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Exact computation of the matching distance on 2-parameter persistence modules

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— Abstract

The matching distance is a pseudometric on multi-parameter persistence modules, defined in terms of the weighted bottleneck distance on the restriction of the modules to affine lines. It is known that this distance is stable in a reasonable sense, and can be efficiently approximated, which makes it a promising tool for practical applications. In this work, we show that in the 2-parameter setting, the matching distance can be computed exactly in polynomial time. Our approach subdivides the space of affine lines into regions, via a line arrangement. In each region, the matching distance restricts to a simple analytic function, whose maximum is easily computed. As a byproduct, our analysis establishes that the matching distance is a rational number, if the bigrades of the input modules are rational.

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1 Introduction

Multi-parameter persistent homology is receiving growing attention, both from the theoret-12 ical and computational points of view. Its motivation lies in the possibility of extending 13 the success of topological data analysis to settings where the structure of data is best cap-14 tured by 2-parameter rather than 1-parameter constructions. The basic algebraic objects 15 of study in multi-parameter persistence are certain commutative diagrams of vector spaces 16 called *persistence modules*. In the 1-parameter setting, persistence modules decompose in an 17 essentially unique way into simple summands called *interval modules*. The decomposition 18 is specified by a discrete invariant called a *persistence diagram*. In contrast, the algebraic 19 structure of a 2-parameter persistence module (henceforth, *bipersistence module*) can be 20

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²¹ far more complex. As a result, a good definition of persistence diagram is unavailable for ²² bipersistence modules [5].

Nevertheless, it is still possible to define meaningful notions of distance between multiparameter persistence modules. Distances on 1-parameter persistence modules play an essential role in both theory and applications. To extend such theory and applications to the multi-parameter setting, one needs to select a suitable distance on multi-parameter persistence modules. However, progress on finding well-behaved, efficiently computable distances on multi-parameter persistence modules has been slow, and this is been an impediment to progress in practical applications.

The most widely studied and applied distances in the 1-parameter setting are the *bot*-30 tleneck distance and the Wasserstein distance [10]. Both can be efficiently computed via 31 publicly available code [13]. In the multi-parameter setting, the distance that has received 32 the most attention is a generalization of the bottleneck distance called the *interleaving* 33 distance. This distance is theoretically well-behaved; in particular, among all distances 34 satisfying a certain stability condition, it is the most discriminative distance on modules 35 over prime fields [15]. However, it was proven recently that the interleaving distance on 36 bipersistence modules is NP-hard to compute, and even to approximate to any constant 37 factor less than three [4]. This motivates the search for a more computable surrogate for 38 the interleaving distance. 39

The matching distance, introduced by Cerri et al. [6], is a natural candidate for such a 40 surrogate. It is a lower bound for the interleaving distance; this is implicit in [6] and shown 41 explicitly in [14]. In the 2-parameter setting, the matching distance is defined as follows: 42 Given a pair of bipersistence modules, we call an affine line ℓ in parameter space with 43 positive slope a *slice*. Restricting the modules to ℓ yields a pair of 1-parameter persistence 44 modules, which we call *slice modules*. These slice modules have a well-defined bottleneck 45 distance, which we multiply by a positive weight depending only on the slope of ℓ . (The 46 weights are chosen in a way that ensures that the matching distance is a lower bound for the 47 interleaving distance.) The matching distance is defined as the supremum of these weighted 48 49 bottleneck distances over all slices. See Section 3 for the precise definition. The definition generalizes readily to n-parameter persistence modules, for any $n \ge 1$; when n = 1, the 50 matching distance is equal to the bottleneck distance. 51

As Cerri et al. have observed, to approximate the matching distance up to any (ab-52 solute) precision, it suffices to sample the space of slices sufficiently densely and to return 53 the maximum weighted bottleneck distance encountered. For a constant number of scale 54 parameters and approximation quality ϵ , a polynomial number of slices are sufficient in 55 terms of module size and $\frac{1}{\epsilon}$, yielding a polynomial time approximation algorithm. [3]. This 56 approach has been recently applied to the virtual ligand screening problem in computational 57 chemistry [12]. To the best of our knowledge, there is no other previous work in which the 58 problem of computing the matching distance has been considered. 59

⁶⁰ **Our contribution.** We give an algorithm that computes the exact matching distance ⁶¹ between a pair of bipersistence modules in time polynomial with respect to the size of the ⁶² input. We assume that each persistence module is specified by a *presentation*. Concretely, ⁶³ this means that the module is specified by a matrix, with each row and each column labeled ⁶⁴ by a point in \mathbb{R}^2 ; see Section 2.

To explain our strategy for computing the matching distance, consider the function Fthat assigns a slice to its weighted bottleneck distance. The matching distance is then simply the supremum of F, taken over all slices. F has a rather complicated structure, since it depends on the longest edge of a perfect matching in a bipartite graph whose edges lengths

⁶⁹ depend on both the slice and the two modules given as input. When the slice changes, the ⁷⁰ matching realizing the bottleneck distance undergoes combinatorial changes, making the

⁷¹ function F difficult to treat analytically.

We show, however, that the space of slices can be divided into polynomially many regions 72 so that the restriction of F to each region takes a simple closed from. Perhaps surprisingly, if 73 we parameterize the space of slices as a subset $\Omega \subset \mathbb{R}^2$, the boundary between these regions 74 can be expressed by the union of polynomially many lines in Ω , making each region convex 75 and bounded by (possibly unbounded) line segments. (This is analogous to the observation of 76 [17] that for a single persistence module, the locus of lines where the combinatorial structure 77 underlying the slice module can change is described by a line arrangement.) Moreover, the 78 restriction of F to each cell attains its supremum at a boundary vertex of the cell, or as the 79 limit of an unbounded line segment if the cell touches the boundary of Ω ; this follows from 80 a straightforward case analysis. These observations together lead to a simple polynomial 81 time algorithm to compute the matching distance. 82

The characterization of the matching distance underlying our algorithm also makes clear that if the row and column labels of the presentations of the input modules have rational coordinates, then the matching distance is rational as well. We are not aware of a simpler argument for this property.

Outline. We introduce the underlying topological concepts in Section 2, and introduce the matching distance in Section 3. We define the line arrangement subdividing the slice space in Section 4 and give the algorithm to maximize each cell of the arrangement in Section 5. We conclude in Section 6.

91 **2** Persistence modules

Single-parameter modules. Let \mathbb{K} be a fixed finite field throughout. A persistence module M over \mathbb{R} is an assignment of \mathbb{K} -vector spaces M_x to real numbers x, and linear maps $M_{x \to y} : M_x \to M_y$ to a pair of real numbers $x \leq y$, such that $M_{x \to y}$ is the identity and $M_{x \to y} \circ M_{y \to z} = M_{x \to z}$. Equivalently, in categorical terms, a persistence module is a functor from \mathbb{R} (considered as a poset category) to the category of \mathbb{K} -vector spaces.

