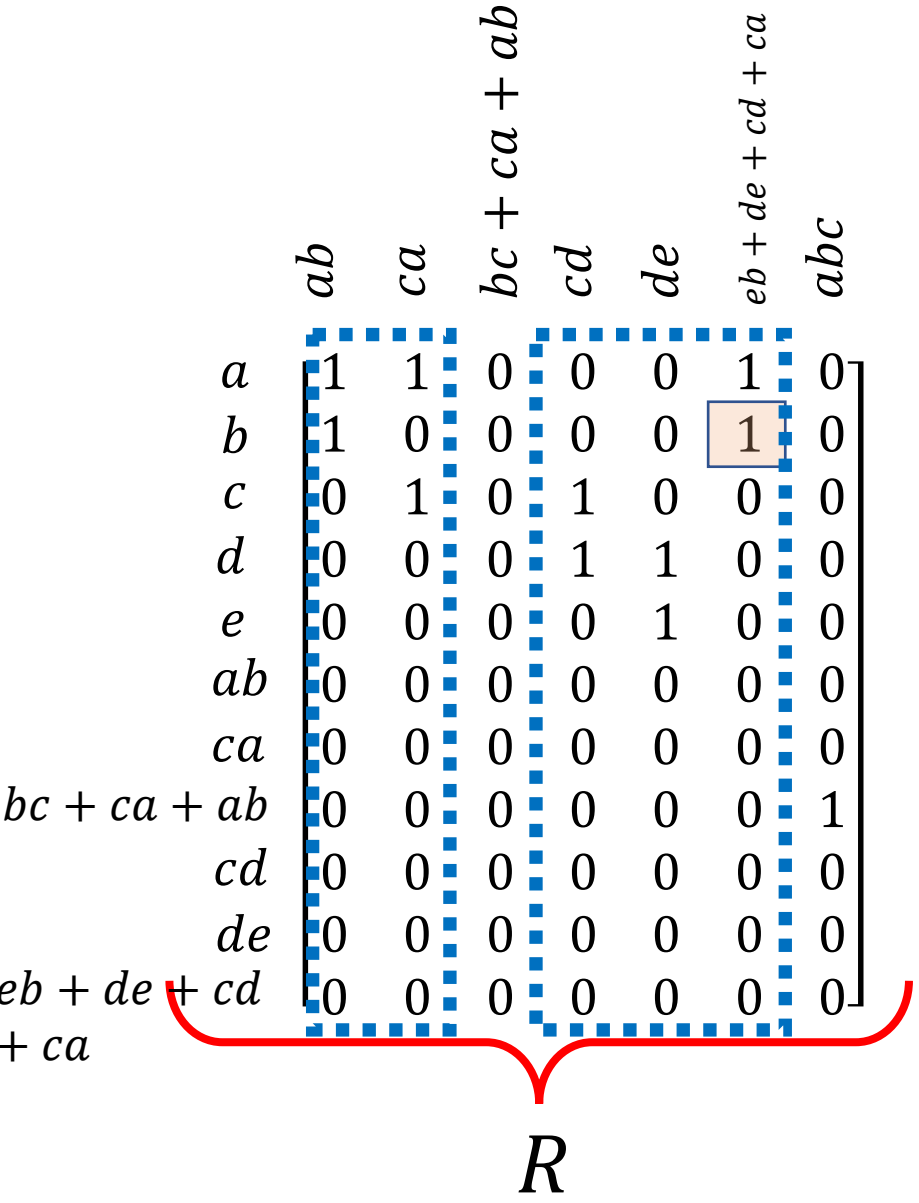
Notation: $low_R(j)$= row index of bottom 1 in column j of matrix R

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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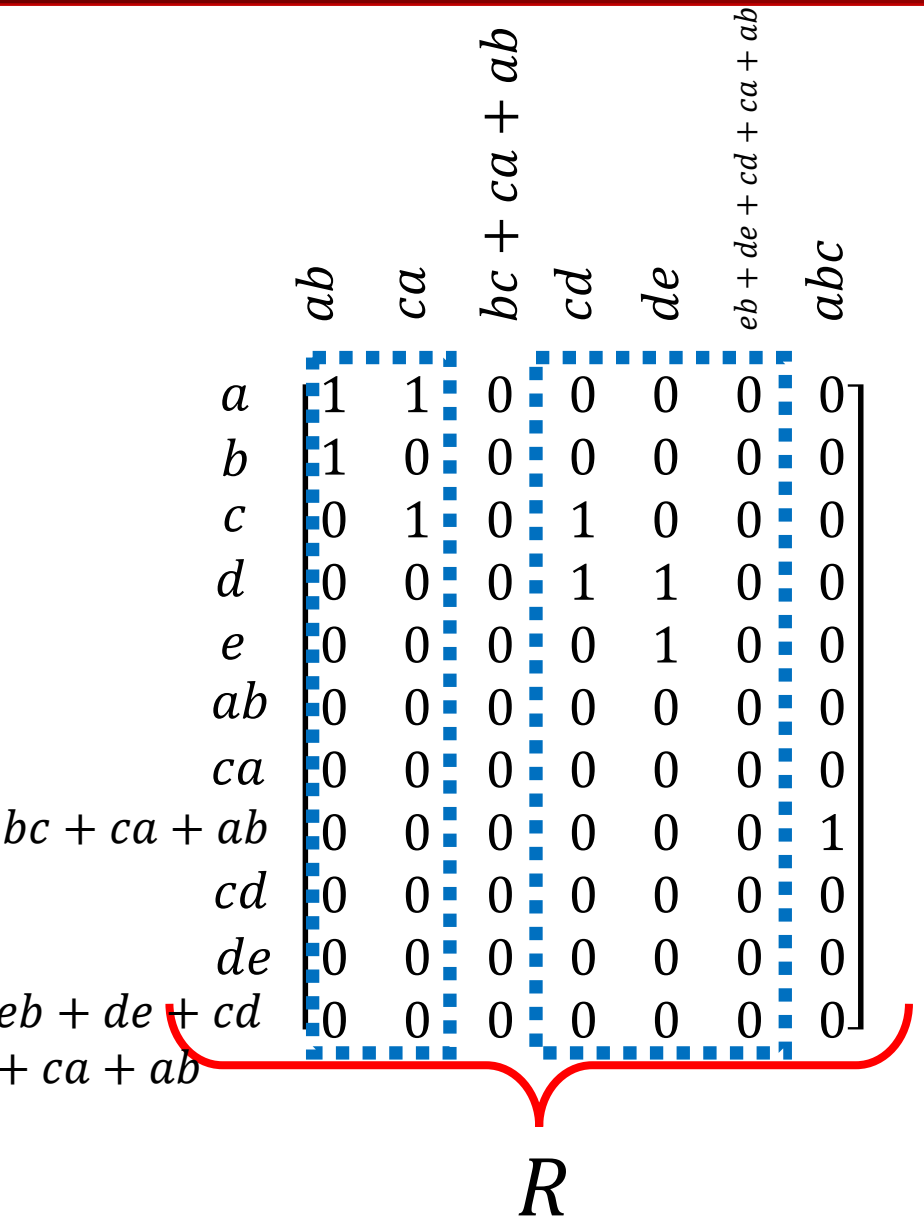
Reduction algorithm for homology



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

Algorithm:

Initialize boundary information in incidence matrix D
Initialize $R := D$

For column $j = 1, 2, \ldots, n$
  while $\exists j' < j, low_R(j') = low_R(j)$ do
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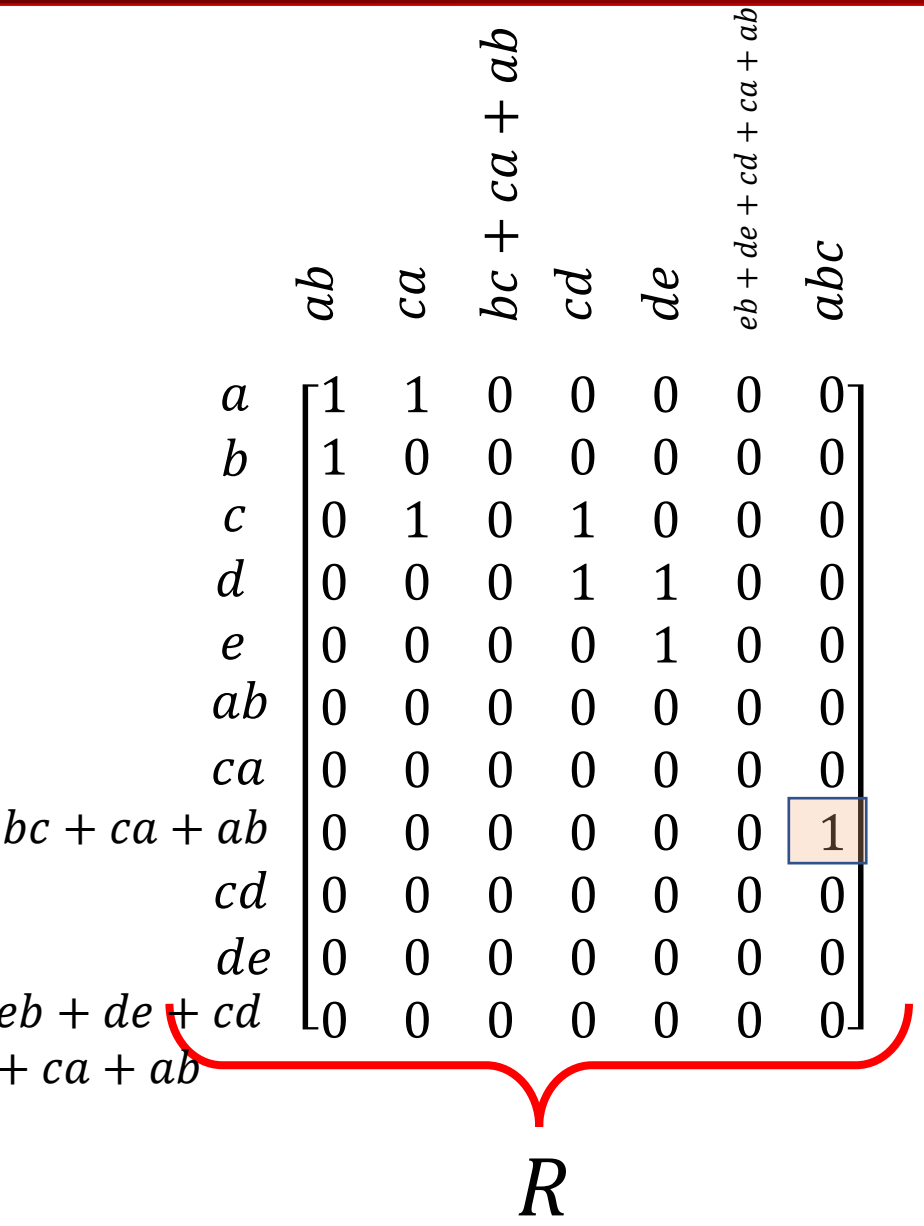
Reduction algorithm for homology



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:

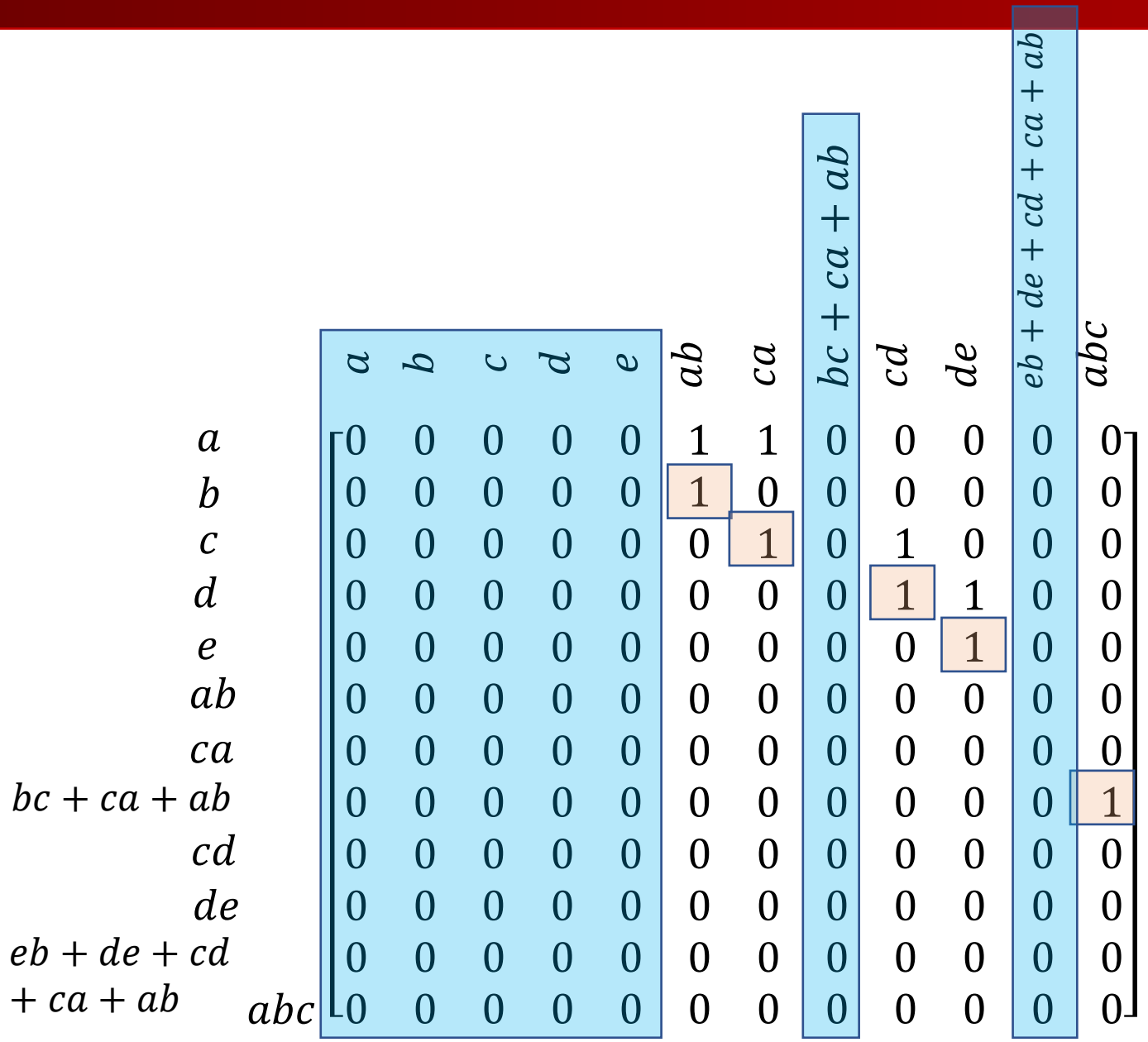
Reduction algorithm for homology

	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

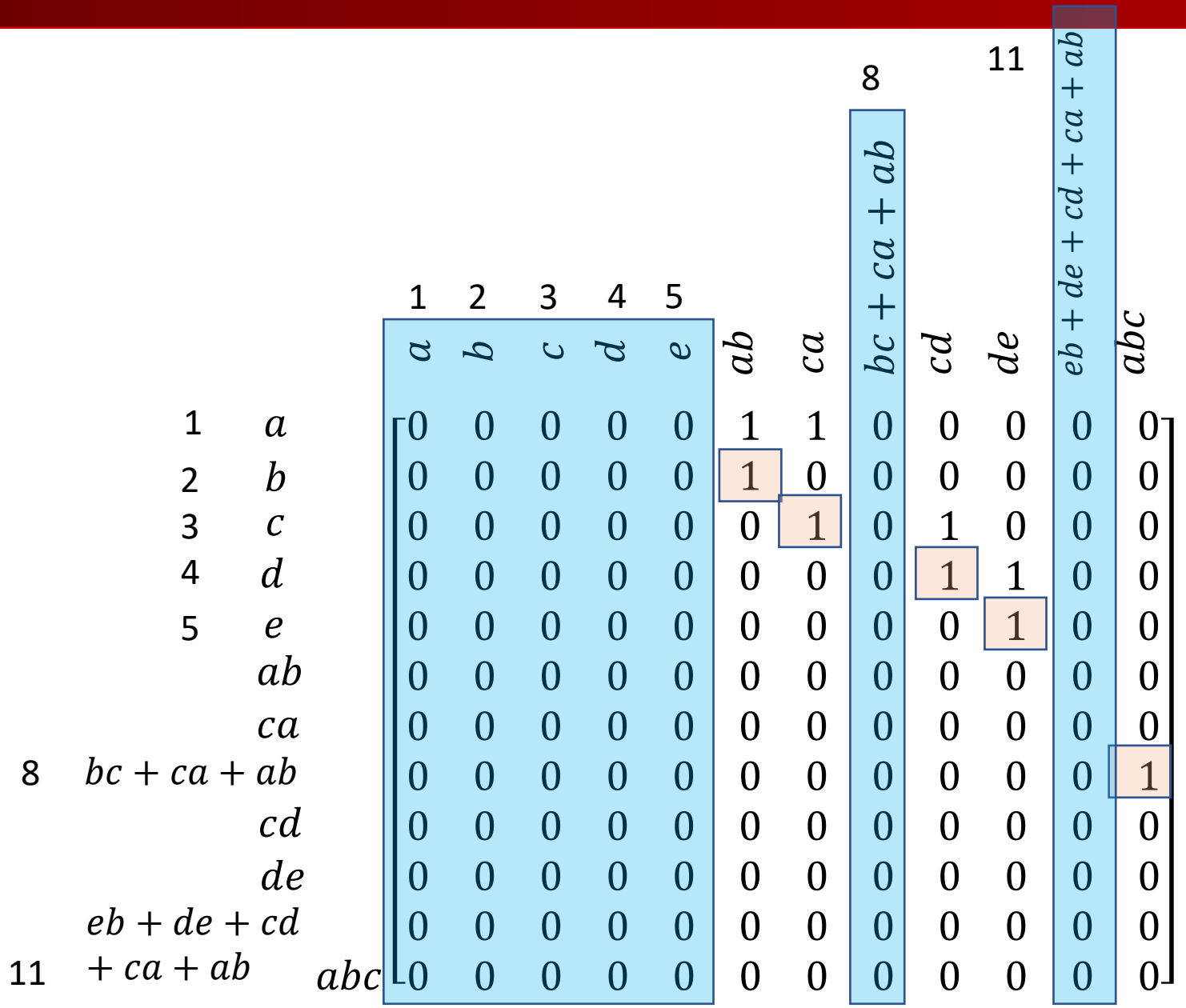
Reduction algorithm for homology



Full matrix at termination. Observe:

- (Proposition) No two columns with the same low_R value
- Zero columns can be read off immediately to get $\ker \partial_p$

