

Ripser

Efficient Computation of Vietoris–Rips Persistence Barcodes

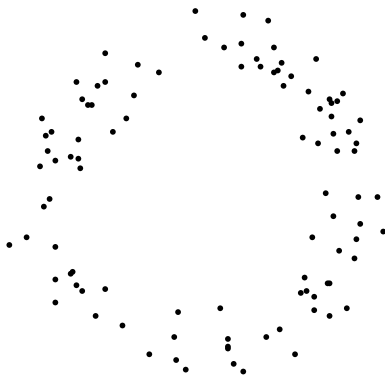
Ulrich Bauer

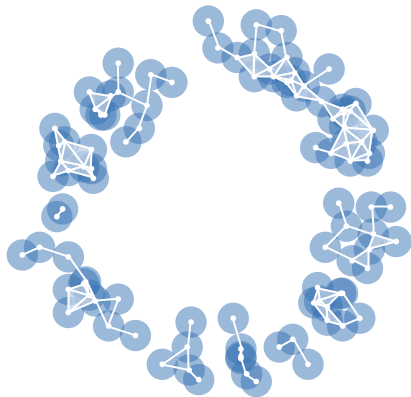
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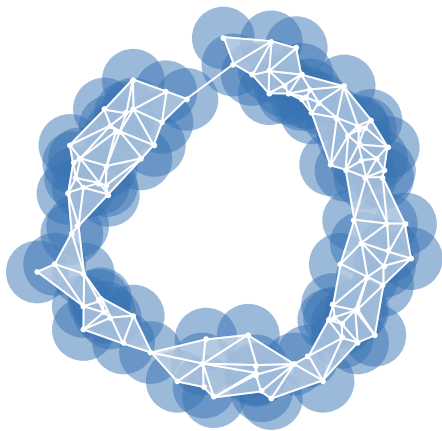
May 2, 2017

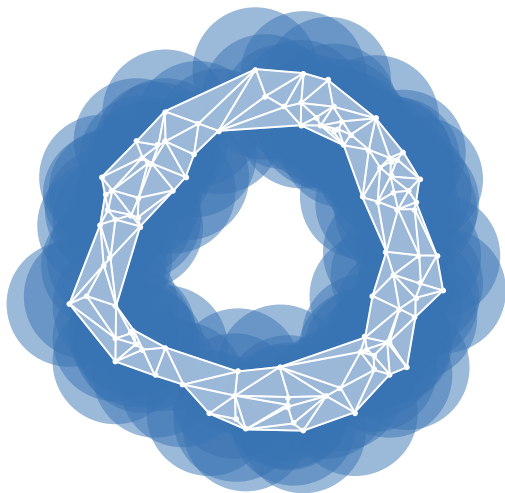
Special Hausdorff Program *Applied and Computational Algebraic Topology*
Hausdorff Research Institute for Mathematics, Bonn