A common way to arrive at a persistence module is to consider a nested sequence of simplicial complexes

99
$$X_1 \subseteq X_2 \subseteq \ldots \subseteq X_n$$

 $_{100}$ and to apply homology with respect to a fixed dimension and base field $\mathbb K.$ This yields a $_{101}$ sequence

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$$H_p(X_1, \mathbb{K}) \to H_p(X_2, \mathbb{K}) \to \ldots \to H_p(X_n, \mathbb{K})$$

of vector spaces and linear maps. To obtain a persistence module over \mathbb{R} , we pick grades $s_1 < s_2 < \ldots < s_n$ and set $M_x := 0$ if $x < s_1$ and $M_x := H_p(X_i, \mathbb{K})$ with $i = \max\{j \mid s_j \leq x\}$ otherwise. For $y \geq x$ and $M_y = H_p(X_j, \mathbb{K})$, we define $M_{x \to y}$ as the map $H_p(X_i, \mathbb{K}) \to$ $H_p(X_j, \mathbb{K})$ induced by the inclusion map $X_i \to X_j$.

Finite presentations. In this work, we restrict our attention to persistence modules that are finitely presented in the following sense. A *finite presentation* is an $\ell \times m$ matrix Pover K, where each row and each column is labeled by a number in R, called the *grade*, such that if $P_{ij} \neq 0$, then $gr(row_i) \leq gr(col_j)$; here gr(-) denotes the grade of a row or column. We refer to the multiset of grades of all rows and columns of P simply as the *set of grades of* P, and denote this set as gr(P). A finite presentation gives rise to a persistence module, as we describe next. The rows of P represent the generators of the module, while the columns of P encode relations (or syzygies) on the generators. Concretely, let e_1, \ldots, e_l denote the standard basis of \mathbb{K}^l , and for $x \in \mathbb{R}$ define the subspace

116
$$\operatorname{Gen}_x := \{e_i \mid \operatorname{gr}(\operatorname{row}_i) \le x\}$$

117 Likewise, define

118
$$\operatorname{Rel}_x := \{\operatorname{col}_j \mid \operatorname{gr}(\operatorname{col}_j) \le x\}$$

119 Then, we define

 $M_x^P := \operatorname{span}(\operatorname{Gen}_x)/\operatorname{span}(\operatorname{Rel}_x)$

and $M_{x \to y}^P$ simply as the map induced by the inclusion map $\operatorname{span}(\operatorname{Gen}_x) \to \operatorname{span}(\operatorname{Gen}_y)$. It 121 can be checked easily that this indeed defines a persistence module M^P . If a persistence 122 module N is isomorphic to M^P , we say that P is a presentation of N. We call a persistence 123 module N finitely presented if there exists a finite presentation of N. For instance, persis-124 tence modules as above arising from a finite simplicial filtration are finitely presented. Also, 125 the representation theorem of persistence [19, 7] states that the category of persistence mod-126 ules over K is isomorphic to the category of graded \mathcal{R} -modules with an appropriately chosen 127 ring \mathcal{R} . With that, a persistence module is finitely presented if and only if the corresponding 128 \mathcal{R} -module is finitely presented (in the sense of a module). 129

For finite presentation via an $\ell \times m$ matrix as above, we call $n := \ell \cdot m$ the *size* of that presentation.

Persistence diagrams. A persistence diagram is a finite multi-set of points of the form (b, d) $\in \mathbb{R} \times (\mathbb{R} \cup \{\infty\})$ with b < d. A well-known structure theorem tells us that we can associate to any finitely presented persistence module M a persistence diagram D(M), and this determines M up to isomorphism [8].

Given a presentation of M, the persistence diagram can be computed by bringing the presentation matrix into echelon form. This process takes cubic time in the size of the presentation using Gaussian elimination [10, 19], or $O(n^{\omega})$ time using fast matrix multiplication, where $\omega \leq 2.373$ [18]. Elimination-based approaches to computing persistent homology perform very well in practice, and are routinely used to study real data.

Lemma 1. For P a finite presentation of a persistence module M,

142 1. The x-coordinates of the points of D(M) form a sub-multiset of the row grades of P,

¹⁴³ 2. The y-coordinates of the points of D(M) form a sub-multiset of the column grades of P.

Proof. This follows from the correctness of the basic matrix reduction algorithm for computing persistent homology, as described in [19].

Bottleneck distance. Consider two persistence diagrams D_1 and D_2 and a bijection $\sigma: D'_1 \to D'_2$ for some $D'_1 \subseteq D_1$ and $D'_2 \subseteq D_2$. For $\delta > 0$, we define $cost(\sigma) := max(A, B)$, where

¹⁴⁹ $A = \max \{ \max(|a - c|, |b - d|) \mid \sigma((a, b)) = (c, d) \},\$

150 $B = \max \{ (b-a)/2 \mid (a,b) \in (D_1 \setminus D_1') \cup (D_2 \setminus D_2') \},\$

and it is understood that $\infty - \infty = 0$. We define the bottleneck distance d_B by

 $d_B(D_1, D_2) = \min\{\epsilon \mid \text{ there exists a matching of cost } \epsilon \text{ between } D_1 \text{ and } D_2\}.$

For persistence modules M and N, we write $d_B(D(M), D(N))$ simply as $d_B(M, N)$.

Lemma 2. Let P^M and P^N be finite presentations of persistence modules M and N, respectively. $d_B(M, N)$ is realized by

- 156 **1.** The difference of a grade of P^M and a grade of P^N ,
- 157 **2.** or half the difference of two grades in P^M ,
- ¹⁵⁸ **3.** or half the difference of two grades in P^N .

¹⁵⁹ **Proof.** This follows immediately from Lemma 1 and the definition of d_B .

◀

Given two finite persistence diagrams D, D', we can compute $d_B(D, D')$ in time to $O(n^{1.5} \log n)$ [11]; see [13] for details, including a report on practical efficiency. Thus, the complexity of computing the bottleneck distance of two persistence modules is dominated by the computation of the persistence diagrams, and has worst-case complexity $O(n^{\omega})$.

Bipersistence modules. The definitions of persistence modules and presentations extend to higher dimensions without problems. In the 2-parameter setting, this goes as follows: Define a partial order \leq on \mathbb{R}^2 by $p \leq q$ if $p_x \leq q_x$ and $p_y \leq q_y$. A bipersistence module is an assignment of K-vector spaces M_p to points $p \in \mathbb{R}^2$, and linear maps $M_{p \to q}$: $M_p \to M_q$ to pairs of points $p \leq q \in \mathbb{R}^2$, such that $M_{p \to p}$ is the identity and $M_{q \to r} \circ M_{p \to q} =$ $M_{p \to r}$ whenever $p \leq q \leq r$. In topological data analysis, 2-dimensional persistence modules typically arise by applying homology to a bifiltered simplicial complex

A finite presentation of a bipersistence module \mathbb{R}^2 is defined in the same way as for oneparameter persistence modules, except that the labels of each row/column are now elements of \mathbb{R}^2 , and the \leq relation appearing in the definition now means the partial order over \mathbb{R}^2 . From now on, we will assume that all bipersistence modules considered are finitely presented.

