

Reducing complexes in Multidimensional Persistence

Claudia Landi

University of Modena and Reggio Emilia

joint work with M. Allili and T. Kaczynski

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- This talk: apply this strategy for multiD persistence in any degree

Outline

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S-Complexes

Multidimensional Persistent Homology

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Partial Matching & Reductions in the framework of persistence

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S-Complexes

1. Let S be a finite set with a gradation S_q such that $S_q = \emptyset$ for $q < 0$. For every element $\sigma \in S$ there exists a unique number q such that $\sigma \in S_q$. This number is called the dimension of σ and denoted $\dim \sigma$.

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3. $C_q(S) := R(S_q)$, the free module over R generated by S_q .
4. We say that (S, κ) is an *S-complex* if $(C_*(S), \partial_*^\kappa)$ with $\partial_q^\kappa : C_q(S) \rightarrow C_{q-1}(S)$ defined on generators $\sigma \in S$ by

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5. By the homology of an S -complex (S, κ) we mean the homology of the chain complex $(C_*(S), \partial_*^\kappa)$, and we denote it by $H_*(S, \kappa)$ or simply by $H_*(S)$.

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 2. define

$$\kappa(\sigma, \tau) := \begin{cases} (-1)^i & \text{if } \sigma = [v_0, v_1, \dots, v_q] \\ & \text{and } \tau = [v_0, v_1, \dots, v_{i-1}, v_{i+1}, \dots, v_q] \\ 0 & \text{otherwise.} \end{cases}$$

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- cubical complexes
 - cell complexes

Multi-filtration of an S-complex

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- A *k-filtration* of S is a family $\mathcal{F} = \{S^a\}_{a \in \mathbb{R}^k}$ of subsets of S with the following properties:
 - \mathcal{F} is nested with respect to inclusions:

$$S^a \subseteq S^b, \text{ for every } a \preceq b$$

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- Given a function $f : S_0 \rightarrow \mathbb{R}^k$, the *sublevel set filtration* is defined by

$$S^a = \{\sigma = [v_0, v_1, \dots, v_q] \in S \mid f(v_i) \preceq a, i = 0, \dots, q\}.$$

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- The i -th persistent homology group of the filtration at (a, b) is image of the map $H_i(j^{(a,b)})$:

$$H_i^{a,b}(S) := \text{im } H_i(j^{(a,b)})$$

Partial matchings

Given an S -complex (S, κ) , a *partial matching* on (S, κ) is a quadruplet (A, B, C, m) where

- A, B, C is a partition of S , and
- $m : A \rightarrow B$ is a map such that, for each $\tau \in A$, $\kappa(m(\tau), \tau)$ is invertible.

In particular, $m(\tau)$ is a primary coface of τ .

Partial matchings

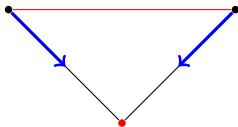
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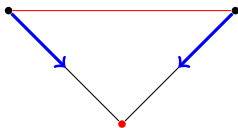
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- A partial matching is called *acyclic* if there is no non-trivial sequence of simplices

$$\sigma_0 \xrightarrow{m} \tau_0 \xrightarrow{>} \sigma_1 \xrightarrow{m} \tau_1 \xrightarrow{>} \dots \xrightarrow{>} \sigma_n \xrightarrow{m} \tau_n \xrightarrow{>} \sigma_0$$

Reductions

Let (A, B, C, m) be a partial matching (not necessarily acyclic) on (S, κ) . A single pair $(m(\sigma), \sigma)$ can be removed so to obtain again an S-complex:

- For $\sigma \in A$, define $(\bar{S}, \bar{\kappa})$ where $\bar{S} = S \setminus \{m(\sigma), \sigma\}$, and $\bar{\kappa} : \bar{S} \times \bar{S} \rightarrow R$,

$$\bar{\kappa}(\eta, \xi) = \kappa(\eta, \xi) - \frac{\kappa(\eta, \sigma)\kappa(m(\sigma), \xi)}{\kappa(m(\sigma), \sigma)}.$$

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Proposition

If (A, B, C, m) is acyclic then, for any $\tau \in A \setminus \{\sigma\}$, $\bar{\kappa}(m(\tau), \tau)$ is invertible. Furthermore, $\bar{\kappa}(m(\tau), \tau) = \kappa(m(\tau), \tau)$.

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Theorem

Fixed $\sigma \in A$, define $\bar{A} = A \setminus \{\sigma\}$, $\bar{B} = B \setminus \{m(\sigma)\}$, $\bar{m} = m|_{\bar{A}}$, and $\bar{C} = C$. If (A, B, C, m) is an acyclic partial matching, then $(\bar{A}, \bar{B}, \bar{C}, \bar{m})$ is an acyclic partial matching too.

