Computation of Persistent Homology

Part 2: Efficient Computation of Vietoris-Rips Persistence

Ulrich Bauer

TUM

August 14, 2018

Tutorial on *Multiparameter Persistence, Computation, and Applications*Institute for Mathematics and its Applications

persistent homology

Vietoris-Rips

Vietoris-Rips filtrations

Consider a finite metric space (X, d). The *Vietoris–Rips complex* is the simplicial complex

$$Rips_t(X) = \{ S \subseteq X \mid diam S \le t \}$$

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

Vietoris-Rips filtrations

Consider a finite metric space (X, d). The *Vietoris–Rips complex* is the simplicial complex

$$Rips_t(X) = \{ S \subseteq X \mid diam S \le t \}$$

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

Goal:

• compute persistence barcodes for $H_d(\operatorname{Rips}_t(X))$ (in dimensions $0 \le d \le k$)

Demo: Ripser

Example data set:

- 192 points on \mathbb{S}^2
- persistent homology barcodes up to dimension 2
- over 56 mio. simplices in 3-skeleton

Demo: Ripser

Example data set:

- 192 points on \mathbb{S}^2
- persistent homology barcodes up to dimension 2
- over 56 mio. simplices in 3-skeleton

Comparison with other software:

- javaplex: 3200 seconds, 12 GB
- Dionysus: 533 seconds, 3.4 GB
- GUDHI: 75 seconds, 2.9 GB
- DIPHA: 50 seconds, 6 GB
- Eirene: 12 seconds, 1.5 GB

Demo: Ripser

Example data set:

- 192 points on \mathbb{S}^2
- persistent homology barcodes up to dimension 2
- over 56 mio. simplices in 3-skeleton

Comparison with other software:

- javaplex: 3200 seconds, 12 GB
- Dionysus: 533 seconds, 3.4 GB
- GUDHI: 75 seconds, 2.9 GB
- DIPHA: 50 seconds, 6 GB
- Eirene: 12 seconds, 1.5 GB

Ripser: 1.2 seconds, 152 MB

Ripser

A software for computing Vietoris–Rips persistence barcodes

- about 1000 lines of C++ code, no external dependencies
- support for
 - coefficients in a prime field \mathbb{F}_p
 - sparse distance matrices for distance threshold
- open source (http://ripser.org)
 - released in July 2016
- online version (http://live.ripser.org)
 - launched in August 2016
- most efficient software for Vietoris–Rips persistence
 - computes H² barcode for 50 000 random points on a torus in 136 seconds / 9 GB (using distance threshold)
- 2016 ATMCS Best New Software Award (jointly with RIVET)

Design goals

Goals for previous persistence software projects:

- PHAT [B, Kerber, Reininghaus, Wagner 2013]: fast persistence computation (matrix reduction only), comparing different algorithms and data sturctures
- DIPHA [B, Kerber, Reininghaus 2014]: distributed persistence computation, based on spectral sequence algorithm

Design goals

Goals for previous persistence software projects:

- PHAT [B, Kerber, Reininghaus, Wagner 2013]: fast persistence computation (matrix reduction only), comparing different algorithms and data sturctures
- DIPHA [B, Kerber, Reininghaus 2014]: distributed persistence computation, based on spectral sequence algorithm

Goals for Ripser:

- Use as little memory as possible
- Be reasonable about computation time

The four special ingredients

Main improvements to the standard reduction algorithm:

- Clearing inessential columns [Chen, Kerber 2011]
- Computing cohomology [de Silva et al. 2011]
- Implicit matrix reduction
- Apparent and emergent pairs

The four special ingredients

Main improvements to the standard reduction algorithm:

- Clearing inessential columns [Chen, Kerber 2011]
- Computing cohomology [de Silva et al. 2011]
- Implicit matrix reduction
- Apparent and emergent pairs

Lessons from PHAT:

- Clearing and cohomology yield considerable speedup,
- but only when both are used in conjuction!

Filtrations and refinements

Simplexwise filtrations

Call a filtration $(K_i)_{i \in I}$ of simplicial complexes (*I* totally ordered)

- essential if $i \neq j$ implies $K_i \neq K_j$,
- simplexwise if for all $i \in I$ with $K_i \neq \emptyset$ there is some index $j < i \in I$ and some simplex $\sigma \in K$ such that $K_i \setminus K_j = \{\sigma\}$.