Example 3. Let M be the bipersistence module given by

$$M_{p} = \begin{cases} \mathbb{K} & \text{if } p \in [0,1) \times [0,1) \\ 0 & \text{otherwise,} \end{cases} \qquad M_{p \to q} = \begin{cases} \mathrm{Id}_{\mathbb{K}} & \text{if } p, q \in [0,1) \times [0,1) \\ 0 & \text{otherwise.} \end{cases}$$

¹⁷⁷ Then a presentation of M is given by

 $\begin{array}{ccc} (1,0) & (0,1) \\ & & (0,0) & \left[\begin{array}{cc} 1 & 1 \end{array} \right] \cdot \end{array}$

In topological data analysis, we do not typically have immediate access to a presentation of a bipersistence module M, but rather to a chain complex of bipersistence modules for which M is a homology module. However, it has recently been observed that from such a chain complex, a (minimal) presentation of M can be computed in cubic time [16]. The algorithm for this is practical, and has been implemented in the software package RIVET [9].

¹⁸⁴ **3** The Matching distance

Slices. We define a slice as a line $\ell : y = sx + t$ where s and t are real numbers with s > 0. Let $\lambda : \mathbb{R} \to \ell$ be an isometric parameterization of the slice, i.e. one such that $\|\lambda(y) - \lambda(x)\|_2 = |y - x|$ for all $x, y \in \mathbb{R}$. Concretely, such a parameterization is given by $\lambda(x) = \frac{1}{\sqrt{1+s^2}}(x, sx + t)$. Given a bipersistence module M and slice ℓ , we define a (1parameter) persistence module M^{ℓ} via $M_x^{\ell} := M_{\lambda(x)}$, with its linear maps induced by M. We call M^{ℓ} a slice module. It is easy to check that if M is finitely presented, then so is M^{ℓ} .

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¹⁹¹ Matching distance. For a slice $\ell : y = sx + t$, we define a weight

192
$$w(\ell) := \begin{cases} \frac{1}{\sqrt{1+s^2}} & s \ge 1\\ \frac{1}{\sqrt{1+\frac{1}{s^2}}} & 0 < s < 1 \end{cases}$$

Note that $w(\ell)$ is maximized for slices with slope 1, and gets smaller when the slope goes to 0 or to ∞ .

Let Λ denote the set of all slices. For two persistence modules M, N over \mathbb{R}^2 , we define a function $F^{M,N} : \Lambda \to [0,\infty)$ via

197
$$F^{M,N}(\ell) := w(\ell) \cdot d_B(M^{\ell}, N^{\ell}).$$

and we define the matching distance between M and N as $d_{\text{match}}(M, N) := \sup F^{M,N}$. As noted in the introduction, the weights $w(\ell)$ are chosen to ensure that d_{match} is a lower bound for the interleaving distance.

≥ Lemma 4. Given two bipersistence modules M, N, the map $F^{M,N}$ is continuous.

Proof. w is clearly continuous, so it suffices to show that the function $\ell \mapsto d_B(M^\ell, N^\ell)$ is 202 continuous. Let \mathcal{D} denote the metric space of all finite persistence diagrams, with metric 203 the bottleneck distance. It follows from [14, Theorem 2] that the map sending a slice ℓ to 204 the persistence diagram $D(M^{\ell})$ is continuous with respect to the topology on \mathcal{D} . Thus the 205 map sending ℓ to the pair $(D(M^{\ell}), D(N^{\ell}))$ is also continuous. Moreover, the bottleneck 206 distance is clearly continuous as a map $\mathcal{D} \times \mathcal{D} \to [0, \infty)$, thanks to the triangle inequality. 207 Since the composition of continuous functions is continuous, it follows that the function 208 $\ell \mapsto d_B(M^\ell, N^\ell)$ is continuous. 209

²¹⁰ **4** The arrangement

In what follows, we fix two bipersistence modules M, N and write the map $F^{M,N}$ simply as F. Let $\Omega := (0, \infty) \times \mathbb{R}$ and $\alpha : \Omega \to \Lambda$ be the bijection sending (s, t) to the line y = sx + t. Clearly, α parameterizes the set of slices. By a slight abuse of notation, we write the map $F \circ \alpha$ simply as F.

In this section, we construct a line arrangement in Ω in such a way that it is simple to compute sup F on each face. Recall that a *line arrangement* of Ω is the subdivision of Ω into vertices, edges, and faces induced by a finite set of distinct lines L_1, \ldots, L_n . The vertices of the arrangement are the intersection points of (at least) two lines, the edges are maximal connected subsets of lines not containing any vertex, and the faces are the connected components of $\Omega \setminus \bigcup_{i=1}^{n} L_i$. Clearly, each vertex, edge, and face of the arrangement is a convex set. The boundary of each face consists of a finite number of edges and vertices.

A first line arrangement. For $v \in \mathbb{R}^2$, let L_v denote the line $y = -v_x x + v_y$. Note that $L_{v} \cap \Omega$ is exactly the set of parameterizations of slices containing v. Now, fix presentations P^M and P^N of M and N. Let \mathcal{A}_0 denote the arrangement in Ω induced by the set of lines

$$_{225} \qquad \{L_v \mid v \in \operatorname{gr}(P^M) \cup \operatorname{gr}(P^N)\}$$

In what follows, we will refine \mathcal{A}_0 by adding more lines into the arrangement. For this we first need to introduce some definitions.

Pushes. For a point $p = (p_x, p_y) \in \mathbb{R}^2$ and a slice $\ell : y = sx + t$, we define the *push of p* onto ℓ as

push
$$(p, \ell) := \begin{cases} (p_x, s \cdot p_x + t) & \text{if } p \text{ lies below } \ell \\ (\frac{p_y - t}{s}, p_y) & \text{if } p \text{ lies on or above } \ell \end{cases}$$



Figure 1 The pushes of two points p and q to three different slices. The length of the thick (red) 234 line corresponds to the $\delta_{p,q}$ value of the corresponding slice. 235

Geometrically, $push(p, \ell)$ gives the intersection point of ℓ and a vertical upward ray emanat-231 ing from p in the first case, and the intersection of ℓ with a horizontal right ray emanating 232 from p in the second case. See Figure 1 for an illustration. 233

A finite presentation of M induces a finite presentation of M^{ℓ} with the same underlying 236 matrix, and each row or column grade $p \in \mathbb{R}^2$ replaced with $\lambda^{-1}(\operatorname{push}(p,\ell))$. Clearly, this 237 presentation can be obtained in linear time in the size of the presentation of M. 238

For
$$p, q \in \mathbb{R}^2$$
, define $\delta_{p,q} : \Omega \to [0, \infty)$ by

$$\delta_{p,q}(s,t) := \|\operatorname{push}(p,\ell) - \operatorname{push}(q,\ell)\|_2 = |\lambda^{-1} \circ \operatorname{push}(p,\ell) - \lambda^{-1} \circ \operatorname{push}(q,\ell)|$$

with ℓ the slice defined by s and t. Again, see Figure 1 for an illustration. 241

We now give piecewise analytic formulae for $\delta_{p,q}$, which depend on whether the slice ℓ is 242 above or below p and q. 243

(I) slice is above both p and q:

$$\delta_{p,q}(s,t) = \|(\frac{p_y - t}{s}, p_y) - (\frac{q_y - t}{s}, q_y)\|_2 = \sqrt{\left(\frac{p_y - q_y}{s}\right)^2 + (p_y - q_y)^2} = |p_y - q_y|\sqrt{1 + \frac{1}{s^2}}$$