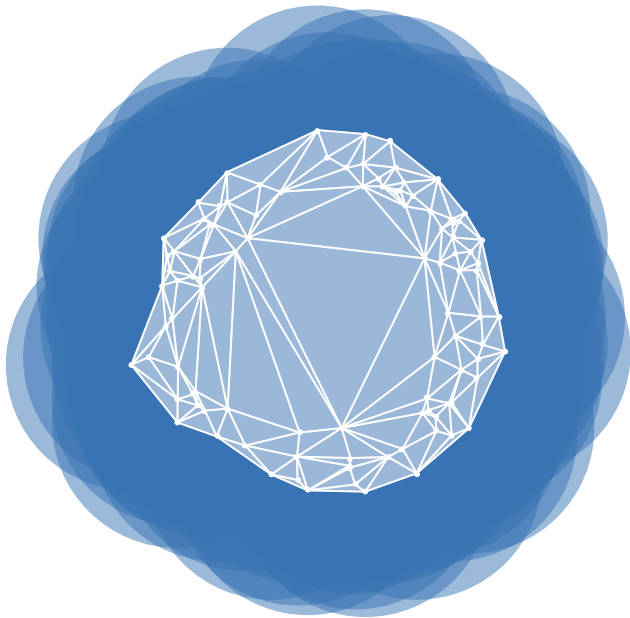
Persistent homology

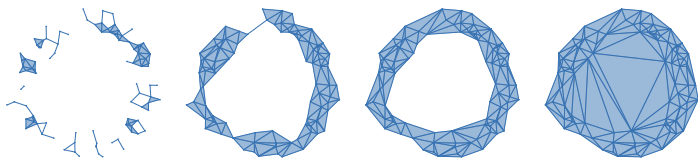


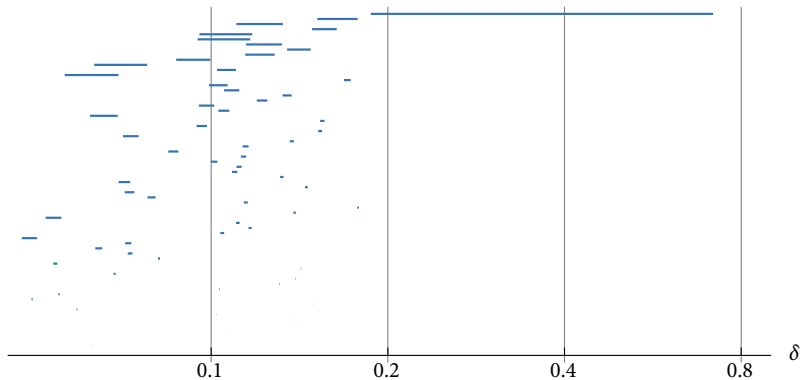
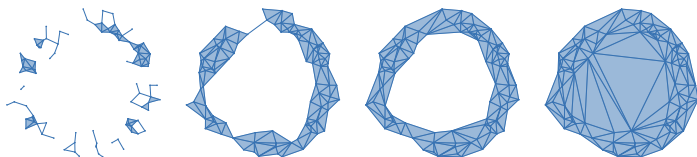


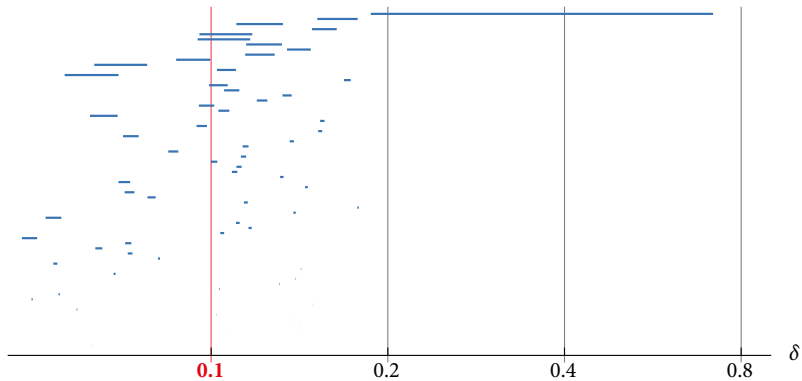
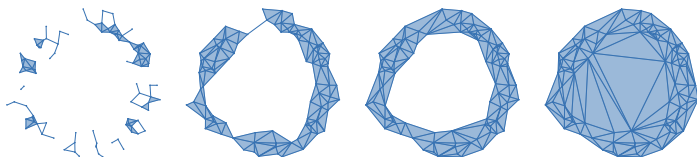


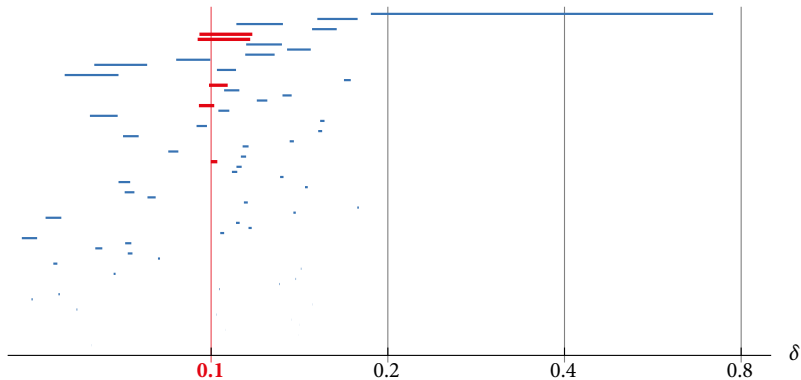
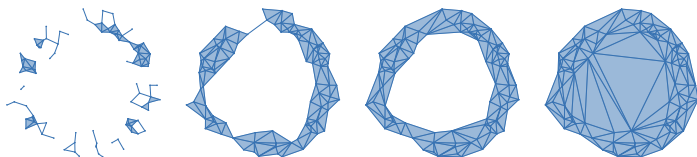


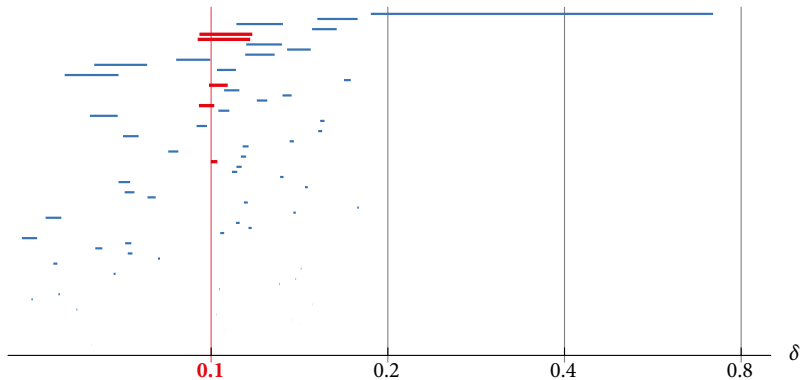
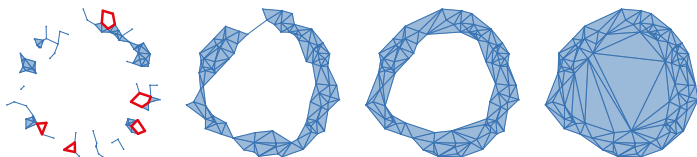