Simplexwise filtrations

Call a filtration $(K_i)_{i \in I}$ of simplicial complexes (*I* totally ordered)

- essential if $i \neq j$ implies $K_i \neq K_j$,
- simplexwise if for all $i \in I$ with $K_i \neq \emptyset$ there is some index $j < i \in I$ and some simplex $\sigma \in K$ such that $K_i \setminus K_j = \{\sigma\}$.

Note:

- These properties are natural assumptions for computation.
- The *Vietoris–Rips filtration* (indexed by \mathbb{R}) is not simplexwise (and not essential).
- To compute Vietoris–Rips persistence, we will reindex and refine.

Reindexing and refinement

A filtration $K: I \to \mathbf{Simp}$ is a *reindexing* of another filtration $F: R \to \mathbf{Simp}$ if $F = K \circ r$ for some monotonic map $r: R \to I$.

- If r is injective, we call K a refinement of F;
- if *r* is surjective, we call *K* a *reduction* of *F*.

Reindexing and refinement

A filtration $K: I \to \mathbf{Simp}$ is a *reindexing* of another filtration $F: R \to \mathbf{Simp}$ if $F = K \circ r$ for some monotonic map $r: R \to I$.

- If r is injective, we call K a refinement of F;
- if r is surjective, we call K a reduction of F.

The Vietoris–Rips filtration can be reindexed:

- reduced to an essential filtration (over the set of pairwise distances), and further
- refined to a simplexwise filtration

Reindexing and refinement

A filtration $K: I \to \mathbf{Simp}$ is a *reindexing* of another filtration $F: R \to \mathbf{Simp}$ if $F = K \circ r$ for some monotonic map $r: R \to I$.

- If r is injective, we call K a refinement of F;
- if r is surjective, we call K a reduction of F.

The Vietoris–Rips filtration can be reindexed:

- reduced to an essential filtration (over the set of pairwise distances), and further
- refined to a simplexwise filtration

Ripser use the lexicographic refinement: simplices ordered by

- diameter, then
- · dimension, then
- (decreasing) lexicographic order of vertices $\{v_{i_k}, \dots, v_{i_0}\}$ (induced by fixed total order $v_0 < \dots < v_{n-1}$ on vertices)

Enumerating (co)faces in lexicographic order

There is an order-preserving bijection

from *k*-simplices (as ordered tuples, ordered lexicographically) to natural numbers (called *combinatorial number system*).

One direction is given by

$$\left[\nu_{i_k},\ldots,\nu_{i_0}\right]\mapsto\sum_{j=0}^k\binom{i_j}{j+1}$$

- The other direction can also be computed quickly
- Using this bijection, faces and cofaces can be efficiently enumerated in (decreasing) lexicographic order

Persistence barcodes through reindexing

Consider a filtration $F : \mathbb{R} \to \mathbf{Simp}$ with reindexing $F = K \circ r$, $K : I \to \mathbf{Simp}$, $r : \mathbb{R} \to [n]$. The persistence barcode of K_{\bullet} determines the persistence barcode of F_{\bullet} :

$$B(H_*(F_{\bullet})) = \{r^{-1}(I) \neq \emptyset \mid I \in B(H_*(K_{\bullet}))\}.$$

Matrix reduction

Computing homology

Computing homology $H_* = Z_*/B_*$:

- compute basis for boundaries $B_* = \operatorname{im} \partial_*$
- extend to basis for cycles $Z_* = \ker \partial_*$
- new (non-boundary) basis cycles generate quotient Z_*/B_*

Computing homology

Computing homology $H_* = Z_*/B_*$:

- compute basis for boundaries $B_* = \operatorname{im} \partial_*$
- extend to basis for cycles $Z_* = \ker \partial_*$
- new (non-boundary) basis cycles generate quotient Z_*/B_*

Computing *persistent* homology $H_* = Z_*/B_*$ (for a simplexwise filtration $K_i \subseteq K$):

- compute *filtered* basis for boundaries $B_* = \operatorname{im} \partial_*$
- extend to basis for cycles $Z_* = \ker \partial_*$
- all basis cycles generate persistent homology

Persistence by matrix reduction

Given:

• D: matrix of boundary ∂_d for a simplexwise filtration $(K_i)_i$ (for canonical basis in filtration order, indexed by $I \times J$)

Wanted:

• persistence barcode of homology $H_d(K_i; \mathbb{F})$ for some (prime) field \mathbb{F} , in dimensions $d = 0, \dots, k$

Notation:

- m_i : jth column of M, m_{ij} : entry in ith row and jth column
- Pivot $m_j = \min\{i \in I : m_{kj} = 0 \text{ for all } k > i\}.$

