MULTIPARAMETER PERSISTENT HOMOLOGY

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The amount of the existing data is increasing rapidly and any way to understand
the shape of the given data is welcomed. In this thesis, we examine a method of
Topological Data Analysis which is called Persistent Homology. After a detailed
overview of 1-parameter case, we extend the structures to the multiparameter case
arising as a natural necessity. We present the similarities and differences between 1-
parameter and multiparameter persistent homology in an expository way. At the last
stage, we work on the interleaving, bottleneck, matching distances and their stability
properties. We also analyze the relations between these pseudometrics, and consider
some examples that help us to calculate them.

Keywords: persistent homology, distance, stability, multiparameter
ÖZ

ÇOK DEĞİŞKENLİ KALICI HOMOLOJİ

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Anahtar Kelimeler: kalıcı homoloji, mesafe, istikrar, çok değişkenli
To my family
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CHAPTER 1

INTRODUCTION

The amount of data (discrete finite set of points in a metric space) we produce is increasing rapidly and any way to understand the data at hand is welcomed. The data can come from many different areas such as an engineering testbed, a biological experiment or results of a questionnaire etc. A relatively new branch of mathematics, called Topological Data Analysis (TDA), proposes to use topology to study properties of data. It is an interdisciplinary field which has intersections with algebraic topology, computational geometry, data analysis, computer science and statistics. The main idea in TDA is to exploit topology to find out the features of the shape of data set and present these features through an easily implementable summaries. In TDA, one also defines (pseudo)metrics to distinguish data sets from each other again by examining their shapes.

Persistent Homology (PH) is one of the most widely used methods in TDA. PH uses homology which is a tool in algebraic topology to detect holes in topological spaces. If we only consider a finite set of points, applying the homology functor directly to this discrete set does not yield any interesting result. In this case, the only non-trivial homology is the 0-th homology group which only counts the number of points. For such a construction, one of the methods that PH suggests is instead of looking at the data set directly, we consider the union of closed balls where centers are the data points, and the radius is $\epsilon \geq 0$ (This is a very naive way to study data sets and we do not mention this method in our thesis, but for motivational purposes, we want to point this out here in the introduction section). However, we should not look for a single $\epsilon$ since working with a fixed $\epsilon$ is unstable with respect to perturbations of data. Also, such an approach cannot distinguish big holes from small ones. In fact, there exists
no canonical $\epsilon$ \cite{23}. For these reasons, we examine all topological spaces that change with respect to the proximity parameter $\epsilon$. With this way, we obtain a nested sequence of topological spaces called a filtration. Then, we apply the homology functor to these topological spaces, or to simplicial complexes obtained from these data sets.

Now, we are ready to track changes in topological features via homology such as where a homology class emerges and what happens to it along the filtration. After using homology, we obtain persistence modules and by passing through their decompositions, we obtain a complete invariant called the barcode as a list of indecomposables giving necessary information about lifespans of connected components, loops and higher dimensional holes in 1-parameter case. Hence, by starting from low dimensional data, we can deduce higher dimensional results. In addition to a set of discrete points, PH also works on data obtained by digital images, real valued functions defined on a chosen topological space and so on.

We also compare persistence modules and measure "how far from being isomorphic" by using stable metrics. We introduce the bottleneck and the interleaving distances, and see that they are equal to each other in 1-parameter setting.

Although 1-parameter persistent homology has many beneficial sides, working on a single parameter gives missing or unstable information for some type of data. For instance, if we have the data with different density, then our ordinary parameter cannot detect the differences caused by density. Therefore, adding a few new data points behaving different than others, called as outliers in the literature, can make significant changes in our results. That means ordinary persistence is very weak to outliers in the data. To overcome this problem, the multiparameter persistent homology is considered by Carlsson and Zomorodian \cite{9} in 2009.

Shifting focus to the multiparameter setting brings new problems to us. The algebraic structure of multiparameter persistence modules is much more complex, and there exists no complete invariant for them, recall that for the 1-parameter case, barcode is a complete invariant. This increases the importance of distances. We extend the bottleneck and the interleaving distances to the multiparameter case. Moreover, by the example of Bjerkevik \cite{4}, we see that they are no more equal to each other, and unlike the interleaving distance, the bottleneck distance is not stable. Since computation of
the interleaving distance is so hard, this leads us to the matching distance as a stable surrogate of the previously mentioned distances in the multiparameter setting [20].

