The coherent matching distance in 2D persistent homology

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Outline

Let us recall some concepts in persistent homology

The importance of lines with slope 1 in 2D persistent homology

The need for coherent matchings

The phenomenon of monodromy

The coherent 2-dimensional matching distance

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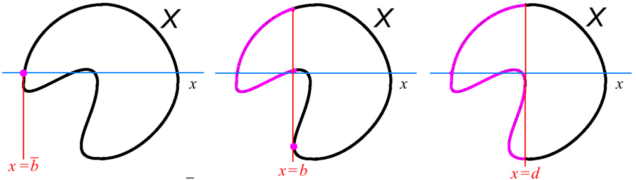
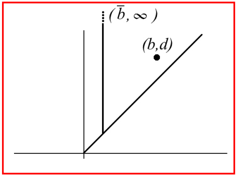
Let us recall what a persistence diagram is

A persistence diagram is a collection of points associated with a continuous filtering function $\varphi : X \to \mathbb{R}$. An example for $\varphi = x$:



birth of a component at $x = \overline{b}$ birth of a component at $x = b$ death of a component at $x = d$



Persistence diagram of the function x

The presence of a point (b,d)

in the persistence diagram of $\varphi : X \to \mathbb{R}$

means that a class of a cycle exists

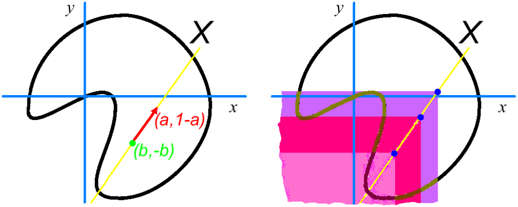
whose birth and death happen

at $\varphi = b$ and $\varphi = d$, respectively.

Persistence diagrams can be compared by a matching distance d_{match}.

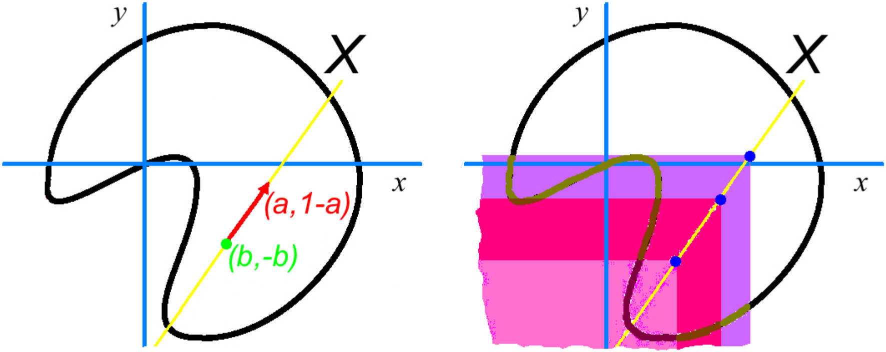
Persistence diagram associated with the pair (P, w)

What can we do in the case $\varphi : X \to \mathbb{R}^2$?



If we have a bifiltration given by a function $\varphi = (\varphi_1, \varphi_2) : X \to \mathbb{R}^2$, we can consider a unit vector (w.r.t. $\|.\|_\infty$) $w = (a, 1-a)$ with a positive slope, and a point $P = (b, -b)$. Every choice of P and w defines a filtration $\{X_t\}$ of X, where X_t is the set of points of X that are both under and on the left of the point $P + tw$. As a consequence, each choice of P and w defines a persistence diagram $\mathscr{D}_\varphi(a, b)$.

The 2-dimensional matching distance



By multiplying the coordinates of each point in $\mathscr{D}_\varphi(a,b)$ by $\min\{a, 1-a\}$ we obtain the normalized persistence diagram $\hat{\mathscr{D}}_\varphi(a,b)$.

The 2-dimensional matching distance $D_{match}(\varphi, \psi)$

Now, we can define the $2D$ matching distance $D_{match}(\varphi, \psi)$ between φ and ψ by setting

$$\boxed{D_{match}(\varphi, \psi) := \sup_{(a,b)} d_{match}(\hat{\mathscr{D}}_\varphi(a,b), \hat{\mathscr{D}}_\psi(a,b)).}$$

Theorem

$D_{match}(\varphi, \psi) \leq \|\varphi - \psi\|_\infty$.