Persistence by matrix reduction

Given:

• D: matrix of boundary ∂_d for a simplexwise filtration $(K_i)_i$ (for canonical basis in filtration order, indexed by $I \times J$)

Wanted:

• persistence barcode of homology $H_d(K_i; \mathbb{F})$ for some (prime) field \mathbb{F} , in dimensions d = 0, ..., k

Notation:

- m_j : jth column of M, m_{ij} : entry in ith row and jth column
- Pivot $m_j = \min\{i \in I : m_{kj} = 0 \text{ for all } k > i\}.$

Computation: barcode is obtained by matrix reduction of D

- $R = D \cdot V$ reduced (non-zero columns have distinct pivots)
- V is regular upper triangular

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

 $I_b = \{i : r_i = 0\}$ birth indices,

 $I_d = \{j : r_j \neq 0\}$ death indices,

 $I_e = I_b \setminus \text{Pivots } R$ essential indices

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

$$I_b = \{i : r_i = 0\}$$
 birth indices,

$$I_d = \{j : r_j \neq 0\}$$
 death indices,

$$I_e = I_b \setminus \text{Pivots } R$$
 essential indices

(note:
$$i = \text{Pivot } r_i \text{ implies } r_i = 0$$
, thus $\text{Pivots } R \subseteq I_b$). Then

$$\Sigma_B = \{r_j \mid j \in I_d\}$$
 is a basis of B_* ,

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

$$I_b = \{i : r_i = 0\}$$
 birth indices,

$$I_d = \{j : r_j \neq 0\}$$
 death indices,

$$I_e = I_b \setminus \text{Pivots } R$$
 essential indices

$$\Sigma_B = \{r_j \mid j \in I_d\}$$
 is a basis of B_* ,

$$\Sigma_Z = \Sigma_B \cup \{v_i \mid i \in I_e\}$$
 is a compatible basis of Z_* .

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

$$I_b = \{i : r_i = 0\}$$
 birth indices,
 $I_d = \{j : r_j \neq 0\}$ death indices,
 $I_e = I_b \setminus \text{Pivots } R$ essential indices

(note: $i = \text{Pivot } r_j \text{ implies } r_i = 0$, thus $\text{Pivots } R \subseteq I_b$). Then

$$\Sigma_B = \{r_j \mid j \in I_d\}$$
 is a basis of B_* ,
 $\Sigma_Z = \Sigma_B \cup \{v_i \mid i \in I_e\}$ is a compatible basis of Z_* .

• Persistent homology is generated by the basis cycles Σ_Z .

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

$$I_b = \{i : r_i = 0\}$$
 birth indices,

$$I_d = \{j : r_j \neq 0\}$$
 death indices,

$$I_e = I_b \setminus \text{Pivots } R$$
 essential indices

$$\Sigma_B = \{r_j \mid j \in I_d\}$$
 is a basis of B_* ,

$$\Sigma_Z = \Sigma_B \cup \{ \nu_i \mid i \in I_e \}$$
 is a compatible basis of Z_* .

- Persistent homology is generated by the basis cycles Σ_Z .
- Persistence intervals: $\{[i,j) \mid i = \text{Pivot } r_j\} \cup \{[i,\infty) \mid i \in I_e\}$

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

$$I_b = \{i : r_i = 0\}$$
 birth indices,

$$I_d = \{j : r_j \neq 0\}$$
 death indices,

$$I_e = I_b \setminus \text{Pivots } R$$
 essential indices

$$\Sigma_B = \{r_j \mid j \in I_d\}$$
 is a basis of B_* ,

$$\Sigma_Z = \Sigma_B \cup \{v_i \mid i \in I_e\}$$
 is a compatible basis of Z_* .

- Persistent homology is generated by the basis cycles Σ_Z .
- Persistence intervals: $\{[i,j) \mid i = \text{Pivot } r_j\} \cup \{[i,\infty) \mid i \in I_e\}$
- Matrix V not used for barcode

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

$$I_b = \{i : r_i = 0\}$$
 birth indices,

$$I_d = \{j : r_j \neq 0\}$$
 death indices,

$$I_e = I_b \setminus \text{Pivots } R$$
 essential indices

$$\Sigma_B = \{r_j \mid j \in I_d\}$$
 is a basis of B_* ,

$$\Sigma_Z = \Sigma_B \cup \{v_i \mid i \in I_e\}$$
 is a compatible basis of Z_* .