(II) slice is below both p and q:

$$\delta_{p,q}(s,t) = \|(p_x, sp_x+t) - (q_x, sq_x+t)\|_2 = \sqrt{(p_x - q_x)^2 + (sp_x - sq_x)^2} = |p_x - q_x|\sqrt{1 + s^2}.$$

(III) slice is between p and q: There are two subcases, which we will call (IIIa) and (IIIb): 246 Assuming p lies above the slice (IIIa), the formula is 247

$$\delta_{p,q}(s,t) = \|(\frac{p_y - t}{s}, p_y) - (q_x, sq_x + t)\|_2 = \sqrt{\left(\frac{p_y - t}{s} - q_x\right)^2 + (p_y - sq_x - t)^2} = \sqrt{\frac{1}{s^2}(p_y - t - sq_x)^2 + (p_y - sq_x - t)^2} = |p_y - t - sq_x|\sqrt{1 + \frac{1}{s^2}}.$$

2

If p lies below the slice (IIIb), the formula is the same, except with the roles of p and q 250 exchanged. 251

The push map is easily seen to be continuous with respect to the slice ℓ , so these formulae 252 also extend to boundaries of the cases, i.e., when the slice contains p or q. 253

▶ Lemma 5. If $p, q \in \operatorname{gr}(P^M) \cup \operatorname{gr}(P^N)$, then in each face of \mathcal{A}_0 , exactly one of the conditions 254 (I), (II), (IIIa), (IIIb) holds everywhere. Hence, $\delta_{p,q}$ can be expressed on the entire face by 255 one of the analytic formulae above. 256

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Proof. Clearly, the closures of the regions in Ω described by the various cases intersect at points (s,t) such that p or q (or both) lie on the line y = sx + t, i.e. such that (s,t) is on the line L_p or L_q . The result follows.

In view of Lemma 5, for $p, q \in \operatorname{gr}(P^M) \cup \operatorname{gr}(P^N)$ we may define the p, q-type of a face \mathcal{A}_0 to be the case (I), (II), (IIIa), or (IIIb) which holds on that face.

Refinement of the arrangement. Now we further subdivide the arrangement A_0 . For that, consider the set of equations of the form

$$\delta_{p,q}(s,t) = 0 \qquad \text{for } p, q \in \operatorname{gr}(P^M) \text{ or } p, q \in \operatorname{gr}(P^N),$$

$$c_{pq}\delta_{p,q}(s,t) = c_{p'q'}\delta_{p',q'}(s,t) \qquad \text{for } p, q, p', q' \in \operatorname{gr}(P^M) \sqcup \operatorname{gr}(P^N),$$
(1)

265 where

264

$$c_{pq} := \begin{cases} \frac{1}{2} & \text{if } p, q \in \operatorname{gr}(P^M) \text{ or } p, q \in \operatorname{gr}(P^N), \\ 1 & \text{otherwise.} \end{cases}$$

Lemma 6. The solution set of each of the above equations restricted to f is either the empty set, the entire face, the intersection of f with a line, or intersection of f with the union of two lines.

Proof. First we show the statement for equations of the form $\delta_{p,q}(s,t) = 0$. There are three cases:

 $\delta_{p,q}$ is of type (I): the equation becomes

273
$$|p_y - q_y| \sqrt{1 + \frac{1}{s^2}} = 0$$

for which either all $(s,t) \in f$ are a solution (if $p_y = q_y$), or no (s,t) is a solution. $\delta_{p,q}$ is of type (II): the same argument holds for the equation

276
$$|p_x - q_x|\sqrt{1 + s^2} = 0.$$

 $\delta_{p,q}$ is of type (III): Swapping p and q if necessary, we obtain the equation

$$p_{y} - t - sq_x | \sqrt{1 + \frac{1}{s^2}} = 0$$

and the solution set is made of all $(s,t) \in f$ for which $p_y - t - sq_x = 0$, which is the equation of a line.

For the remaining equations, we give the proof in the special case that $c_{pq} = c_{p'q'}$; the proof in the other cases is essentially the same. For equations of the form $\delta_{p,q}(s,t) = \delta_{p',q'}(s,t)$, there are six cases to check, depending on the type of the δ -functions on the left and right sides of the equation:

Both $\delta_{p,q}(s,t)$ and $\delta_{p',q'}(s,t)$ are of type (I): the equation is

286
$$|p_y - q_y| \sqrt{1 + \frac{1}{s^2}} = |p'_y - q'_y| \sqrt{1 + \frac{1}{s^2}}$$

and the equation is satisfied if and only if $|p_y - q_y| = |p'_y - q'_y|$, independent of s and t. Hence, the solution set is either f or \emptyset .

Both $\delta_{p,q}(s,t)$ and $\delta_{p',q'}(s,t)$ are of type (II): the same argument as in the previous case applies, so the solution set is either f or \emptyset .

 $\delta_{p,q}$ is of type (I) and $\delta_{p',q'}$ of type (II): we get the equation

²⁹²
$$|p_y - q_y| \sqrt{1 + \frac{1}{s^2}} = |p'_x - q'_x| \sqrt{1 + s^2}$$

293 Since $1 + \frac{1}{s^2} = \frac{1+s^2}{s^2}$, this simplifies to

$$|p_y - q_y| = s|p'_x - q'_x|$$

and the solution set is either all of f (if both absolute values vanish), the empty set (if only $p'_x - q'_x = 0$), or the intersection of f with the vertical line $s = \frac{|p_y - q_y|}{|p'_x - q'_x|}$ (otherwise). Both $\delta_{p,q}$ and $\delta_{p',q'}$ are of type (III): Swapping p, q or p', q' if necessary, we get

²⁹⁸
$$|p_y - t - sq_x| \sqrt{1 + \frac{1}{s^2}} = |p'_y - t - sq'_x| \sqrt{1 + \frac{1}{s^2}}$$

hence, (s,t) is a solution if and only if $p_y - t - sq_x = p'_y - t - sq'_x$ or $p_y - t - sq_x = -(p'_y - t - sq'_x)$. The first equations yields again either f, \emptyset , or a vertical line as solution set, the second equation always defines a line. Exchanging the roles of p and q, or the roles of p' and q', or both, does not change the conclusion.

 $\delta_{p,q}$ is of type (I) and $\delta_{p',q'}$ is of type (III): Swapping p' and q' if necessary, the formula is

305
$$|p_y - q_y| \sqrt{1 + \frac{1}{s^2}} = |p_y - t - sq_x| \sqrt{1 + \frac{1}{s^2}}$$

 $(s,t) \in f \text{ is a solution if } p_y - t - sq_x = p_y - q_y \text{ or } p_y - t - sq_x = q_y - p_y, \text{ which is a line equation in both cases.}$

 $\delta_{p,q}$ is of type (II) and $\delta_{p',q'}$ is of type (III): Swapping p' and q' if necessary, we get

³⁰⁹ $|p_x - q_x|\sqrt{1 + s^2} = |p'_y - t - sq'_x|\sqrt{1 + \frac{1}{s^2}}$

310 which simplifies to

311
$$s|p_x - q_x| = |p'_y - t - sq'_x|$$

Here $(s,t) \in f$ is a solution if and only if $s(p_x - q_x) = p'_y - t - sq'_x$ or $s(p_x - q_x) = -(p'_y - t - sq'_x)$. Again, we obtain a line in both cases.

