Ripser

or: the unexpected efficiency of persistent cohomology

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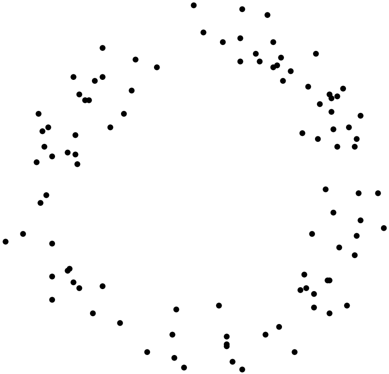
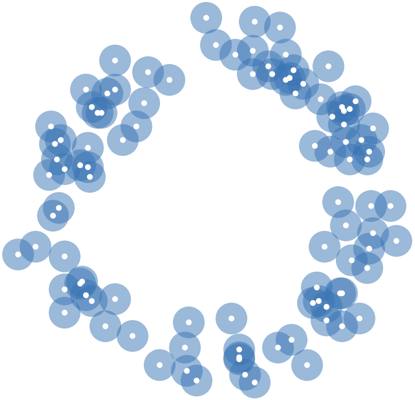
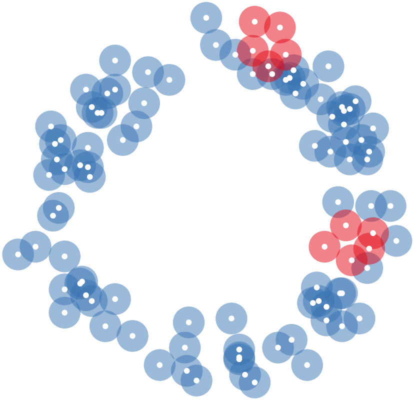
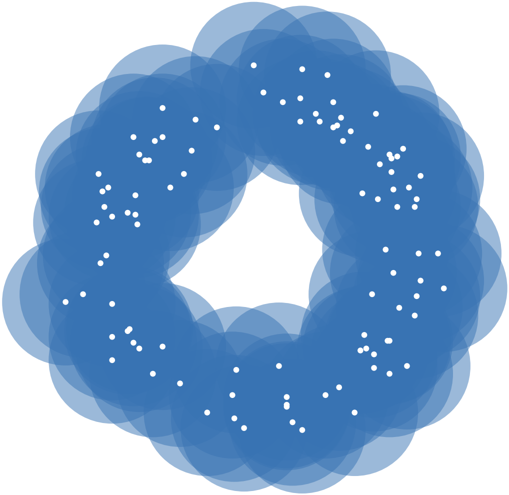
TU Graz

