Chunk Reduction for Multi-Parameter Persistent Homology

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Der Wissenschaftsfonds.

Multi-Parameter Persistent Homology

Multi-parameter persistence describes the *changes in homology* of datasets evolving along *two or more (independent) scale parameters*

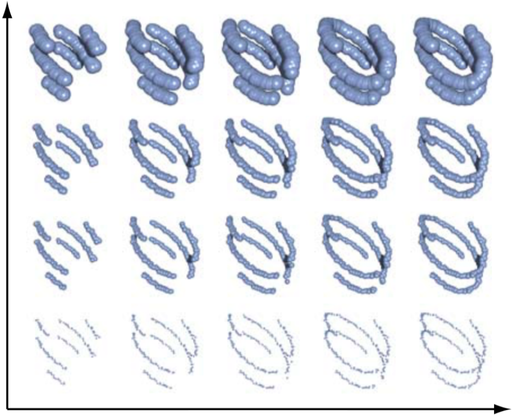


Image courtesy of [Carlsson & Zomorodian 2009]

Multi-Parameter Persistent Homology

Formally:

Given a *d*-filtered chain complex $C := (C_*^p)_{p \in \mathbb{R}^d}$,

the *multi-parameter persistence* k^{th} *module* $H_k(C)$ consists of:

- A collection of *homology spaces* $H_k(C_*^p)$ for $p \in \mathbb{R}^d$
- A collection of *linear maps* $\iota_k^{p,q} : H_k(C_*^p) \to H_k(C_*^q)$ induced by the inclusion maps at *k*-chain level for $p, q \in \mathbb{R}^d$ and $p \leq q$

Multi-parameter persistent homology provides a ***stable and discriminative information*** *but…*

Multi-Parameter Persistent Homology

But…

Computations scale badly with the size of the input complex

Our Goal

Design and implement a *simplification process*

drastically reducing the size of the input complex while

preserving its multi-parameter persistent homology

Outline

- *Multi-Chunk Algorithm*
- *Optimality Result*
- *Experimental Evaluation*
- *Conclusions and Future Developments*

Multi-Chunk Algorithm

Inspired by the chunk algorithm for persistent homology [Bauer et al. 2014],

We propose a ***reduction algorithm*** such that

given a *d*-filtered chain complex C returns a *d*-filtered chain complex $\bar{C}$

- *drastically smaller* than C
- *homology-equivalent* to C

C and $\bar{C}$ are *homology-equivalent* if, for any $k \in \mathbb{N}$ and any $p, q \in \mathbb{R}^d$ with $p \leq q$,

$H_k(C_*^p)$ and $H_k(\bar{C}_*^p)$ are ***isomorphic*** via a map φ_k^p and each diagram

$$\begin{tikzcd} H_k(C_*^p) \arrow[r] \arrow[d, "\varphi_k^p"] & H_k(C_*^q) \arrow[d, "\varphi_k^q"] \\ H_k(\bar{C}_*^p) \arrow[r] & H_k(\bar{C}_*^q) \end{tikzcd}$$

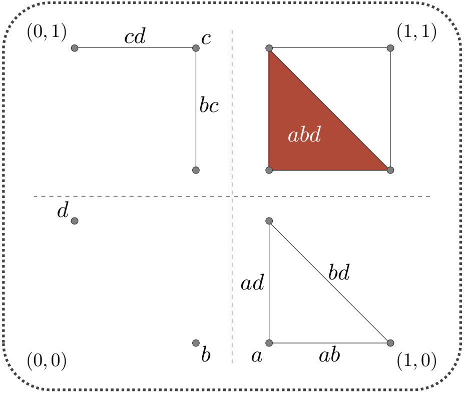
commutes where horizontal maps are induced by inclusion maps

Multi-Chunk Algorithm

Initialization:

Given a *d*-filtered simplicial complex,

each ***k*-simplex *σ*** can be represented by a ***k*-column** encoding:



- Boundary of ***σ***
- Dimension *k*
- Filtration value ***v(σ)***
- Index ***i(σ)***

where *i* is a ***total order*** on the simplices compatible with the filtering function *v*