This thesis is organized as follows:

In Chapter 2, we provide the necessary background for 1-parameter persistent homology. We start Chapter 3 with the motivation of multiparameter persistent homology and construct filtrations and persistence modules. Chapter 4 is all about pseudometrics and their stability results in multiparameter setting. We give some examples to understand how we can use them in practice. In this chapter, we also show that the matching distance on different parametrizations of a line is always equal. Thus, restricting the set of admissible lines to the suitable set having unique parametrization for each line does not change $d_{\text{match}}$. 
CHAPTER 2

ONE-PARAMETER PERSISTENT HOMOLOGY

2.1 Filtration

Definition 1. [27] A filtration indexed by \{0, 1, \ldots, n\} is a nested sequence of topological spaces:

\[ \mathcal{K} : K_0 \subseteq K_1 \subseteq \cdots \subseteq K_n \]

where the number \( n \) is not necessarily finite.

Example 2.1.1. Let \( K \) be a compact topological space lying in some Euclidean space, and \( h : K \to \mathbb{R} \) be a real valued function. For \( a_i \in \mathbb{R} \), define the sublevel set \( K_{a_i} \) as

\[ K_{a_i} := h^{-1}(-\infty, a_i] = \{ x \in K \mid h(x) \leq a_i \} \]

where \( i \in \mathbb{N} \). Clearly, \( K_{a_i} \) is a subspace of \( K \) for all \( a_i \in \mathbb{R} \), and \( K_{a_i} \subseteq K_{a_j} \) for all \( a_i < a_j \). Moreover, \( K = K_{a_n} \) for some \( a_n \in \mathbb{R} \) since \( K \) is compact. Hence, we construct a filtration of \( K \) indexed by \{0, 1, \ldots, n\} by setting \( K_i := K_{a_i} \) for \( i = 0, 1, \ldots, n \). In addition, it is called a sublevel set filtration.

Note here that \( a_0 < a_1 < \ldots < a_n \) are the function values, and the filtering function \( h \) is not necessarily continuous. One example of a filtering function, a height function, is given in Figure 2.2.

Sometimes, to study complex geometric objects, it is more convenient to consider them as discrete objects. We want to see them as the union of simple building blocks glued together in a well defined set of rules. Our simple building blocks are called simplices.

Definition 2. [5] Let \( x_0, \ldots, x_k \in \mathbb{R}^n \). An affine combination of these points is a
finite linear combination
\[
\sum_{i=0}^{k} \lambda_i x_i \text{ such that } \sum_{i=0}^{k} \lambda_i = 1,
\]
where \(\lambda_0, \ldots, \lambda_k \in \mathbb{R}\). We say that \(k + 1\) points \(x_0, \ldots, x_k\) are **affinely independent** if
\[
\sum_{i=0}^{k} \lambda_i x_i = 0 \in \mathbb{R}^n \text{ and } \sum_{i=0}^{k} \lambda_i = 0,
\]
then \(\lambda_i = 0\) for all \(i \in \{0, 1, \ldots, k\}\). An affine combination is called as a **convex combination** if \(\lambda_i\) is non-negative for all \(i \in \{0, 1, \ldots, k\}\). The set of all convex combinations is said to be the **convex hull** of \(x_0, \ldots, x_k\), and it is denoted by \(\text{conv}\{x_0, x_1, \ldots, x_k\}\).

A \(k\)-**simplex** \(\sigma\) is the convex hull of \(k + 1\) affinely independent points. Note that 0-simplex is a vertex, 1-simplex is an edge, 2-simplex is a triangle and 3-simplex is a tetrahedron. A face \(\tau\) of a simplex \(\sigma\) is the convex hull of a non-empty subset of the vertex set of \(\sigma\), and it is denoted by \(\tau \leq \sigma\).

Now, we put simplices together to form more complex shapes, called simplicial complexes which are suitable for combinatorial purposes.

