Computing the matching distance of multi-parameter persistence from Morse critical values

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Outline

Brief introduction to persistence

Persistence-preserving discrete gradients

Critical cells for ..
... Detecting gradient anti-alignment
... Fibering persistence modules
... Computing the matching distance

Conclusions

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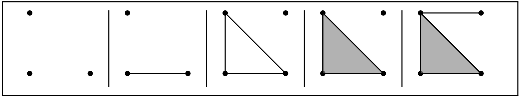
The pipeline of 1-parameter persistence

Geometry	functions	$f : \Sigma \to \mathbb{R}$
$\downarrow$	$\downarrow$	$\downarrow$
Topology	sublevel sets	$\Sigma^u = \{\sigma \in \Sigma : f(\sigma) \leq u\}$
$\downarrow$	$\downarrow$	$\downarrow$
Algebra	vector spaces	$M = \{H_k(\Sigma^u), i^{u,v}\}$
$\downarrow$	$\downarrow$	$\downarrow$
Combinatorics	invariants	decomposition: $M \cong \bigoplus_i \mathbb{I}_{[b_i,d_i)}$ barcodes: $B(M) = \{[b_i, d_i)\}$



The pipeline of 1-parameter persistence

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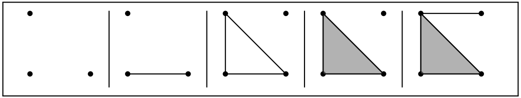


Decomposition	$\Leftrightarrow$	barcodes
Interleaving distance	$=$	bottleneck distance

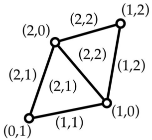
The pipeline of multi-parameter persistence

Geometry	functions	$f : \Sigma \to \mathbb{R}^n$
$\downarrow$	$\downarrow$	$\downarrow$
Topology	sublevel sets	$\Sigma^u = \{\sigma \in \Sigma : f(\sigma) \preceq u\}$
$\downarrow$	$\downarrow$	$\downarrow$
Algebra	vector spaces	$M = \{H_k(\Sigma^u), i^{u,v}\}$
$\downarrow$	$\downarrow$	$\downarrow$
Combinatorics	invariants	decomposition: $M \cong \bigoplus_i M_i$ fibered barcodes: $\{B(M_L)\}_L$

Decomposition	$\not\Leftrightarrow$	fibered barcodes
Interleaving distance	$\geq$	matching distance

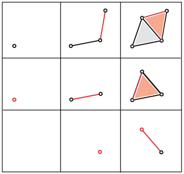
[L18]

More in detail



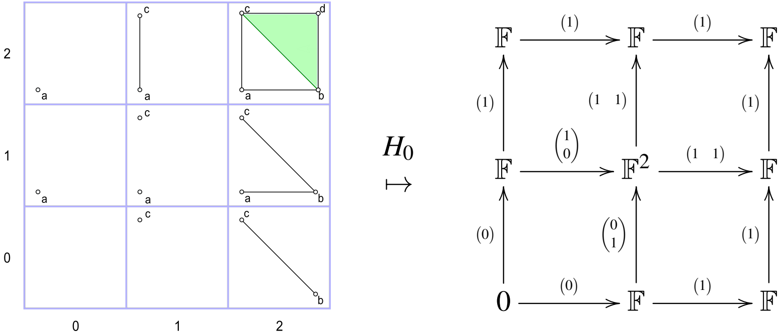
- Σ simplicial complex
- $f = (f_1, \dots, f_n) : \Sigma \to \mathbb{R}^n$
- Lower level subcomplexes: for $u \in \mathbb{R}^n$,

$$\Sigma^u := \{\sigma \in \Sigma : f(\sigma) \preceq u\}$$



- Nested: $u \preceq v$ implies $\Sigma^u \subseteq \Sigma^v$
- E.g., f defined on vertices and extended to any σ by

$$f_i(\sigma) = \max_{v \in \sigma} f_i(v)$$



- $M = \{H(\Sigma^u), i^{u,v}\}_{u \preceq v}$ persistence module of (Σ, f)

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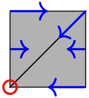
Discrete gradients