Multi-Chunk Algorithm

Initialization:

Given a *d*-filtered simplicial complex,

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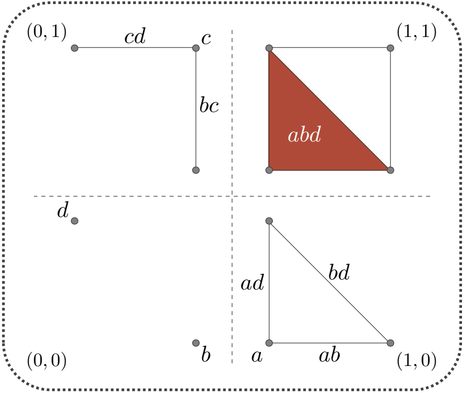

	bd
– Boundary of ***σ***	$\{b, d\}$
– Dimension *k*	1
– Filtration value ***v(σ)***	$(1, 0)$
– Index ***i(σ)***	9

where *i* is a ***total order*** on the simplices compatible with the filtering function *v*

Multi-Chunk Algorithm

			$(0,0)$		$(0,1)$			$(1,0)$				$(1,1)$
	i		1	2	3	4	5	6	7	8	9	10
		σ	b	d	c	bc	cd	a	ab	ad	bd	abd
$(0,0)$	1	b				1			1		1	
	2	d					1			1	1	
$(0,1)$	3	c				1	1					
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$(1,1)$	10	abd										

Multi-Chunk Algorithm

Multi-chunk algorithm offers an immediate *parallelization* scheme in shared memory and it consists of *three phases*:

I - Local Reduction

II - Compression

III - Removal of Local Pairs

Local Pivot:

A column σ has a *local pivot* iff the element τ with *maximal index* in the boundary of σ is such that $v(\tau)=v(\sigma)$

Multi-Chunk Algorithm

			(0,0)		(0,1)			(1,0)			(1,1)
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Multi-Chunk Algorithm

Phase I: Local Reduction

Proceed in ***decreasing dimension*** *k* and traverse the *k*-columns in ***increasing order w.r.t. i***

Goal: *Label the columns as local or global*

Given an ***unlabeled*** *k*-column σ, while

- σ has a local pivot and
- there is a *k*-column σ' with the same local pivot and $i(\sigma) < i(\sigma')$

perform the ***column addition*** $\sigma \leftarrow \sigma + \lambda\sigma'$ (λ is s.t. the local pivot of σ disappears)

If, at the end of the loop, the column σ ***does not have a local pivot***

- σ is labeled as ***global***

otherwise,

- σ is labeled as ***local negative*** and its local pivot as ***local positive***

Multi-Chunk Algorithm

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Multi-Chunk Algorithm

Phase II: Compression

Goal: ***Simplify the boundary*** *of the global columns*

Given a ***global*** *k*-column σ, while

- the boundary of σ contains local positive or negative elements

pick the local *(k-1)*-column τ in the boundary of σ with maximal index *i*

If τ is ***local negative***,

- remove τ from the boundary of σ

If τ is **local positive**

- perform the column addition $\sigma \leftarrow \sigma + \lambda\sigma'$

  where σ' is s.t. (τ,σ') is a local pair and λ is such that τ disappears

Multi-Chunk Algorithm

			$(0,0)$		$(0,1)$			$(1,0)$				$(1,1)$
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Multi-Chunk Algorithm

Phase III: Removal of Local Pairs

*Traverse the columns and **remove** all the columns labeled as **local positive** or **local negative***

Theorem

Remaining columns generate a d-filtered chain complex having the same multi-parameter persistent homology as the input (they are homotopy-equivalent)