**Definition 3.** [5] A **simplicial complex** \(K\) in \(\mathbb{R}^n\) is a finite collection of simplices such that \(\sigma \in K\) and \(\tau \leq \sigma\) implies that \(\tau \in K\), and if \(\sigma_0, \sigma_1 \in K\), then \(\sigma_0 \cap \sigma_1\) is either empty or a face of both \(\sigma_0\) and \(\sigma_1\). A subcollection \(L\) of the simplicial complex \(K\) is a **subcomplex** of \(K\) if it is a simplicial complex itself.

The above construction for the simplicial complex is geometric. In combinatorics, we have a similar definition which is more abstract:

**Definition 4.** [27] An **abstract simplicial complex** \(\mathcal{A}\) is a finite collection of sets such that \(\alpha \in \mathcal{A}\) and \(\beta \subseteq \alpha\) implies that \(\beta \in \mathcal{A}\). The sets in \(\mathcal{A}\) are called simplices and a **subcomplex** \(\mathcal{B}\) of \(\mathcal{A}\) is an abstract simplicial complex such that \(\mathcal{B} \subseteq \mathcal{A}\).

**Example 2.1.2.** Let us see an example of a filtration obtained from a simplicial complex \(K\). Let \(h: K \to \mathbb{R}\) be a non-decreasing function, that is, for \(\tau \leq \sigma\), we have \(h(\tau) \leq h(\sigma)\).
Consider the sublevel set \( K_{a_i} := h^{-1}(-\infty, a_i] \). Since \( h \) is non-decreasing, \( K_{a_i} \) is a subcomplex of \( K \) for any \( a_i \in \mathbb{R} \). Then, we have a filtration of \( K \) that is a nested sequence of subcomplexes:

\[
K_0 \subseteq K_1 \subseteq \cdots \subseteq K_n = K
\]

where \( K_i := K_{a_i} \) for some \( a_i \in \mathbb{R} \).

Until now, we have seen examples in which a filtration ends up with a topological space whose properties we want to understand. On the other hand, we may start with a set of discrete points sitting in \( \mathbb{R}^n \). In this case, instead of attaining it as an ultimate space, it becomes the initial subspace in the filtration. We can consider points in the set as vertices, and by a proximity parameter which we will define, we can obtain a filtration of simplicial complexes. There are many ways to obtain such a filtration, and we introduce the Vietoris-Rips complex.

**Definition 5.** [17] Let \( X \) be a finite collection of points in \( \mathbb{R}^n \). The **Vietoris-Rips complex**, denoted by \( Rips(X)_\epsilon \), is an abstract simplicial complex whose \( k \)-simplices are made of unordered \((k+1)\) distinct points such that all pairwise distances between these points are less than or equal to \( \epsilon \).

From now on throughout this thesis, \( X \) denotes a finite set of points in some Euclidean space unless otherwise stated.

Here, \( \epsilon \) is called the proximity parameter. When \( \epsilon = 0 \), we just have discrete set of points, \( X = \{x_i\}_{i=1}^n \). When \( \epsilon > 0 \), we need to specify pairwise distances between points. If two points have a distance less than or equal to \( \epsilon \), then we add an edge between them. After adding all possible edges, we obtain its 1-skeleton. Since Vietoris-Rips complex is a flag complex, which means that it is maximal among all abstract simplicial complexes with its 1-skeleton, it is enough to have 1-skeleton to construct \( Rips(X)_\epsilon \).

Clearly, as \( \epsilon \) is increasing, the simplicial complex is getting bigger, so we can construct a filtration by considering the corresponding Vietoris-Rips complexes for different values of the proximity parameter \( \epsilon \). Moreover, since we start with finitely many points, for \( \epsilon \) large enough, all the vertices in \( X \) get connected to each other. As
Figure 2.1: A filtration consisting of Vietoris-Rips complexes for some values of $\epsilon$ between $\epsilon = 0$ and $\epsilon = 2.1$ where we start with discrete set of points, but for $\epsilon \geq 2.1$, the complex turns into a solid disk, [25].