Remark. The previous theorem strongly depends on the **normalization** of persistence diagrams.

The distance $D_{match}(\varphi, \psi)$ has been introduced in the paper [S. Biasotti, A. Cerri, P. Frosini, D. Giorgi, C. Landi, *Multidimensional size functions for shape comparison*, Journal of Mathematical Imaging and Vision, vol. 32 (2008), n. 2, 161–179.]

Computation of the 2D matching distance

In the paper

S. Biasotti, A. Cerri, P. Frosini, D. Giorgi,
A new algorithm for computing the 2-dimensional matching distance between size functions,
Pattern Recognition Letters, vol. 32 (2011), n. 14, 1735–1746

we proposed a method to compute $D_{match}(\varphi, \psi)$ for 2D persistent homology in degree 0 and made our first experiments.

The results showed a strange phenomenon that we are going to illustrate in the next slides.

Remark: As for the generalization of the previously cited algorithm to multidimensional persistence in any degree see the paper [A. Cerri, P. Frosini, *A new approximation algorithm for the matching distance in multidimensional persistence*, AMS Acta, 2971 (2011)].

Computation of the 2D matching distance

Remarks:

- In principle, 2D persistent homologies can be also compared by using the interleaving distance ([M. Lesnick, *The theory of the interleaving distance on multidimensional persistence modules*, Foundations of Computational Mathematics, vol. 15 (2015), n. 3, 613–650]). Unfortunately, as noted in that paper, the question of if and how the interleaving distance on multidimensional persistence modules can be computed remains open. This fact justifies the interest in the 2D matching distance $D_{match}(\varphi, \psi)$.
- As for the visualization of 2D persistence modules we point out the interesting paper [M. Lesnick, M. Wright, *Interactive Visualization of 2-D Persistence Modules*, arXiv:1512.00180].

Our first experiments in 3D shape comparison

Let us have a look at some pictures taken from the previously cited paper on the 2D matching distance, illustrating the first results that we obtained in 3D shape comparison.

The objects that we compare are displayed on the left of each figure.

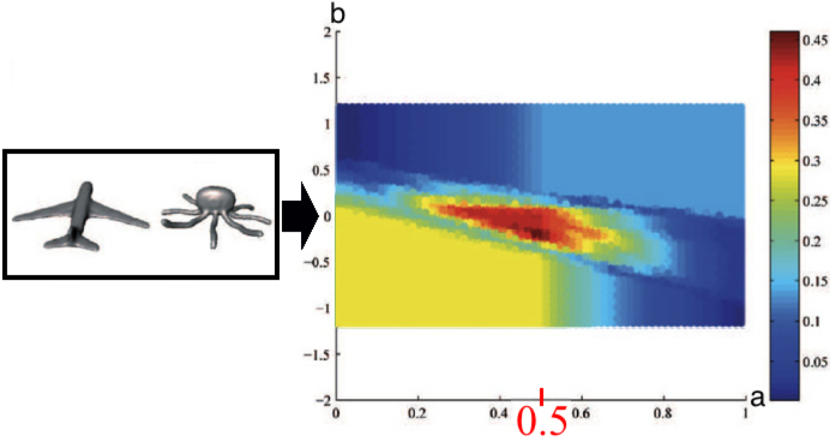
The color at (a,b) represents the value $d_{match}(\hat{\mathscr{D}}_\varphi(a,b),\hat{\mathscr{D}}_\psi(a,b))$.

The largest values are in **red** and **brown**, the lowest ones are in **blue**.

The values at points (a,b) with $|b|$ large are not displayed, since they just represent the 1-dimensional persistence of the two components of $\varphi=(\varphi_1,\varphi_2)$ and are not relevant for our exposition.