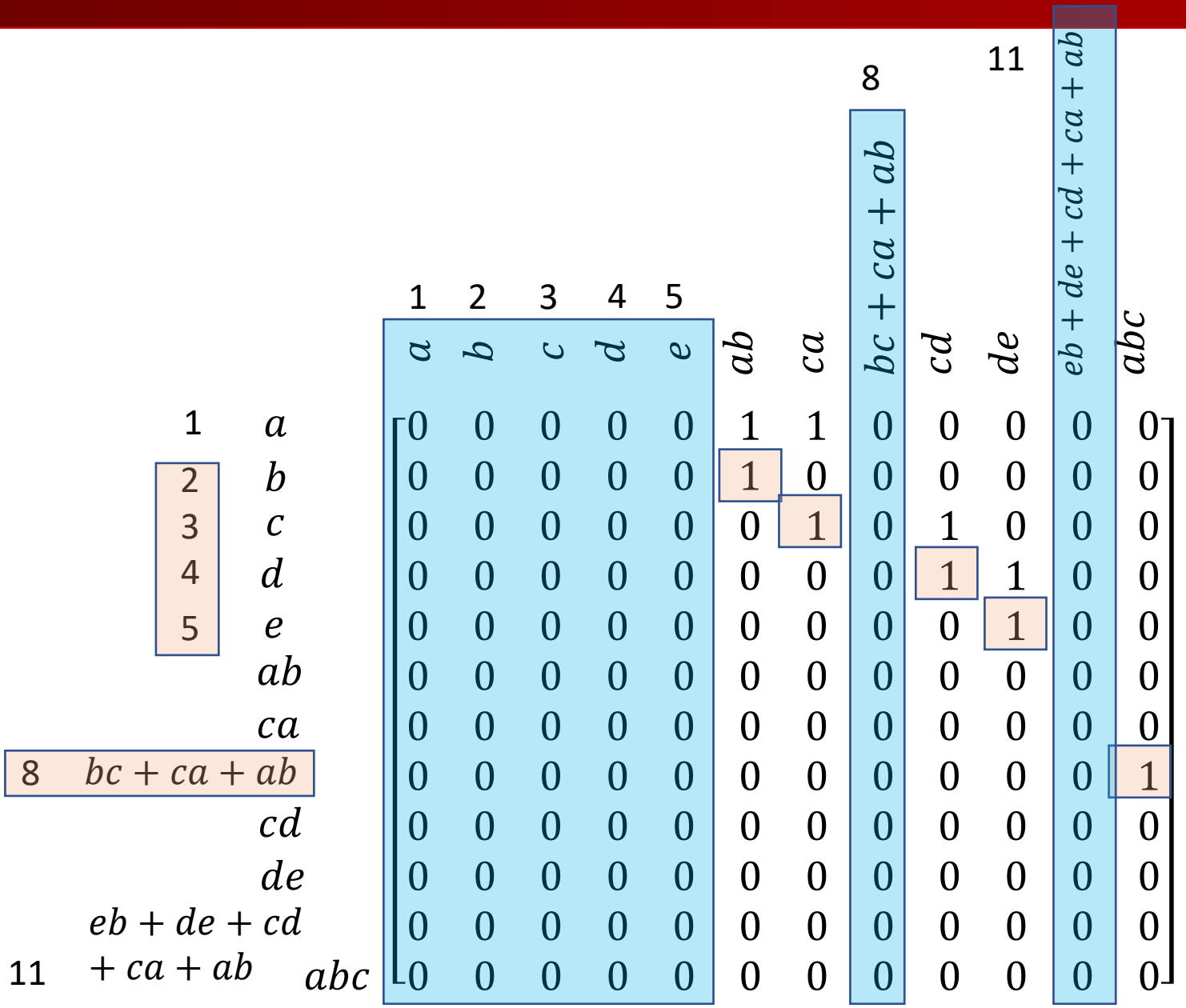
Reduction algorithm for homology



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

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

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

		1	2	3	4	5	6	7	8	9	10	11	12
		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

Full matrix at termination. Observe:

- (Proposition) No two columns with the same low_R value
- Zero columns can be read off immediately to get $\ker \partial_p$
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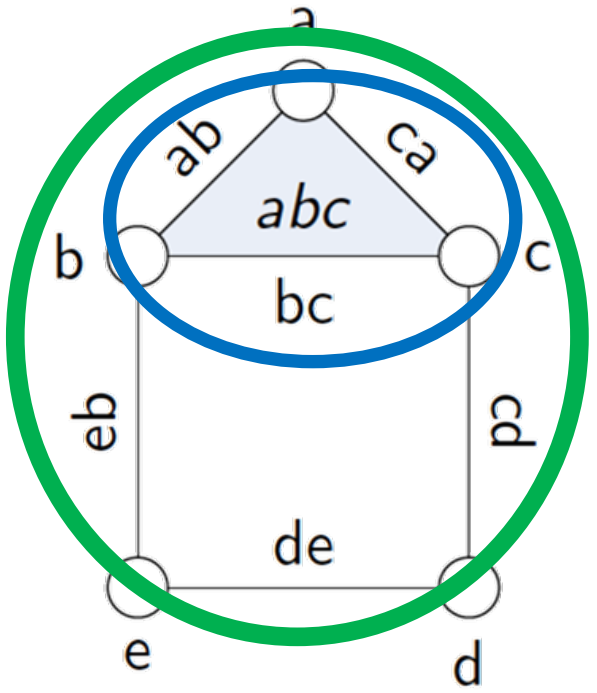
$H_0 \cong \mathbb{F}[a]$

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

		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
	$eb + de + cd$	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												

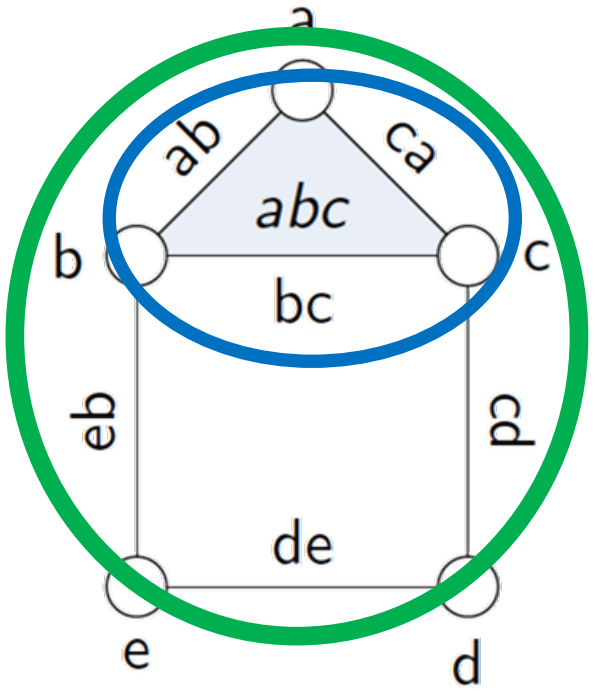


The bases we deserve, not the bases we need

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

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

		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



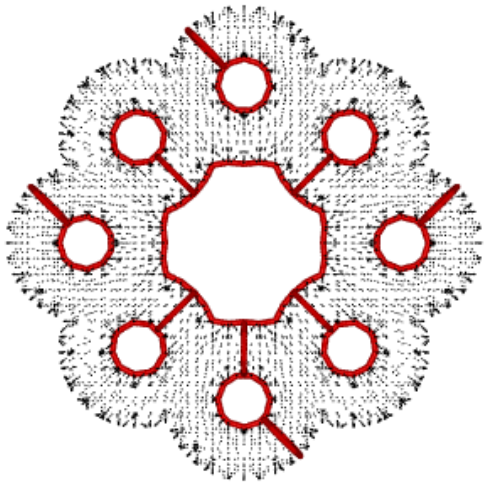
Caveat: homology involves an equivalence class, so we get "representative cycles". E.g. we got $eb + de + cd + cca + ab$ instead of $eb + de + cd + bc$.

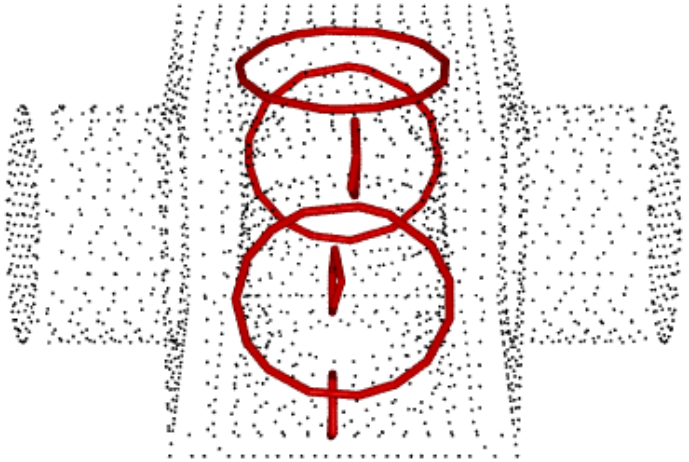
Operating at the algebraic level gives up some control over geometric correspondence.

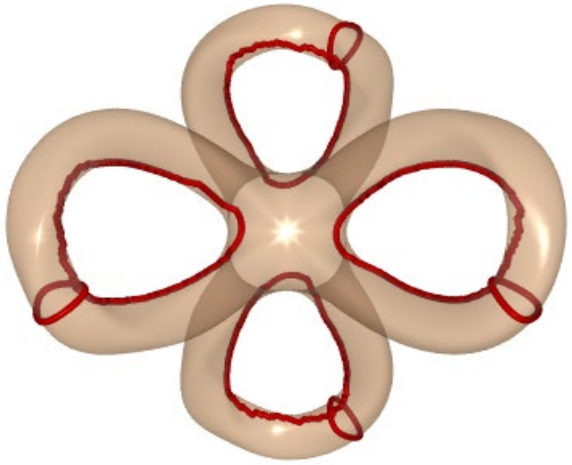
ShortLoop

Oleksiy Busaryev, Tamal Dey, Jian Sun, Yusu Wang

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







Persistent homology

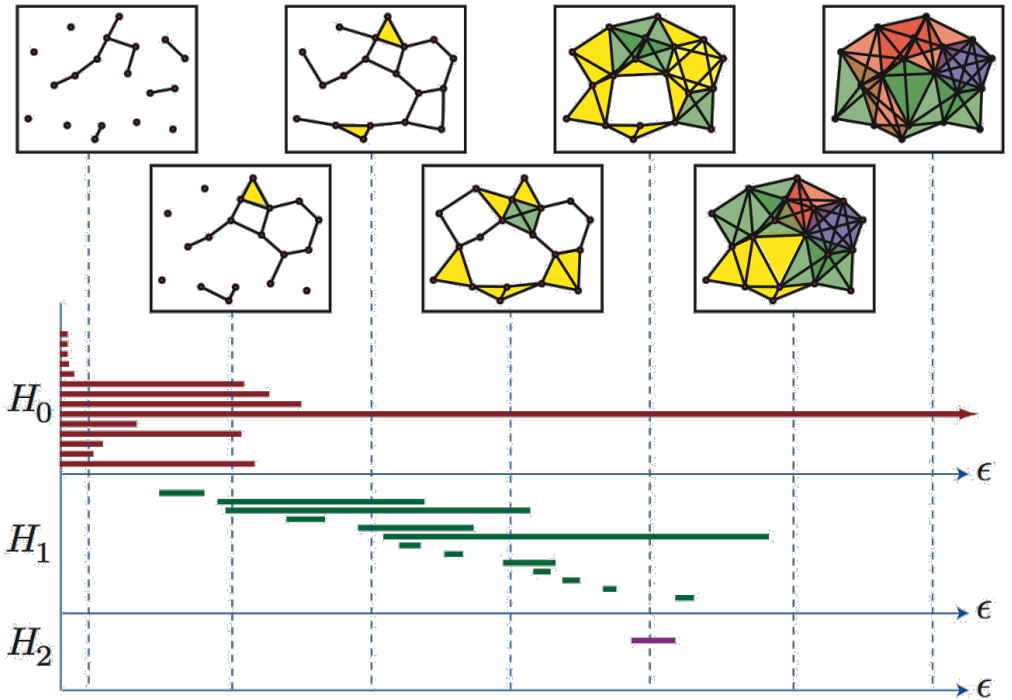
Pipeline

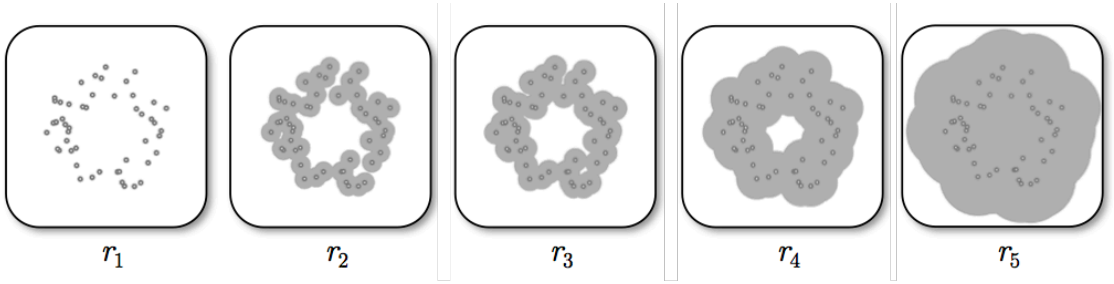
Dataset:
- **Euclidean point cloud data**
- **Metric spaces**
- **Triangulated shape**
- Graphs, matrices…

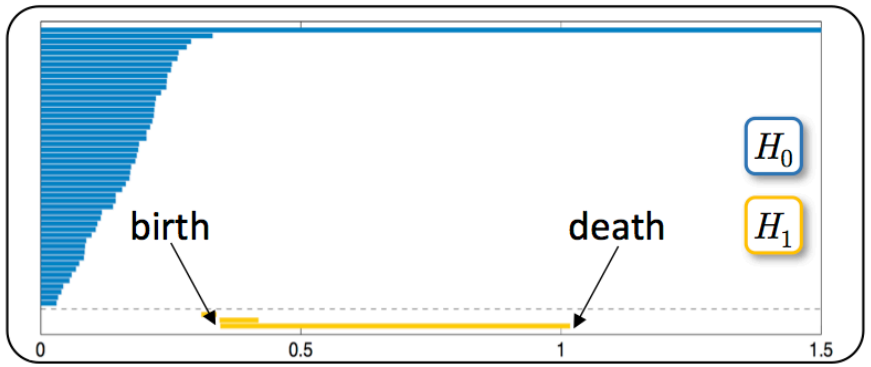
Filtered simplicial complex
- Possible to have both inclusions and deletions (dynamic data)

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

Visual summary: a **persistence diagram** or **persistence barcode**
- Persistence landscapes for ML-friendly output







Reduction algorithm for persistent homology

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

Persistence algorithm:

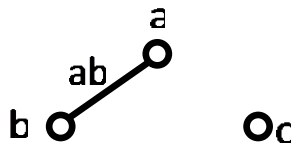
- When setting up boundary matrices/overall incidence matrix, order basis vectors according to order of appearance of simplices
- Apply reduction algorithm from before
- Read off persistence pairs $\{(i,j) \mid i = low_R(j) \neq 0\}$ and essential indices $\{i \mid R[:,i] = 0,\ i \neq low_R(j) \text{ for any } j\}$
- 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)

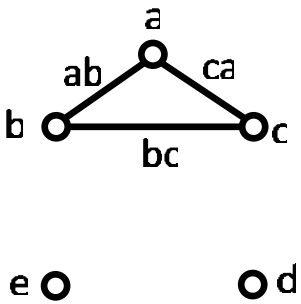
Back to the house example

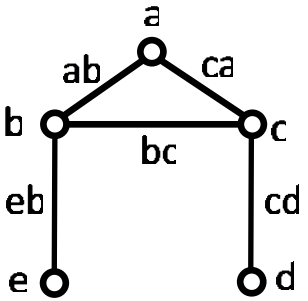
Entry time: 1 1 1 1 1 1 2 2 3 3 4 5

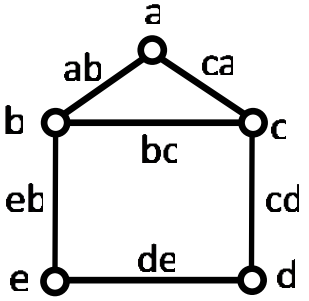
Index: 1 2 3 4 5 6 7 8 9 10 11 12

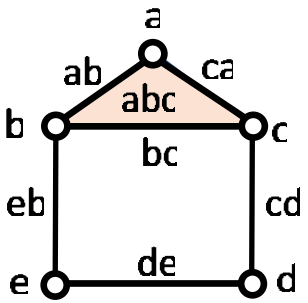
	a	b	c	d	e	ab	ca	bc	cd	eb	de	abc
a	0	0	0	0	0	1	1	0	0	0	0	0
b	0	0	0	0	0	1	0	1	0	1	0	0
c	0	0	0	0	0	0	1	1	1	0	0	0
d	0	0	0	0	0	0	0	0	1	0	1	0
e	0	0	0	0	0	0	0	0	0	1	1	0
ab	0	0	0	0	0	0	0	0	0	0	0	1
ca	0	0	0	0	0	0	0	0	0	0	0	1
bc	0	0	0	0	0	0	0	0	0	0	0	1
cd	0	0	0	0	0	0	0	0	0	0	0	0
eb	0	0	0	0	0	0	0	0	0	0	0	0
de	0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





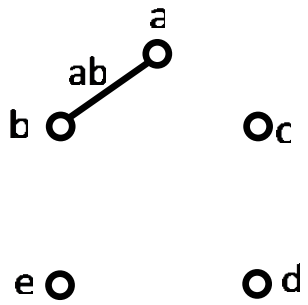


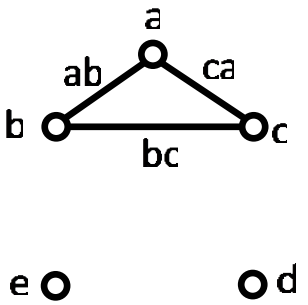


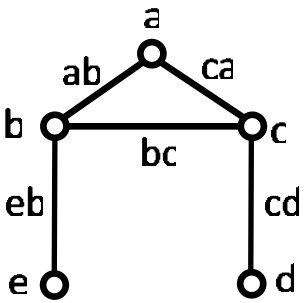


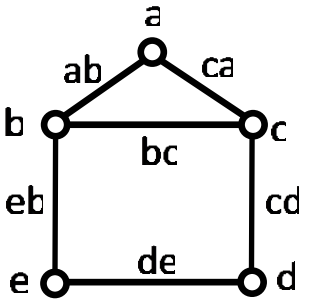
Back to the house example

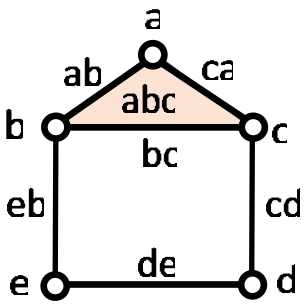
		1	2	3	4	5	ab	ca	8 $bc+ca+ab$	cd	eb	11 $de+eb+cd+ca+ab$	abc
		a	b	c	d	e							
1	a	0	0	0	0	0	1	1	0	0	0	0	0
2	b	0	0	0	0	0	1	0	0	0	1	0	0
3	c	0	0	0	0	0	0	1	0	1	0	0	0
4	d	0	0	0	0	0	0	0	0	1	0	0	0
5	e	0	0	0	0	0	0	0	0	0	1	0	0
	ab	0	0	0	0	0	0	0	0	0	0	0	0
	ca	0	0	0	0	0	0	0	0	0	0	0	0
8	$bc+ca+ab$	0	0	0	0	0	0	0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