As a result, the corresponding Vietoris-Rips complex becomes a solid disk eventually. An example of a filtration using these complexes is given in Figure 2.1.

### 2.2 Persistent Homology

Thanks to the following filtration of topological spaces:

\[ \mathcal{K} : K_0 \subseteq K_1 \subseteq \cdots \subseteq K_n, \]

we can consider the corresponding sequence of homology groups to gain more information. For $i \leq j$, there exists an inclusion map $K_i \hookrightarrow K_j$ which induces a homomorphism between homology groups: $f_{i,j}^p : H_p(K_i) \to H_p(K_j)$ for each dimension $p$. Therefore, any filtration induces a sequence of homology groups connected by homomorphisms induced by inclusions

\[ H_p(\mathcal{K}) : H_p(K_0) \to H_p(K_1) \to \cdots \to H_p(K_n). \]

**Remark 2.2.1.** When we pass to induced maps, we actually apply homology functor to inclusion maps with coefficients in $\mathbb{Z}$. Moreover, all of $H_p(K_i)$ can also be seen as $\mathbb{Z}$-modules with scalar multiplication. In fact, if we take homology with field coefficients, then all the homology groups become vector spaces, and homomorphisms between them are linear maps. We revisit these points when we define what a persistence module is.

Now, let us give the formal definition of persistent homology groups:
Definition 6. [16] The $p$-th persistent homology groups $H_{p}^{i,j}(K)$ of $K$ are the images of the homomorphisms induced by the inclusions $K_i \hookrightarrow K_j$,

$$H_{p}^{i,j}(K) := \text{im}\{f_{p}^{i,j} : H_{p}(K_i) \to H_{p}(K_j)\}$$

for $0 \leq i \leq j \leq n$. Note that $H_{p}^{i,j}(K)$ is not defined for $i > j$. Furthermore, the $p$-th persistent Betti numbers are defined as the rank of the corresponding persistent homology groups:

$$\beta_{p}^{i,j} := \text{rank}(H_{p}^{i,j}(K)).$$

In fact, $H_{p}^{i,j}(K)$ measures the homology classes which persist or disappear through the filtration levels. More specifically, we count the homology classes of $K_i$ which are still alive in $K_j$. Thus, $H_{p}^{i,j}(K)$ can also be defined as

$$H_{p}^{i,j}(K) = Z_{p}(K_i)/(B_{p}(K_j) \cap Z_{p}(K_i)),$$

where $Z_{p}(K_i)$ shows $p$-cycles in $K_i$, and $B_{p}(K_j)$ are $p$-boundaries in $K_j$.

Definition 7. [16] Let $\alpha \in H_{p}(K_i)$. We say that $\alpha$ is born at $K_i$, if $\alpha \notin H_{p}^{i-1,i}(K)$. Moreover, $\alpha$ dies at $K_j$, if $f_{p}^{i-1,j}(\alpha)$ is a nontrivial element in $H_{p}(K_{j-1})$ while $f_{p}^{i,j}(\alpha)$ is a trivial element in $H_{p}(K_j)$. Alternatively, we say that $\alpha$ dies at $K_j$ if it merges with an older class (a class that is born earlier) when we pass through from $K_{j-1}$ to $K_j$. In other words, $f_{p}^{i-1,j}(\alpha) \notin H_{p}^{i-1,j-1}(K)$ but $f_{p}^{i,j}(\alpha) \in H_{p}^{i-1,j}(K)$.

Whenever we say that two homology classes merge together at a particular level, we mean that they become equal as homology group elements, and turns into a single class. In such cases, we keep the class which is born earlier to keep better track of the persistence of homology classes. If these two classes are born at the same time, then we make a choice by keeping one of them. This rule is known as Elder Rule.