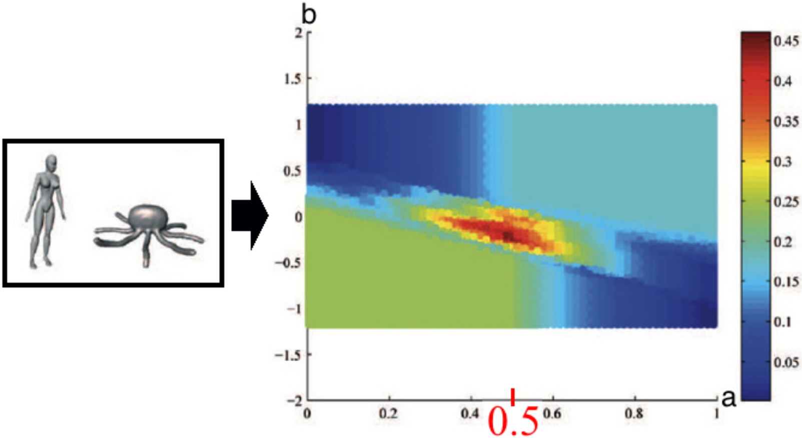
We recall that we are interested in $D_{match}(\varphi,\psi)$, i.e. the supremum of $d_{match}(\hat{\mathscr{D}}_\varphi(a,b),\hat{\mathscr{D}}_\psi(a,b))$, for $0<a<1$ and $b\in\mathbb{R}$.

Result 1



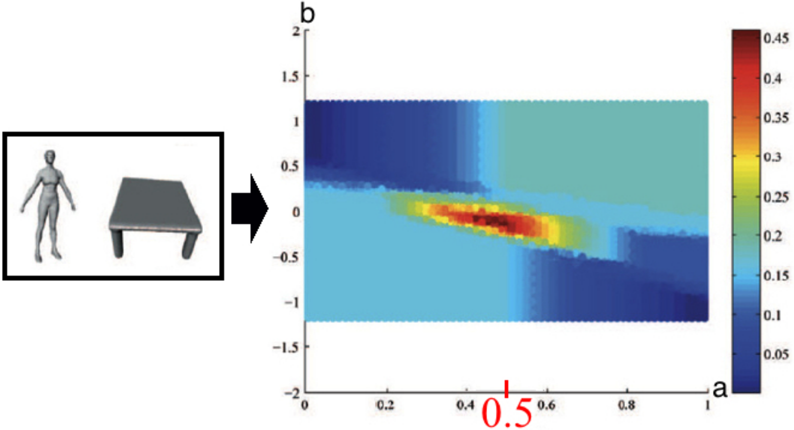
Please note that the largest value (i.e. the 2-dimensional matching distance) is taken at a point (a, b) with a approximately equal to $1/2$.

Result 2



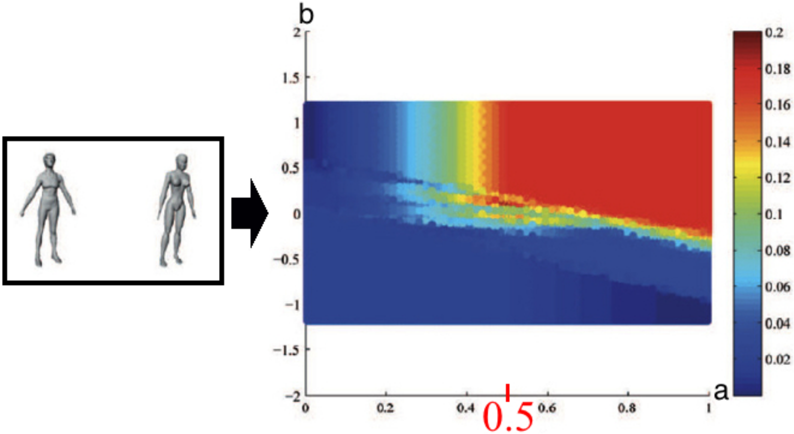
Please note that the largest value (i.e. the 2-dimensional matching distance) is taken at a point (a, b) with a approximately equal to $1/2$.

Result 3



Please note that the largest value (i.e. the 2-dimensional matching distance) is taken at a point (a, b) with a approximately equal to $1/2$.