- Persistent homology is generated by the basis cycles Σ_Z .
- Persistence intervals: $\{[i,j) \mid i = \text{Pivot } r_j\} \cup \{[i,\infty) \mid i \in I_e\}$
- Matrix V not used for barcode
- Columns with indices Pivots R not used at all

Matrix reduction algorithm

return R, V

Require: $D: I \times I$ matrix **Ensure:** $R = D \cdot V$: reduced, V: regular upper triangular, P: persistence pairs R := D $V := \operatorname{Id}(J \times J)$ **for** $j \in J$ in increasing order **do while** $\exists k < j$ with $i := \text{Pivot } r_k = \text{Pivot } r_i$ **do** $\lambda = \frac{r_{ij}}{r_{ij}}$ $r_i := r_i - \lambda \cdot r_k$ \triangleright eliminate pivot entry r_{ii} $v_i := v_i - \lambda \cdot v_k$ **if** $i := Pivot r_i \neq 0$ **then** append (i, j) to P

Clearing

Clearing non-essential positive columns

Idea [Chen, Kerber 2011]:

- Don't reduce at non-essential birth indices
- Use the fact that $i = \text{Pivot } r_i \text{ implies } r_i = 0$
- Reduce boundary matrices of $\partial_d : C_d \to C_{d-1}$ in decreasing dimension $d = k + 1, \dots, 1$
- Whenever $i = \text{Pivot } r_j$ (in matrix for ∂_d)
 - Set r_i to 0 (in matrix for ∂_{d-1})

Clearing non-essential positive columns

Idea [Chen, Kerber 2011]:

- Don't reduce at non-essential birth indices
- Use the fact that $i = \text{Pivot } r_i \text{ implies } r_i = 0$
- Reduce boundary matrices of $\partial_d : C_d \to C_{d-1}$ in decreasing dimension $d = k+1, \ldots, 1$
- Whenever $i = \text{Pivot } r_i$ (in matrix for ∂_d)
 - Set r_i to 0 (in matrix for ∂_{d-1})
 - Set v_i to r_j (if V is needed)

Clearing non-essential positive columns

Idea [Chen, Kerber 2011]:

- Don't reduce at non-essential birth indices
- Use the fact that $i = \text{Pivot } r_i \text{ implies } r_i = 0$
- Reduce boundary matrices of $\partial_d: C_d \to C_{d-1}$ in decreasing dimension $d = k+1, \ldots, 1$
- Whenever $i = \text{Pivot } r_j$ (in matrix for ∂_d)
 - Set r_i to 0 (in matrix for ∂_{d-1})
 - Set v_i to r_j (if V is needed)
- Still yields $R = D \cdot V$ reduced, V regular upper triangular

Note:

- reducing *birth* columns typically harder than death columns: $O(j^2)$ (birth) vs. $O((j-i)^2)$ (death)
- · with clearing: need only reduce essential columns

Counting homology column reductions

Consider k + 1-skeleton of n - 1-simplex (Rips filtration) Number of columns in boundary matrix:

$$\sum_{d=1}^{k+1} \binom{n}{d+1} = \sum_{d=1}^{k+1} \binom{n-1}{d} + \sum_{d=1}^{k+1} \binom{n-1}{d+1}$$
total total death

Counting homology column reductions

Consider k + 1-skeleton of n - 1-simplex (Rips filtration) Number of columns in boundary matrix:

$$\sum_{d=1}^{k+1} \binom{n}{d+1} = \sum_{d=1}^{k+1} \binom{n-1}{d} + \sum_{d=1}^{k+1} \binom{n-1}{d+1}$$

$$= \sum_{d=1}^{k+1} \binom{n-1}{d} + \binom{n-1}{k+2} + \sum_{d=1}^{k} \binom{n-1}{d+1}$$
death essential essential cleared

Counting homology column reductions

Consider k + 1-skeleton of n - 1-simplex (Rips filtration) Number of columns in boundary matrix:

$$\sum_{d=1}^{k+1} \binom{n}{d+1} = \sum_{d=1}^{k+1} \binom{n-1}{d} + \sum_{d=1}^{k+1} \binom{n-1}{d+1}$$

$$= \sum_{d=1}^{k+1} \binom{n-1}{d} + \binom{n-1}{k+2} + \sum_{d=1}^{k} \binom{n-1}{d+1}$$
death essential cleared

$$k = 2, n = 192$$
: $56\,050\,096 = 1\,161\,471 + 53\,727\,345 + 1161\,280$

Clearing didn't help much!

Cohomology

How is persistent cohomology related to persistent homology?