Definition 8. [16] Let $\alpha$ be born at $K_i$ and die at $K_j$. If $K$ is a sublevel set filtration, then the difference in the corresponding function values, $a_j - a_i$, is called the persistence of $\alpha$, and it is denoted by $\text{pers}(\alpha) = a_j - a_i$. In the case of a filtration consisting of Vietoris-Rips complexes, it is taken to be $\epsilon_j - \epsilon_i$. We call the difference in index, $j - i$, as the index persistence of the class. Furthermore, if $\alpha$ is born at $K_i$ but never dies, then $\alpha$ is called an essential class and its persistence and index persistence are infinite. Even if we have a filtration consisting of finitely many spaces, we call the classes that live in the homology group of the very last space as an essential class.
Definition 9. \[16\] Let $\mu^{i,j}_p$ be the number of $p$-dimensional classes that are born at $K_i$ and die at $K_j$. This number is called the multiplicity at $(i, j)$.

Observe that we can express $\mu^{i,j}_p$ as a linear combination of the $p$-th persistent Betti numbers:

$$
\mu^{i,j}_p = (\beta^{i,j-1}_p - \beta^{i,j}_p) - (\beta^{i-1,j-1}_p - \beta^{i-1,j}_p)
$$

for all $i < j$ and for all $p$. We can consider the meaning of $\beta^{i,j}_p$ as the number of $p$-dimensional classes born before or at $K_i$ and die after $K_j$. So, in the equality above, the left parenthesis gives the number of classes born before or at $K_i$ and die exactly at $K_j$ while the right parenthesis gives the number of classes born before or at $K_{i-1}$ and die exactly at $K_j$.

2.3 Algebraic Background

We can compute persistent homology groups at each filtration level, and by studying the lifespans of homology classes, we may draw some conclusions. Our aim is to have a meaningful summary showing us the information coming from each filtration level in a gathered form. However, as a first thing, we need to recall basic terminology of the category theory. Let us define necessary parts:

Definition 10. \[23\] A partially ordered set (poset for short) is a set $P$ with a binary relation $\leq$ (the partial order) satisfying

i) $x \leq x$ (Reflexivity),

ii) $x \leq y$ and $y \leq x$ implies $x = y$ (Anti-symmetry),

iii) $x \leq y$ and $y \leq z$ implies $x \leq z$ (Transivity),

for all $x, y, z \in P$. If $x \leq y$ or $y \leq x$, then we say $x$ and $y$ are comparable. A partially ordered set is called totally ordered if each pair of elements from the set is comparable with each other. Furthermore, $P^{op}$ is the opposite poset of $P$, that is, $x \leq y$ in $P^{op}$ if and only if $y \leq x$ in $P$. 

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Definition 11. A category $C$ consists of:

i) A collection $\text{Ob}C$ of objects,

ii) A set $\text{Mor}(X, Y)$ of morphisms for each pair $X, Y \in \text{Ob}C$ and a distinguished identity morphism $\text{id}_X \in \text{Mor}(X, X)$ for each $X \in \text{Ob}C$,

iii) Compositions of morphisms, that is, for each $f \in \text{Mor}(X, Y)$ and $g \in \text{Mor}(Y, Z)$, we have $g \circ f \in \text{Mor}(X, Z)$, satisfying

$$f \circ \text{id}_X = f, \text{id}_Y \circ f = f \text{ and } (h \circ g) \circ f = h \circ (g \circ f)$$

for $h \in \text{Mor}(Z, W)$ where $X, Y, Z, W \in \text{Ob}C$.

Remark 2.3.1. A poset $(P, \leq)$ can be considered as a category with objects $i, j \in P$ and morphisms $i \leq j$. Throughout this thesis, when we write the poset in bold, $P$, it means the poset category of $P$.

Definition 12. Let $C$ and $D$ be categories. A functor $F : C \to D$ is a mapping consisting of:

i) A choice of object $F(X) \in \text{Ob}D$ for each $X \in \text{Ob}C$,

ii) A choice of morphism $F(f) \in \text{Mor}(F(X), F(Y))$ for each $f \in \text{Mor}(X, Y)$, satisfying $F(g \circ f) = F(g) \circ F(f)$ and $F(\text{id}_X) = \text{id}_{F(X)}$.

Remark 2.3.2. For notational purposes, later in the thesis, we might opt to denote $F(X)$ by $F_X$.