Result 4



Please note that the largest value (i.e. the 2-dimensional matching distance) is taken at a point (a, b) with a approximately equal to $1/2$.

A conjecture

In our experiments, it seemed that all the relevant information was given by lines with $a = 1/2$, i.e. lines with slope 1.

At the beginning we thought that this phenomenon was just a coincidence. So we looked for other examples, showing global maxima at points (a, b) with $a \neq 1/2$, but our search was unsuccessful.

After that, we started to think that some interesting principle might be hidden in the results of our experiments.
We formulated this conjecture:

Conjecture

$$\sup_{0<a<1, b\in\mathbb{R}} d_{match}(\hat{\mathscr{D}}_\varphi(a,b), \hat{\mathscr{D}}_\psi(a,b)) = \sup_{b\in\mathbb{R}} d_{match}(\hat{\mathscr{D}}_\varphi(\tfrac{1}{2},b), \hat{\mathscr{D}}_\psi(\tfrac{1}{2},b)).$$

In other words: Can we confine ourselves to assume $a = 1/2$?

Another reason supporting our conjecture

In the paper [A.Cerri, C. Landi, *Hausdorff stability of persistence spaces*, Foundations of Computational Mathematics, vol. 16 (2016), n. 2, 343–367] the authors show that the computation of the **Hausdorff distance** between persistent spaces can be made by matching points in the persistence spaces along lines having direction $(1, \ldots, 1)$.

Remark: The concept of persistence space is a generalization of the concept of persistence diagram to the case of filtering functions taking values in $\mathbb{R}^k$.

The previous result suggests that something special happens in the direction $(1, 1)$, when we consider the 2-dimensional case.

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Looking for a proof of our conjecture

We started to look for a proof of our conjecture but we realized that we needed to change our definition of matching distance in order to proceed.

Indeed the classical definition of matching distance *does not require* that the matchings between the persistence diagrams $\hat{\mathscr{D}}_{\varphi}(a, b)$, $\hat{\mathscr{D}}_{\psi}(a, b)$ are COHERENT to each other as a and b change. This means that the classical definition does not require that the matchings change "continuously" when a and b change continuously.

To proceed in our proof we needed this property.

The problem of incoherent matchings

At the beginning of our research we thought that the matchings $\sigma_{a,b}$ between $\hat{\mathscr{D}}_\varphi(a,b)$ and $\hat{\mathscr{D}}_\psi(a,b)$ would be coherent to each other in a natural way, and tried to prove this property.

We observe that the concept of coherent matchings is of topological nature and depends on the stability of persistence diagrams with respect to the bottleneck distance: in other words, it is based on the fact that the persistence diagrams $\hat{\mathscr{D}}_\varphi(a,b)$, $\hat{\mathscr{D}}_\psi(a,b)$ change continuously with respect to a and b. Indeed, without this continuity we could not establish which point in $\hat{\mathscr{D}}_\varphi(a,b)$ corresponds to which point in $\hat{\mathscr{D}}_\varphi(a',b')$, for (a',b') close to (a,b).

A naïve (and wrong) solution to the coherence problem

Our first (and naïve) idea was the following one. We should fix a pair $(\bar{a}, \bar{b})$ and a matching $\sigma_{\bar{a},\bar{b}}$ between $\hat{\mathscr{D}}_{\varphi}(\bar{a}, \bar{b})$ and $\hat{\mathscr{D}}_{\psi}(\bar{a}, \bar{b})$. Then we should construct a coherent family of matchings $\sigma_{a,b}$ between $\hat{\mathscr{D}}_{\varphi}(a, b)$ and $\hat{\mathscr{D}}_{\psi}(a, b)$, by means of this procedure:

1. We choose a path c, going from $(\bar{a}, \bar{b})$ to (a, b).
2. For each $\bar{P} \in \hat{\mathscr{D}}_{\varphi}(c(0))$ we follow the path $P(t) \in \hat{\mathscr{D}}_{\varphi}(c(t))$ such that $P(0) = \bar{P}$. Similarly, we follow the path $Q(t) \in \hat{\mathscr{D}}_{\psi}(c(t))$, such that $Q(0) = \sigma_{\bar{a},\bar{b}}(\bar{P})$. We assume that these paths are continuous.
3. We define $\sigma_{a,b}(P(1)) := Q(1)$.