▶ **Definition 7.** Let \mathcal{A} denote the line arrangement in Ω formed by the lines in \mathcal{A}_0 , all lines from the case analysis above, and the vertical line s = 1.

Lemma 8. The arrangement \mathcal{A} consists of $O(n^4)$ lines.

Proof. The case analysis in the proof of Lemma 6 was performed relative to a choice of face f in \mathcal{A}_0 . However, for a fixed choice of an equation in the set of equations (1), the lines which arise in the case analysis depend only on the p, q-type or p', q'-type of f. There are at most $4 \times 4 = 16$ possible way of jointly choosing the p, q-type and p', q'-type of f, and for a given choice, at most two lines are added to the arrangement. Hence, each of the $O(n^4)$ equations in the set of equations (1) contributes at most a constant number of lines to \mathcal{A} . The result now follows easily.

Note that the arrangement \mathcal{A} depends on the choice of presentations for M and N.

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Figure 2 An arrangement of lines. The lightly shaded regions show outer regions, the darkly shaded region is an example of an inner region. The outer segments of the marked outer regions are drawn more thickly.

Theorem 9. For any face f of \mathcal{A} , there is some choice of $p, q \in \operatorname{gr}(P^M) \cup \operatorname{gr}(P^N)$ such that $d_B(M^{\ell}, N^{\ell}) = c_{pq} \delta_{p,q}(\ell)$ for all $\ell \in \alpha(f)$.

327 The formal proof of this result is deferred to Appendix A. It can be summarized as follows:

1. The order of the pushes of the grades of P^M and P^N along ℓ is the same across f. This is because whenever this order changes, we need to cross one of lines of the arrangement \mathcal{A} . Since the combinatorial structure of the persistence diagram only depends on the order of the grades of the presentations, that combinatorial structure is constant across f.

³³² 2. Each birth or death coordinate of the combinatorial persistence diagram associated to

³³³ M is indexed by an element of P^M , and similarly for N.

334 **3.** The order of the values of the functions $\delta_{p,q}$ remains the same across f. This is because any change in their order will result again in crossing one of the lines of the arrangement \mathcal{A} . As a result, the combinatorial bottleneck matching remains the same across f, and so do the longest edge of the matching and the pair of grades (p,q) that realizes the bottleneck. The bottleneck distance along any slice ℓ in f is $c_{pq}\delta_{p,q}(\ell)$.

339 **5** Maximization

We define a *region* of \mathcal{A} as the closure of a face of \mathcal{A} within Ω . We can compute the matching distance by determining sup F(s,t) separately for each region in \mathcal{A} . We will show now that in each region, sup F(s,t) is either realized at a boundary vertex, or as the limit of an unbounded boundary edge, which can be computed easily.

We fix the following notation: A region $R \subseteq \Omega$ is an *inner region* if it is bounded as a set in \mathbb{R}^2 and it has a positive distance to the vertical line s = 0 in \mathbb{R}^2 (in other words, R does not reach the boundary of Ω). An inner region is a convex polygon. Regions that are not inner region are called *outer regions*. Outer regions have exactly two *outer segments* in their boundary, which are infinite or converge to a point on the vertical line s = 0. See Figure 2 for illustrations of these concepts.

For a fixed region R of \mathcal{A} , Theorem 9 ensures that there is a pair of grades (p,q) whose δ -function realizes d_B within the interior of R (a face of \mathcal{A}). By continuity, this implies that $\delta_{p,q}$ also realizes d_B on the entire region.

Lemma 10. The supremum of F within R is attained either at a vertex on the boundary of R, or as the limit of F along an unbounded segment. In the latter case, the limit

can be expressed in simple terms based on the equation of the line segment and one of the functions $\delta_{p,q}$.

Proof. We distinguish 6 cases based on the type of the δ -function and on whether $s \leq 1$ or $s \geq 1$ (note that each cell belongs to one of these cases, because the line s = 1 is in \mathcal{A}).

 $\delta_{p,q}$ of type (I), $s \leq 1$ In that case,

363
$$F(\ell) = w(\ell)\delta_{p,q}(\ell) = \frac{1}{\sqrt{1 + \frac{1}{s^2}}} |p_y - q_y| \sqrt{1 + \frac{1}{s^2}} = |p_y - q_y|,$$

a constant function. Clearly, the supremum is attained everywhere, in particular at the boundary vertices of R.

 $_{_{366}}$ $\delta_{p,q}$ of type (I), $s\geq 1$ We get

367
$$F(\ell) = \frac{1}{\sqrt{1+s^2}} |p_y - q_y| \sqrt{1+\frac{1}{s^2}} = \frac{1}{s} |p_y - q_y|$$

Clearly, this function becomes larger when s gets smaller. Moreover, because $s \ge 1$ within the cell, there is a leftmost vertex on the boundary, which minimizes s and therefore attains the supremum within the cell.

 $_{_{371}}$ $\delta_{p,q}$ of type (II), $s\leq 1$ We obtain

372
$$F(\ell) = \frac{1}{\sqrt{1 + \frac{1}{s^2}}} |p_x - q_x| \sqrt{1 + s^2} = s |p_x - q_x|.$$

Similarly to the previous case, there exists a rightmost boundary vertex in the cell (because $s \leq 1$), which realizes the supremum.

 $_{_{375}}$ $\delta_{p,q}$ of type (II), $s \geq 1$ The function simplifies to

376
$$F(\ell) = \frac{1}{\sqrt{1+s^2}} |p_x - q_x| \sqrt{1+s^2} = |p_x - q_x|,$$

a constant function, which attains its supremum at any boundary vertex. $\delta_{p,q}$ of type (III), $s \leq 1$ Assuming that p lies above the slice, we get

379
$$F(\ell) = \frac{1}{\sqrt{1 + \frac{1}{s^2}}} |p_y - t - sq_x| \sqrt{1 + \frac{1}{s^2}} = |p_y - t - sq_x|.$$

If R is an inner region, we are maximizing the above function over a closed convex polygon, and the maximum is achieved at a boundary vertex, because $|p_y - t - sq_x|$ is the maximum of two linear functions in s and t.

It remains to analyze the case that R is an outer region. We argue first that R is bounded in t-direction from above and below: Since $\delta_{p,q}$ is of type (III), with p lying above ℓ , (s,t)must be below the (non-vertical) line $t = -sp_x + p_y$ in the dual space. Likewise, since q is below ℓ , (s,t) must be above $t = -sq_x + q_y$. Moreover, we have $0 < s \leq 1$. If the above lines intersect at a point r with s-value in (0,1), R is contained in the triangle spanned by the two lines and the vertical line s = 0. Otherwise, R is contained in the trapezoid induced by these two lines and the vertical lines s = 0 and s = 1.