A *discrete gradient* V is a partition of Σ into

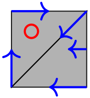
- singletons $\{\sigma\}$ (critical cells), and
- pairs $\{\sigma, \tau\}$, where σ is a facet of τ

such that

- V is acyclic: $\nexists$ closed path $\{\sigma_i, \tau_i\}_{1 \le i \le r}$ with σ_{i+1} facet of τ_i



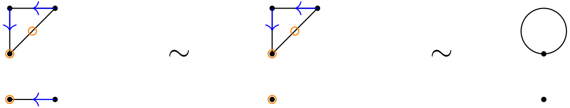
Discrete gradient vector field



Not a discrete gradient vector field

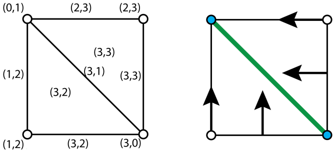
Discrete Morse Theory

- Any pair $(\sigma, \tau) \in V$ defines a simplical collapse which preserves homotopy type.



- Homotopy equivalent $\implies$ isomorphic homology groups.
- Therefore, critical values can help identify the steps of the filtration where the associated subcomplex may undergo a change in homology.

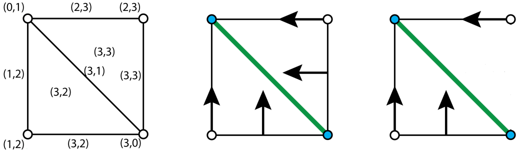
Compatible discrete gradients



A discrete gradient V is *compatible* with $f : \Sigma \to \mathbb{R}^n$ if

$$\forall(\sigma, \tau) \in V,\ f(\sigma) = f(\tau).$$

Compatible discrete gradients



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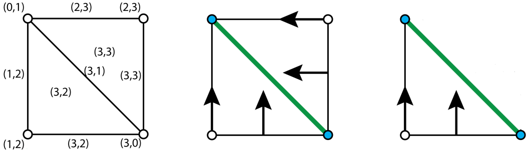

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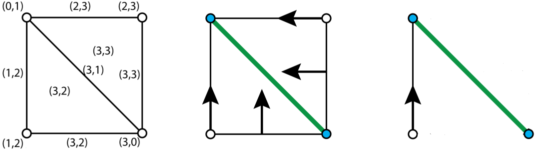

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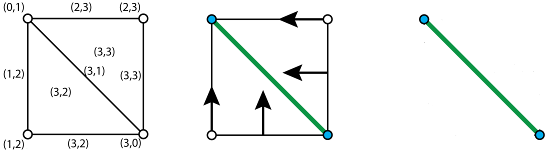

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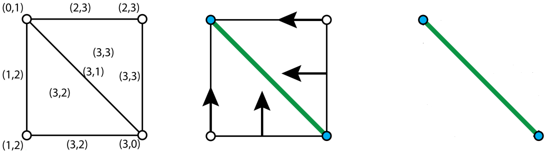

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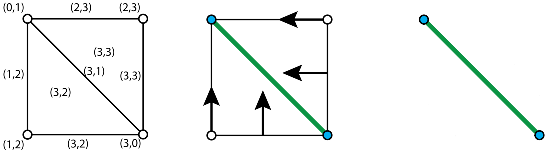
[AKL'17]: The persistence module of (Σ, f) and that of its Morse complex formed by critical cells only are isomorphic

Compatible discrete gradients



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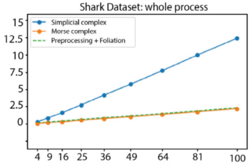
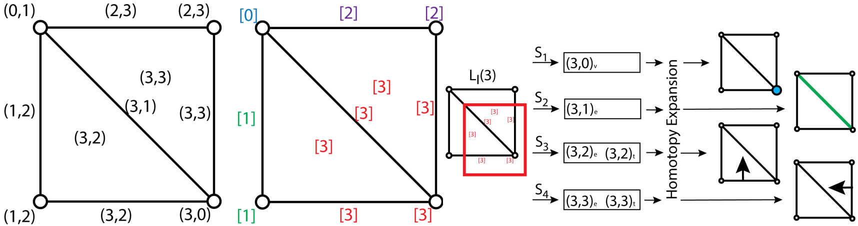
- Convenient to speed up computations, e.g. of the fibered barcode



[SIDL'2020]

Construction of a compatible discrete gradient

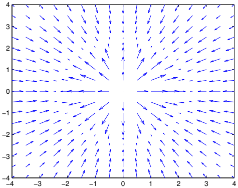
[SIDL'20]: A discrete gradient compatible with a generic f can be built in linear time on the number of vertices.