Roughly speaking, we could try to transport the matching $\sigma_{\bar{a},\bar{b}}$ to other pairs (a, b) by using the stability of the normalized persistence diagrams $\hat{\mathscr{D}}_{\varphi}(a, b)$ and $\hat{\mathscr{D}}_{\psi}(a, b)$, i.e. the fact that they depend continuously on a and b.

A naïve solution to the coherence problem

The previously proposed approach has a problem. If $\hat{\mathscr{D}}_\varphi(c(\bar{t}))$ contains a multiple point for a $\bar{t} \in [0,1]$, the path $P(t)$ is not well-defined. An analogous problem holds for $Q(t)$. Indeed, during collisions the identity of points is not preserved and we are not able to follow them.

The consequent natural idea is the one of following the movements of points of $\hat{\mathscr{D}}_\varphi(a,b)$ avoiding the pairs (a,b) for which points of $\hat{\mathscr{D}}_\varphi(a,b)$ with multiplicity greater than one exist.

Therefore, we restrict ourselves to consider pairs (a,b) in the set $Reg(\varphi) := \{(a,b) : \hat{\mathscr{D}}_\varphi(a,b) \text{ does not contain multiple points}\}$.

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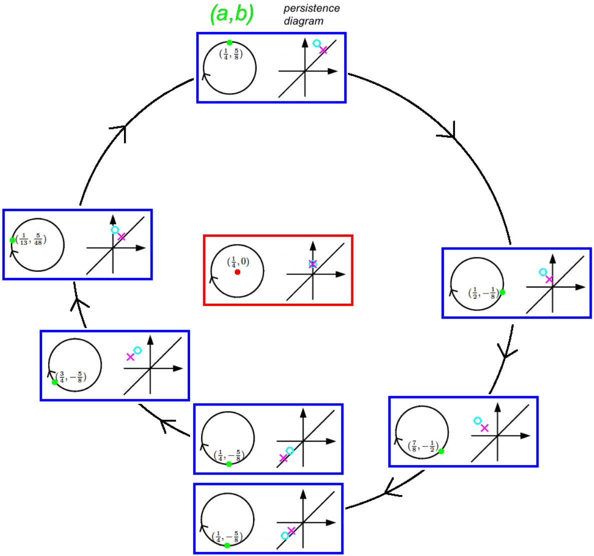
A key difficulty in our naïve solution

Unfortunately, the previous approach still has a problem.
Indeed, the definition of $\sigma_{a,b}(P(1)) := Q(1)$ depends on the choice of the path $c : [0,1] \to Reg(\varphi) \cap Reg(\psi)$, going from $(\bar{a}, \bar{b})$ to (a, b). Precisely, it depends on the homotopy class of c relative to $(\bar{a}, \bar{b})$ and (a, b).

We call this fact the monodromy phenomenon in 2-dimensional persistent homology.

For more details about the monodromy phenomenon in 2-dimensional persistent homology we refer the interested reader to the paper [A. Cerri, M. Ethier, P. Frosini, *A study of monodromy in the computation of multidimensional persistence*, Proceedings of the 17th IAPR International Conference on Discrete Geometry for Computer Imagery, LNCS 7749, 2013, 192–202].

An example of monodromy in 2D persistent homology



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The monodromy phenomenon as an obstruction

The existence of monodromy implies that each loop in $Reg(\varphi)$ induces a permutation on $\hat{\mathscr{D}}_\varphi(\bar{a},\bar{b})$. In other words, we cannot establish which point in $\hat{\mathscr{D}}_\varphi(\bar{a},\bar{b})$ corresponds to which point in $\hat{\mathscr{D}}_\varphi(a,b)$, since the answer depends on the path that we follow from $(\bar{a},\bar{b})$ to (a,b) in the parameter space $Reg(\varphi)\cap Reg(\psi)$. As a consequence, different paths going from $(\bar{a},\bar{b})$ to (a,b) can "transport $\sigma_{\bar{a},\bar{b}}$ to (a,b) in a different way".