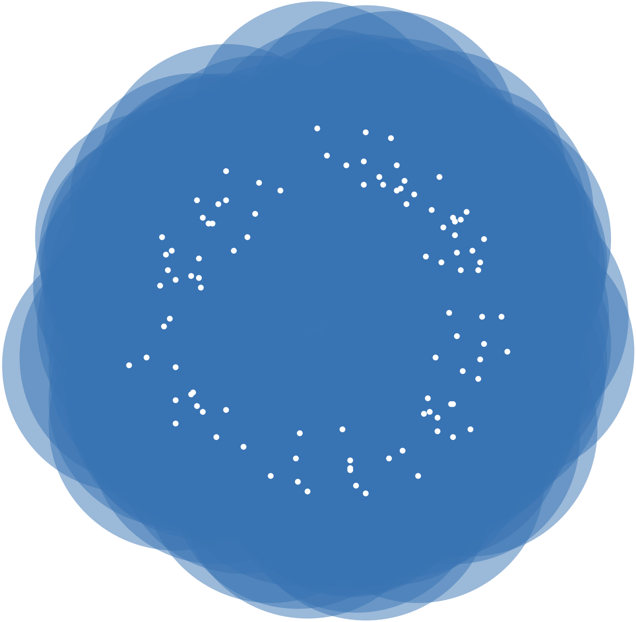
Persistent homology

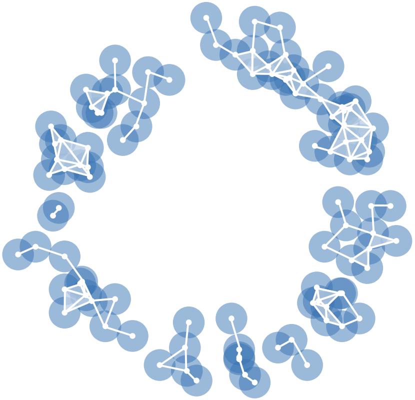


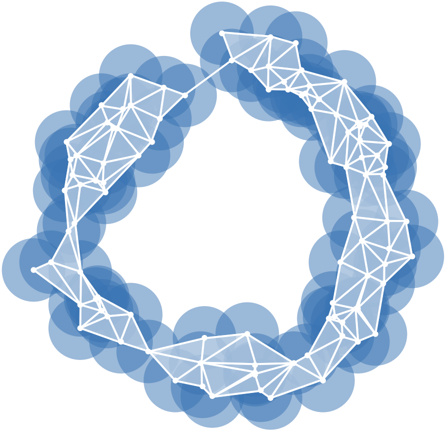


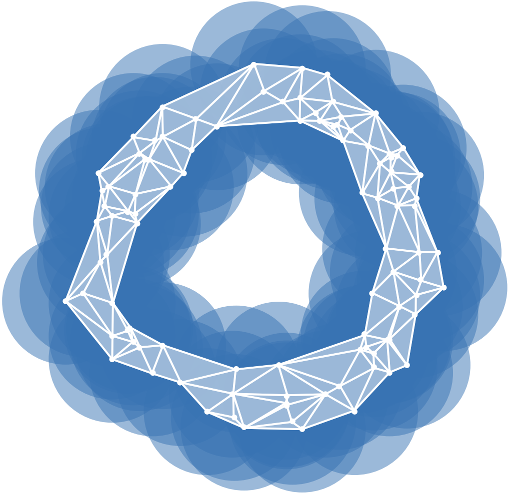


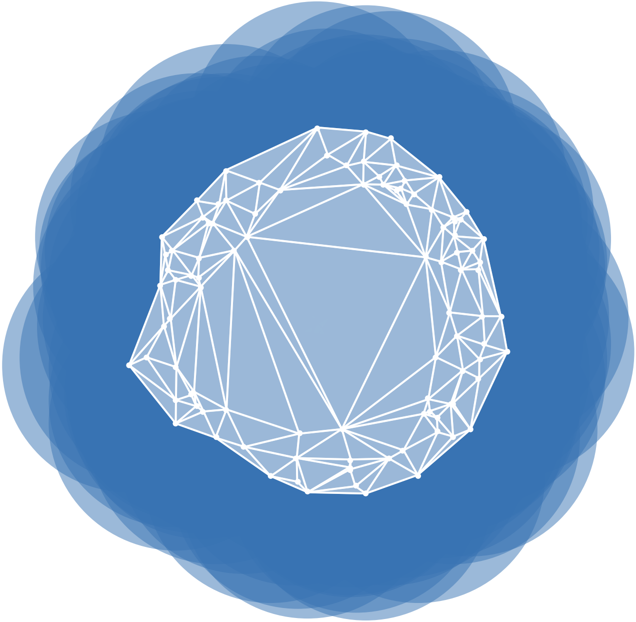












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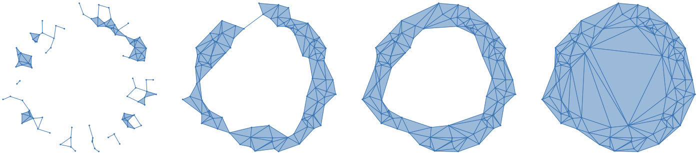