It follows that the two outer segments of R converge to the vertical line s = 0. Let $(0, t_1)$ denote the limit of the lower outer segment and $(0, t_2)$ the limit of the upper outer

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segment. Clearly $t_1 \leq t_2$. Let \bar{R} denote the union of R with the vertical line segment 392 from $(0, t_1)$ to $(0, t_2)$; note that \overline{R} is the closure of R considered as a subset of \mathbb{R}^2 . Observe 303 that $|p_y - t - sq_x|$ is continuous over \mathbb{R}^2 ; therefore F can be continuously extended to \overline{R} . 394 It follows that the supremum of F over \overline{R} is attained at a boundary vertex, since \overline{R} is a 395 convex closed polygon. There are two cases: either the maximum is attained at a vertex 396 of \mathcal{A} , or at $(0, t_1)$ or $(0, t_2)$. As we can readily see, the function values at the latter two 397 points are $|p_y - t_1|$ and $|p_y - t_2|$, respectively. The case where p is below the slice and q 398 is above is analyzed in the same way, with the roles of p and q swapped. 399

 $\delta_{p,q}$ of type (III), $s \ge 1$ Assuming that p lies above the slice, we get

$$F(\ell) = \frac{1}{\sqrt{1+s^2}} |p_y - t - sq_x| \sqrt{1 + \frac{1}{s^2}} = |\frac{p_y}{s} - \frac{t}{s} - q_x|$$

We first consider the case where R is an inner region, and we show that the function is 402 maximized at a boundary vertex of R. The function $\left|\frac{p_y}{s} - \frac{t}{s} - q_x\right|$ has no local maximum 403 over \mathbb{R}^2 since it is the absolute value of a linear function in t for any fixed s. Hence, the 404 supremum over R must be attained on the boundary. We have to exclude the case that 405 the maximum lies in the interior of an edge. For vertical edges this is obvious, because 406 for a constant s, the function simplifies to the absolute value of a linear function in t407 which must be maximized at a boundary vertex. For a non vertical line of the form 408 t = as + b, plugging in this equation for t yields a function of the form 409

$$\left|\frac{p_y}{s} - \frac{as+b}{s} - q_x\right| = \left|\frac{1}{s}(p_y - b) - a - \frac{1}{s}(p_y - b)\right| = \frac{1}{s}(p_y - b) - a - \frac{1}{s}(p_y - b) - \frac{1}{s}(p_y - b$$

401

410

424

This is the absolute value of a monotone function in s and hence has no local maximum.
Again, this implies that it is maximized at a boundary vertex.

 $q_x|.$

Consider now the case where R is an outer region. As in the previous case, R is upper 413 and lower bounded by two non-vertical lines, because we assume type (III). Hence, the 414 two outer segment of R cannot be vertical; the lower outer segment has a slope r_1 and 415 the upper outer segment has a slope r_2 with $r_1 < r_2$. We argue next that the supremum 416 of $\frac{p_y}{s} - \frac{t}{s} - q_x$ is either attained at a boundary vertex, or equal to $|r_1 + q_x|$, or equal 417 to $|r_2 + q_x|$. Let (s_i, t_i) denote a sequence of points in R such that $F(s_i, t_i)$ converges 418 to the supremum. If (s_i, t_i) converges to a point in R (or has at least a convergent 419 subsequence), it follows (similarly to the case of an inner region) that the limit point is 420 a boundary vertex. Otherwise, we can assume (by passing to a subsequence) that the 421 sequence s_i is unbounded. Moreover, the sequence $\frac{t_i}{s_i}$ is bounded by $[r_1, r_2]$ and therefore 422 has a convergent subsequence with limit r'. Passing to this subsequence, we obtain that 423

$$\lim_{i \to \infty} F(s_i, t_i) = \lim_{i \to \infty} \left| \frac{p_y}{s_i} - \frac{t_i}{s_i} - q_x \right| = \left| -r' - q_x \right| = \left| r' + q_x \right|$$

Hence, the supremum must be of the form $|r' + q_x|$ for some $r' \in [r_1, r_2]$. On the other hand, this expression is clearly maximized for either $|r_1 + q_x|$ or $|r_2 + q_x|$, and there exist sequences attaining these values, for instance when choosing (s_i, t_i) on either of the outer segments. The case where p lies below the slice and q lies above is treated similarly, with the roles of p and q exchanged.

⁴³⁰ **The algorithm.** We now give the algorithm to compute the matching distance:

 $_{431}$ Compute the arrangement induced by \mathcal{A} from Definition 7.

For each vertex (s,t) in the arrangement, compute F(s,t). Let m be the maximum among all the values.

For each outer region R, pick a point (s,t) in the interior. Compute the bottleneck distance and identify a pair (p,q) of grades that realizes the bottleneck. Determine whether p and q are above or below the slice (s,t). If the region is of type (III) with respect to p and q, then do the following:

⁴³⁸ If R is on the left of s = 1, compute the intersections $(0, t_1)$, $(0, t_2)$ of the outer ⁴³⁹ segments of R with the vertical line s = 0. Set $m := \max\{m, |p_y - t_1|, |p_y - t_2|\}$.

If R is on the right of s = 1, let r_1, r_2 denote the slopes of the outer segments of R.

441

Set $m := \max\{m, |r_1 + q_x|, |r_2 + q_x|\}.$

442 \blacksquare Return m.

⁴⁴³ By "computing the arrangement", we mean to store the planar subdivision induced by ⁴⁴⁴ the lines of the arrangement (e.g.[2, Ch.2]). In fact, it not too difficult to implement the ⁴⁴⁵ algorithm without explicitly constructing the line arrangement \mathcal{A} , nor even storing its whole ⁴⁴⁶ set of vertices. This reduces the space complexity of the algorithm by a polynomial factor, ⁴⁴⁷ while leaving its time complexity unchanged. See Appendix B for the details.

448 • Theorem 11. The above algorithm computes the matching distance in polynomial time.

449 Proof. Correctness follows from Lemma 10: as we check all vertices of the arrangement, we
 450 cover the supremum of all inner regions. The outer regions are handled separately in the
 451 last steps of the algorithm.

Running time: recall from Lemma 8 that we have $O(n^4)$ lines in the arrangement \mathcal{A} . Hence, the arrangement has $O(n^8)$ vertices, $O(n^4)$ outer regions, and can be computed in $O(n^8 \log n)$ time using an extension of the Bentley-Ottman sweep-line algorithm [1]. For each vertex and each outer region, we have to compute two persistence diagrams, which can be done in $O(n^3)$ time, and a bottleneck distance whose complexity can be neglected. The remaining computations are negligible. Hence, we arrive at a $O(n^{11})$ algorithm.