Does monodromy prevent us from proceeding in our research and from defining a coherent 2-dimensional matching distance?

Fortunately, the answer is no, as we will show in the next slides.

Working assumptions

To simplify the exposition, in what follows we state our results by assuming that the topological space X is a manifold M homeomorphic to the m-sphere S^m, with $m \geq 2$.

In particular, this implies that all normalized persistence diagrams $\hat{\mathscr{D}}_\varphi(\bar{a}, \bar{b})$, $\hat{\mathscr{D}}_\psi(\bar{a}, \bar{b})$ contain a single point at infinity in degree 0 and m, and no point at infinity in the other homology degrees.

In this way, the problem of continuously extending a matching can be restricted to considering only proper points, as there are no ambiguities in following the evolution of points at infinity.

Working assumptions

Also, we assume that

1. the functions $\varphi, \psi : M \to \mathbb{R}^2$ are *normal*, i.e. the sets of singular pairs for φ and ψ are discrete;
2. a real value $\varepsilon > 0$ exists such that if two proper points P_1, P_2 of $\hat{\mathscr{D}}_\varphi(\bar{a}, \bar{b})$ have Euclidean distance less than ε from the diagonal $\Delta := \{(u,v) \in \mathbb{R}^2 : u = v\}$, then the Euclidean distance between P_1 and P_2 is not smaller than ε, for all regular (a,b). The same property holds for $\hat{\mathscr{D}}_\psi(\bar{a}, \bar{b})$. In plain words, this assumption means that the diagonal Δ "does not contain double points of the persistence diagrams of φ and ψ".

Transporting a matching along a homotopy

Now, we need to specify the concept of transporting a proper point $\bar{P}$ of the persistence diagram of f along a homotopy $f_\tau := H(\tau, \cdot)$ between two continuous functions $f, g : M \to \mathbb{R}$.

Let us consider a continuous path $P(\tau)$ describing the "movement of the point $\bar{P}$" in the persistent diagrams of the functions $H(\tau, \cdot)$, while τ changes in an interval $[0, \bar{\tau}]$.

We say that the path $P(\tau)$ is admissible for H if

1. $P(\tau)$ belongs to the persistence diagram of f_τ for every $\tau \in [0, \bar{\tau}]$;
2. $P(\tau)$ meets Δ at a finite number of points;
3. $P(\tau)$ "does not stop" at any point of Δ if it can "move on" in the set $\Delta^+ := \{(u, v) \in \mathbb{R}^2 : u < v\}$.

Transporting a matching along a homotopy

The following important statement holds.

Proposition

Let $H(\tau,\cdot)$ be a homotopy between two continuous functions $f,g:M\to\mathbb{R}$. For every point $\bar{P}$ that belongs to the persistence diagram of f and has multiplicity 1, an $\varepsilon>0$ and a unique path $P:[0,\varepsilon]\to\Delta^+\cup\Delta$ exist, such that $P(0)=\bar{P}$ and the path $P(\tau)$ is admissible for the restriction of $H(\tau,\cdot)$ to the set $[0,\varepsilon]$.

We say that *the homotopy H transports $\bar{P}$ to $P(\varepsilon)$*.
The previous statement guarantees that we can follow the movements of each point in the persistence diagram, during the homotopy H.

Transporting a matching along a path

In particular, the following statement holds for any continuous filtering function $\varphi : M \to \mathbb{R}^2$.

Proposition

Let $c : [0,1] \to Reg(\varphi)$ be a continuous path with $c(0) = (a,b)$. For every proper point $\bar{P} \in \hat{\mathscr{D}}_\varphi(a,b)$, a unique path $P : [0,1] \to \Delta^+ \cup \Delta$ admissible for c exists, such that $P(0) = \bar{P}$.

We say that c transports $\bar{P}$ to $P(1)$ with respect to φ.

