Ripser

Efficient Computation of Vietoris–Rips Persistence Barcodes

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Vietoris–Rips persistence

Vietoris–Rips filtrations

Consider a finite metric space (X, d).

The *Vietoris–Rips complex* is the simplicial complex

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

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

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Goal:

- compute persistence barcodes for $H_d(\mathrm{Rips}_t(X))$
  (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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- javaplex: 3200 seconds, 12 GB
- Dionysus: 533 seconds, 3.4 GB
- GUDHI: 75 seconds, 2.9 GB
- DIPHA: 50 seconds, 6 GB
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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 H^2 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 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 conjuction!

Matrix reduction

Matrix reduction algorithm

Setting:

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

Notation:

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

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- $R = D$, $V = I$
- while $\exists i < j$ with $\mathrm{pivot}\, R_i = \mathrm{pivot}\, R_j$
  - add R_i to R_j, add V_i to V_j

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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

$$P = \{i : R_i = 0\} \qquad \textit{positive} \text{ indices,}$$

$$N = \{j : R_j \neq 0\} \qquad \textit{negative} \text{ indices,}$$

$$E = P \setminus \operatorname{pivots} R \qquad \textit{essential} \text{ indices.}$$

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- Persistence intervals: $\{[i, j) \mid i = \operatorname{pivot} R_j\} \cup \{[i, \infty) \mid i \in E\}$
- 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 $\partial_d : C_d \to C_{d-1}$ in decreasing dimension $d = k+1, \dots, 1$
- Whenever $i = \operatorname{pivot} R_j$ (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

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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 (and very expensive)
- The resulting persistence barcode is the same

  [de Silva et al. 2011]

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Example ($k = 2, n = 192$):

- $\underbrace{1\,161\,471}_{\text{negative}} + \underbrace{1\,161\,471}_{\text{skipped}} + \underbrace{53\,727\,345}_{\text{essential}}$ columns in homology
- $\underbrace{1\,161\,471}_{\text{negative}} + \underbrace{18\,336}_{\text{skipped}} + \underbrace{1}_{\text{essential}}$ columns in cohomology

Observations

For a typical input:

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

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

Implicit matrix reduction

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- Boundary matrix D for filtration-ordered basis
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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 $j = 1, \ldots, n$
  - while $\exists i < j$ with $\operatorname{pivot} R_i = \operatorname{pivot} R_j$
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- current column R_j
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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)
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• simplexwise filtration	persistence (computation)

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Typical assumptions on the filtration:

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

Conclusion:

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

Apparent pairs

Definition

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

- σ is the youngest face of τ
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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

Emergent persistent pairs

Consider the *lexicographically refined Rips filtration:*

- increasing diameter, refined by
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Assume that

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

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

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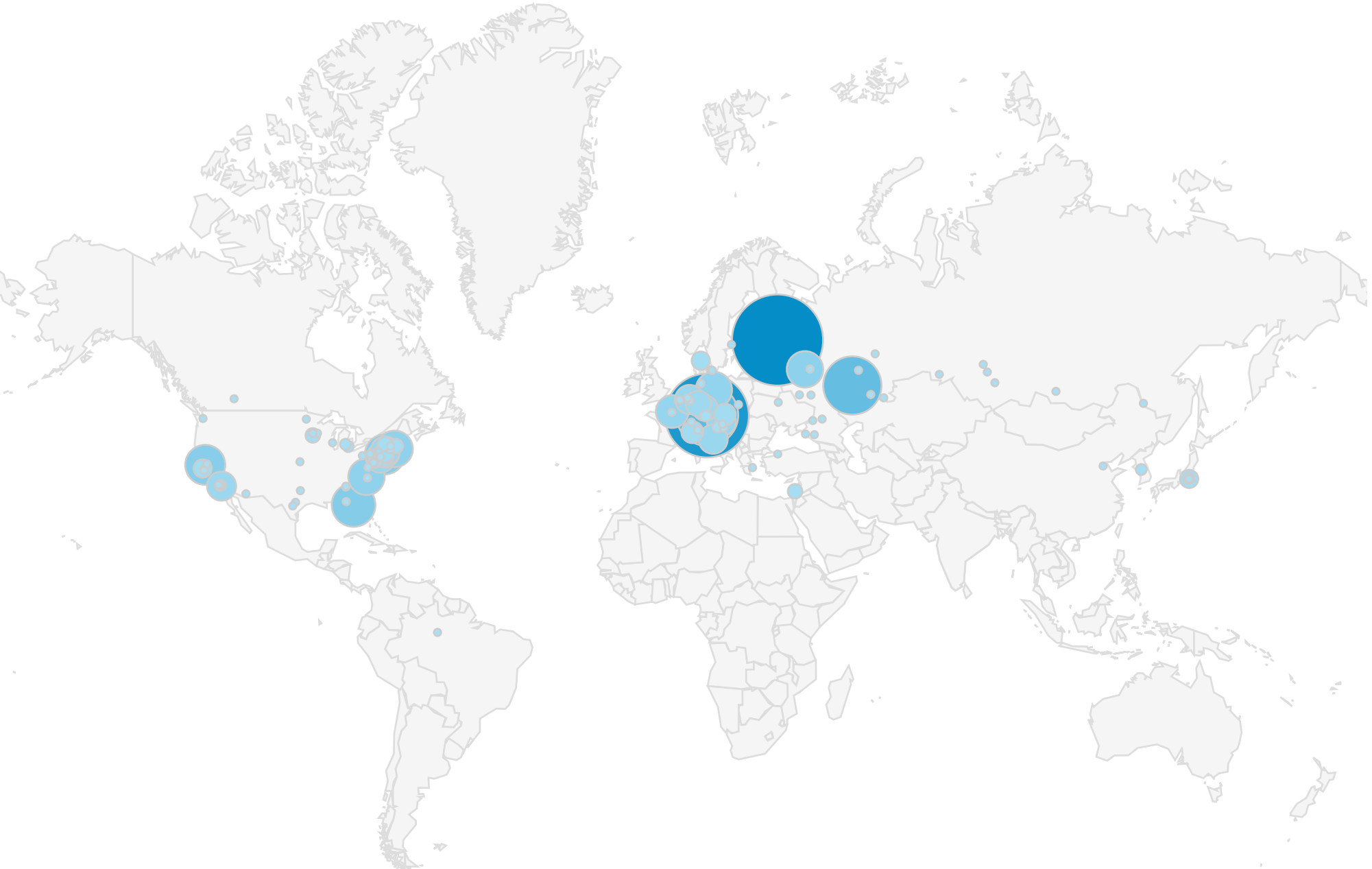
Then (σ, τ) *is an* emergent *persistence pair.*

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

Ripser Live: users from 156 different cities



http://ulrich-bauer.org/ripser-talk-dagstuhl.pdf