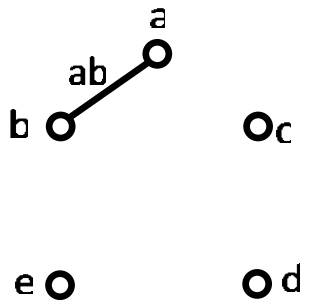
Persistence pairs: $\{(2,6),(3,7),(4,9),(5,10),(8,12)\}$
(column indices)

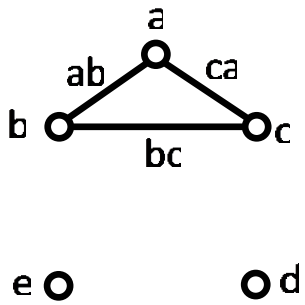
Lifetimes (dim 0): $\{[1,1),[1,2),[1,3),[1,3)\}$
(time indices)

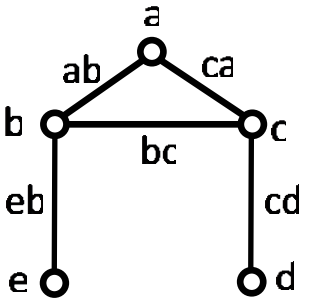
Lifetimes (dim 1): $\{[2,5)\}$
(time indices)

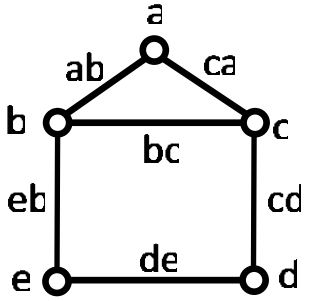
Essential indices: $\{1,11\}$
(column indices)

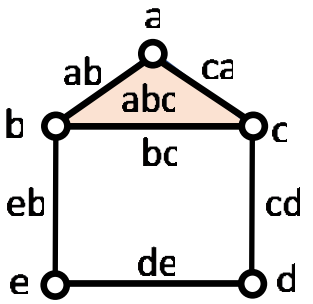
Lifetimes: $\{[1,\infty)$ (connected component), $[4,\infty)$ (loop)$\}$
(time indices)











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

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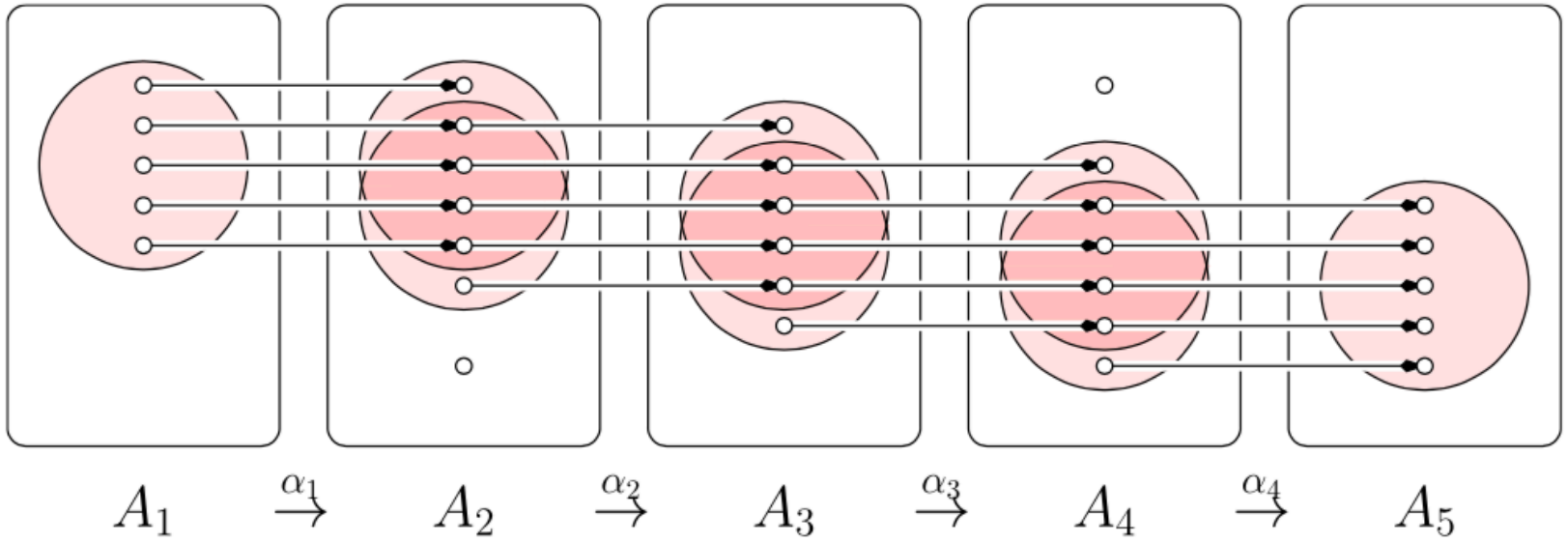
Obtaining bases for the individual vector spaces is not sufficient. To encode linear maps, we need compatible bases.

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

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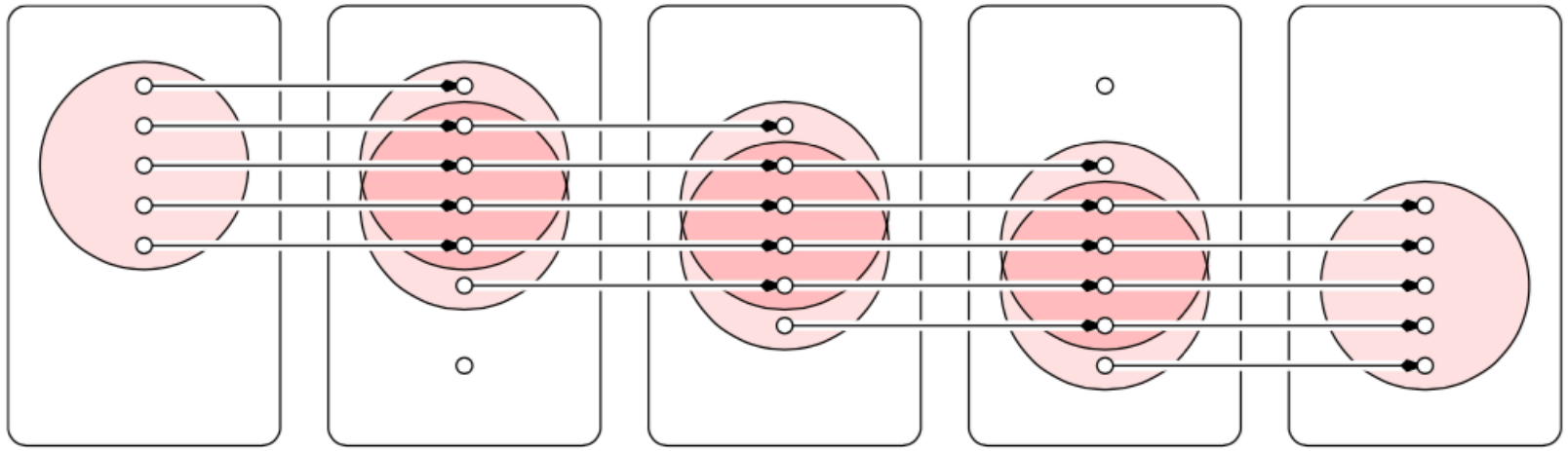

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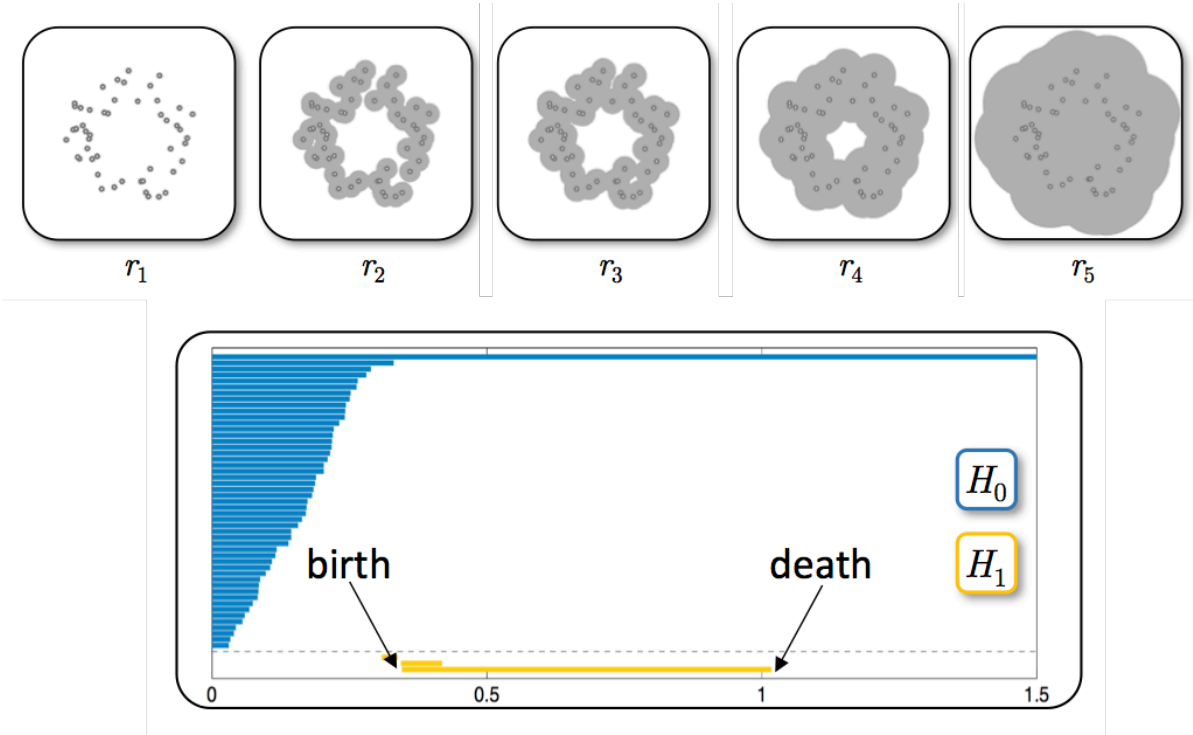
Theorem (Krull-Remak-Schmidt): Such a decomposition is unique up to relabeling.

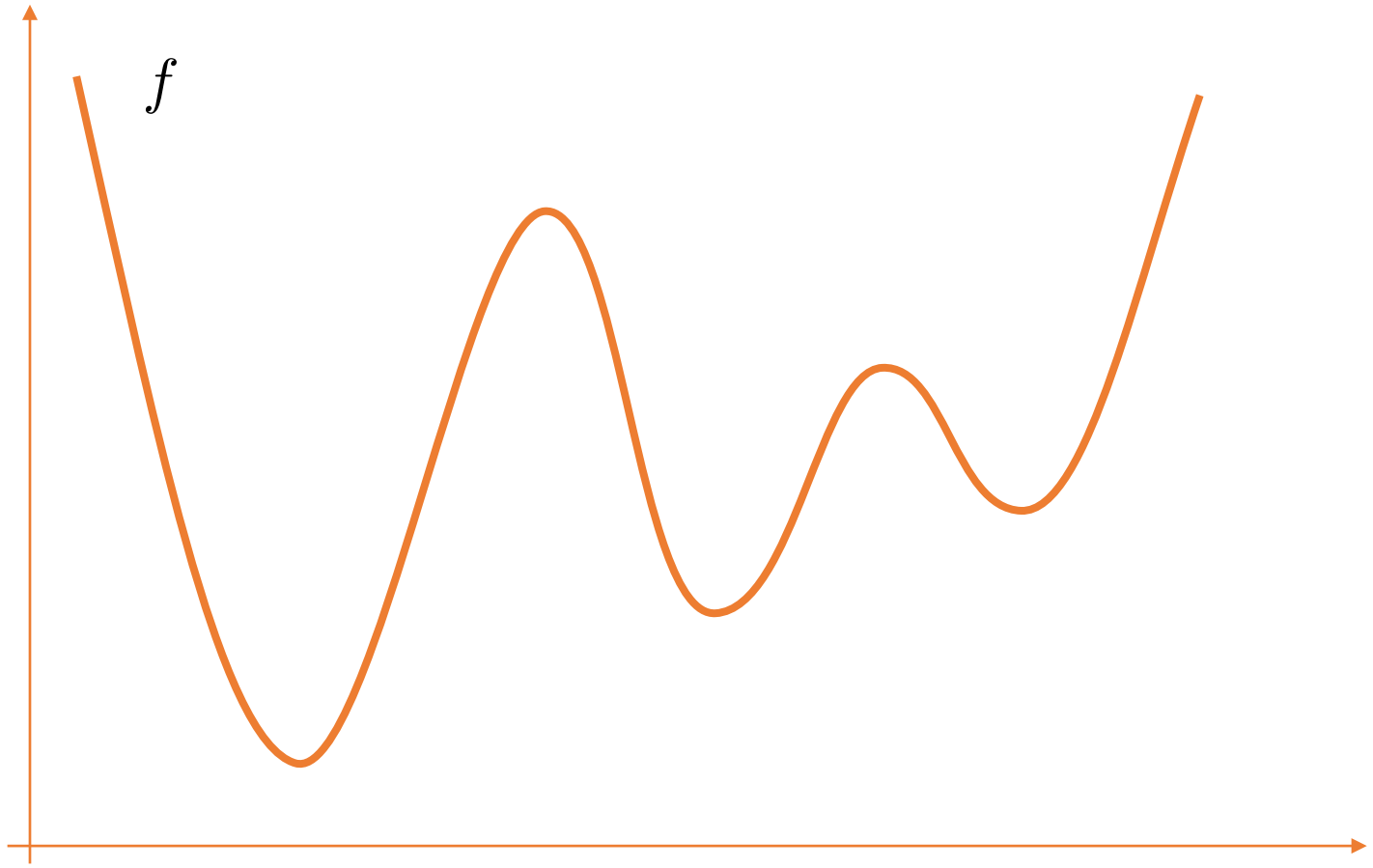
Sublevel Set Persistence

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

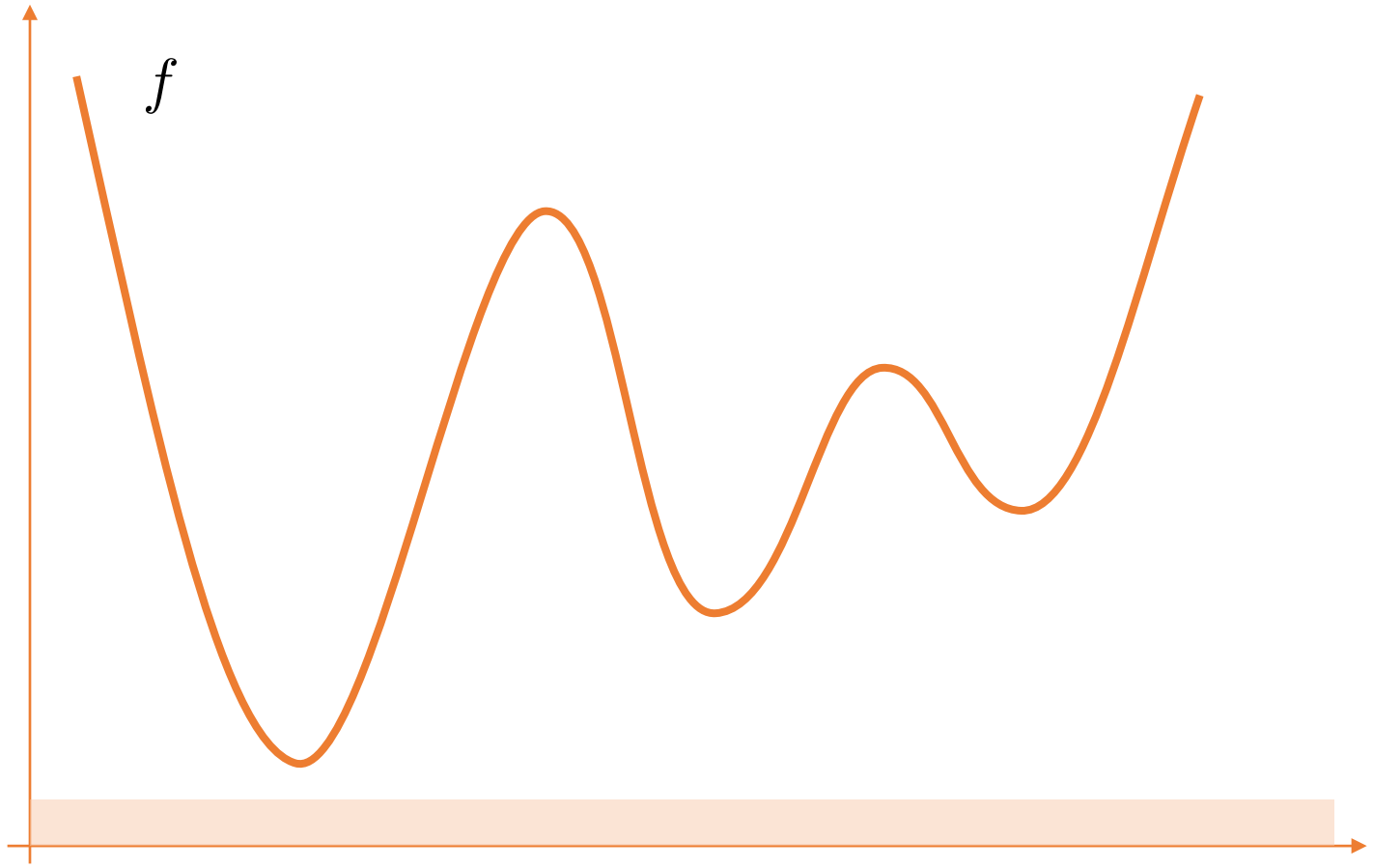


- When given a function $f: \mathcal{M} \to \mathbb{R}$ where $\mathcal{M}$ is a triangulated space (i.e. a simplicial complex at the outset), we can use f as a filter