We remark that the algorithm can be realized entirely with rational arithmetic if all 458 grades are rational numbers. Indeed, all lines in the arrangement have rational coefficients, 459 and so do their intersection points. An intersection points corresponds to a slice along which 460 we are required to compute the bottleneck distance. Recall from Section 3 that the definition 461 of the slice ℓ module introduces a grade of $\lambda^{-1}(\operatorname{push}(p,\ell))$ where $\lambda^{-1}(p_x,p_y) = \sqrt{1+s^2}p_x$. 462 Hence, these grades are not rational numbers. However, the bottleneck distance is multiplied 463 with the weight $w(\ell)$ of the slice afterwards, and instead of doing so, one can as well scale all 464 grades with $w(\ell)$ in advance. A simple calculation shows that this indeed turns the grades 465 into rational values. 466

⁴⁶⁷ A simple analysis also reveals that if the input coordinates are rational and of bitsize ⁴⁶⁸ $\leq b$, all intermediate computations in the algorithm can be performed with a bitsize of $\leq cb$, ⁴⁶⁹ with c a (small) constant. Hence, the algorithm is strongly polynomial.

470 **6** Discussion

We have presented the first polynomial time algorithm to exactly compute the matching distance for 2-parameter persistent modules. It is natural to ask about practicality of our approach. The large exponent of n^{11} seems discouraging at first, but we mention first that the worst-case running time of $O(n^3)$ for persistent homology is usually not appearing for real instances; indeed an almost linear behavior can be expected. Still, the large number of

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- $O(n^4)$ lines in the arrangement constitutes a computational barrier in practice. There are several possibilities, however, to reduce this effect:
- ⁴⁷⁸ Instead of computing the arrangement \mathcal{A} globally, we could compute the intermediate ⁴⁷⁹ arrangement \mathcal{A}_0 and refine each face of it separately, using only those lines that affect
- 480 the δ -functions within this face.
- ⁴⁸¹ As a follow-up to the previous point, it might be possible to compute a smaller arrange-⁴⁸² ment per face adaptively. The idea is to start at some interior point in a face of \mathcal{A}_0 , ⁴⁸³ identifying a pair (p,q) that realizes the bottleneck distance and then to determine the
- boundary of the region where (p,q) realizes the bottleneck distance.
- As a preprocessing step, we can move from the input presentations to *minimal presentations*, which represent isomorphic persistent module (that is, yielding the same matching
- distance), but with the smallest number of generators and relations (hence minimizing n).
 We pose the question of whether an implementation realizing the above ideas is competitive
 to an approximative, sampling-based approach for computing the matching distance.
- Our algorithm needs to treat the outer edges of the arrangement \mathcal{A} separately since our analysis does not rule out the possibility that the supremum is realized at the boundary of Ω . On the other hand, we are not aware of an example of two finite presentations whose matching distance is not realized by a particular slice in Ω . A proof that the supremum in the definition of the matching distance is in fact a maximum would greatly simplify our algorithm, since it would boil down to computing the intersection points of all lines and searching for the maximal F-value among them.
- Finally, we have restricted attention to the case of two-parameter persistence modules. It is natural to conjecture that our algorithm extends to more parameters by constructing a hyperplane arrangement. It would be worthwhile to check this conjecture in future work.
- Acknowledgments. This work was initiated at the Banff workshop "Multiparameter Persistent Homology" (18w55140) in Oaxaca, Mexico (Aug. 2018). We thank Jan Reininghaus and the other members of the discussion group on this topic for fruitful initial exchanges. We thank Matthew Wright for helpful discussions about line arrangements, slices, and the computational aspects of 2-parameter persistence.

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A Appendix: proof of Theorem 9

Let $G^M = \operatorname{gr}(P^M)$ and let $G^N = \operatorname{gr}(P^N)$. As an intermediate result, we prove that the combinatorial structure of each persistence diagram stays the same across the face f:

551 Lemma 12. For each face f of A, there exist multisets

552
$$\mathcal{T}_M^f \subset G^M \times (G^M \cup \{(\infty, \infty)\}),$$

553
$$\mathcal{T}_N^f \subset G^N \times (G^N \cup \{(\infty, \infty)\})$$

such that for any $\ell \in \alpha(f)$,

where by convention $push((\infty,\infty),\ell) := (\infty,\infty)$ and $\lambda^{-1}((\infty,\infty)) := \infty$. We call \mathcal{T}_M^f and \mathcal{T}_N^f diagram templates.

⁵⁵⁹ **Proof.** This is a variant of [17, Theorem 4.1]. We give a succinct, algorithmically flavored ⁵⁶⁰ proof here. We prove the result for M; the proof for N is the same.

First, note that the restriction of the partial order on \mathbb{R}^2 to any $\ell \in \alpha(f)$ is a total order. This total order pulls back under the map $\operatorname{push}(-,\ell) : \operatorname{gr}(P^M) \to \ell$ to a totally ordered partition of $\operatorname{gr}(P^M)$, (i.e., elements of the partition are level sets). It can be checked that, because \mathcal{A} refines \mathcal{A}_0 and also contains all lines of the form $\delta_{p.q} = 0$ for $p, q \in \operatorname{gr}(P^M)$ with p and q incomparable in the partial order on \mathbb{R}^2 , this totally ordered partition is the same for all $\ell \in \alpha(f)$; see [17, Corollary 3.4]. Thus, we obtain a unique totally ordered partition of $\operatorname{gr}(P^M)$ associated to all of f. Let us refine this to a fixed total order on $\operatorname{gr}(P^M)$.

Permuting the row or columns of a presentation for M yields another presentation for M, so we may assume without loss of generality that the order of rows and columns for P^M is consistent with our total order on $gr(P^M)$. Applying the matrix reduction underlying the standard persistence algorithm [19] to the matrix underlying P^M yields a matching σ of row and column indices, where a non-zero column in the reduced matrix is matched to the row of its pivot. We may define

$$\mathcal{T}_{M}^{j} := \{ \operatorname{gr}(\operatorname{row}_{i}), \operatorname{gr}(\operatorname{col}_{j}) \mid (i, j) \in \sigma, \ \operatorname{gr}(\operatorname{row}_{i}), \operatorname{gr}(\operatorname{col}_{j}) \text{ not together in the partition} \}$$

$$\cup \{ (\operatorname{gr}(\operatorname{row}_{i}), (\infty, \infty)) \mid i \text{ is unmatched in } \sigma \}.$$

(As an aside, we remark that this is not the only way to define \mathcal{T}_M^f such that the property in the statement of the lemma is satisfied.)

As mentioned earlier, P^M induces a finite presentation P^{ℓ} for M^{ℓ} ; the presentation matrix remains the same, and we simply replace each row and column grade g by $\lambda^{-1} \circ$ push (g, ℓ) . From this, and the correctness of the standard algorithm for computing persistent homology [19], it follows that

$$D(M^{\ell}) = \left\{ (\lambda^{-1} \circ \operatorname{push}(a, \ell), \lambda^{-1} \circ \operatorname{push}(b, \ell)) \mid (a, b) \in \mathcal{T}_M^f \right\},$$

583 as desired.