• Cohomology (over \mathbb{F}) is vector space dual to homology:

$$H^p(K) \cong H_p(K)^* = \operatorname{Hom}(H_p(K), \mathbb{F}).$$

How is persistent cohomology related to persistent homology?

• Cohomology (over \mathbb{F}) is vector space dual to homology:

$$H^p(K) \cong H_p(K)^* = \operatorname{Hom}(H_p(K), \mathbb{F}).$$

• Duality preserves ranks of linear maps (in finite dimensions): for $f:V\to W$ with dual $f^*:W^*\to V^*$,

$$\operatorname{rank} f^* = \operatorname{rank} f$$
.

How is persistent cohomology related to persistent homology?

• Cohomology (over \mathbb{F}) is vector space dual to homology:

$$H^p(K) \cong H_p(K)^* = \operatorname{Hom}(H_p(K), \mathbb{F}).$$

• Duality preserves ranks of linear maps (in finite dimensions): for $f:V\to W$ with dual $f^*:W^*\to V^*$,

$$\operatorname{rank} f^* = \operatorname{rank} f$$
.

 The persistence barcode of a persistence module is uniquely determined by the ranks of the internal maps.

How is persistent cohomology related to persistent homology?

• Cohomology (over \mathbb{F}) is vector space dual to homology:

$$H^p(K) \cong H_p(K)^* = \operatorname{Hom}(H_p(K), \mathbb{F}).$$

• Duality preserves ranks of linear maps (in finite dimensions): for $f:V\to W$ with dual $f^*:W^*\to V^*$,

$$\operatorname{rank} f^* = \operatorname{rank} f$$
.

 The persistence barcode of a persistence module is uniquely determined by the ranks of the internal maps.

Thus, persistent homology and persistent cohomology have the same barcode [de Silva et al 2011].

Persistent (relative) homology

How is persistent relative homology related to persistent homology?

 The short exact sequence of filtered chain complexes (with coefficients in F)

$$0 \to C_p(K_\bullet) \to C_p(K) \to C_p(K,K_\bullet) \to 0$$

induces a long exact sequence in persistent homology

$$\cdots \to H_{p+1}(K,K_{\bullet}) \to H_p(K_{\bullet}) \to H_p(K) \to H_p(K,K_{\bullet}) \to \cdots$$

and analogously for persistent cohomology.

Consider the long exact sequence

$$\cdots \to H_{p+1}(K) \stackrel{r}{\to} H_{p+1}(K, K_{\bullet}) \stackrel{\partial}{\to} H_p(K_{\bullet}) \stackrel{i}{\to} H_p(K) \to \cdots$$

•
$$B(\ker(i)) = \{[b,d) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(\partial))$$

Consider the long exact sequence

$$\cdots \to H_{p+1}(K) \stackrel{r}{\to} H_{p+1}(K, K_{\bullet}) \stackrel{\partial}{\to} H_p(K_{\bullet}) \stackrel{i}{\to} H_p(K) \to \cdots$$

- $B(\ker(i)) = \{[b,d) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(\partial))$
- $B(\operatorname{im}(i)) = \{[b, \infty) \in B(H_p(K_{\bullet}))\}$

Consider the long exact sequence

$$\cdots \to H_{p+1}(K) \stackrel{r}{\to} H_{p+1}(K,K_{\bullet}) \stackrel{\partial}{\to} H_p(K_{\bullet}) \stackrel{i}{\to} H_p(K) \to \cdots$$

- $B(\ker(i)) = \{[b,d) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(\partial))$
- $B(\operatorname{im}(i)) = \{[b, \infty) \in B(H_p(K_{\bullet}))\}$
- $H_p(K_{\bullet}) \cong \operatorname{im}(\partial) \oplus \operatorname{im}(i)$

Consider the long exact sequence

$$\cdots \to H_{p+1}(K) \stackrel{r}{\to} H_{p+1}(K, K_{\bullet}) \stackrel{\partial}{\to} H_p(K_{\bullet}) \stackrel{i}{\to} H_p(K) \to \cdots$$

- $B(\ker(i)) = \{[b,d) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(\partial))$
- $B(\operatorname{im}(i)) = \{[b, \infty) \in B(H_p(K_{\bullet}))\}$
- $H_p(K_{\bullet}) \cong \operatorname{im}(\partial) \oplus \operatorname{im}(i)$
- $B(\operatorname{coker}(i)) = \{(-\infty, b) \mid [b, \infty) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(r))$