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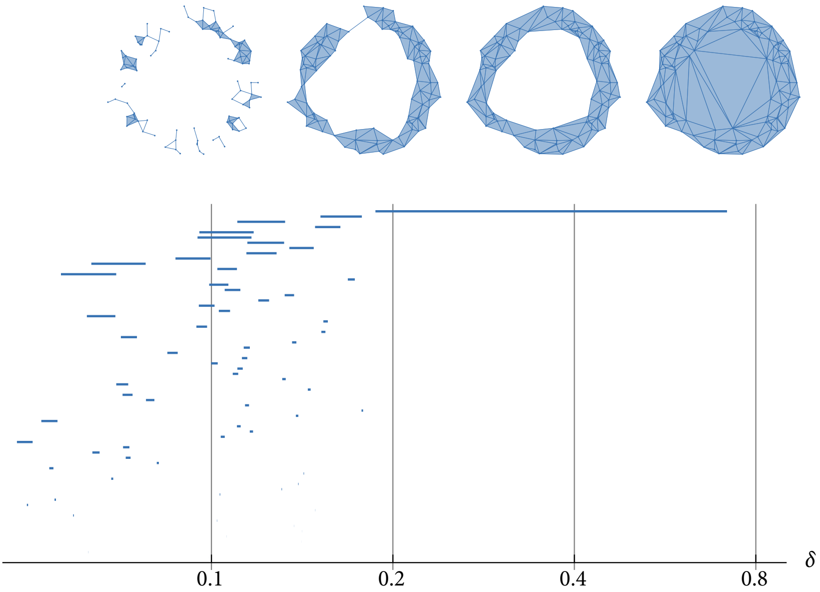

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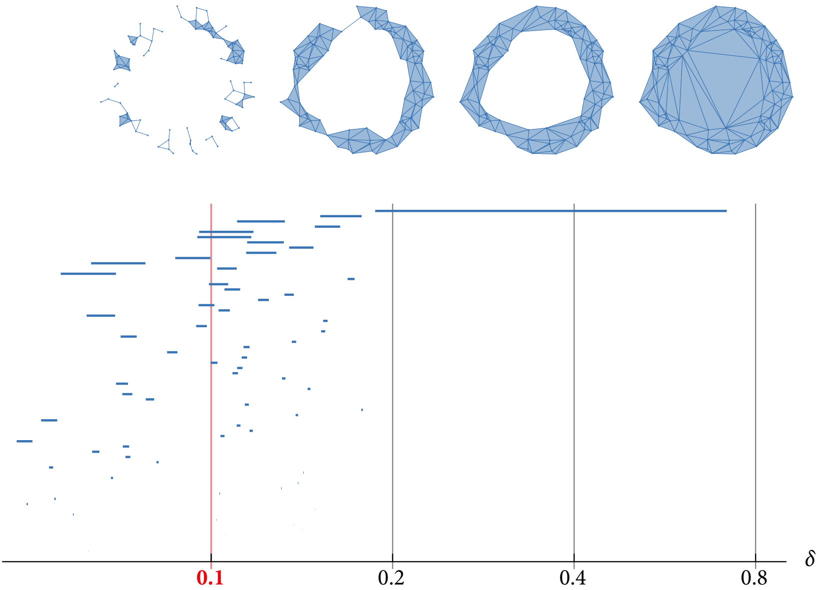

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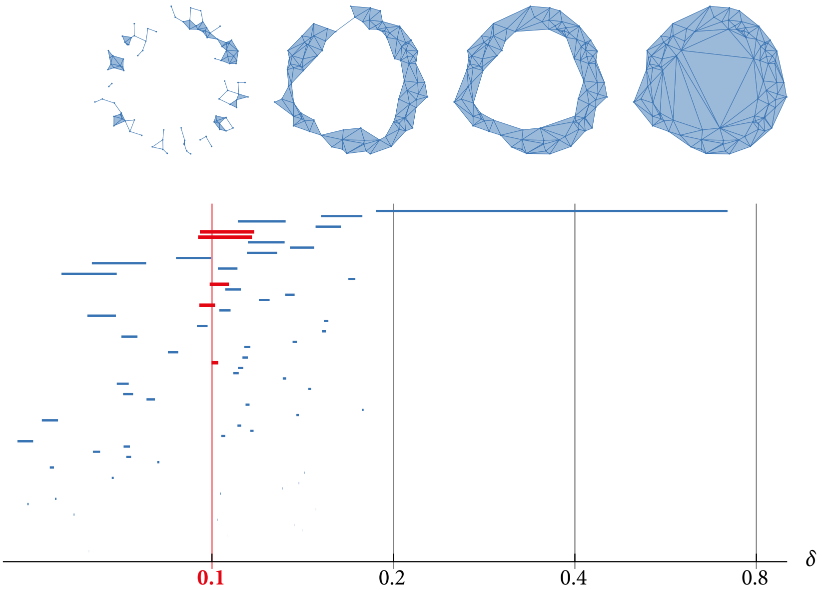