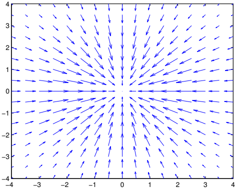
[LS'21]: For 2D simplicial complexes and 3D cubical complexes, it is also persistence-perfect.

Critical cells for ... detecting gradient anti-alignment

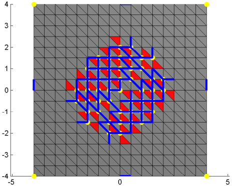
Critical cells localize the regions where the gradient vector fields of f_1 and f_2 disagree:



∇f_1



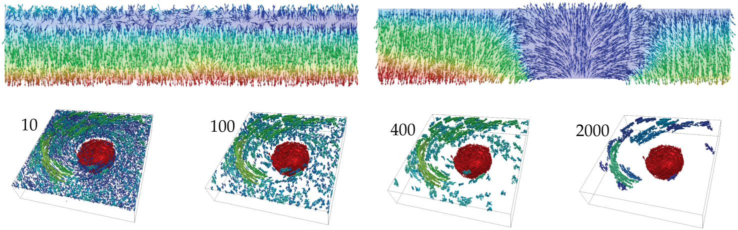
∇f_2



(color=dim)

[AKLM'19]

Hurricane Isabel dataset: temperature and pressure on cubical grid

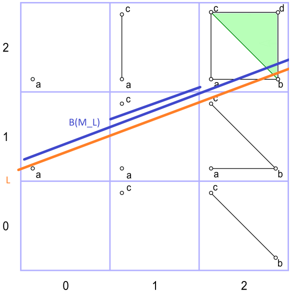


Clusters with $\geq$ 10, 100, 400, 2000 critical cells (color encodes size)

[ISLD'16]

Critical cells ... for fibering persistence modules

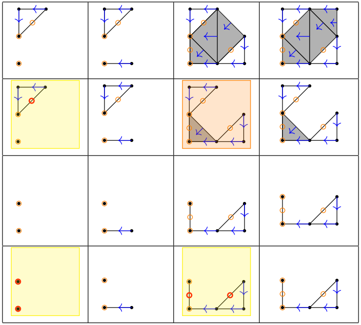
- Each increasing line L in $\mathbb{R}^n$ induces a 1-parameter filtration with associated persistence module M_L.
- The *fibered barcode* of M maps each line L to the barcode of M_L.



Note: $O(m^2)$ lines to consider with m number of simplices

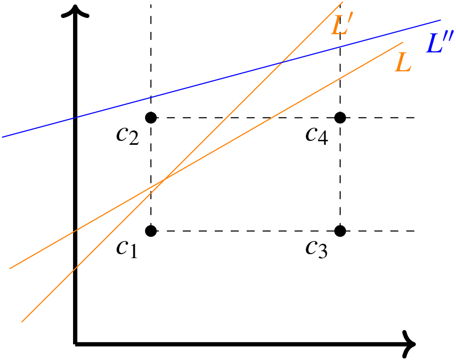
Note: Barcode computations repeated across different lines, each taking $O(m^3)$ time

- A *critical value* is the value of the parameter at which a critical simplex enters into the filtration.
- $\overline{C}$ is the closure of the set of critical values C under least upper bound.



We can use critical values to partition the set of all lines of $\mathbb{R}^n$ into equivalence classes:

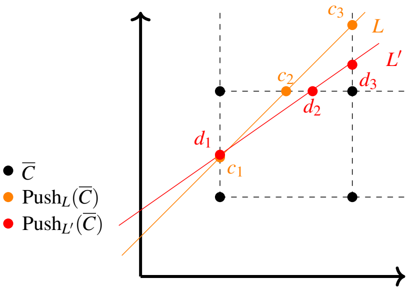
- We write $L \sim_{\overline{C}} L'$, if L and L' have the same reciprocal position with respect to c for all $c \in \overline{C}$.