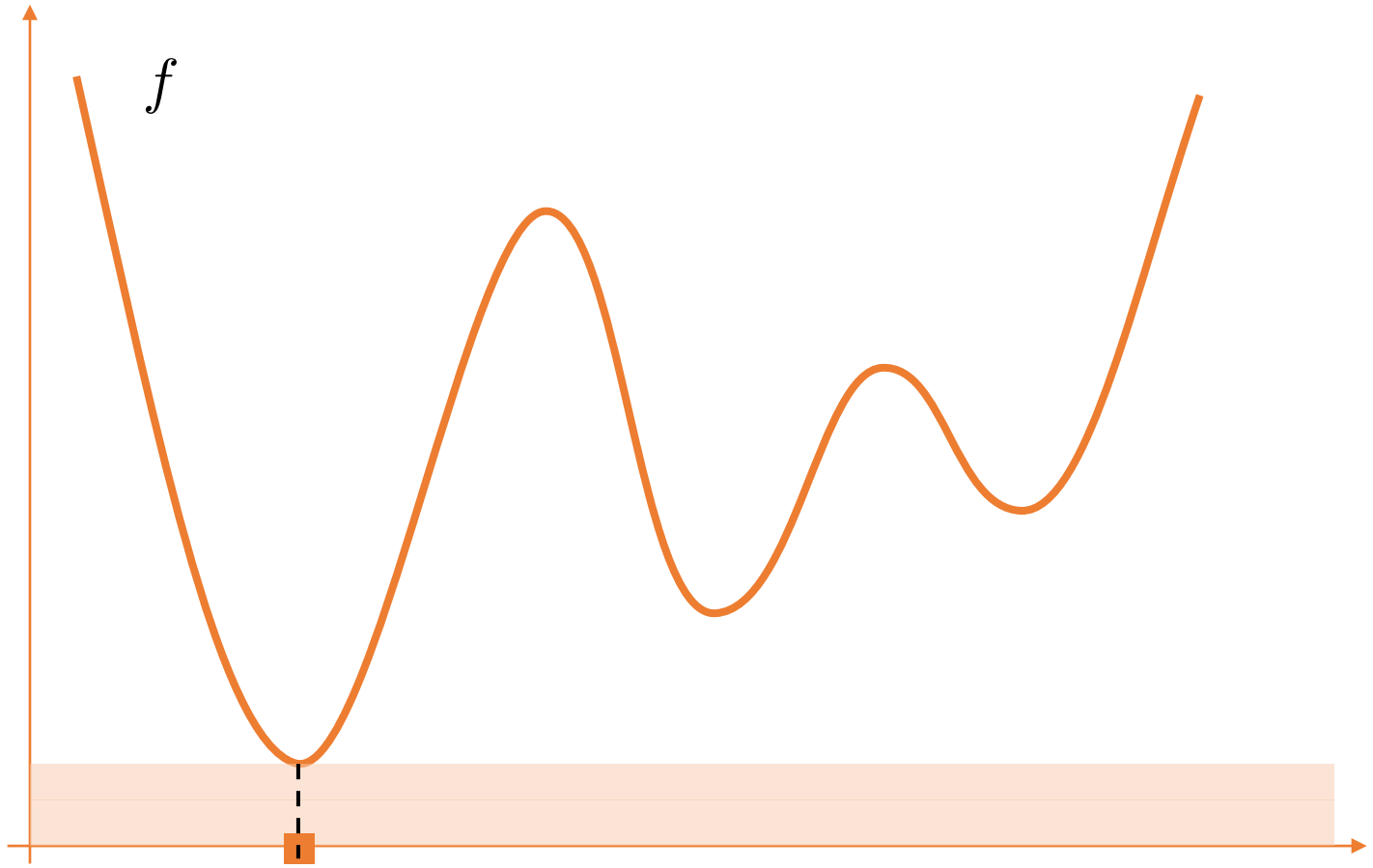
Sublevel Set Persistence



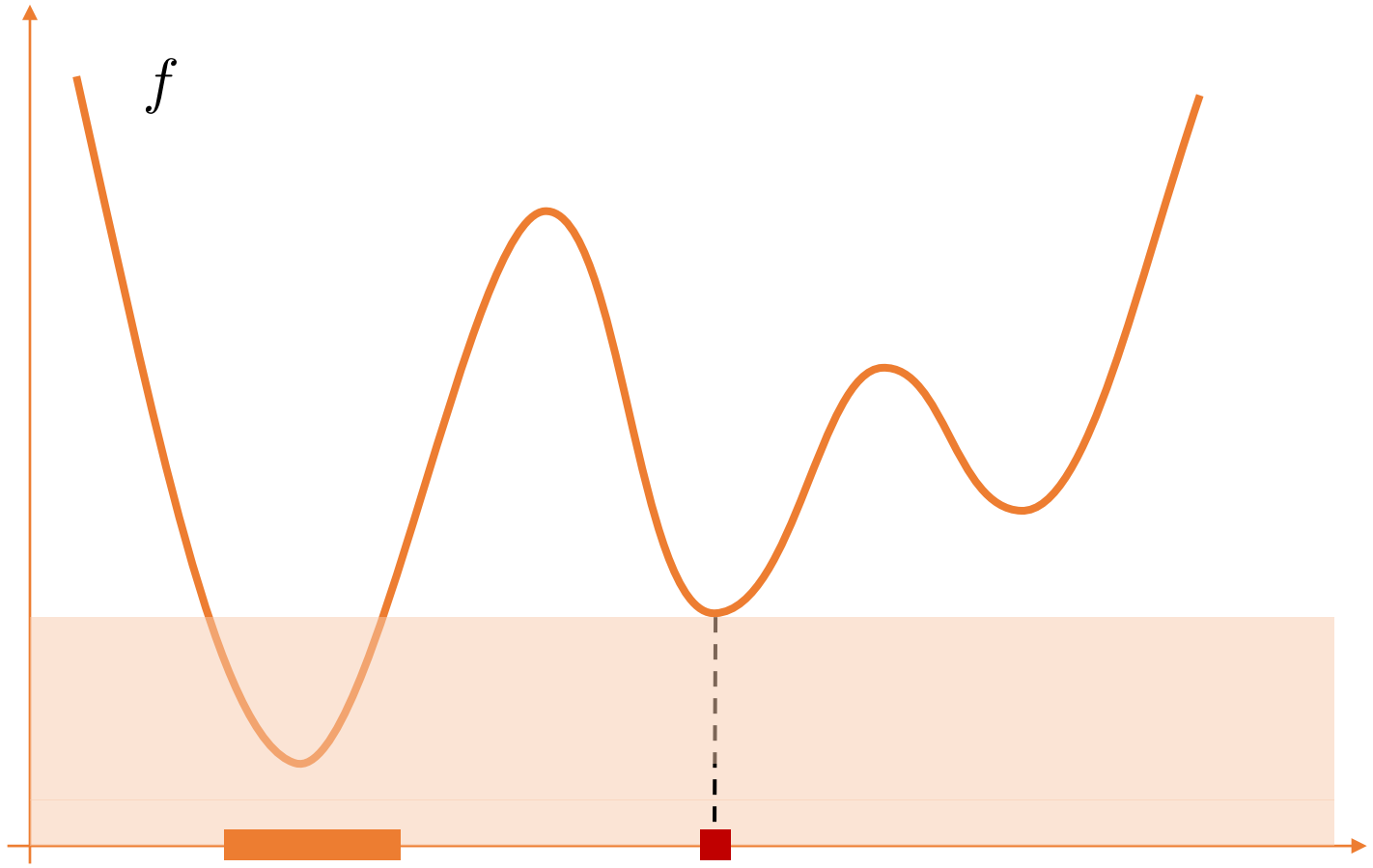
Sublevel Set Persistence



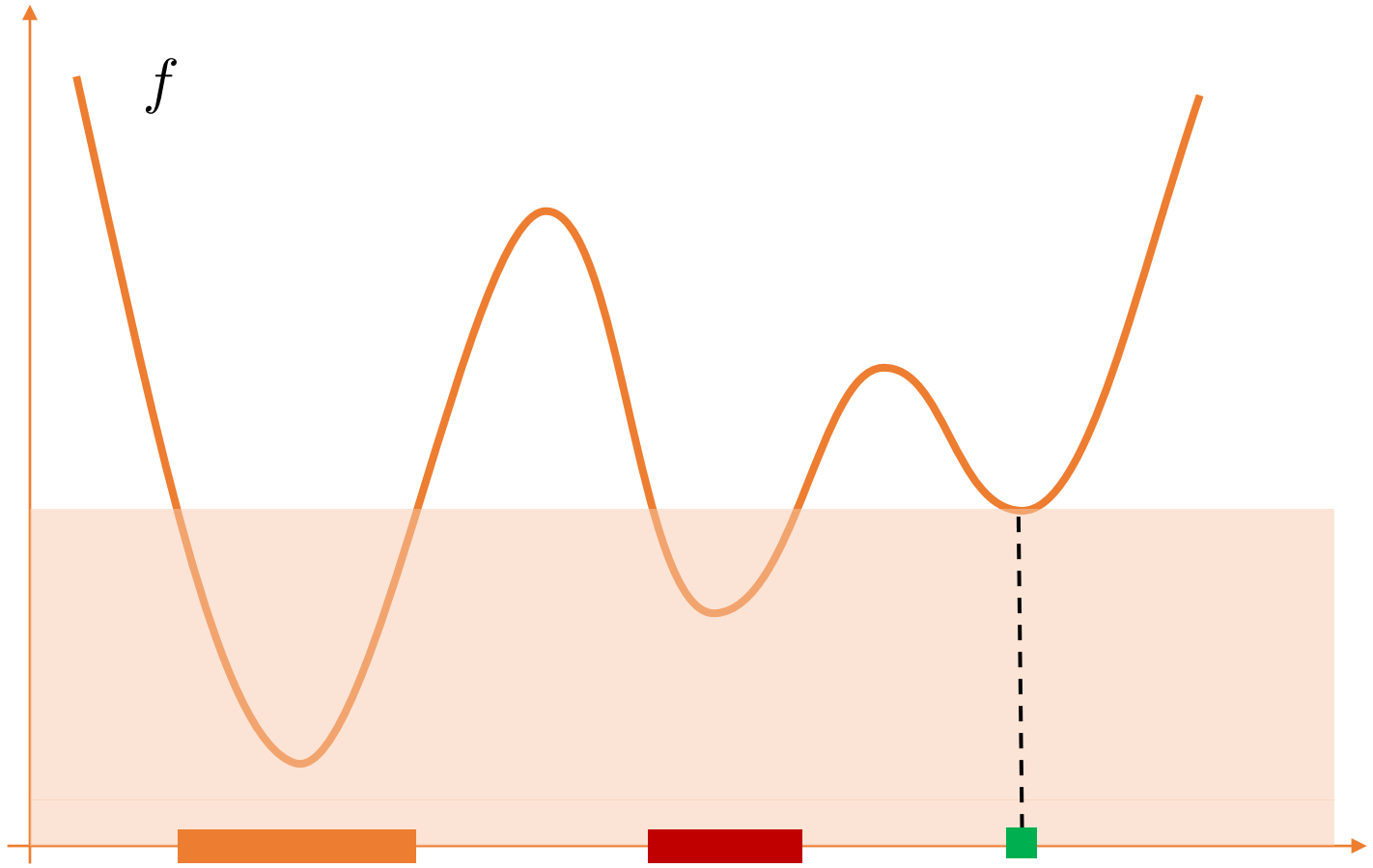
Sublevel Set Persistence



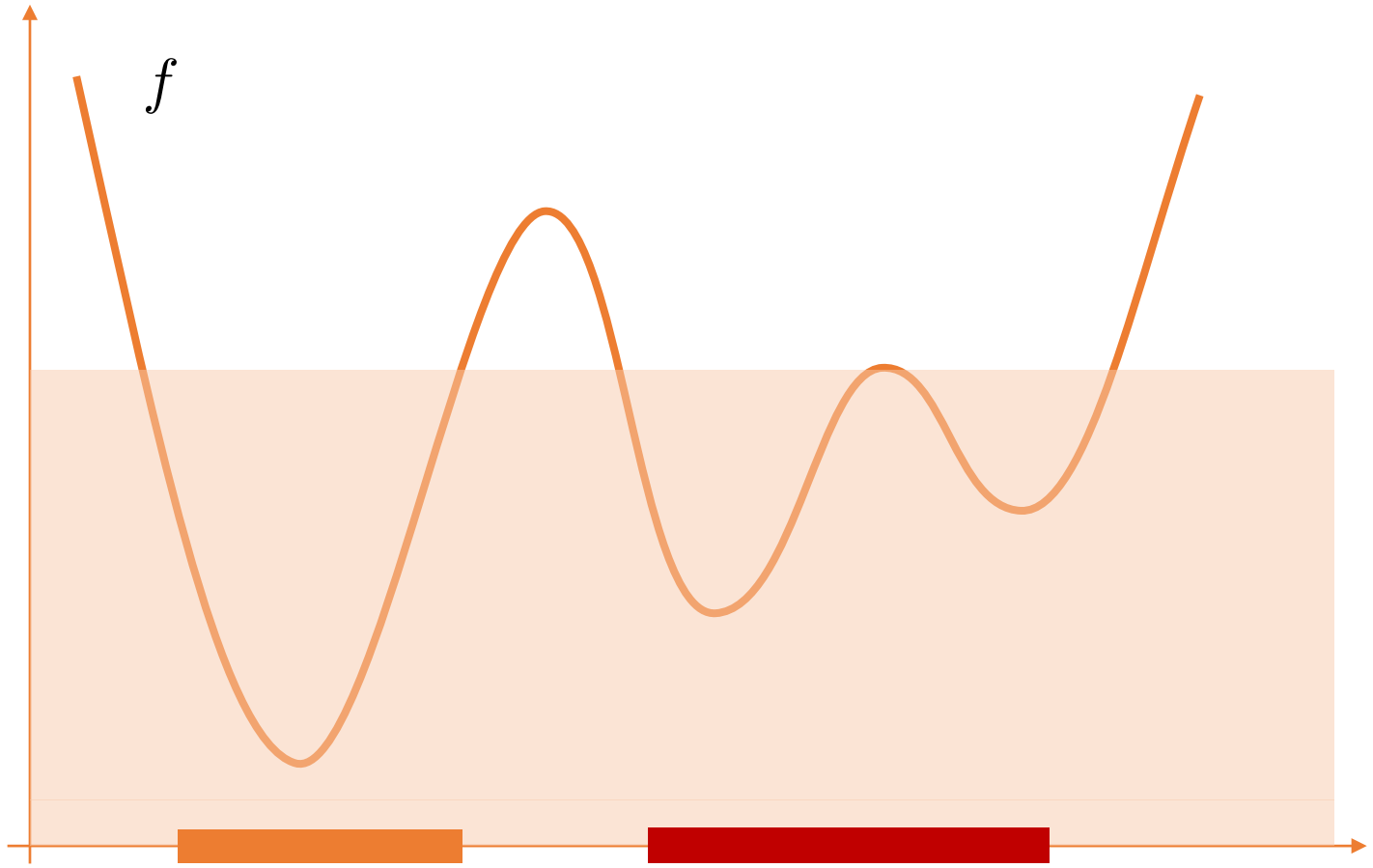
Sublevel Set Persistence



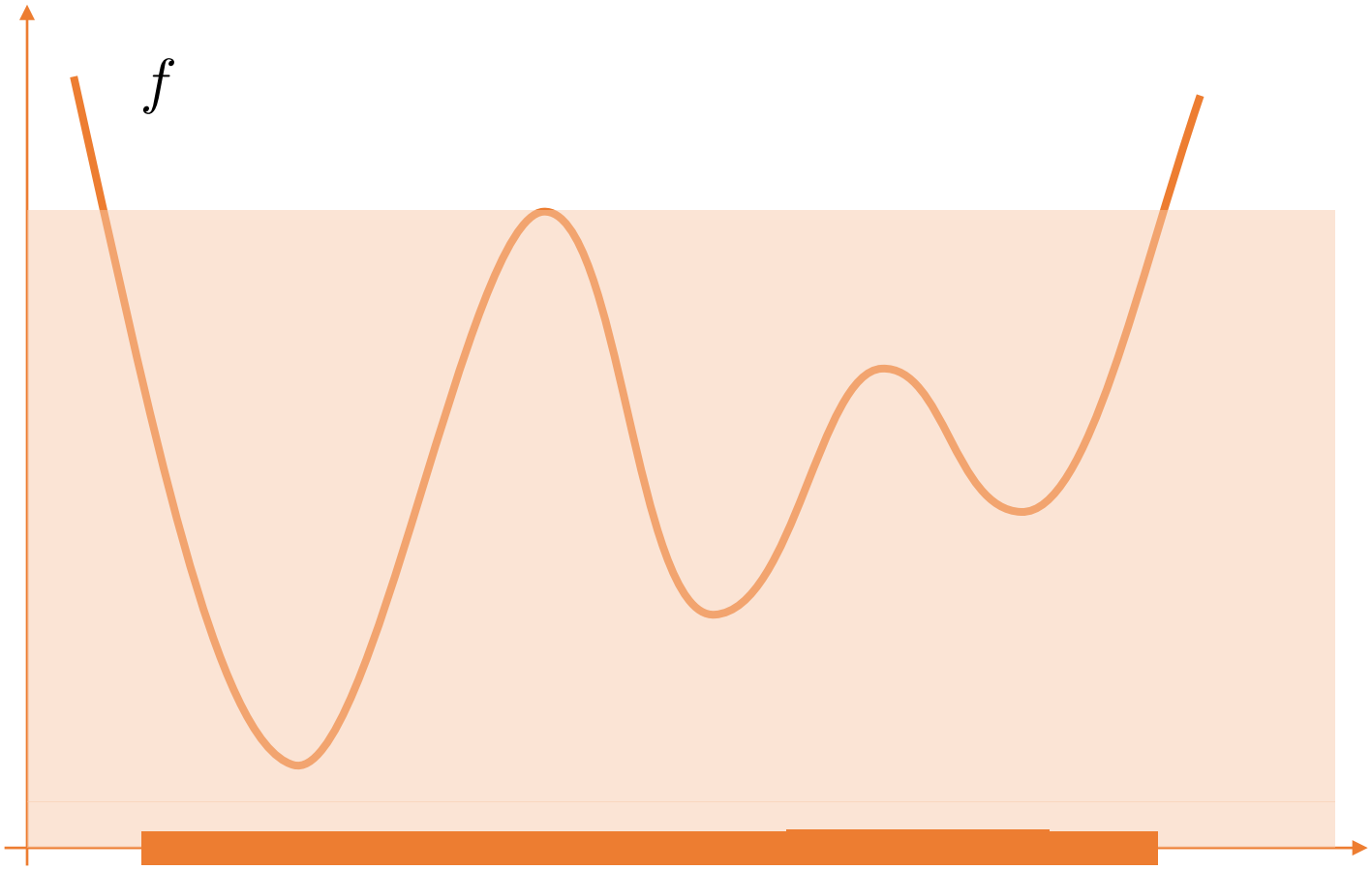
Sublevel Set Persistence