Multi-Chunk Algorithm

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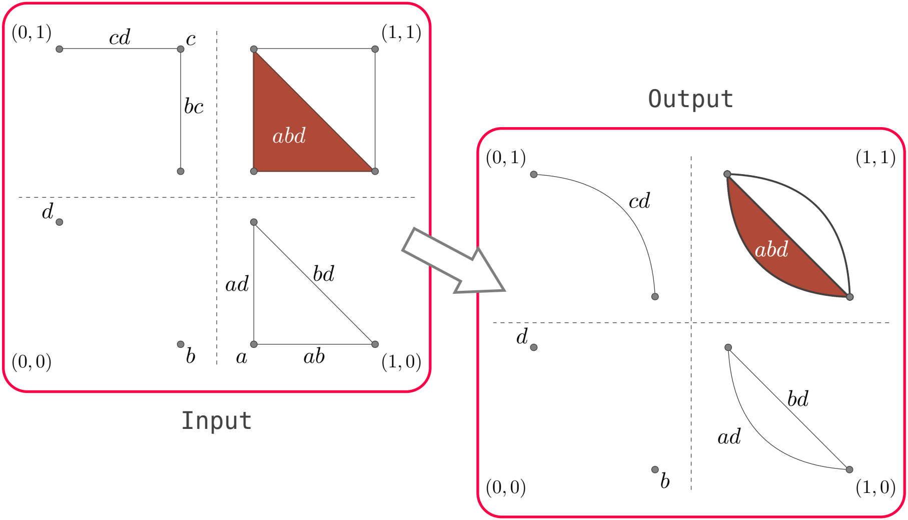
Multi-Chunk Algorithm



Multi-Chunk Algorithm

Remarks

- *In Phase I, to proceed in decreasing dimension avoids performing any column additions on local positive columns*
- *Algorithm operates independently on columns of the same value (called chunks)*

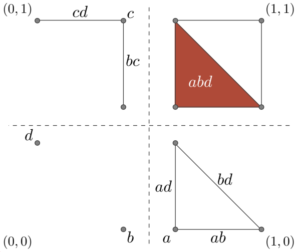
Proposition

Multi-chunk algorithm has time complexity $O(m\ell^3 \log \ell + gn\ell \log \ell)$ *and space complexity* $O(n\ell + g^2)$ *where:*

- n *is the size of the input complex*
- m *is the number of chunks*
- ℓ *is the maximal size of a chunk*
- g *is the number of global columns*

Optimality Result

- $C_*^{<p} := \sum_{q<p} C_*^q$
- $\gamma_k^p(C) := \dim C_k^p - \dim C_k^{<p}$
- $\delta_k^p(C) := \dim(\ker\ \iota_{k-1}^p) + \dim(\text{coker}\ \iota_k^p)$



$$\gamma_1^{(1,0)}(C) = 3 > 2 = \delta_1^{(1,0)}(C)$$

Proposition

For any d-filtered chain complex D quasi-isomorphic to the input complex C,

$$\gamma_k^p(D) \geq \delta_k^p(C)$$

Theorem

Let $\bar{C}$ be the d-filtered chain complex complex obtained as output, then

$$\gamma_k^p(\bar{C}) = \delta_k^p(C)$$

Optimality Result

- $C_*^{<p} := \sum_{q<p} C_*^q$
- $\gamma_k^p(C) := \dim C_k^p - \dim C_k^{<p}$
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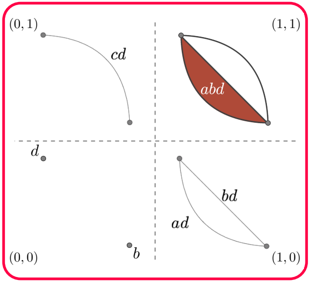

$$\gamma_1^{(1,0)}(\bar{C}) = 2 = \delta_1^{(1,0)}(C)$$

Proposition

For any d-filtered chain complex D quasi-isomorphic to the input complex C,

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Theorem

Let $\bar{C}$ be the d-filtered chain complex complex obtained as output, then

$$\gamma_k^p(\bar{C}) = \delta_k^p(C)$$

Experimental Evaluation

We have experimentally compared the performances of our approach with the simplification process based on *discrete Morse theory* proposed in [Scaramuccia et al. 2018]