- Here, $L \sim_{\overline{C}} L'$, but $L'' \nsim_{\overline{C}} L'$ and $L'' \nsim_{\overline{C}} L$

Barcodes of restrictions along equivalent lines $L \sim_{\overline{C}} L'$ are in bijection:

$$\gamma : B(M_L) \to B(M_{L'})$$



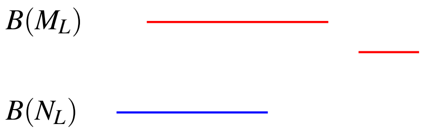
So, it is sufficient to compute $B(M_L)$ on representative lines

[BBHLM'21]

Critical cells for ... computing the matching distance

Let M, N be 2-parameter persistence modules, L a line with positive slope. Given the barcodes $B(M_L)$ and $B(N_L)$,

- the cost $c(\sigma)$ of a partial matching $\sigma : B(M_L) \to B(N_L)$ is the maximum amount one has to enlarge or shrink the ends of each interval $[b,d]$ in B in order to obtain the interval $\sigma([b,d])$, or $[\frac{d-b}{2}, \frac{d-b}{2}]$ if $[b,d)$ is unmatched



- Their bottleneck distance d_B is the minimum cost over all partial matchings σ.
- The matching distance between M and N is defined as

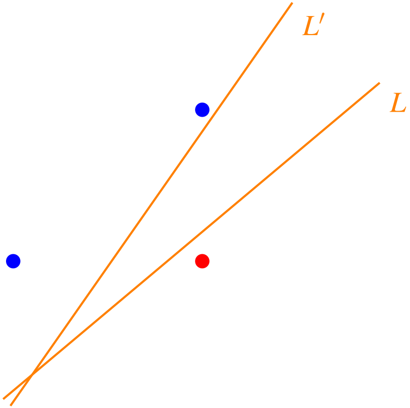
$$\sup_L w_L d_B(B(M_L), B(N_L))$$

where the weight w_L is given by the slope of L.

Critical values determine the matching distance

Theorem

The critical values of M and N determine a finite set $\Omega \subset \mathbb{R}^2$ such that the matching distance between M and N is realized by a line (not necessarily unique) through two points in $\overline{C \cup \Omega}$, or by a line through one point in $\overline{C \cup \Omega}$ having diagonal direction.



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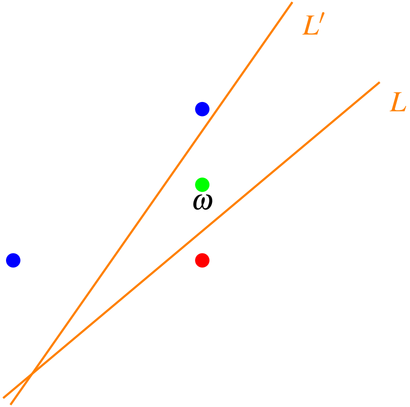
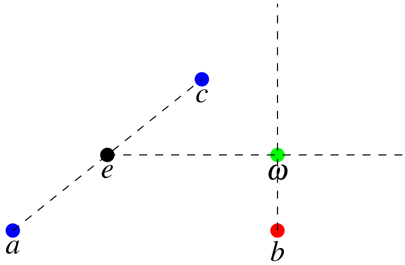


Computation of the switch points ω

3 points case: given three points $a, c \in C_M$ and $b \in C_N$, add ω such that for any line L through ω,

$$\|push_L(b) - push_L(a)\| = \|push_L(b) - push_L(c)\|$$

- If a and c both push rightwards to L while b pushes upwards, then $\omega = (x_b, (y_c + y_a)/2)$



- a and b both push rightwards to L while c pushes upwards, then $\omega = (x_c, 2y_b - y_a)$
- ...

Complexity

In the worst case, taking m to be the number of critical cells of the persistence modules M and N,

- the number of switch points is $\binom{m}{4} \sim m^4$
- the number of lines to consider is $O(m^8)$
- the cost of computing the bottleneck distance along one line is $O(m^{1.187})$ [Katz&Sharir22]
- the cost of computing $B(M_L)$ and $B(N_L)$ for a fixed line L is $O(m^3)$ which dominates that of the bottleneck distance
- the total runtime cost is $O(m^{11})$
- the space cost is $O(m^4)$ for storing the set of critical and switch values

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Take-home message:

- Critical cells capture diverse and fundamental aspects of multi-parameter persistence
- In particular, critical points determine the matching distance for bi-persistence

Open questions:

- reduction of the number of switch points
- computation of matching distance for n-persistence modules

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Thank you for your attention!