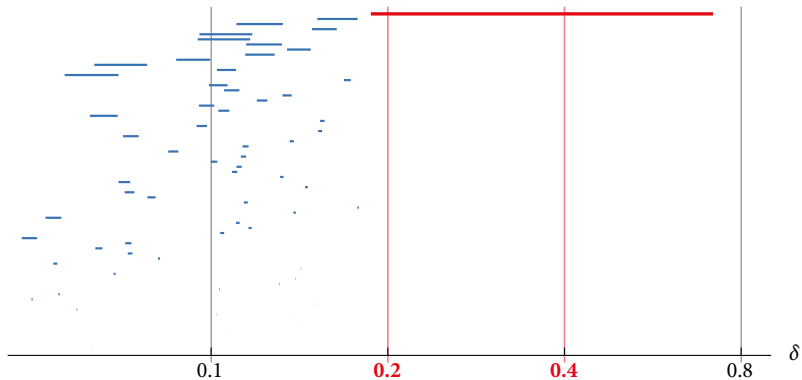
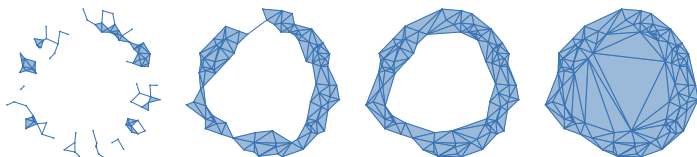


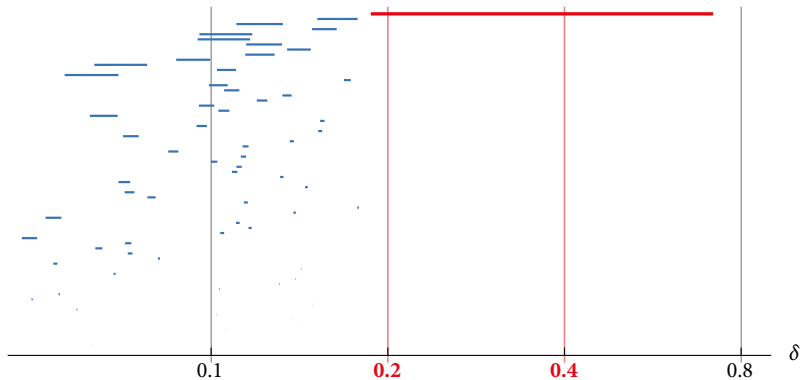
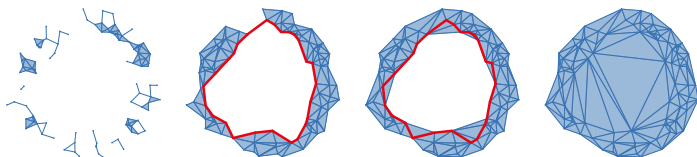












Vietoris–Rips persistence

Vietoris–Rips filtrations

Consider a finite metric space (X, d) .

The *Vietoris–Rips complex* is the simplicial complex

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

- 1-skeleton: all edges with pairwise distance $\leq t$
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Goal:

- compute persistence barcodes for $H_d(\text{Rips}_t(X))$
(in dimensions $0 \leq d \leq k$)

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

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Comparison with other software:

- javaplex: 3200 seconds, 12 GB
- Dionysus: 533 seconds, 3.4 GB
- GUDHI: 75 seconds, 2.9 GB
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Ripser: 1.2 seconds, 152 MB

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- 2016 ATMCS Best New Software Award (jointly with RIVET)

Design goals

Goals for previous projects:

- PHAT [B, Kerber, Reininghaus, Wagner 2013]:
fast persistence computation (matrix reduction only)
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Goals for Ripser:

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

The four special ingredients

The improved performance is based on 4 insights:

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

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Lessons from PHAT:

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

Matrix reduction

Matrix reduction algorithm

Setting:

- finite metric space X , n points
- persistent homology $H_d(\text{Rips}_t(X); \mathbb{F}_2)$ in dimensions $d \leq k$

Notation:

- D : boundary matrix of filtration
- R_i : i th column of R

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Result:

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

Compatible basis cycles

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

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

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$\Sigma_Z = \Sigma_B \cup \{V_i \mid i \in E\}$	is <i>another</i> basis of Z_* .