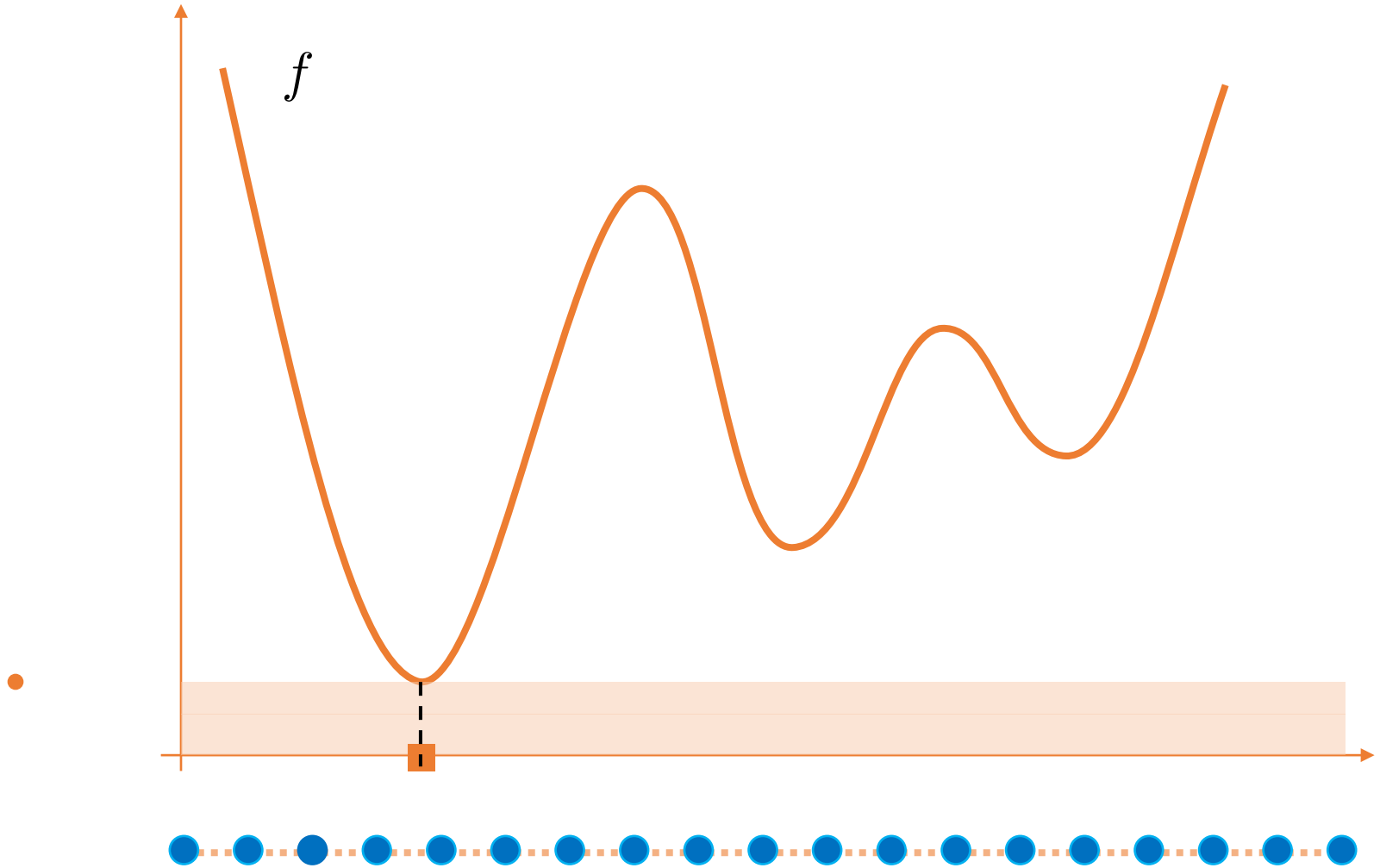
Sublevel Set Persistence



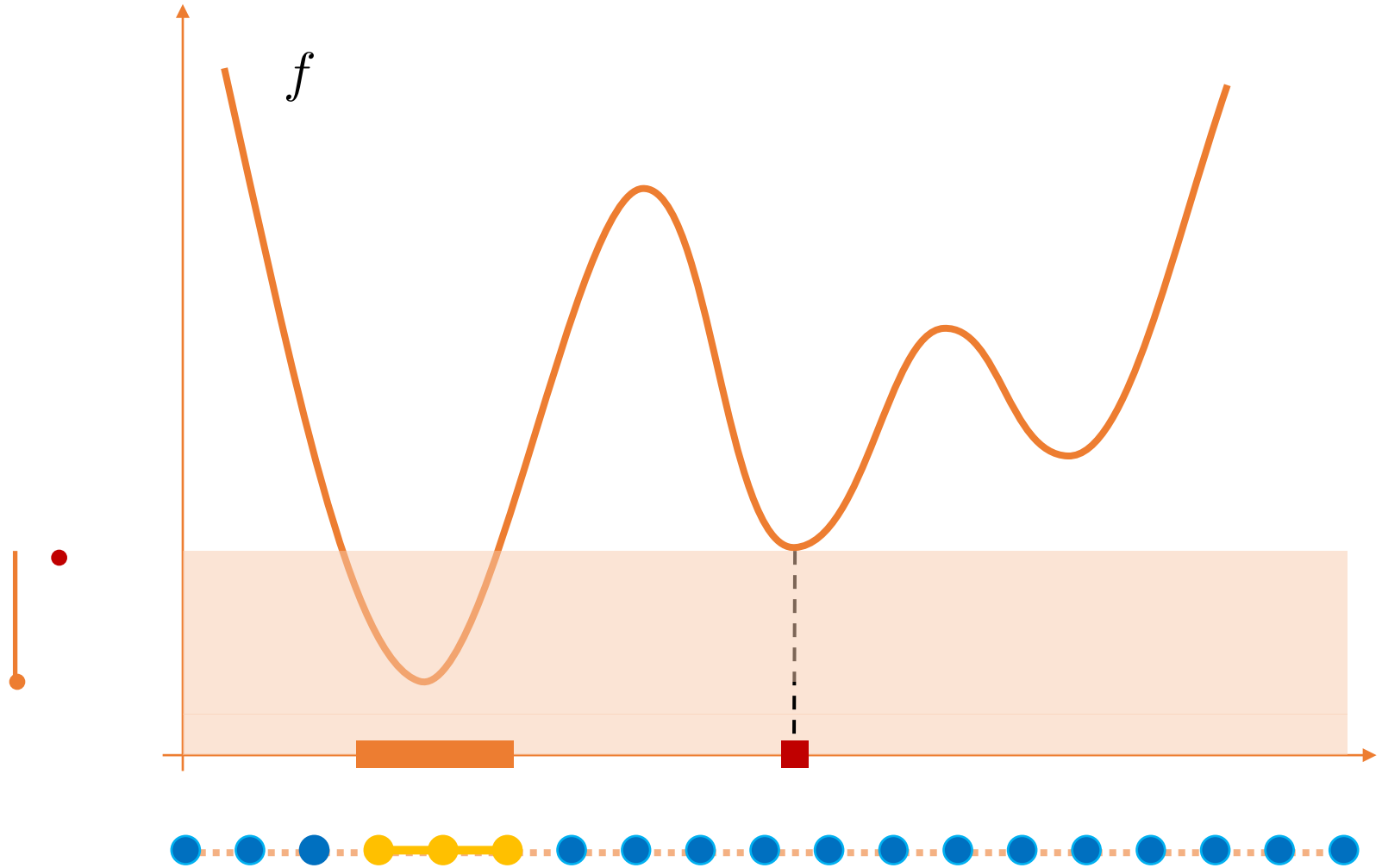
Sublevel Set Persistence



Sublevel Set Persistence



Sublevel Set Persistence



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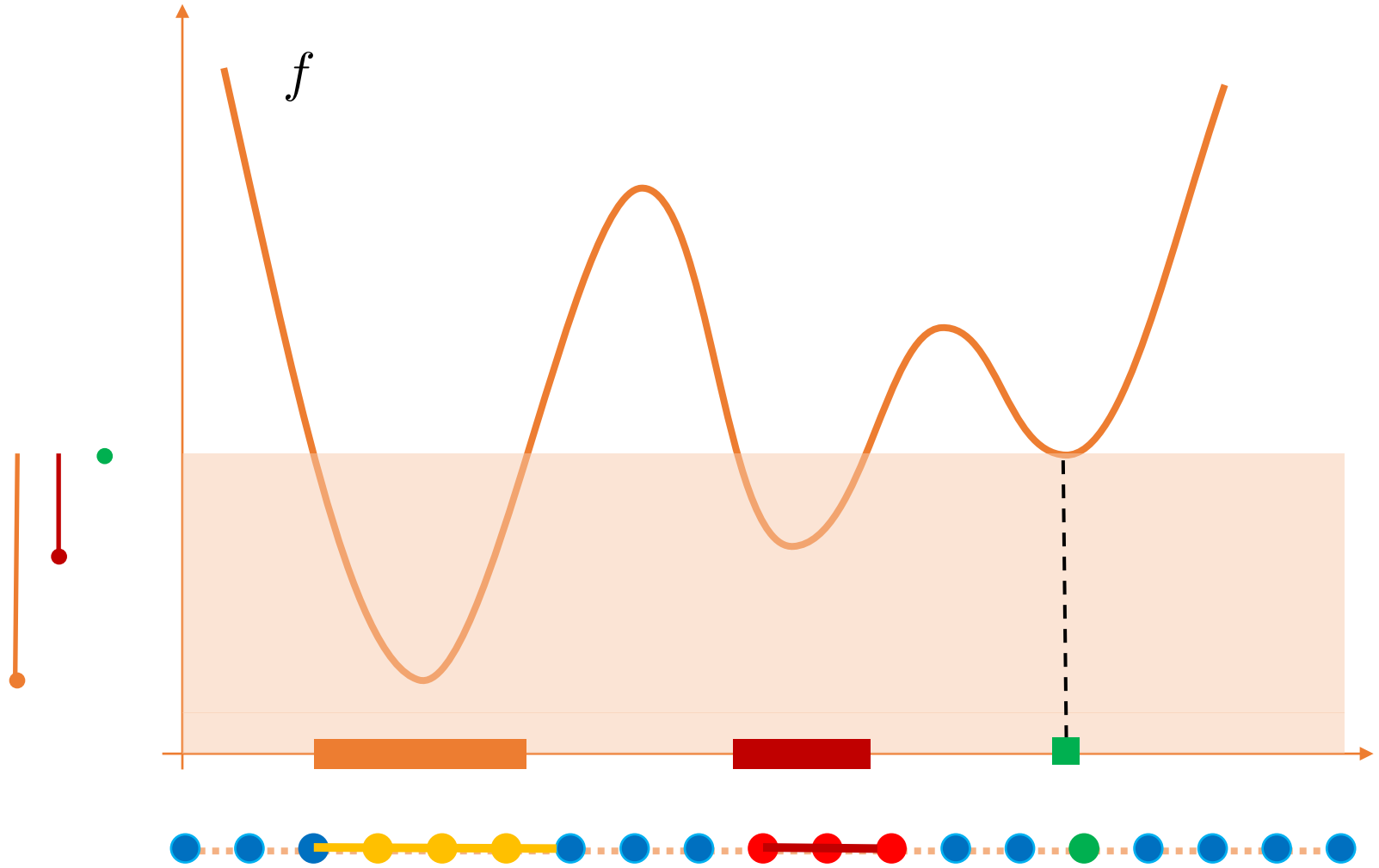

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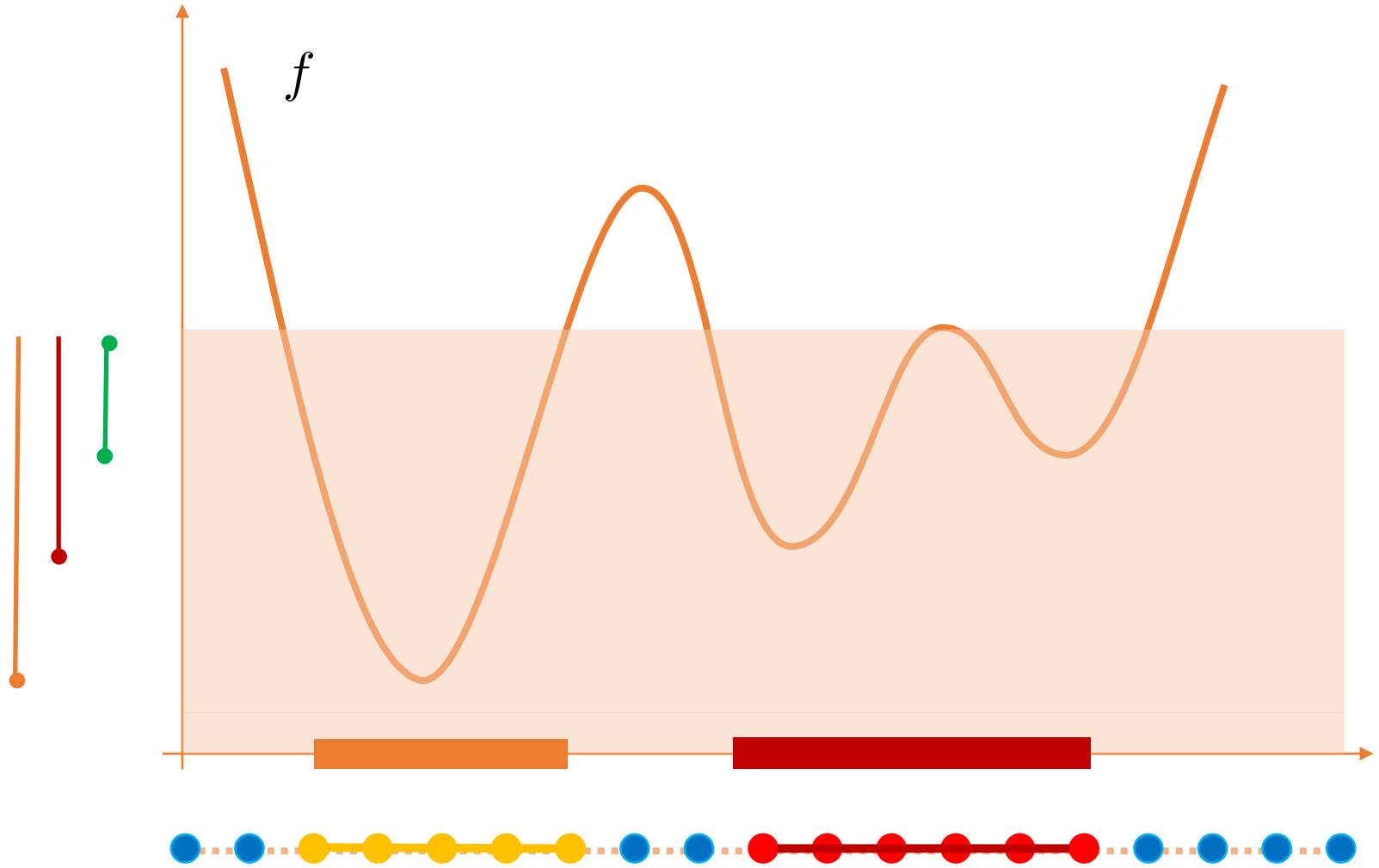