Suppose we are given two persistence diagrams D and D'. For each $(x, y) \in D \cup D'$, let $w_0(x, y) := \frac{y-x}{2}$, and for each $(x, y), (x', y') \in D \times D'$, let $w_1(x, x') := \max(|x - x'|)$, and

 $w_2(y, y') := \max(|y - y'|)$. We call these (possibly infinite) numbers the weights of the pair 586 (D, D'). Denoting the set of pairs indexing these weights as I(D, D'), the weights define a 587 function $w^{D,D'}: I^{D,D} \to [0,\infty)$. Note that $d_B(D,D') = w^{D,D'}(x,y)$ for some $(x,y) \in I^{D,D'}$. 588 Clearly, a pair of bijections of persistence diagrams $\zeta_1 : D \to E$ and $\zeta_2 : D' \to E'$ induces 589 a bijection 590

The following is an easy consequence of the definition of d_B . 592

▶ Lemma 13. If $d_B(D, D') = w^{D,D'}(x, y)$ and ζ_1, ζ_2 preserve the order of the weights, in 593 the sense that 594

595
$$w^{D,D'}(x,y) \le w^{D,D'}(x',y')$$
 if and only if $w^{E,E'}(\zeta(x,y)) \le w^{E,E'}(\zeta(x',y')),$

596 then
$$d_B(E, E') = w^{E, E'}(\zeta(x, y))$$
.

Proof of Theorem 9. Let \mathcal{T}_M^f and \mathcal{T}_N^f be diagram templates for the cell f. For any $\ell \in \alpha(f)$, 597 Lemma 12 gives us distinguished bijections 598

599
$$\gamma: \mathcal{T}_M^f \to D(M^\ell), \qquad \gamma': \mathcal{T}_N^f \to D(N^\ell).$$

It is easily checked that for $(x, y) \in D(M^{\ell})$, and $(p, q) = \gamma^{-1}(x, y)$, we have 600

601
$$w_0(x,y) = \frac{1}{2}\delta_{p,q}(\ell) = c_{pq}\delta_{p,q}(\ell).$$
 (2)

Similarly, for 602

$$(x,y) \in D(M^{\ell}), \ (x',y') \in D(N^{\ell}), \ (p,p') = \gamma^{-1}(x,y), \ \text{and} \ (q,q') = \gamma'^{-1}(x',y'),$$

we have 604

605
$$w_1(x, x') = \delta_{p,q}(\ell) = c_{pq}\delta_{p,q}(\ell),$$
 (3)

606
$$w_2(y,y') = \delta_{p',q'}(\ell) = c_{p'q'}\delta_{p',q'}(\ell).$$
 (4)

Note that as we move the slice ℓ inside f, the order of the values taken by the functions 607 7}

$$\{c_{pq}\delta_{p,q} \mid p,q \in P^M \cup P^N$$

cannot change. Indeed, the functions $\ell \to \delta_{p,q}(\ell)$ are continuous, and by Lemma 6 and the 609 definition of the arrangement \mathcal{A} , the intersection of f with the solution set of each equation 610 $c_{pq}\delta_{p,q} = c_{p'q'}\delta_{p',q'}$ is either f or \emptyset . 611

The diagram templates provide bijections $D(M^{\ell}) \to D(M^{\ell'})$ and $D(N^{\ell}) \to D(N^{\ell'})$ for 612 all $\ell, \ell' \in \alpha(f)$. It now follows from equations (2-4) that for each ℓ, ℓ' , these preserve the 613 order on weights. Thus, by Lemma 13, if 614

615
$$d_B(D(M^{\ell}), D(N^{\ell})) = w^{D(M^{\ell}), D(N^{\ell})}(x, y)$$

for some $\ell \in \alpha(f)$, then 616

$${}^{_{617}} \qquad d_B(D(M^{\ell'}), D(N^{\ell'})) = w^{D(M^{\ell'}), D(N^{\ell'})}(\zeta^{\ell, \ell'}(x, y))$$

for all $\ell' \in \alpha(f)$, where 618

$$_{619} \qquad \zeta^{\ell,\ell'}: I^{D(M^{\ell}),D(N^{\ell})} \to I^{D(M^{\ell'}),D(N^{\ell'})}$$

is the bijection induced by the barcode templates. The result now follows from equations 620 (2-4).621

622 **B** A more-space efficient algorithm

The algorithm described in Section 5 consists of two major steps: we first find the maximal 623 value of F over all intersection points of lines in the arrangement \mathcal{A} , and then check the 624 convergence along outer segments for certain outer regions of \mathcal{A} . To decide whether an 625 outer region needs to be considered, we require one interior point of that region, to decide 626 the type of the region. The arrangement \mathcal{A} (stored as a planar subdivision as in [2, Ch.2]) 627 contains enough information to access all necessary data conveniently. However, its space 628 complexity is $O(n^8)$ because the arrangement is induced by $O(n^4)$ lines. We show next how 629 to implement the algorithm without constructing \mathcal{A} in memory, yielding a space complexity 630 of $O(n^4)$: 631

Reporting the intersection points of a set of lines in the plane is one of the oldest prob-632 lems in computational geometry. The Bentley-Ottmann sweep-line algorithm [1] reports all 633 intersection points in time proportional to the number of such points. Note that there are 634 up to $O(n^8)$ intersections, so storing all such points is space consuming. However, there is 635 no need to do so – whenever the sweep-line algorithm reports a new point, we compute F636 at this point and compare the value with the maximal F-value seen before, updating the 637 maximum if the newly encountered value is larger. There is no need to store the intersection 638 beyond this moment. In this way, we obtain the maximal F-value among all intersection 639 points using only $O(n^4)$ space. 640

For handling outer regions, note that we can extend the sweep-line algorithm such that it also returns the leftmost intersection point with positive s-coordinate, and the rightmost intersection point, among all pairs of lines in \mathcal{A} . Let $0 < s_{min} \leq s_{max}$ denote the scoordinates of these intersection points. Now, consider the vertical line $s = \frac{s_{min}}{2}$, which is partitioned into open intervals

$$_{646} \qquad (-\infty, b_1), (b_1, b_2), \dots, (b_{m-1}, b_m), (b_m, \infty) \tag{5}$$

where m is the number of $O(n^4)$ lines in \mathcal{A} that intersect the vertical line, and b_1, \ldots, b_m are 647 the intersection points of these (non-vertical) lines with the vertical line. The intervals in the 648 sequence can be computed in $O(n^4 \log n)$ time, just by sorting the b_i 's. The intervals in the 649 sequence (5) are in one-to-one correspondence with the outer segments of \mathcal{A} that have the 650 line s = 0 in their boundary. More precisely, each interval is contained in the corresponding 651 outer segment, and for $i \in \{1, \ldots, m-1\}$, the point $(\frac{s_{min}}{2}, \frac{b_i+b_{i+1}}{2})$ is an interior point of 652 the corresponding outer region, whose outer segments of the lines of \mathcal{A} contain the points 653 b_i and b_{i+1} . This information suffices to determine the type of the region, and to compute 654 the limit values of the F-function if necessary. The two infinite regions corresponding to 655 $(-\infty, b_1)$ and (b_m, ∞) can be ignored, because these regions must be of type (I) or type 656 (II). The same construction provides interior points of outer regions that are unbounded in 657 s-direction, considering the vertical line at $s = 2s_{max}$. 658

⁶⁵⁹ With this variant, we compute the matching distance with space complexity $O(n^4)$. The ⁶⁶⁰ time complexity remains $O(n^{11})$ as in the original algorithm, because we still iterate over ⁶⁶¹ $O(n^8)$ vertices and compute the bottleneck distance in each position in $O(n^3)$ time.