Consider the long exact sequence

$$\cdots \to H_{p+1}(K) \stackrel{r}{\to} H_{p+1}(K, K_{\bullet}) \stackrel{\partial}{\to} H_p(K_{\bullet}) \stackrel{i}{\to} H_p(K) \to \cdots$$

- $B(\ker(i)) = \{[b,d) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(\partial))$
- $B(\operatorname{im}(i)) = \{[b, \infty) \in B(H_p(K_{\bullet}))\}$
- $H_p(K_{\bullet}) \cong \operatorname{im}(\partial) \oplus \operatorname{im}(i)$
- $B(\operatorname{coker}(i)) = \{(-\infty, b) \mid [b, \infty) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(r))$
- $H_{p+1}(K, K_{\bullet}) \cong \operatorname{im}(\partial) \oplus \operatorname{im}(r)$

Consider the long exact sequence

$$\cdots \to H_{p+1}(K) \stackrel{r}{\to} H_{p+1}(K,K_{\bullet}) \stackrel{\partial}{\to} H_p(K_{\bullet}) \stackrel{i}{\to} H_p(K) \to \cdots$$

We have:

- $B(\ker(i)) = \{[b,d) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(\partial))$
- $B(\operatorname{im}(i)) = \{[b, \infty) \in B(H_p(K_{\bullet}))\}$
- $H_p(K_{\bullet}) \cong \operatorname{im}(\partial) \oplus \operatorname{im}(i)$
- $B(\operatorname{coker}(i)) = \{(-\infty, b) \mid [b, \infty) \in B(H_p(K_{\bullet}))\} = B(\operatorname{im}(r))$
- $H_{p+1}(K, K_{\bullet}) \cong \operatorname{im}(\partial) \oplus \operatorname{im}(r)$

Thus, the *absolute* and *relative* persistence barcodes determine each other [de Silva et al 2011; Schmahl 2018].

 Cohomology allows for clearing starting from dimension 0 (avoiding the initial overhead)

- Cohomology allows for clearing starting from dimension 0 (avoiding the initial overhead)
- Persistence in dimension 0 has special algorithms (Kruskal's algorithm for MST, union-find data structure)

- Cohomology allows for clearing starting from dimension 0 (avoiding the initial overhead)
- Persistence in dimension 0 has special algorithms (Kruskal's algorithm for MST, union-find data structure)
- Persistent cohomology arises from a reverse filtration

$$C^*(K_0) \twoheadleftarrow C^*(K_1) \twoheadleftarrow \cdots \twoheadleftarrow C^*(K_n)$$

- Cohomology allows for clearing starting from dimension 0 (avoiding the initial overhead)
- Persistence in dimension 0 has special algorithms (Kruskal's algorithm for MST, union-find data structure)
- Persistent cohomology arises from a reverse filtration

$$C^*(K_0) \twoheadleftarrow C^*(K_1) \twoheadleftarrow \cdots \twoheadleftarrow C^*(K_n)$$

Persistent relative cohomology arises from a filtration

$$C^*(K, K_0) \leftarrow C^*(K, K_1) \leftarrow \cdots \leftarrow C^*(K, K_n)$$

- Cohomology allows for clearing starting from dimension 0 (avoiding the initial overhead)
- Persistence in dimension 0 has special algorithms (Kruskal's algorithm for MST, union-find data structure)
- Persistent cohomology arises from a reverse filtration

$$C^*(K_0) \twoheadleftarrow C^*(K_1) \twoheadleftarrow \cdots \twoheadleftarrow C^*(K_n)$$

Persistent relative cohomology arises from a filtration

$$C^*(K, K_0) \leftarrow C^*(K, K_1) \leftarrow \cdots \leftarrow C^*(K, K_n)$$

 Can be computed by reduction of coboundary matrix: transpose of boundary matrix, with reversed index orders

Counting cohomology column reductions

Consider K: k + 1-skeleton of n - 1-simplex, Rips filtration Number of columns in coboundary matrix:

$$\sum_{d=0}^{k} \underbrace{\binom{n}{d+1}}_{\text{total}} = \sum_{d=0}^{k} \underbrace{\binom{n-1}{d+1}}_{\text{death}} + \sum_{d=0}^{k} \underbrace{\binom{n-1}{d}}_{\text{birth}}$$

Counting cohomology column reductions

Consider K: k + 1-skeleton of n - 1-simplex, Rips filtration Number of columns in coboundary matrix:

$$\sum_{d=0}^{k} \binom{n}{d+1} = \sum_{d=0}^{k} \binom{n-1}{d+1} + \sum_{d=0}^{k} \binom{n-1}{d}$$

$$= \sum_{d=0}^{k} \binom{n-1}{d+1} + \binom{n-1}{0} + \sum_{d=1}^{k} \binom{n-1}{d}$$
death essential essential cleared