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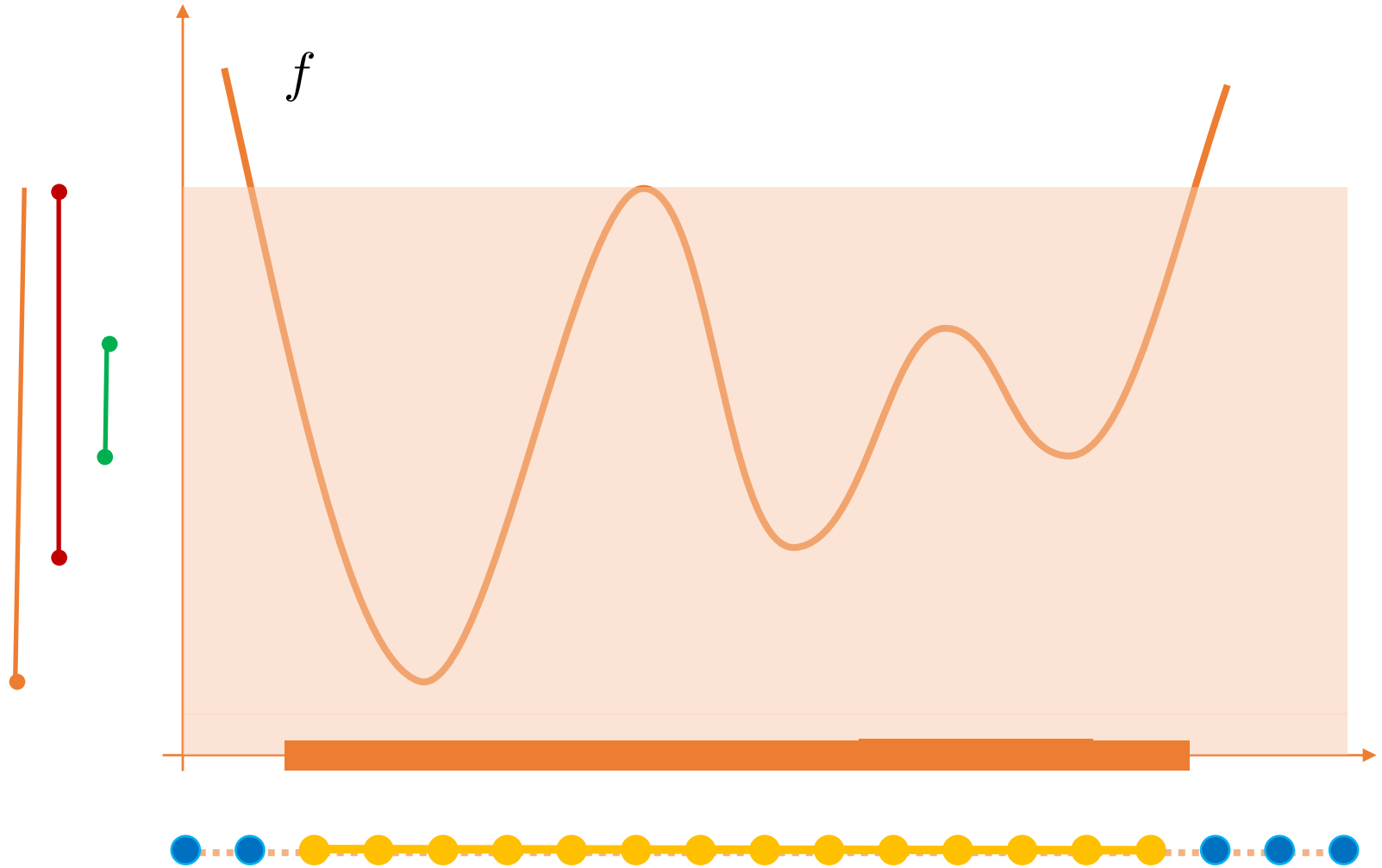
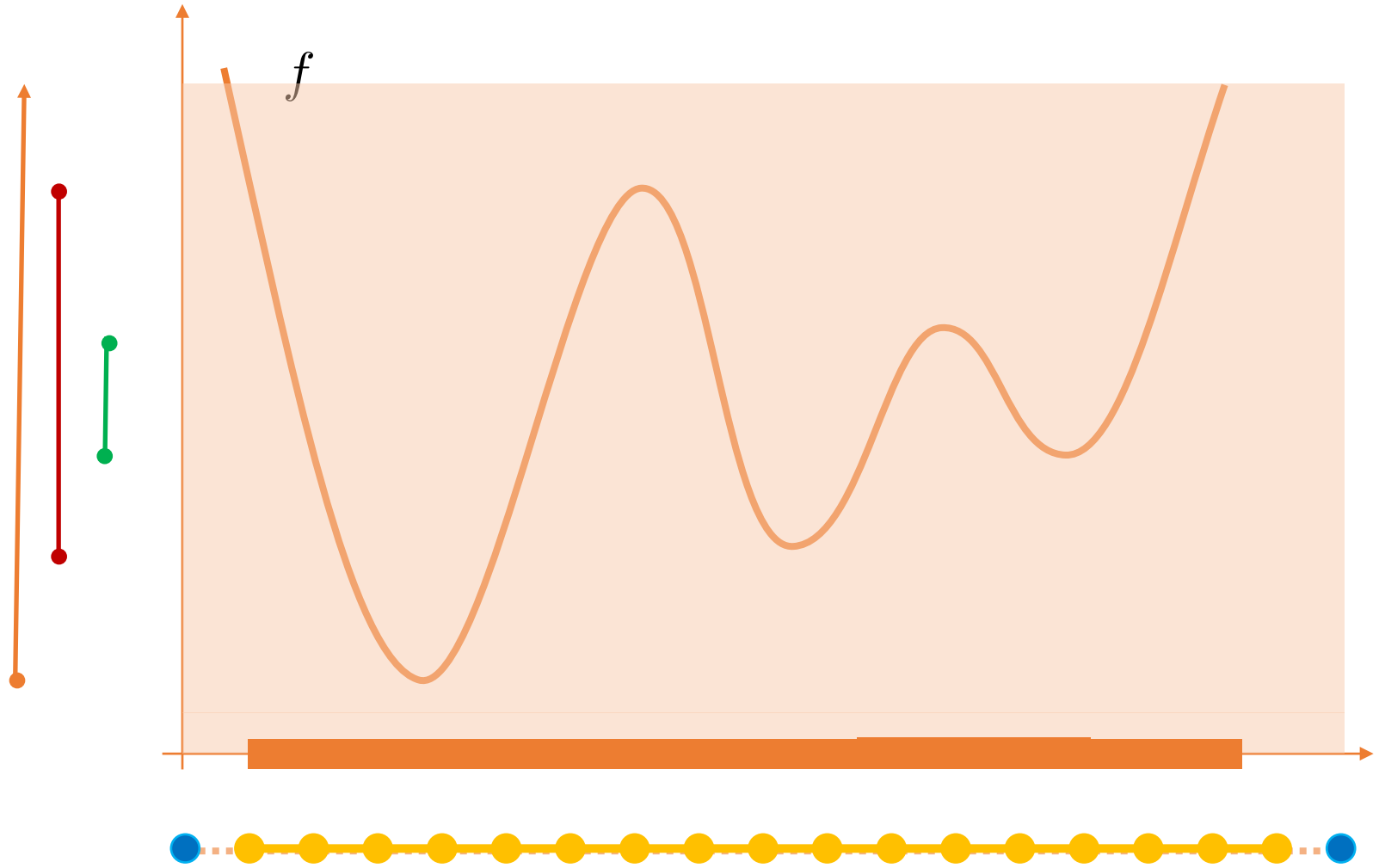
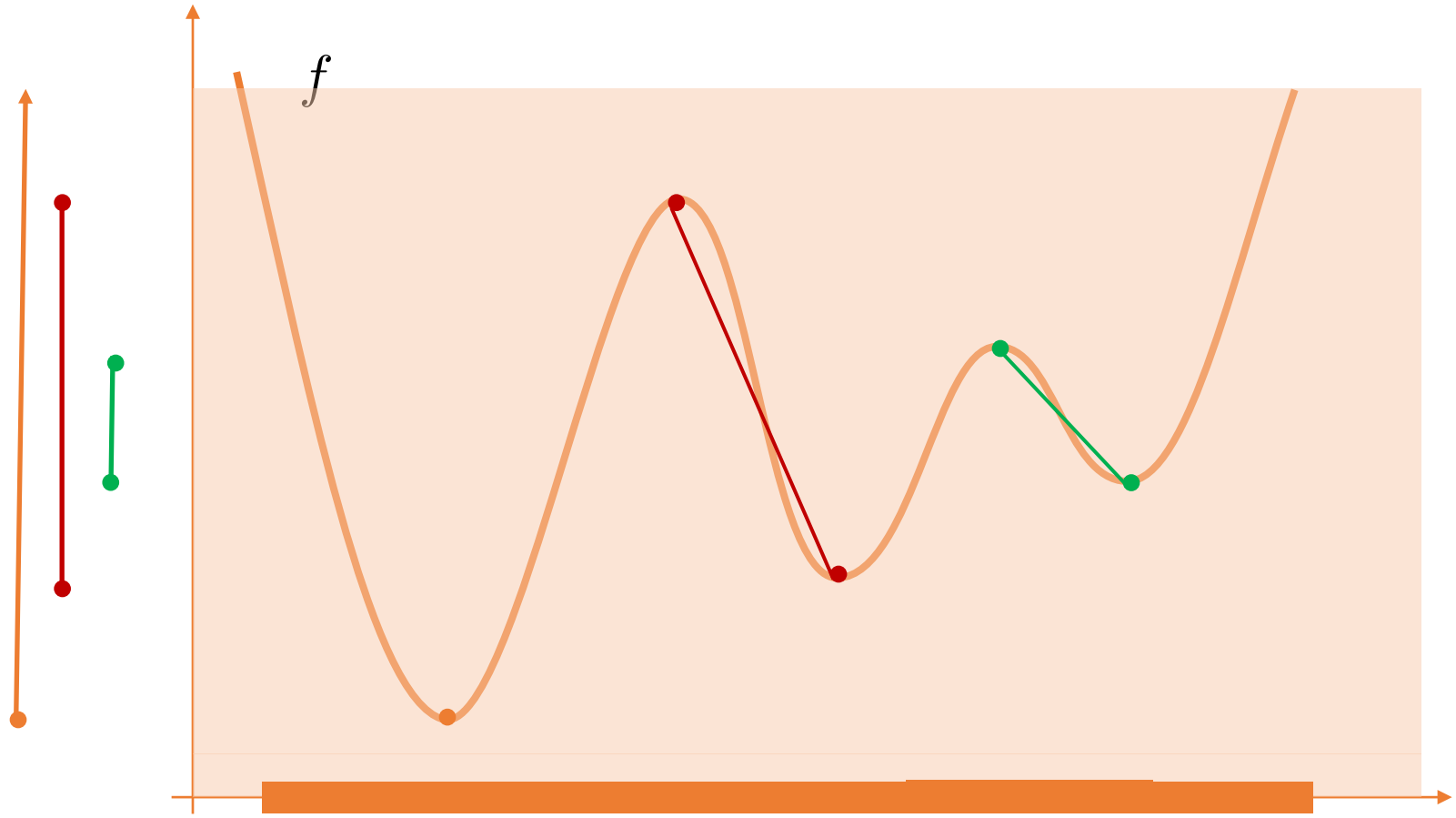


Persistence Gives a Pairing



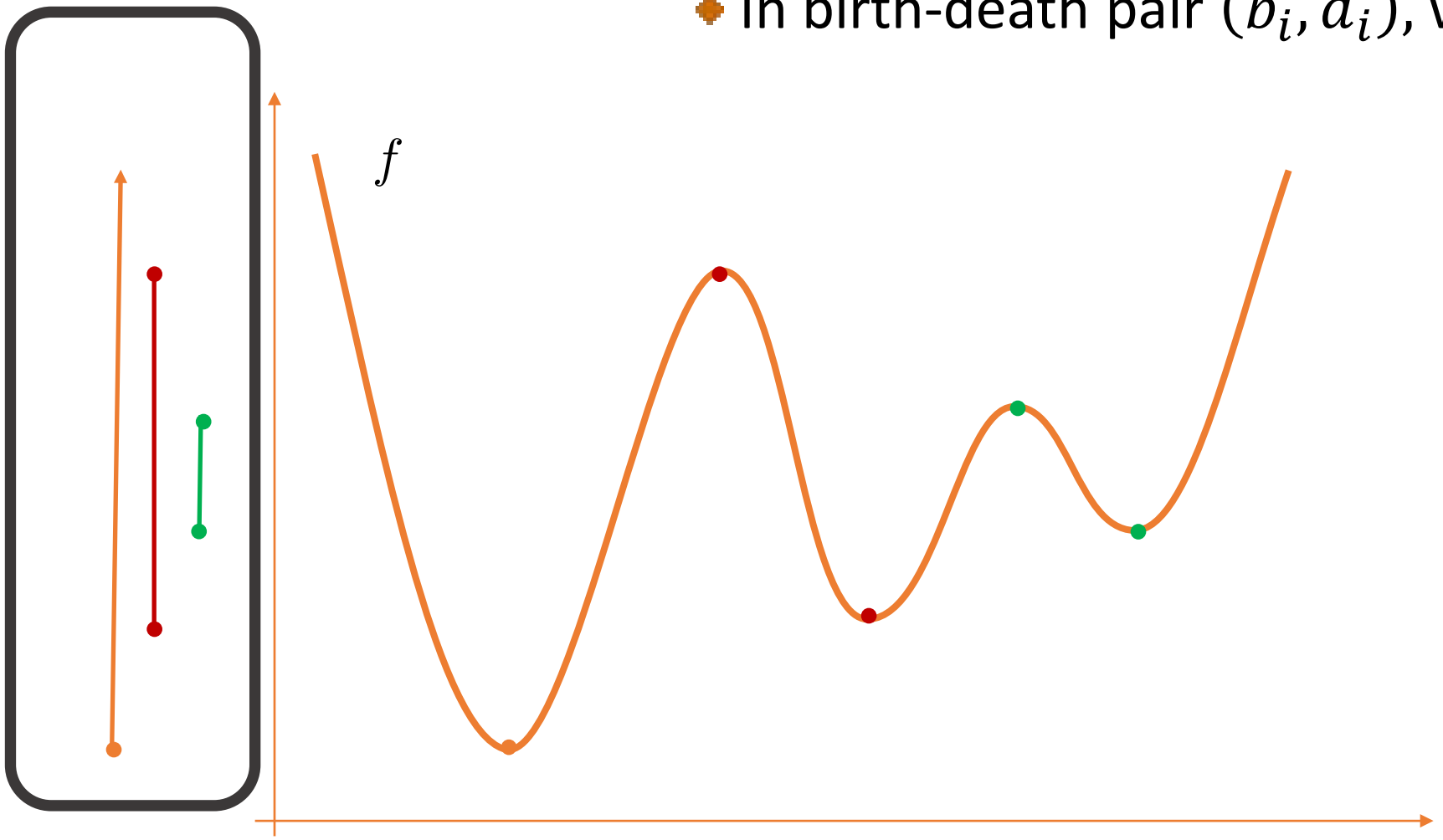
Elder Rule



Persistence barcodes and diagrams

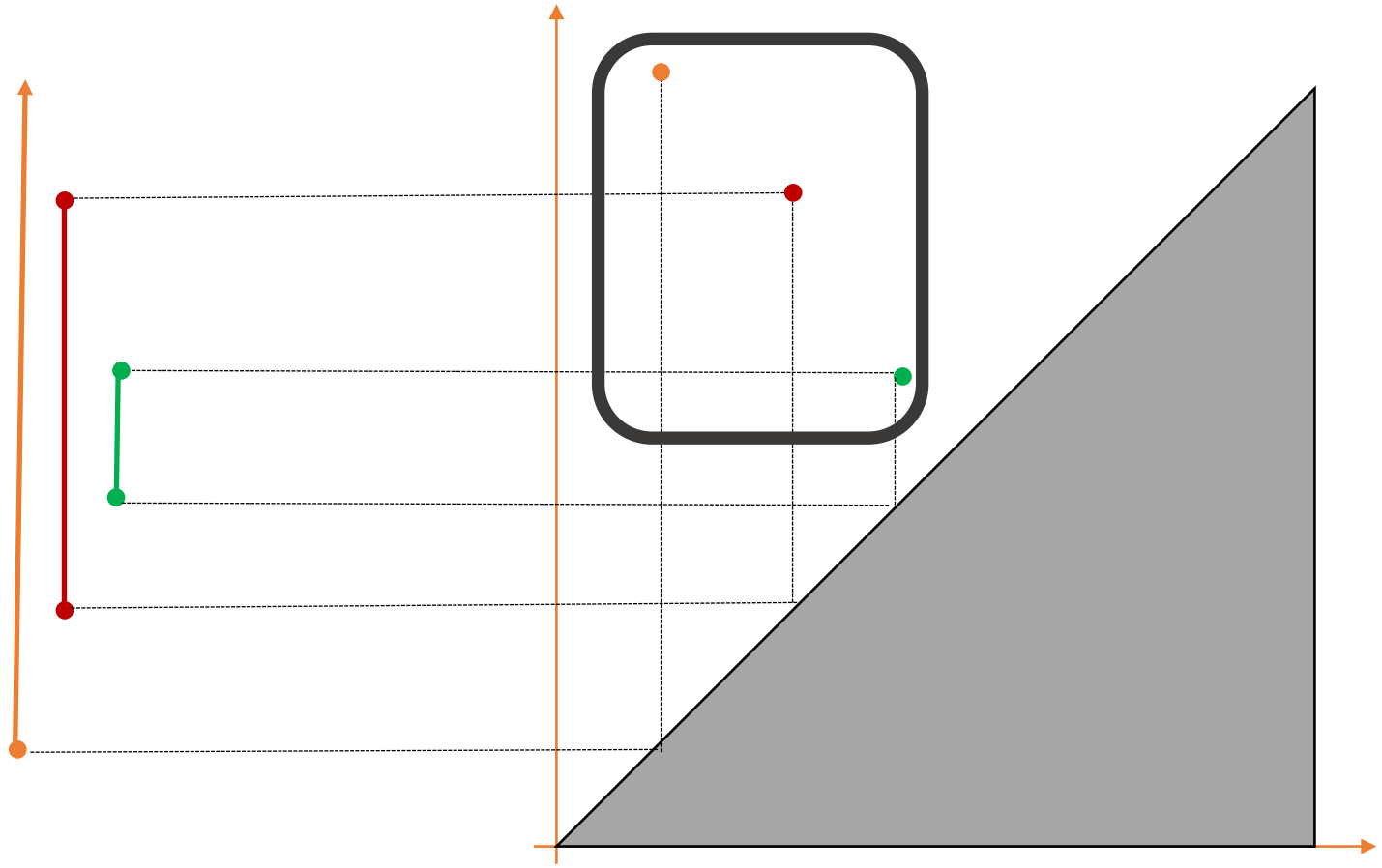
Persistence pairing yields a barcode

- 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

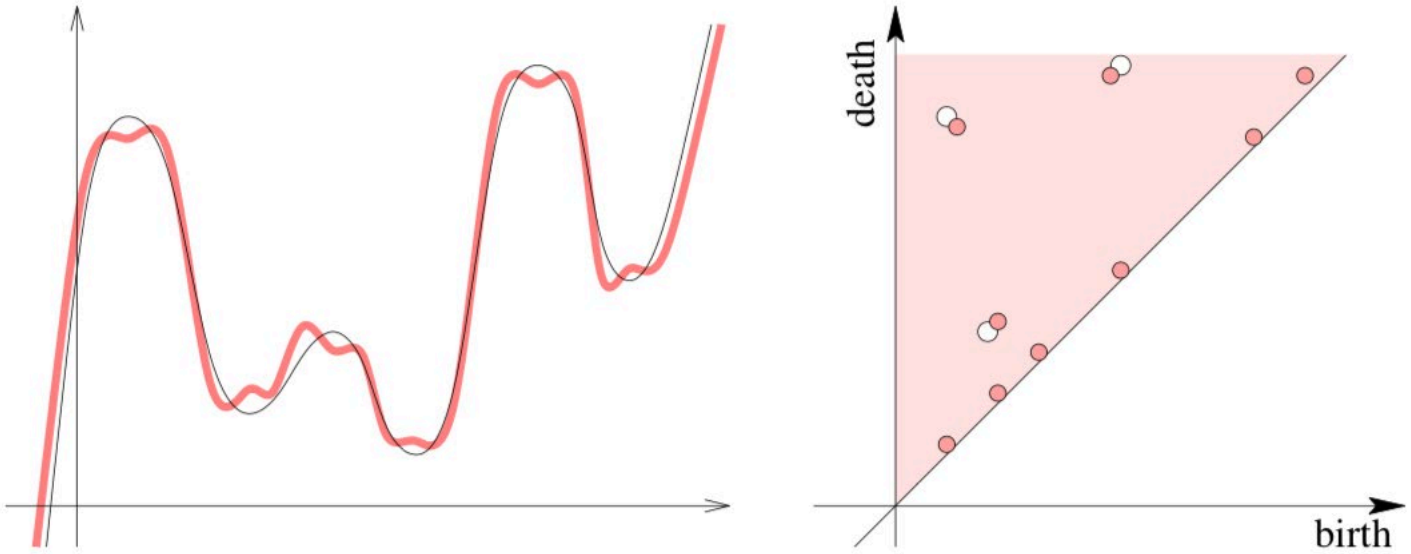


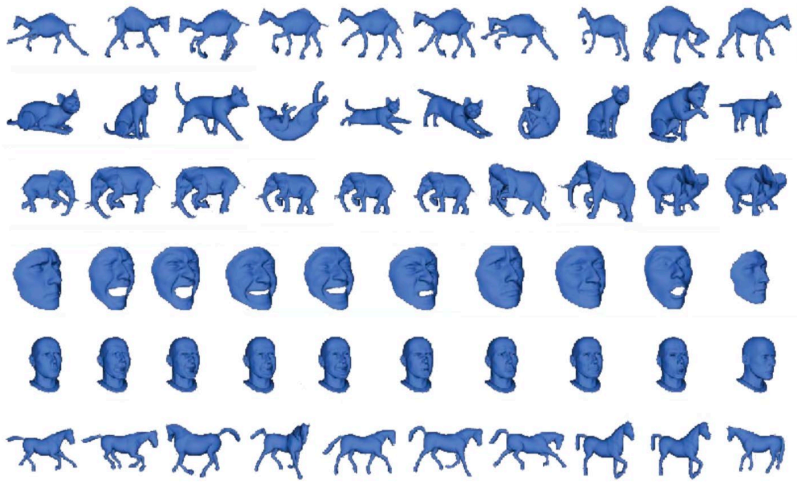
Figure from Edelsbrunner, Harer, *Computational Topology*

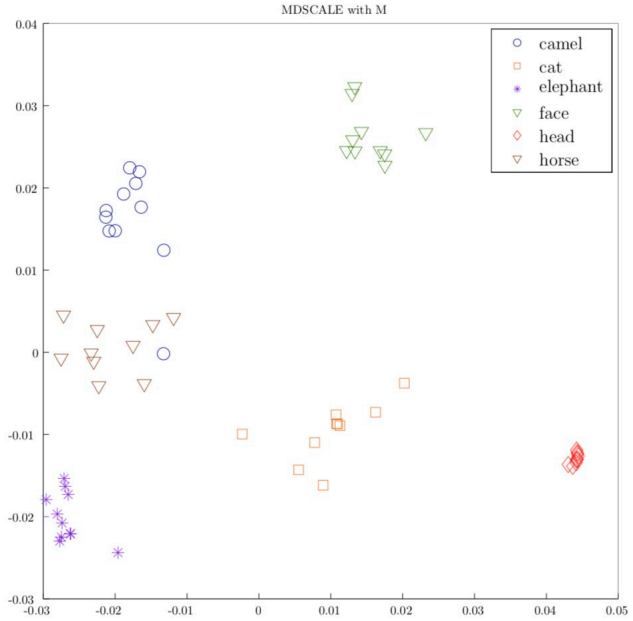
- Theorem (Cohen-Steiner, Edelsbrunner, Harer): $\mathcal{M}$ a triangulable space, $f, g: \mathcal{M} \to \mathbb{R}$ "nice". Then,
$$d_B\big(D_k(f), D_k(g)\big) \leq \|f - g\|_\infty.$$