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- Persistence intervals: $\{[i, j) \mid i = \text{pivot } R_j\} \cup \{[i, \infty) \mid i \in E\}$
- Columns with non-essential positive indices never used!

Clearing

Clearing non-essential positive columns

Idea [Chen, Kerber 2011]:

- Don't reduce at non-essential positive indices
- Reduce boundary matrices of $\partial_d : C_d \rightarrow C_{d-1}$ in decreasing dimension $d = k + 1, \dots, 1$
- Whenever $i = \text{pivot } R_j$ (in matrix for ∂_d)
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Note:

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

Cohomology

Persistent cohomology

We have seen: many columns of $R = D \cdot V$ are not needed

- Skip those inessential columns in matrix reduction

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For persistence barcodes in low dimensions $d \leq k$:

- Number of skipped indices for reducing D^T (cohomology) is much larger than for D (homology)
 - reducing boundary matrix produces basis for $H_{k+1}(K_{k+1})$, which is not needed
- The resulting persistence barcode is the same
[de Silva et al. 2011]

Counting homology column reductions

- standard matrix reduction:

$$\underbrace{\sum_{d=1}^{k+1} \binom{n}{d+1}}_{\dim C_d(K)} = \underbrace{\sum_{d=1}^{k+1} \binom{n-1}{d}}_{\dim B_{d-1}(K)} + \underbrace{\sum_{d=1}^{k+1} \binom{n-1}{d+1}}_{\dim Z_d(K)}$$

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Observations

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

- Only 845 out of 1 161 471 columns have to be reduced

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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

Oblivious matrix reduction

Algorithm variant:

- $R = D$
- for $j = 1, \dots, n$
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Corollary

The rank of an $m \times n$ matrix can be computed in $O(n)$ memory.

Apparent and emergent pairs

Natural filtration settings

Typical assumptions on the filtration:

- | | |
|-------------------------------------|---------------------------|
| • general filtration | persistence (in theory) |
| • filtration by singletons or pairs | discrete Morse theory |
| • simplexwise filtration | persistence (computation) |

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Conclusion:

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

Discrete Morse theory

Definition (Forman 1998)

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

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

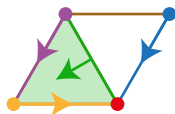


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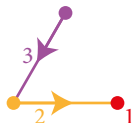
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Discrete Morse theory

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

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



A function $f : K \rightarrow \mathbb{R}$ on a cell complex is a *discrete Morse function* if

- sublevel sets are subcomplexes, and



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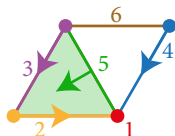
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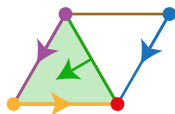


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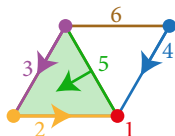
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A function $f : K \rightarrow \mathbb{R}$ on a cell complex is a *discrete Morse function* if

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



Fundamental theorem of discrete Morse theory

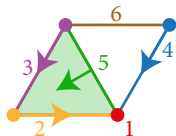
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$K \simeq M$ for some cell complex M built from the critical cells of f .

This homotopy equivalence is compatible with the filtration.

Corollary

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

Morse pairs and persistence pairs

Consider a *Morse filtration* (one or two simplices at a time).

Morse pair (σ, τ) :

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Consider a *simplexwise filtration* (one simplex at a time).

Persistence pair (σ, τ) :

- inserting simplex σ creates a new *homological* feature
- inserting τ destroys that feature again

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

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Lemma

Any apparent pairs is a persistence pair.

Lemma

The apparent pairs form a discrete gradient.

- Generalizes a construction proposed by [Kahle 2011] for the study of random Rips filtrations

From Morse theory to persistence and back

Proposition (from Morse to persistence)

The pairs of a Morse filtration are apparent 0-persistence pairs for the canonical simplexwise refinement of the filtration.

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The pairs of a Morse filtration are apparent 0-persistence pairs for the canonical simplexwise refinement of the filtration.

Proposition (from persistence to Morse)

Consider an arbitrary filtration with a simplexwise refinement. The apparent 0-persistence pairs yield a Morse filtration

- refining the original one, and*
- refined by the simplexwise one.*

Emergent persistent pairs

Consider the *lexicographically refined Rips filtration*:

- increasing diameter, refined by
- lexicographic order

This is the simplexwise filtration for computations in Ripser.

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Lemma

Assume that

- τ is the lexicographically minimal proper coface of σ with $\text{diam}(\tau) = \text{diam}(\sigma)$,
- and there is no persistence pair (ρ, τ) with $\sigma < \rho$.

Then (σ, τ) is an emergent persistence pair.

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Then (σ, τ) is an emergent persistence pair.

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

Ripsers Live: users from 156 different cities