Reductions preserve homology [KMS 1998]

- Define $\pi : C_*(S) \rightarrow C_*(\bar{S})$ and $\iota : C_*(\bar{S}) \rightarrow C_*(S)$ on generators by setting

$$\pi(\tau) = \begin{cases} 0 & \text{if } \tau = m(\sigma) \\ -\sum_{\xi \in \bar{S}} \frac{\kappa(m(\sigma), \xi)}{\kappa(m(\sigma), \sigma)} \xi & \text{if } \tau = \sigma \\ \tau & \text{otherwise} \end{cases}$$

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- π and ι are chain equivalences with the chain homotopy $D_* : C_*(S) \rightarrow C_{*+1}(S)$ given on generators $\tau \in S_q$, $q \in \mathbb{Z}$, by

$$D_q(\tau) = \begin{cases} \frac{1}{\kappa(m(\sigma), \sigma)} m(\sigma) & \text{if } \tau = \sigma \\ 0 & \text{otherwise} \end{cases}$$

Filtration-preserving matching

A partial matching (A, B, C, m) on a filtered S -complex is said to *preserve the filtration* when, for every $a \in \mathbb{R}^k$,

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A filtration-preserving partial matching on S naturally induces a filtration on \bar{S} : for each $\tau \in \bar{S}$,

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Proposition

Let $(\bar{S}, \bar{\kappa})$ be obtained from (S, κ) by reduction of the pair $(m(\sigma), \sigma)$.
Then, for each $q \in \mathbb{Z}$,

$$\pi(C_q(S^a)) \subseteq C_q(\bar{S}^a), \quad \iota(C_q(\bar{S}^a)) \subseteq C_q(S^a), \quad D_q(C_q(S^a)) \subseteq C_{q+1}(\bar{S}^a)$$

Reductions preserve persistent homology

Proposition

The maps $\pi|_{C_*(S^a)} : C_*(S^a) \rightarrow C_*(\bar{S}^a)$ and $\iota|_{C_*(\bar{S}^a)} : C_*(\bar{S}^a) \rightarrow C_*(S^a)$ defined by restriction are chain homotopy equivalences. Moreover, the diagram

$$\begin{array}{ccc} H_*(S^a) & \xrightarrow{H_*(j^{(a,b)})} & H_*(S^b) \\ \downarrow \cong & & \downarrow \cong \\ H_*(\bar{S}^a) & \xrightarrow{H_*(j^{(a,b)})} & H_*(\bar{S}^b) \end{array}$$

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Theorem

For every $a \preceq b \in \mathbb{R}^k$, $H_*^{a,b}(S)$ is isomorphic to $H_*^{a,b}(\bar{S})$.

The matching algorithm: introduction

- We start from the matching algorithm of [King-Knudson-Mramor 2005] [for homology](#)
 - input: a simplicial complex and [an \$\mathbb{R}\$ -valued function on its vertices](#)
 - output: an acyclic partial matching
 - recursive
 - vertex-based and lower-link-based
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 - **cancels pairs of critical cells to achieve optimality**
- and extend it **for multidimensional persistent homology**
 - input: a simplicial complex, **an \mathbb{R}^k -valued function and an ordering on its vertices**
 - output: a **filtration-preserving** acyclic partial matching
 - recursive
 - vertex-based and lower-link-based
 - **without cancellation**

Indexing map for vertices

Lemma

There exists an injective function $I : S_0 \rightarrow \mathbb{N}$ such that, for each $v, w \in S_0$ with $v \neq w$, $f(v) \not\preceq f(w)$ implies $I(v) < I(w)$.

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- apply the topological sorting algorithm
- this algorithm has linear complexity

The matching algorithm for multiD persistence

Input: A finite simplicial complex S with a function $f : S_0 \rightarrow \mathbb{R}^k$ and an indexing $l : S_0 \rightarrow \mathbb{N}$ on its vertices.

Output: Three lists A, B, C of simplices of S , and a function $m : A \rightarrow B$.

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function Partition (complex S , function f , indexing map l)

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Output: Three lists A, B, C of simplices of S , and a function $m : A \rightarrow B$.
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Set w_0 as the vertex with smallest index l' in D' .

Add $[v, w_0]$ to B and define $m(v) = [v, w_0]$.

For each $\sigma \in C' \setminus \{w_0\}$, add $v * \sigma$ to C .

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4. **return** A, B, C, m .

Correctness, reduction, and complexity

Theorem

The matching algorithm produces a partial matching (A, B, C, m) that is acyclic. Moreover, if $\sigma \in S^a$ then $m(\sigma) \in S^a$.

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Theorem

The algorithm produces (A, B, C, m) in less than $2\gamma^d(d+1)!N$ steps, where

d : dimension of S





N : cardinality of S_0

γ : upper bound on the number of cofaces of any simplex in S

Numerical tests

- Considered four simplicial complexes.
- Each complex was filtered by the \mathbb{R}^2 -valued function defined on vertices by $f(v) = (|x|, |y|)$.
- Present the results in a table where
 - row 1 shows the number of vertices, edges, faces, and the total number of cells of each considered mesh S ,
 - while row 2 shows the same quantities referred to the cell complex C obtained by using our matching algorithm to reduce S .
 - Finally, row 3 shows the ratio between the second and the first rows, expressing them in percentage points. In other words, the lower are those ratios, the higher is the reduction rate.

Numerical tests

				
	tie	space_shuttle	x_wing	space_station
#S ₀	2014	2376	3099	5749
#C ₀	228	121	175	1879
%	11.3	5.1	5.6	32.7
#S ₁	5944	6330	9190	15949
#C ₁	3343	3699	3605	11158
%	56.2	58.4	39.2	70.0
#S ₂	3827	3952	6076	10237
#C ₂	3012	3576	3415	9316
%	78.7	90.5	56.2	91.0
#S	11785	12658	18365	31935
#C	6583	7396	7195	22353
%	55.9	58.4	39.2	70.0

Conclusions

- The reduction algorithm has linear complexity vs polynomial complexity of persistence computation
- May be a convenient pre-processing technique
- Full paper available at [arXiv:1310.8089v2](https://arxiv.org/abs/1310.8089v2)
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Thank you for your attention!