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

Stability of persistent homology

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

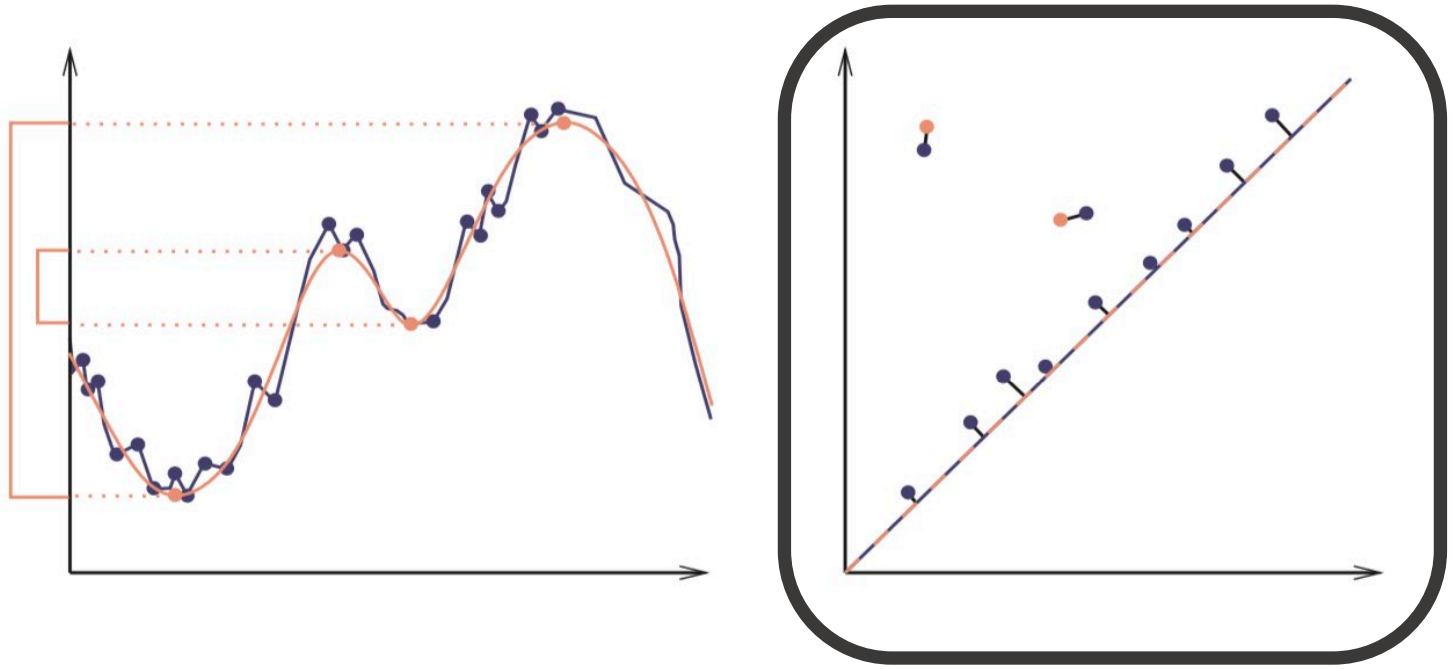




- Theorem (Chazal, Cohen-Steiner, Guibas, Mémoli, Oudot): $(X, d_X), (Y, d_Y)$ finite metric spaces. Then,
$$d_B\big(D_k(VR(X)), D_k(VR(Y))\big) \leq 2d_{GH}(X, Y).$$

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

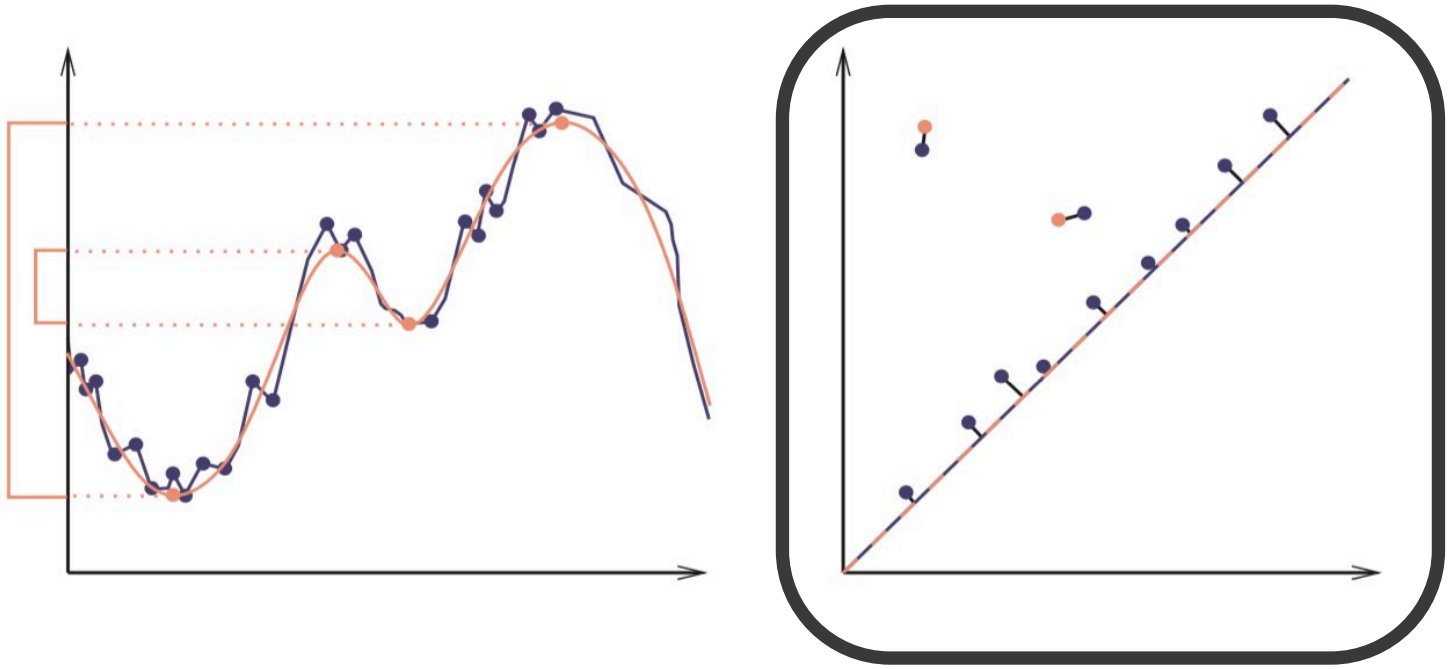
The bottleneck distance



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.

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

Gromov-Hausdorff stability

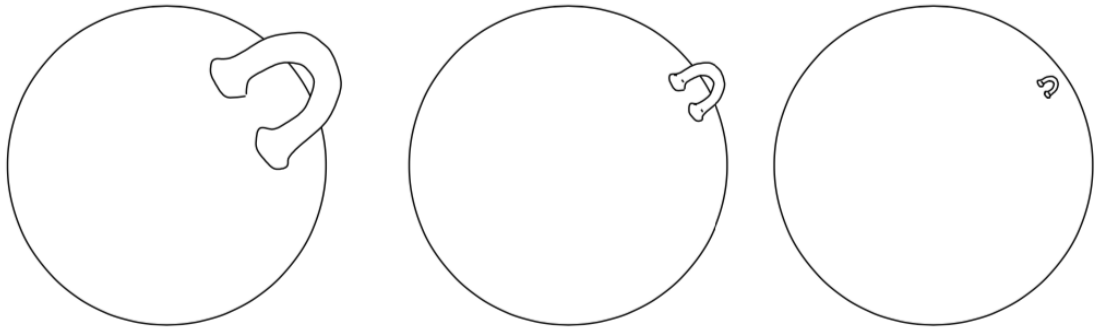


Figure from Burago, Burago, Ivanov, *A course in metric geometry*

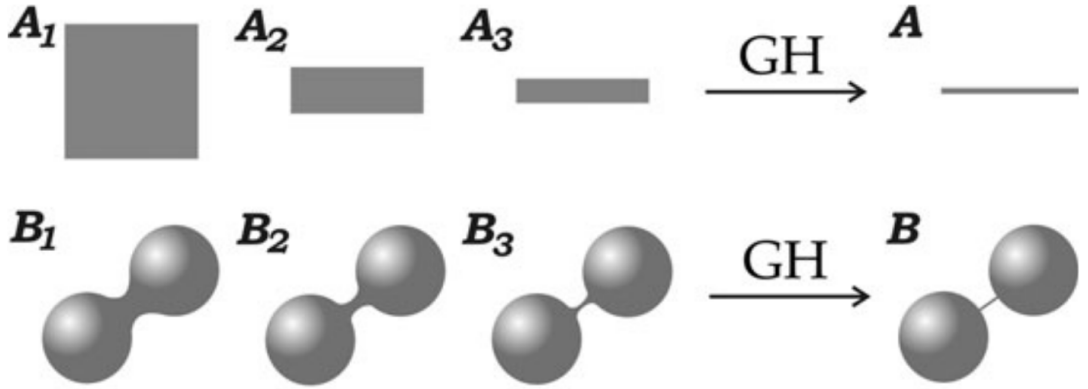


Figure from Sormani, *How Riemannian manifolds converge*

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

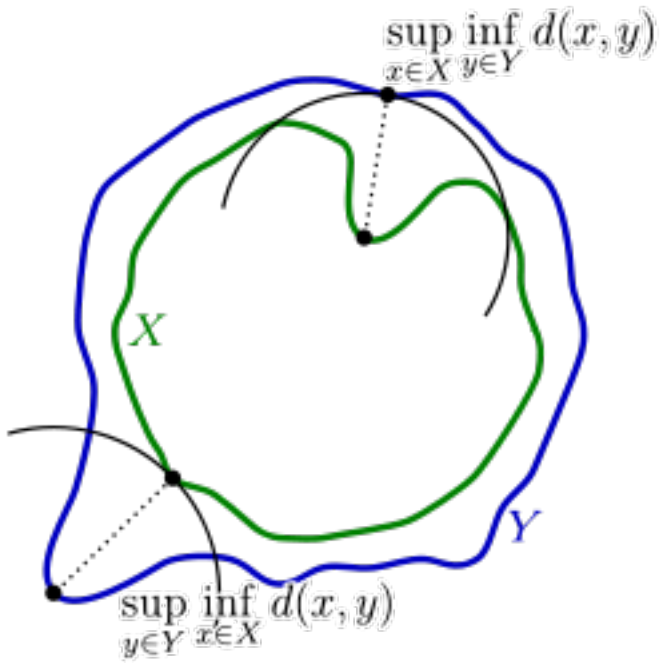
- Used to study convergence of spaces
- Popularized by Gromov in the context of geometric group theory

Gromov-Hausdorff stability

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

Hausdorff distance:

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

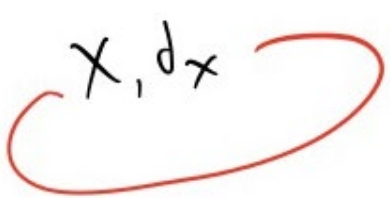


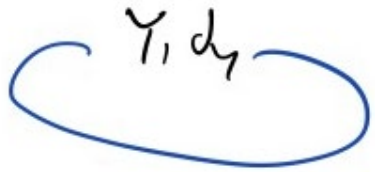
$(X, d_X), (Y, d_Y)$ finite metric spaces

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





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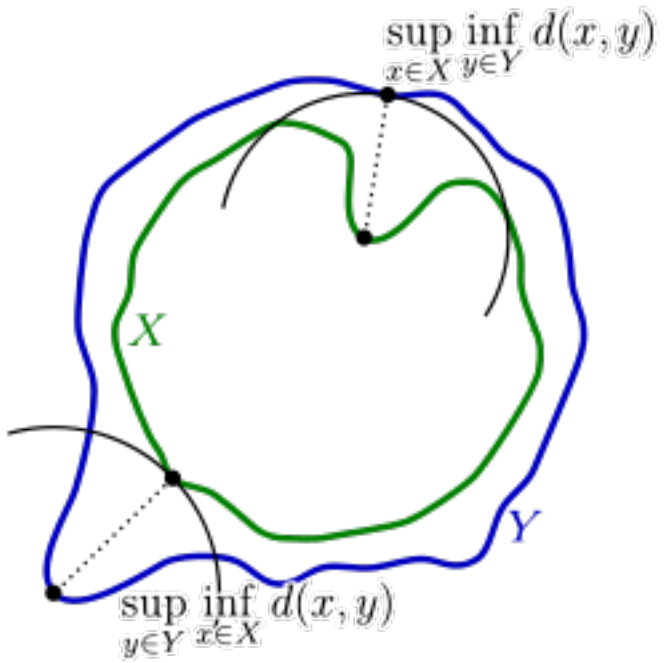

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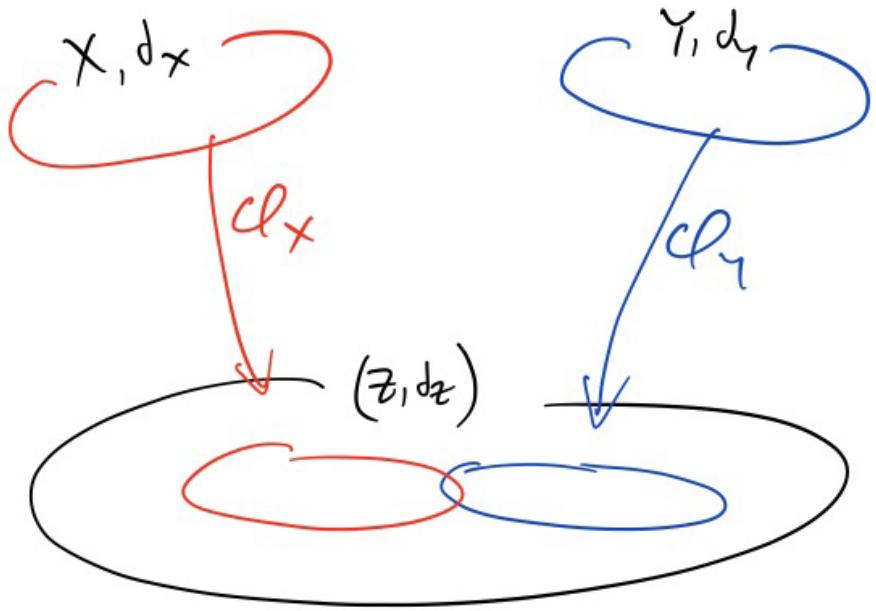
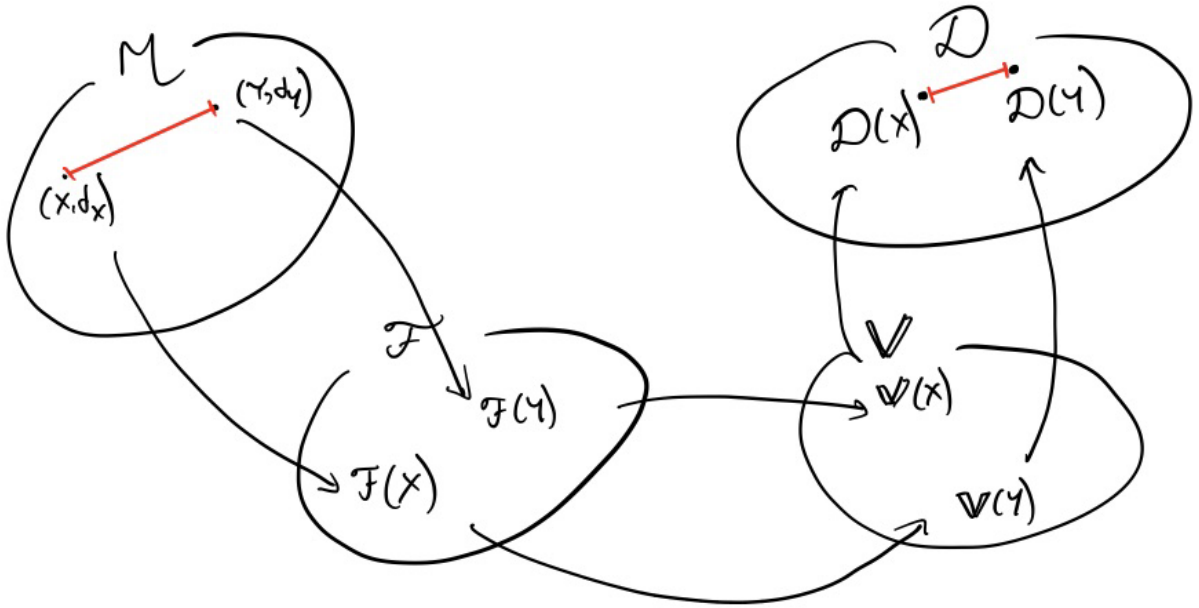


Gromov-Hausdorff stability



$\mathcal{M}$ = 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,

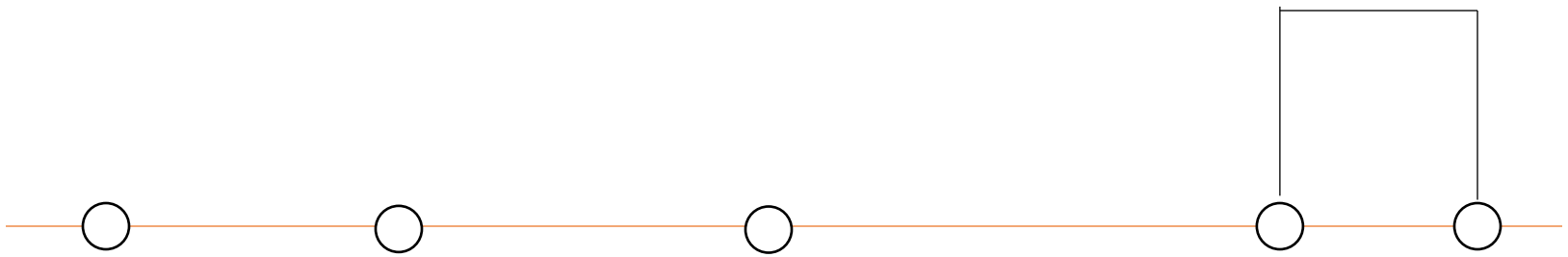
$$d_B\big(D_k(VR(X)), D_k(VR(Y))\big) \leq 2d_{GH}(X, Y).$$