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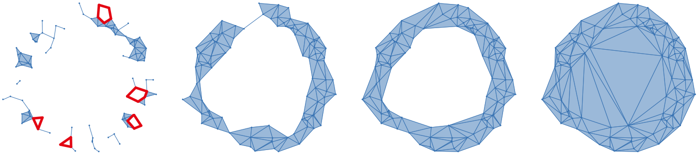

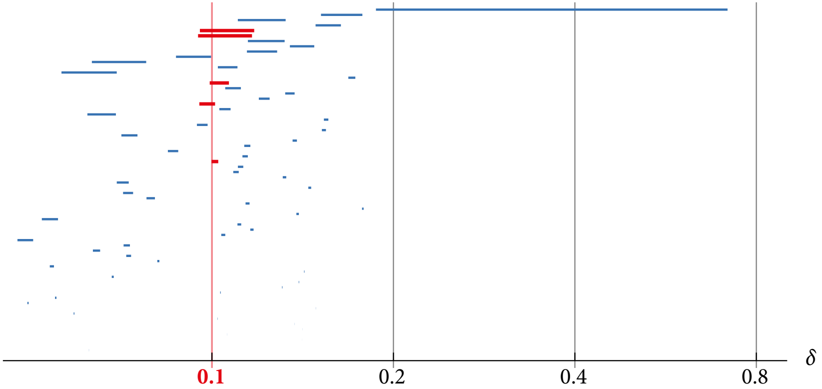

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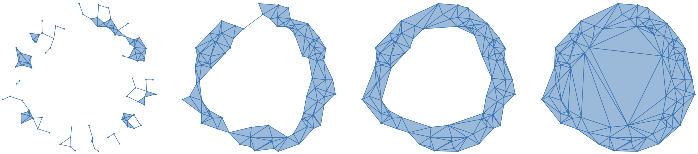

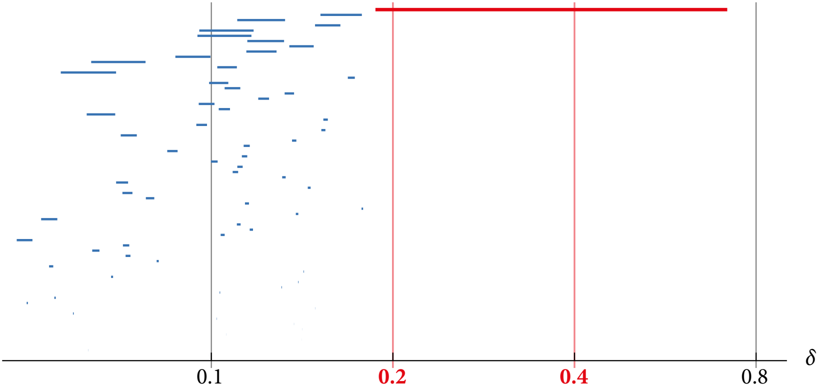

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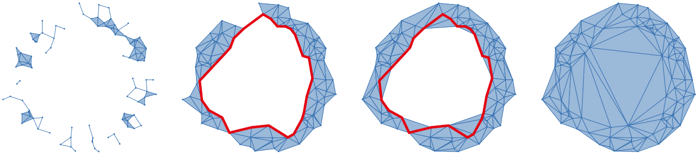