Counting cohomology column reductions

Consider K: k + 1-skeleton of n - 1-simplex, Rips filtration Number of columns in coboundary matrix:

$$\sum_{d=0}^{k} \binom{n}{d+1} = \sum_{d=0}^{k} \binom{n-1}{d+1} + \sum_{d=0}^{k} \binom{n-1}{d}$$

$$= \sum_{d=0}^{k} \binom{n-1}{d+1} + \binom{n-1}{0} + \sum_{d=1}^{k} \binom{n-1}{d}$$
death essential cleared

$$k = 2$$
, $n = 192$: $1179808 = 1161471 + 1 + 18336$

Observations

For a typical input:

- V has very few off-diagonal entries
- most death columns of D are already reduced

Observations

For a typical input:

- V has very few off-diagonal entries
- most death columns of D are already reduced

Previous example (k = 2, n = 192):

• Only 79 + 42 + 1 = 122 out of 192 + 18145 + 1143135 = 1161471 columns are actually modified in matrix reduction

Standard approach:

- Boundary matrix D for filtration-ordered basis
 - Explicitly generated and stored in memory

Standard approach:

- Boundary matrix D for filtration-ordered basis
 - Explicitly generated and stored in memory
- Matrix reduction: store only reduced matrix R
 - transform D into R by column operations

Standard approach:

- Boundary matrix D for filtration-ordered basis
 - Explicitly generated and stored in memory
- Matrix reduction: store only reduced matrix R
 - transform D into R by column operations

Approach for Ripser:

- Boundary matrix D for lexicographically ordered basis
 - Implicitly defined and recomputed when needed

Standard approach:

- Boundary matrix D for filtration-ordered basis
 - Explicitly generated and stored in memory
- Matrix reduction: store only reduced matrix R
 - transform D into R by column operations

Approach for Ripser:

- Boundary matrix D for lexicographically ordered basis
 - Implicitly defined and recomputed when needed
- Matrix reduction in Ripser: store only coefficient matrix V
 - recompute previous columns of $R = D \cdot V$ when needed
 - Typically, V is much sparser and smaller than R
 - · Also used in Dionysus, Gudhi

Require: $D: I \times J$ matrix

Ensure: $R = D \cdot V$: reduced, V: regular upper triangular,

P: persistence pairs

for $j \in J$ in increasing order **do**

$$v_j \coloneqq e_j, r_j \coloneqq d_j$$

while $\exists k < j$ with $i := \text{Pivot } r_j \text{ and } (i, k) \in P \text{ do}$

$$\lambda = r_{ij}$$

$$r_j := r_j - \lambda \cdot D \cdot \nu_k$$

 \triangleright eliminate pivot entry r_{ij}

 $v_i := v_i - \lambda \cdot v_k$

if $i := \text{Pivot } r_i \neq 0 \text{ then}$

$$v_j = r_{ij}^{-1} \cdot v_j$$

append (i, j) to P

 \triangleright make pivot entry $r_{ij} = 1$

return V

Require: $D: I \times J$ matrix

Ensure: $R = D \cdot V$: reduced, V: regular upper triangular,

P: persistence pairs

for $j \in J$ in increasing order **do**

$$v_j := e_j, r_j := d_j$$

while $\exists k < j$ with $i := \text{Pivot } r_j \text{ and } (i, k) \in P \text{ do}$

$$\lambda = r_{ij}$$

$$r_i := r_i - \lambda \cdot D \cdot \nu_k$$

 $v_i := v_i - \lambda \cdot v_k$

if $i := \text{Pivot } r_i \neq 0 \text{ then }$

$$v_j = r_{ij}^{-1} \cdot v_j$$

append (i,j) to P

 \triangleright make pivot entry $r_{ij} = 1$

 \triangleright eliminate pivot entry r_{ii}

return V

Require: $D: I \times J$ matrix

Ensure: $R = D \cdot V$: reduced, V: regular upper triangular,

P: persistence pairs

for $j \in J$ in increasing order **do**

$$v_j := e_j, r_j := d_j$$

while $\exists k < j$ with $i := \text{Pivot } r_j \text{ and } (i, k) \in P \text{ do}$