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

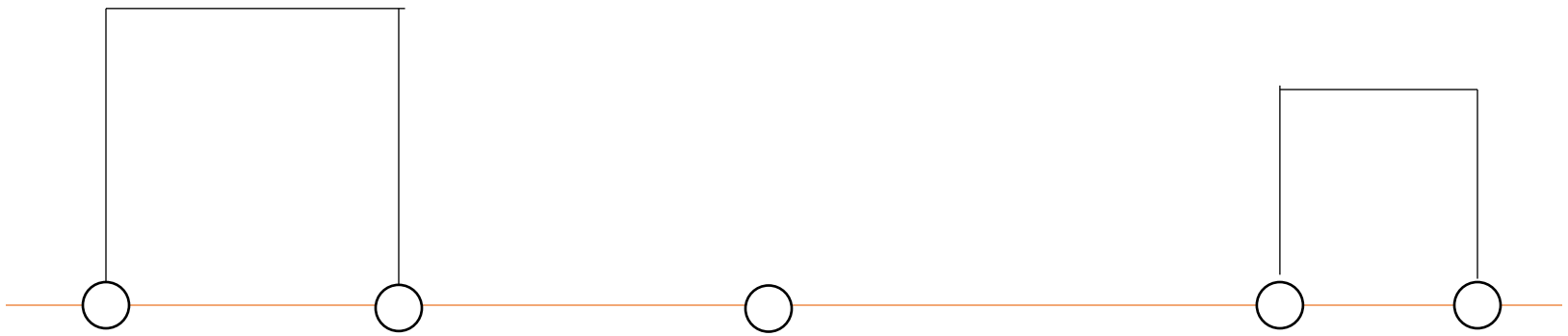
NP-hard

0-dimensional persistence and single linkage clustering

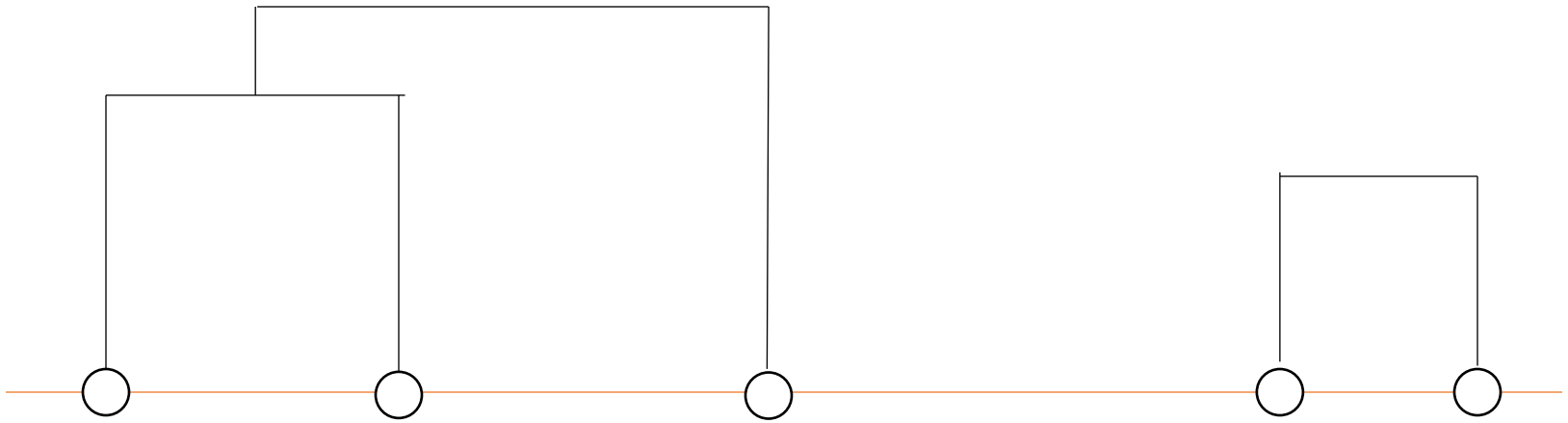
0-dimensional persistence and single linkage clustering



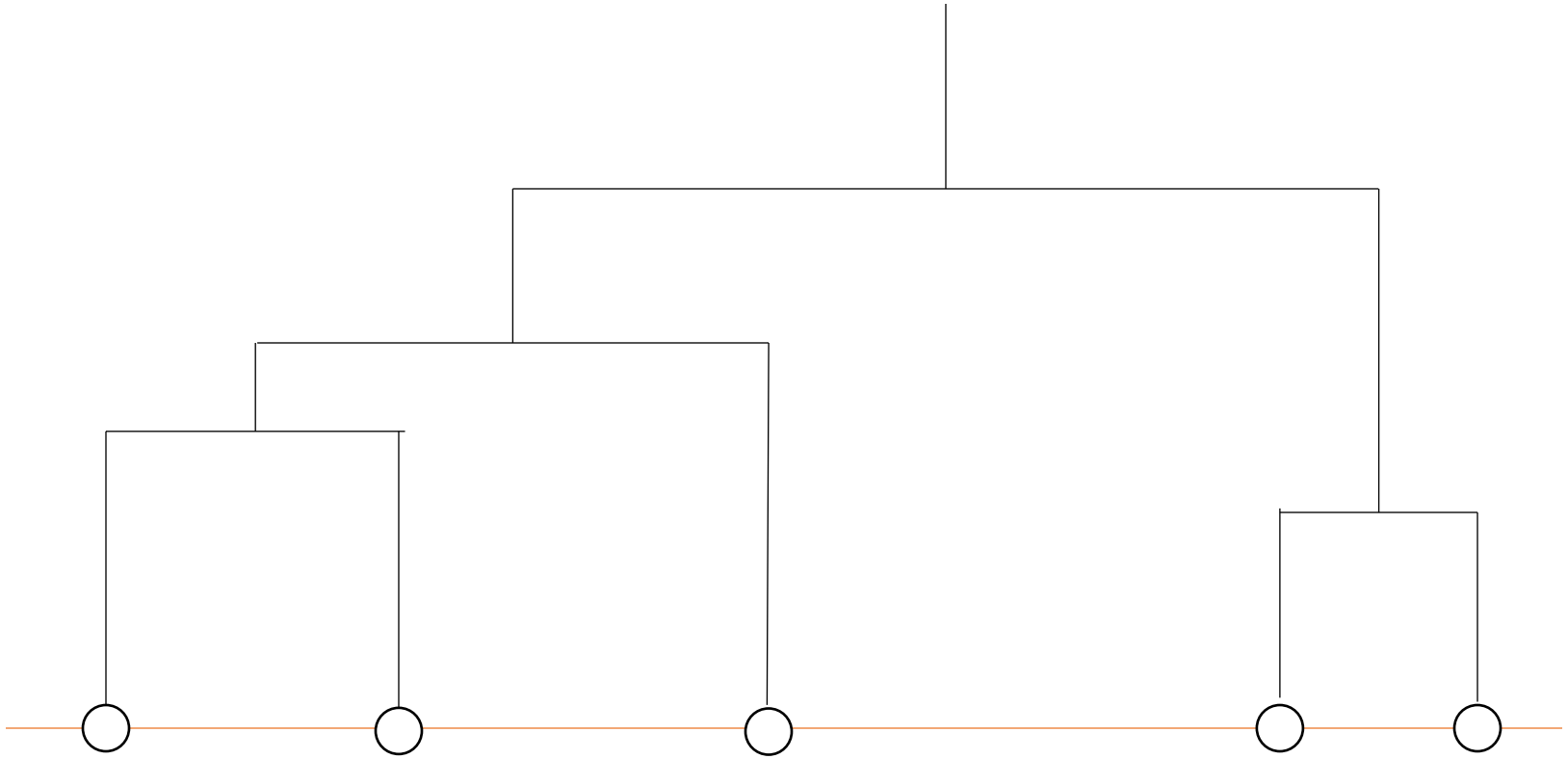
0-dimensional persistence and single linkage clustering



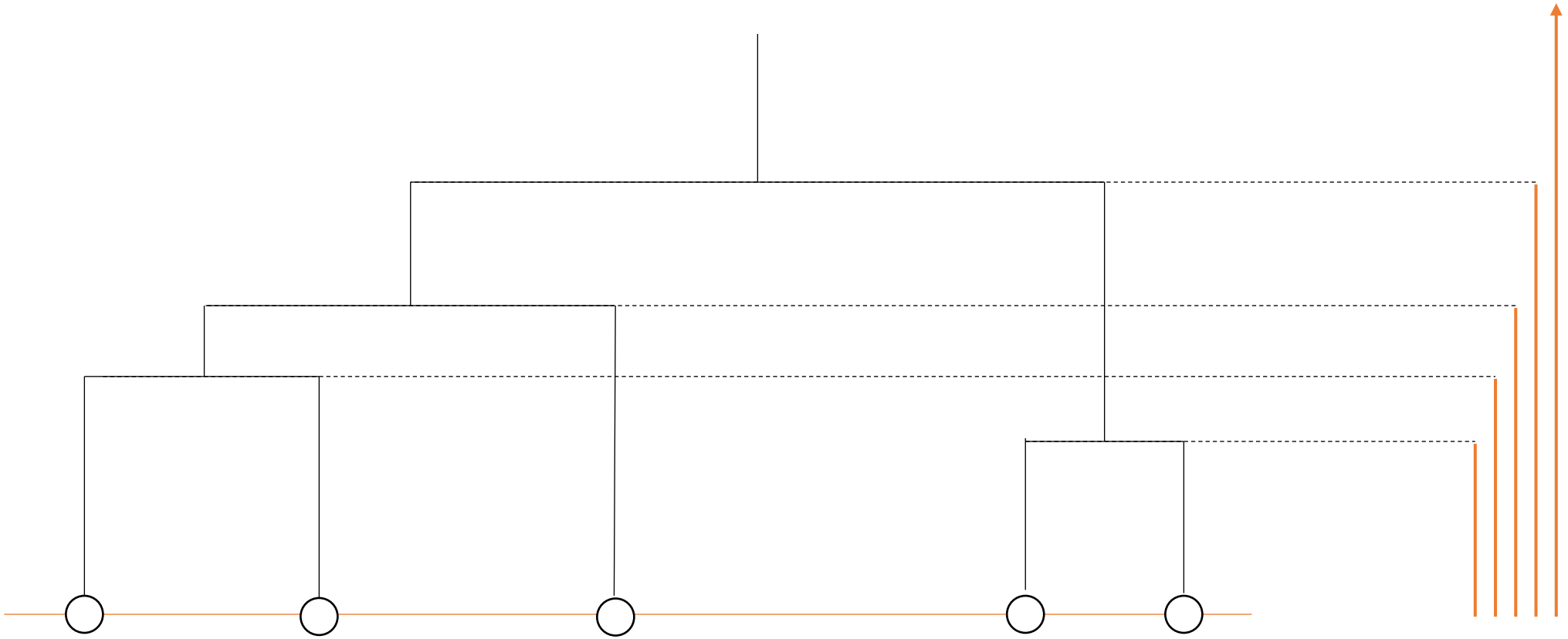
0-dimensional persistence and single linkage clustering



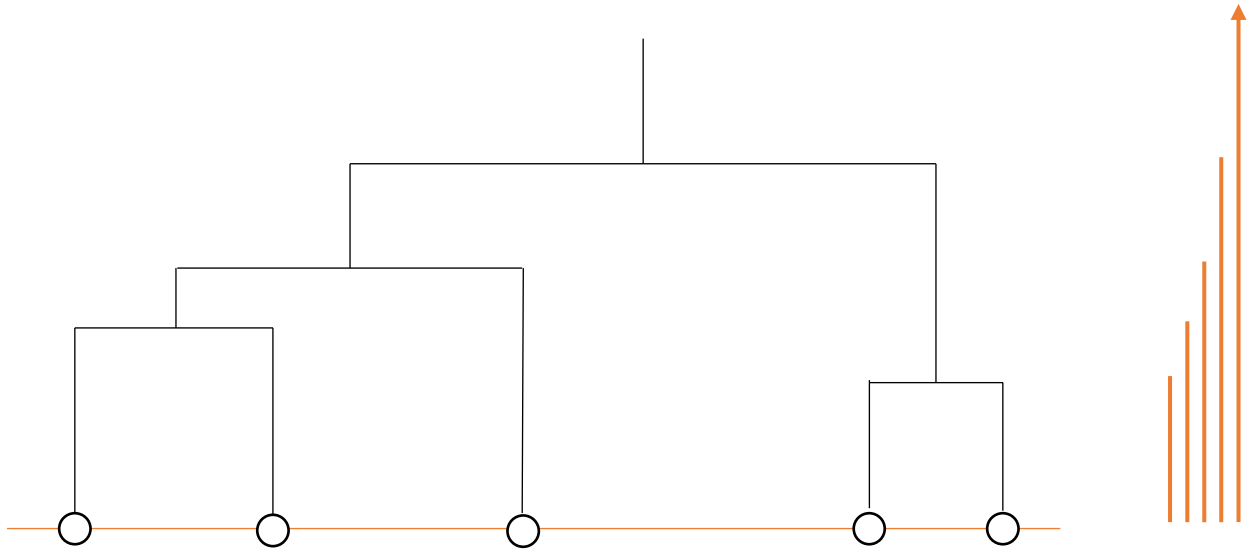
0-dimensional persistence and single linkage clustering



0-dimensional persistence and single linkage clustering



0-dimensional persistence and single linkage clustering



- Fact: { dendrograms } ↔ {ultrametric spaces}
- Theorem (Carlsson, Mémoli): Let (X, u_X) denote the output of SLHC on (X, d_X). Then,

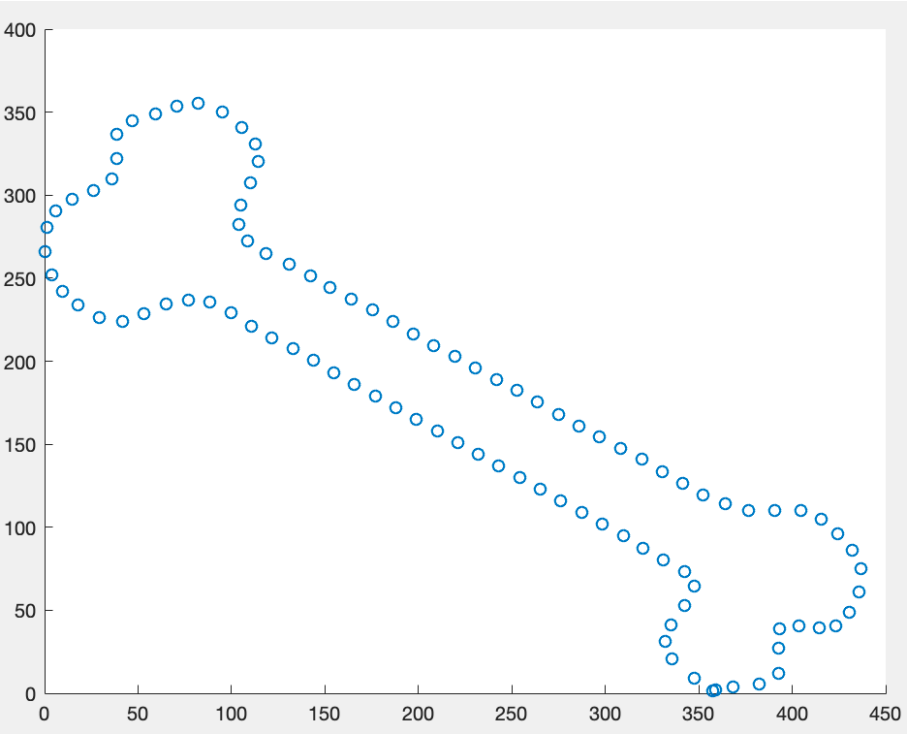
$$d_{GH}\big((X, u_X), (Y, u_Y)\big) \leq d_{GH}\big((X, d_X), (Y, d_Y)\big).$$

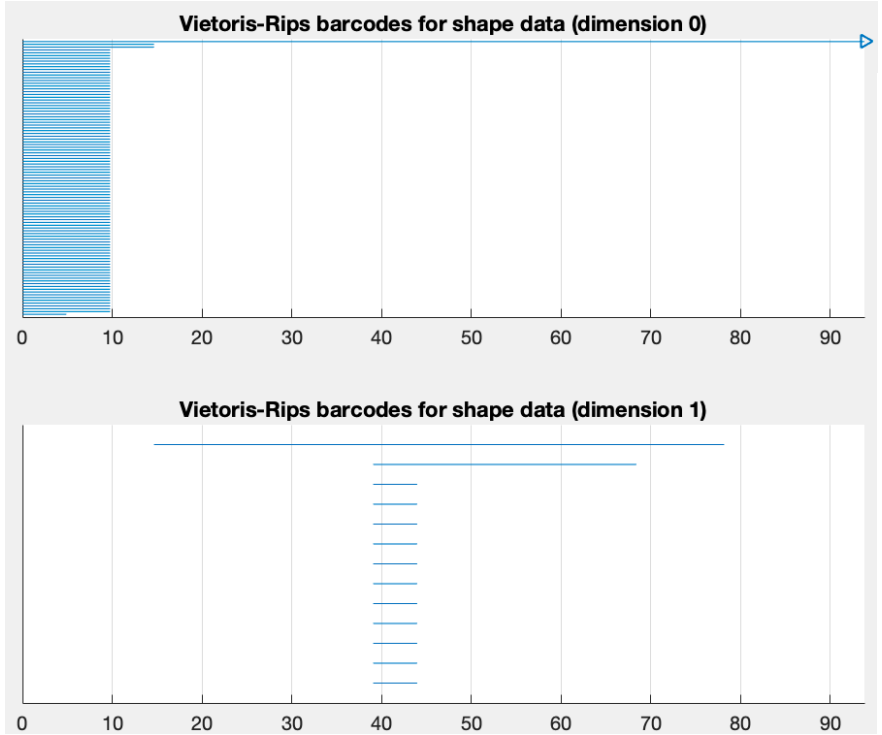
- (Tradeoff) 0-dimensional persistence loses information but permits comparison via d_B (easier than d_{GH})

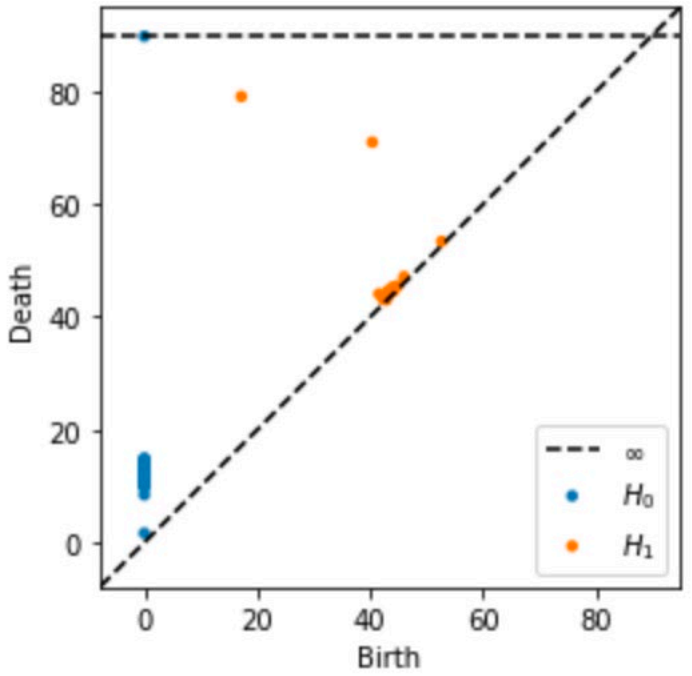
Software packages

- 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
- …many others

Demo – Javaplex and Ripser







The End