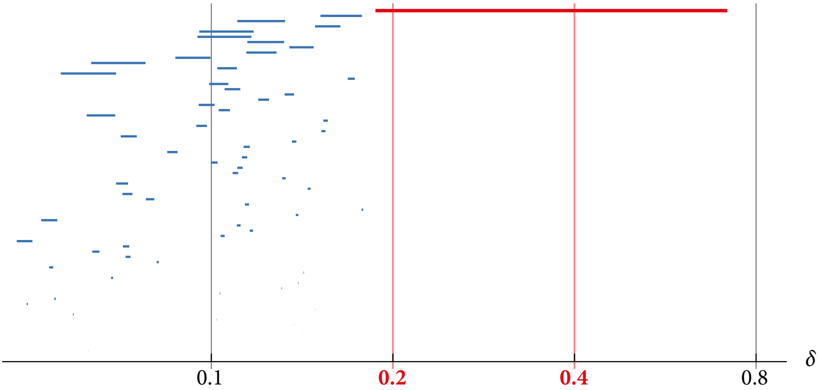

Vietoris–Rips filtrations

Consider a finite metric space (X, d).

The *Vietoris–Rips complex* is the simplicial complex

$$\mathrm{Rips}_t(X) = \{S \subseteq X \mid \mathrm{diam}\, S \leq t\}$$

- 1-skeleton: all edges with pairwise distance $\leq t$
- all possible higher simplices (flag complex)

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Goal:

- compute cohomology $H^d(\mathrm{Rips}_t(X))$
  (for all t and $0 \leq d < k$)
- together with induced maps $H^d(\mathrm{Rips}_s(X) \hookrightarrow \mathrm{Rips}_t(X))$
  (for all $s \leq t$)

Design goals

Goals for previous projects:

- PHAT: fast persistence computation
  (boundary matrix reduction only)
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Features:

- time- and memory-efficient
- less than 1000 lines of code in a single C++ file
- support for coefficients in prime finite fields
- no external dependencies

The past

Matrix reduction

Setting:

- finite metric space, n points
- persistent homology for k-skeleta of *Vietoris–Rips filtration*
- homology H_d in dimensions $0 \leq d < k$

Notation:

- D: boundary matrix of filtration
- R_i: ith column of R

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Algorithm:

- $R = D, V = I$
- while $\exists i < j$ with $\operatorname{pivot} R_i = \operatorname{pivot} R_j$
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Result:

- $R = D \cdot V$ is reduced (unique pivots)
- V is full rank upper triangular

Lessons from PHAT

Two optimizations speed up computation considerably:

- Clearing positive columns
  [Chen, Kerber 2011]
- Persistent cohomology
  [de Silva, Morozov, Vejdemo-Johannson 2011]

But only when *both* are used in conjuction!

Compatible basis cycles

For a reduced boundary matrix $R = D \cdot V$, call

$$P = \{i : R_i = 0\} \qquad \textit{positive} \text{ indices,}$$
$$N = \{j : R_j \neq 0\} \qquad \textit{negative} \text{ indices,}$$
$$E = P \setminus \operatorname{pivots} R \qquad \textit{essential} \text{ indices.}$$

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Persistent homology is generated by the basis cycles Σ_Z.

- Columns with non-essential positive indices never used!