REMARK: If $P(\tau)$ reaches the diagonal $u = v$, the definition of **admissible path** implies that $P(\tau)$ is assumed to stop there until it possibly "comes out from the diagonal" at the same point where it entered. Hence, $P(\tau)$ cannot "move along the diagonal".

Transporting a matching along a path

Now, let us consider two continuous filtering functions $\varphi, \psi : M \to \mathbb{R}^2$. We need to define the concept of transporting a matching between $\hat{\mathscr{D}}_\varphi(a,b)$ and $\hat{\mathscr{D}}_\psi(a,b)$ along a path $c : [0,1] \to \mathrm{Reg}(\varphi) \cap \mathrm{Reg}(\psi)$ with $c(0) = (a,b)$.

Let $\sigma_{a,b}$ be a matching between $\hat{\mathscr{D}}_\varphi(a,b)$ and $\hat{\mathscr{D}}_\psi(a,b)$, with (a,b) an element of $\mathrm{Reg}(\varphi) \cap \mathrm{Reg}(\psi)$. We can naturally associate to $\sigma_{a,b}$ a matching $\sigma_{c(1)} : \hat{\mathscr{D}}_\varphi(c(1)) \to \hat{\mathscr{D}}_\psi(c(1))$. We set $\sigma_{c(1)}(P') = Q'$ if and only if c transports $\bar{P}$ to P' with respect to φ and $\bar{Q}$ to Q' with respect to ψ. We also say that *c transports $\sigma_{a,b}$ to $\sigma_{c(1)}$ along c with respect to the pair (φ, ψ)*.

We are now ready to introduce the **coherent 2D matching distance**.

Coherent 2D matching distance

Definition

Choose a point $(a,b) \in \mathrm{Reg}(\varphi) \cap \mathrm{Reg}(\psi)$. Let Γ be the set of all continuous paths $c : [0,1] \to Reg(\varphi) \cap Reg(\psi)$ with $c(0) = (a,b)$. Let S be the set of all matchings $\sigma : \hat{\mathscr{D}}_\varphi(c(0)) \to \hat{\mathscr{D}}_\psi(c(0))$. For every $\sigma \in S$ and every $c \in \Gamma$, let $T_c^{(\varphi,\psi)}(\sigma)$ be the matching obtained by transporting σ along c with respect to the pair (φ, ψ). We define the *coherent 2D matching distance* $CD_{match}(\varphi,\psi)$ as

$$CD_{match}(\varphi,\psi) := \max\left\{ \min_{\sigma \in S} \sup_{c \in \Gamma} \mathrm{cost}\left(T_c^{(\varphi,\psi)}(\sigma) \right), \gamma_\infty \right\},$$

where γ_∞ is the maximum varying (a,b) of the distance between the point at infinity of $\hat{\mathscr{D}}_\varphi(a,b)$ and the point at infinity of $\hat{\mathscr{D}}_\psi(a,b)$ for degrees 0 and m, and 0 for the other degrees.

Properties of CD_{match}

Proposition

The definition of $CD_{match}(\varphi,\psi)$ does not depend on the choice of the point $(a,b) \in Reg(\varphi) \cap Reg(\psi)$.

Proposition

$CD_{match}(\varphi,\psi)$ is a pseudo-distance.

Theorem

$D_{match}(\varphi,\psi) \leq CD_{match}(\varphi,\psi) \leq \|\varphi-\psi\|_\infty$.

Recap

- Examples suggest that in 2-dimensional persistent homology just filtrations defined by lines with slope 1 might be relevant.
- The attempt of proving the previous statement leads to modify the definition of 2-dimensional matching distance by requiring that the matchings associated with the lines are coherent to each other.
- The search for coherent families of matchings leads to discover the phenomenon of monodromy in 2-dimensional persistent homology, as an obstruction to construct such families.
- The transport of matchings along paths allows to overcome that obstruction and to introduce the coherent 2D matching distance.
- We are working on the proof that just filtrations defined by lines with slope 1 are relevant for the computation of the coherent 2D matching distance.


THANKS
FOR YOUR
ATTENTION!