Dataset	Size		Time (sec.)				Memory Usage (GB)	
			Chunk		DMT			
	Input	Output	Prep.	Simpl.	Prep.	Simpl.	Chunk	DMT
Eros	2.9 M	202 K	1.7	0.8	2.7	15.8	0.36	0.46
Donna	3.0 M	217 K	1.8	0.8	2.8	16.9	0.38	0.48
Chinese Dragon	3.9 M	321 K	2.5	1.1	3.9	22.3	0.52	0.64
Circular Box	4.2 M	365 K	2.9	1.2	4.3	24.0	0.68	0.68
Ramesses	5.0 M	407 K	3.4	1.3	5.5	29.4	0.68	0.81
Pensatore	6.0 M	369 K	3.8	1.6	6.8	34.3	0.76	0.97
Raptor	6.0 M	260 K	4.4	1.7	5.4	32.3	0.73	0.93
Neptune	12.0 M	893 K	8.4	4.4	14.9	69.2	1.52	1.94
Cube 1	590 K	67 K	0.5	0.3	0.7	3.2	0.09	0.10
Cube 2	2.4 M	264 K	1.8	1.1	2.6	13.1	0.35	0.40
Cube 3	9.4 M	1.0 M	7.6	4.8	11.0	53.1	1.37	1.58
Cube 4	37.7 M	4.2 M	31.9	19.4	44.9	216.0	5.50	6.32

Conclusions and Future Developments

In Summary:

We have presented a *pre-processing procedure* for improving the computation of multi-parameter persistent homology and we have provided *theoretical and experimental evidences of its effectiveness*

Future Directions:

- Develop a *parallel implementation* with shared memory of the multi-chunk algorithm
- Evaluate the impact of the chunk algorithm for the computation of the persistence module and of the *persistence space*
- Compare the proposed strategy with the *minimal presentation algorithm* for persistence modules from RIVET [Lesnick & Wright 2019]

Thank you

Ulderico Fugacci
TU Graz, Institute of Geometry

C and $\bar{C}$ are *homology-equivalent* if, for any $k \in \mathbb{N}$ and any $p, q \in \mathbb{R}^d$ with $p \leq q$,

$H_k(C_*^p)$ and $H_k(\bar{C}_*^p)$ are ***isomorphic*** via a map φ_k^p and each diagram

$$\begin{tikzcd} H_k(C_*^p) \arrow[r] \arrow[d, "\varphi_k^p"] & H_k(C_*^q) \arrow[d, "\varphi_k^q"] \\ H_k(\bar{C}_*^p) \arrow[r] & H_k(\bar{C}_*^q) \end{tikzcd}$$

commutes where horizontal maps are induced by inclusion maps

C and $\bar{C}$ are *quasi-isomorphic* if the isomorphisms of the above diagram are induced by a collection of chain maps f_*^p such that each diagram

$$\begin{tikzcd} C_*^p \arrow[r] \arrow[d, "f_k^p"] & C_*^q \arrow[d, "f_k^q"] \\ \bar{C}_*^p \arrow[r] & \bar{C}_*^q \end{tikzcd}$$

commutes where horizontal maps are the inclusion maps

C and $\bar{C}$ are *homotopy-equivalent* if there exist two collections of chain maps f_*^p and g_*^p such that they are ***homotopy-inverse*** (i.e., $g_*^p f_*^p \simeq \mathrm{id}_{C_*^p}$ and $f_*^p g_*^p \simeq \mathrm{id}_{\bar{C}_*^p}$) and each diagram

$$
\begin{tikzcd}
C_*^p \arrow[rr] \arrow[d, shift right, "f_k^p"'] & & C_*^q \arrow[d, shift right, "f_k^q"'] \\
\bar{C}_*^p \arrow[rr] \arrow[u, shift right, "g_k^p"'] & & \bar{C}_*^q \arrow[u, shift right, "g_k^q"']
\end{tikzcd}
$$

commutes where horizontal maps are the inclusion maps

Homotopy-equivalent ⇨ ***Quasi-isomorphic*** ⇨ ***Homology-equivalent***

Filtered chain complexes which are
homology-equivalent but not quasi-isomorphic