$$\lambda = r_{ij}$$

$$r_j := r_j - \lambda \cdot D \cdot \nu_k$$

 \triangleright eliminate pivot entry r_{ij}

$$v_j := v_j - \lambda \cdot v_k$$

if $i := \text{Pivot } r_i \neq 0 \text{ then }$

$$v_j = r_{ij}^{-1} \cdot v_j$$

 \triangleright make pivot entry $r_{ij} = 1$

append (i, j) to P

return V

Require: $D: I \times I$ matrix **Ensure:** $R = D \cdot V$: reduced, V: regular upper triangular, P: persistence pairs **for** $j \in J$ in increasing order **do** $v_i := e_i, r_i := d_i$ while $\exists k < j$ with $i := \text{Pivot } r_i \text{ and } (i, k) \in P \text{ do}$ $\lambda = r_{ii}$ $r_i := r_i - \lambda \cdot D \cdot \nu_k$ \triangleright eliminate pivot entry r_{ii} $v_i := v_i - \lambda \cdot v_k$ **if** $i := Pivot r_i \neq 0$ **then**

if $i := \text{Pivot } r_j \neq 0$ ther $v_j = r_{ii}^{-1} \cdot v_j$

append (i, j) to P

return V

 \triangleright make pivot entry $r_{ii} = 1$

Implementation details

Current (working) columns v_j , r_j :

- priority queue (heap), comparison-based
- representing a linear combination of row basis elements
- elements: tuples consisting of
 - coefficient
 - row index
 - diameter of corresponding simplex
- pivot entry lazily evaluated (when extracting top element)

Previous (finalized) columns v_k (k < j):

sparse matrix data structure

Apparent and emergent pairs

Apparent pairs

Definition

In a simplexwise filtration, (σ, τ) is an *apparent* pair if

- σ is the youngest face of τ
- τ is the oldest coface of σ

Apparent pairs

Definition

In a simplexwise filtration, (σ, τ) is an *apparent* pair if

- σ is the youngest face of τ
- τ is the oldest coface of σ

Lemma

The apparent pairs are persistence pairs.

Lemma

The apparent pairs form a discrete gradient.

- Generalizes a construction proposed by [Kahle 2011] for the study of random Rips filtrations
- Apparent pairs also appear (independently) in Eirene [Henselmann 2016] and in [Mendoza-Smith, Tanner 2017]

Emergent persistent pairs

A persistence pair (σ, τ) for a simplexwise filtration is

- an emergent face pair if σ is the youngest proper face of τ ,
- an emergent coface pair if τ is the oldest proper coface of σ .

Emergent persistent pairs

A persistence pair (σ, τ) for a simplexwise filtration is

- an emergent face pair if σ is the youngest proper face of τ ,
- an emergent coface pair if τ is the oldest proper coface of σ .

Lemma

Consider the lexicographically refined Rips filtration. Assume that

- τ is the lexicographically minimal proper coface of σ with $diam(\tau) = diam(\sigma)$, and
- τ is not already in a persistence pair (ρ, τ) with $\rho > \sigma$.

Then (σ, τ) is a 0-persistence emergent coface pair.

Emergent persistent pairs

A persistence pair (σ, τ) for a simplexwise filtration is

- an emergent face pair if σ is the youngest proper face of τ ,
- an emergent coface pair if τ is the oldest proper coface of σ .

Lemma

Consider the lexicographically refined Rips filtration. Assume that

- τ is the lexicographically minimal proper coface of σ with $diam(\tau) = diam(\sigma)$, and
- τ is not already in a persistence pair (ρ, τ) with $\rho > \sigma$.

Then (σ, τ) *is a* 0-persistence emergent coface pair.

- Includes all apparent pairs with persistence 0
- Can be identified *without* enumerating all cofaces of σ (shortcut for computation)

Speedup from emergent pairs shortcut

Previous example (k = 2, n = 192):

 Only 36 672 + 164 214 + 3 392 039 = 3 592 925 out of 36 672 + 3 447 550 + 216 052 515 = 219 536 737 nonzero entries of the coboundary matrix are actually visited

Speedup from emergent pairs shortcut

Previous example (k = 2, n = 192):

 Only 36 672 + 164 214 + 3 392 039 = 3 592 925 out of 36 672 + 3 447 550 + 216 052 515 = 219 536 737 nonzero entries of the coboundary matrix are actually visited

Using implicit reduction (boundary matrix columns may be revisited multiple times):

 Only 155 474 + 253 134 + 7500 332 = 7908 940 out of 155 474 + 3536 470 + 220 160 808 = 223 852 752 nonzero entries are actually visited

Speedup: 1.2 s vs. 5.6 s (factor 4.7)

Ripser Live: users from 567 different cities