Definition 13. A natural transformation $N : F \to G$ between the two functors $F, G : C \to D$ is a choice of morphism $N_X : F_X \to G_X$ for each $X \in \text{Ob}C$ such that the following diagram commutes:

$$
\begin{array}{ccc}
F_X & \xrightarrow{F(f)} & F_Y \\
\downarrow N_X & & \downarrow N_Y \\
G_X & \xrightarrow{G(f)} & G_Y \\
\end{array}
$$

where $f \in \text{Mor}(X, Y)$. $N$ is called a natural isomorphism if each morphism $N_X$ is an isomorphism.
We also mention the equivalence of two categories $C$ and $D$:

**Definition 14.** \[^{[23]}\] A functor $F : C \to D$ is said to be an **equivalence** between $C$ and $D$ if there exists a functor $G : D \to C$ satisfying

$$G \circ F \cong \text{id}_C \text{ and } F \circ G \cong \text{id}_D.$$ 

Next, we recall some algebraic definitions, but first let us fix some notation. Throughout the rest of this chapter, $R$ always denotes a commutative ring with unity, and $(T, \leq)$ denotes a totally ordered set with $T \subseteq \mathbb{R}$.

**Definition 15.** \(^{[21]}\) A ring $\langle R, +, \times \rangle$ is said to be a **$T$-graded ring** if it is written as a direct sum,

$$R \cong \bigoplus_{i \in T} R_i,$$

such that the ring multiplication in $R$ maps $R_i \times R_j$ to $R_{i+j}$. In particular, $R_0$ is a subring of $R$, and each $R_i$ is a $R_0$-module for all $i \in T$. A graded ring $R$ is **non-negatively** graded if $R_i = 0$ for all $i < 0$.

**Definition 16.** \(^{[21]}\) A **$T$-graded module** $M$ over a graded ring $R$ is a module which is written as a direct sum,

$$M \cong \bigoplus_{i \in T} M_i,$$

so that the ring action is defined by $R_i \times M_j \to M_{i+j}$. Moreover, elements of $M_i$ are said to be **homogeneous of degree** $i$. This degree $i$ is called **grade**. In particular, each $M_i$ is a $R_0$-module for all $i \in T$. A graded module $M$ is **non-negatively** graded if $M_i = 0$ for all $i < 0$.

**Definition 17.** \(^{[15],[21]}\) An $R$-module $M$ is said to be **finitely generated** if it has a finite number of generators, that is, there exists a subset $\{m_1, \ldots, m_n\} \subseteq M$ such that for any $m \in M$,

$$m = \sum_{i=1}^{n} r_i m_i \text{ where } r_i \in R \text{ for all } i.$$ 

The set $\{m_1, \ldots, m_n\}$ is called a generating set of $M$, and it is **minimal** if its cardinality is minimal among its generating sets. The $R$-linear combinations $\sum_{i=1}^{n} r_i m_i$ is called a **relation** if $\sum_{i=1}^{n} r_i m_i = 0$. 

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Definition 18. [21] A free module $M$ is an $R$-module which admits a basis, or the zero module. Since a basis is linearly independent, $M$ does not have any relation, and if $\beta$ is its basis, then

$$M \cong \bigoplus_{b \in \beta} R.$$ 

Definition 19. [21] A sequence of $R$-module homomorphisms

$$\ldots \rightarrow M_{i-1} \xrightarrow{f_{i-1}} M_i \xrightarrow{f_i} M_{i+1} \rightarrow \ldots$$

is called exact if $\ker(f_i) = \text{im}(f_{i-1})$ for all $i$.

Definition 20. [21] A presentation of an $R$-module $M$ is an exact sequence

$$F_1 \xrightarrow{f} F_0 \xrightarrow{g} M \rightarrow 0$$

where $F_0$ and $F_1$ are free $R$-modules. $M$ is said to be finitely presented if $F_0$ and $F_1$ have finite bases.

Remark 2.3.3. Here, $F_0$ is the free $R$-module generated by generators of $M$. Since $\ker(g) = \text{im}(f)$, and $\ker(g)$ corresponds to relations of $M$, $\text{im}(f)$ is the submodule of relations. Furthermore, observe that $\text{coker}(f) = F_0/\text{im}(f) \cong M$.