Clearing non-essential positive columns

Idea [Chen, Kerber 2011]:

- Don't reduce at non-essential positive indices
- Reduce boundary matrices of $\partial_d : C_d \to C_{d-1}$ in decreasing dimension $d = k \dots 1$
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Note:

- reducing *positive* columns typically harder than negative
- with clearing: need only reduce *essential* positive columns

Counting column reductions

- standard matrix reduction:

$$\sum_{d=1}^{k} \binom{n}{d+1} = \underbrace{\sum_{d=1}^{k} \binom{n-1}{d}}_{\text{negative}} + \underbrace{\sum_{d=1}^{k} \binom{n-1}{d+1}}_{\text{positive}}$$

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Clearing for persistent cohomology:

- reduce in increasing dimension $d = 0, \ldots, k-1$
- negative becomes (dual) positive
- positive non-essential becomes (dual) negative
- essential stays (dual) essential

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Natural filtration settings

Typical assumptions on the filtration:

• general filtration	persistence (in theory)
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Conclusion:

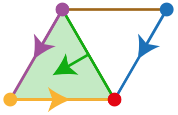
- Discrete Morse theory sits in the middle
  between persistence and persistence (hah!)

Discrete Morse theory

Definition (Forman 1998)

A *discrete vector field* on a cell complex is a partition of the set of simplices into

- singleton sets $\{\phi\}$ *(critical cells)*, and
- pairs $\{\sigma, \tau\}$, where σ is a facet of τ.



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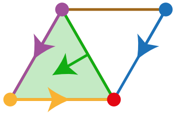

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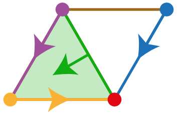

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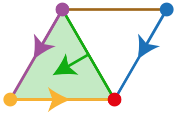

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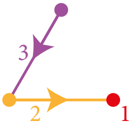

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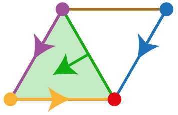

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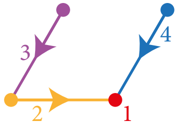

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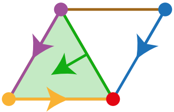

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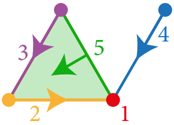

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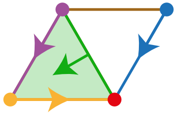

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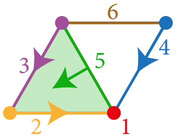

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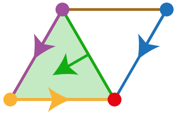

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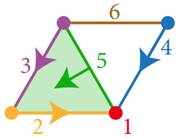
- sublevel sets are subcomplexes, and
- level sets form a discrete vector field.



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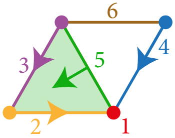
Theorem (Forman 1998)

If $(s, t]$ contains no critical value of f, then the sublevel set K_t collapses to K_s *(written as $K_t \searrow K_s$).*



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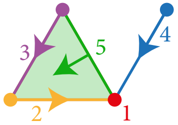

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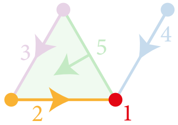

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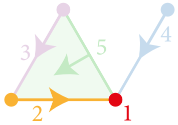

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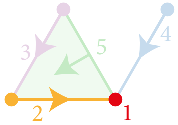

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This homotopy equivalence is compatible with the filtration.

Corollary

K and M have isomorphic persistent homology (with regard to the sublevel set filtration of f).

From Morse theory to persistence and back

Proposition (from Morse to persistence)

The pairs of a Morse filtration are apparent 0*-persistence pairs.*

Apparent persistence pair (σ, τ):

- σ is the youngest face of τ
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You may have seen this before!

- Matt Kahle: random Rips complex in supercritical regime

The present

Ripser design principles

Don't store what you can compute:

- filtration (from distance matrix)
- boundary matrix D (from n, d)
- reduced matrix $R = D \cdot V$ (from matrices D, V)
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- filtration (from distance matrix)
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Store only:

- persistence pairs
- negative column indices (sorted by filtration order)
- current column of R (in heap, comparison based)

Observations

For a typical input:

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Example: $k = 3, n = 192$:

- Only $191 + 53 + 601 = 845$ out of $1\,161\,471$ pairs are not apparent 0-persistence pairs

Conclusion

Can compute much larger instances than previous software

- H^2 persistence for data with 1681 points,
  in about 30 minutes using 20GB RAM
- Available at `http://ripser.org`
- Runs in the browser at `http://live.ripser.org`