Ripser

or: the unexpected efficiency of persistent cohomology

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Design goals

Goals for previous projects:

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

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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 $0 \le d < k$

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

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!

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

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

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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 $d = k \dots 1$
- Whenever $i = pivot R_j$
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Note:

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

standard matrix reduction:

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

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Persistent cohomology

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Clearing for persistent cohomology:

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

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$$k = 3, n = 192$$
: 1161 472 = 1 + 1161 471

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 (from matrices D, V)
- reduction matrix V (from persistence pairs)

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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:

- V has very few off-diagonal entries
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Example: k = 3, n = 192:

 Only 191 + 53 + 601 = 845 out of 1161471 pairs are not apparent 0-persistence pairs

Conclusion

Can compute much larger instances than previous software

- H² persistence for data with 1681 points, in about 30 minutes using 20GB RAM
- Available at http://git.io/ripser
- Bring your own data set to the hands-on demonstration!