Remark 2.3.4. Note that in the above definitions we can replace $T$ which is a totally ordered set with a poset.

2.4 Persistence Module

Definition 21. [28] A persistence module $M$ indexed by $T$ is a collection of $R$-modules $\{M_i\}_{i \in T}$ together with homomorphisms, defined whenever $i \leq j$,

$$\varphi^M_{i,j} : M_i \rightarrow M_j$$

satisfying the conditions:

(i) $\varphi^M_{i,i} = \text{id}_{M_i}$

(ii) $\varphi^M_{i,k} = \varphi^M_{j,k} \circ \varphi^M_{i,j}$ for all $i \leq j \leq k$. 

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Observe that a persistence module $M$ can be seen as a functor from $T$ (the category of $T$) to the category of $R$-modules. Moreover, persistence modules form a category whose morphisms are natural transformations between persistence modules. We denote the category of $T$-indexed 1-parameter persistence modules by $1\text{-mod}$.

Let us choose $T$ as $\mathbb{N}$ for the time being and define a special type of persistence modules:

**Definition 22.** A persistence module $M = \{M_i, \phi_{i,j}\}_{i,j \in \mathbb{N}}$ is of **finite type** if each $M_i$ is a finitely generated $R$-module, and each $\phi_{i,j}$ is an isomorphism for $j \geq i \geq m$ for some $m \in \mathbb{N}$.

Although we see the word module in the definition of persistence module, we have not given a module structure yet. Let us put that structure on $M = \{M_i, \phi_{i,j}\}_{i,j \in \mathbb{N}}$.

Consider the map $\phi_{i,j}$ as the shifting map denoted by

$$x^{j-i} : M_i \rightarrow M_j$$

for each $i \leq j \in \mathbb{N}$. Basically, $x^i$ corresponds to an $i$-shift upward in grading. Moreover, we take $R[x]$ with the standard grading, and we see a persistence module as a graded module over $R[x]$ thanks to the maps $x^i, i \in \mathbb{N}$. Formally, we define a map $\alpha$ taking a persistence module, and sending it to a graded module over $R[x]$:

$$\alpha(M) = \bigoplus_{i \in \mathbb{N}} M_i,$$

such that $R$ acts on $M_i$’s individually, and the action of $x$ is given by

$$x \cdot (m_0, m_1, m_2, \ldots) = (0, x(m_0), x(m_1), \ldots)$$

$$= (0, \phi_{0,1}^M(m_0), \phi_{1,2}^M(m_1), \ldots)$$

where $m_i \in M_i$ for all $i \in \mathbb{N}$.

We define a category of graded modules by taking morphisms as the module homomorphisms $f : M \rightarrow N$ such that $f(M_i) \subseteq N_i$ for all $i \in \mathbb{N}$. In fact, the map $\alpha$ gives the following equivalence when we restrict persistence modules to be of finite type:

**Theorem 2.4.1.** There exists an equivalence between the category of persistence modules indexed by $\mathbb{N}$ of finite type over $R$ and the category of finitely generated non-negatively graded modules over $R[x]$. 

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Thanks to Theorem 2.4.1, we can consider every persistence module indexed by \( \mathbb{N} \) of finite type over \( R \) with a module structure coming from a finitely generated non-negatively graded module over the polynomial ring \( R[x] \). In addition, a persistence module is finitely generated if and only if it is of finite type.

Now, there is a question to answer. How can we decompose a finitely generated graded module in a simple form? Here, the crucial point is the choice of \( R \). For instance, if we take \( R = \mathbb{Z} \), then we have a graded module over \( \mathbb{Z}[x] \). Finding a decomposition of a \( \mathbb{Z}[x] \)-module (or a graded module over \( \mathbb{Z}[x] \)) is extremely hard. Fortunately, we have a structure theorem coming from algebra which points out how to take \( R \):

**Theorem 2.4.2.** [28] Let \( D \) be a principal ideal domain. Then, every finitely generated \( D \)-module decomposes uniquely into cyclic \( D \)-modules in the following form:

\[
D^\beta \oplus \left( \bigoplus_{i=1}^{m} D/d_i D \right),
\]

where \( d_i \in D \) such that \( d_i/d_{i+1} \) and \( \beta \in \mathbb{Z} \). In a similar fashion, every finitely generated graded module \( M \) over a graded ring \( D \) which is a PID decomposes uniquely into the following form:

\[
\left( \bigoplus_{i=1}^{n} x^{\alpha_i} D \right) \oplus \left( \bigoplus_{j=1}^{m} x^{\gamma_j} D/d_j D \right)
\]

where \( d_j \in D \) are homogeneous such that \( d_j/d_{j+1} \) and \( \alpha_i, \gamma_j \in \mathbb{Z} \). Moreover, \( x^{\alpha} \) denotes an \( \alpha \)-shift upward in grading. In both cases, the left and right parts of the middle direct sum correspond to free portion and torsional portion, respectively.

Consider the set of polynomials given by \( \mathbb{k}[x] \) where \( \mathbb{k} \) is a field. It is an \( \mathbb{N} \)-graded ring with the usual polynomial addition and multiplication where \( R_i = \{ kx^i \mid k \in \mathbb{k} \} \). It is also a principal ideal domain (PID) since \( \mathbb{k} \) is a field. Therefore, if we take a finitely generated graded module \( M \) over \( \mathbb{k}[x] \), then by Theorem 2.4.2, \( M \) decomposes into the form:

\[
M \cong \left( \bigoplus_{i=1}^{n} x^{\alpha_i} \mathbb{k}[x] \right) \oplus \left( \bigoplus_{j=1}^{m} x^{\gamma_j} \mathbb{k}[x]/(x^{\beta_j}) \right).
\]

(2.1)

where \( \beta_j \geq 1 \). In other words, the reason behind working over polynomial ring with field coefficients is to obtain a PID, and further a simple decomposition for such persistence modules.
In Remark 2.2.1, we emphasized that if we apply homology functor to a filtration with field coefficients, then homology groups \( H_p(K_i) := M_i, i \in \mathbb{N} \) become vector spaces, and the maps \( f^{i,j}_p : M_i \rightarrow M_j \) are linear for all \( i, j \in \mathbb{N} \). That is to say each homology group becomes a \( k \)-module, and each linear map between them is a module homomorphism. Therefore, we obtain a persistence module.

From now on, we always consider homology with field coefficients. Thus, a persistence module means a collection of vector spaces and linear maps satisfying conditions given in Definition 21. This in turn implies that a persistence module can be seen as a functor from \( T \) to the category of vector spaces, \( \text{Vect} \), over a fixed field \( k \). Furthermore, in the rest of the thesis, for ease of computation, the field \( k \) is chosen as \( \mathbb{Z}_2 \).

Let \( M_1 \) and \( M_2 \) be two persistence modules indexed by the same totally ordered set \( T \). We can define a new persistence module by considering their direct sum given as:

\[
(M_1 \oplus M_2)_i = ((M_1)_i, (M_2)_i) \quad \text{and} \quad \varphi^{M_1 \oplus M_2}_{i,j} = (\varphi^{M_1}_{i,j}, \varphi^{M_2}_{i,j}).
\]

We can further generalize this for a family of persistence modules \( \{M_p | p \in J\} \) with the same index set \( T \) by considering their direct sums:

\[
M = \bigoplus_{p \in J} M_p \text{ where } M_i = \bigoplus_{p \in J} (M_p)_i.
\]

If the cardinality of \( J \) is infinite, then an element of \( M_i \) is a finite linear combination of elements of \( (M_p)_i \), that is,

\[
\bigoplus_{p \in J} (M_p)_i = \{c_1m_1 + \ldots + c_nm_n \mid \text{each } c_j \in k, m_j \in (M_p)_i \text{ for some } i \in J\}.
\]

We define the zero persistence module \( \mathbb{O} \) as the persistence module such that \( \mathbb{O}_i \) is the zero vector space for all \( i \in T \).

A persistence module \( M \) is said to be indecomposable if \( M \cong N_1 \oplus N_2 \) implies that \( N_1 \) or \( N_2 \) is the zero persistence module. \( M \) is called decomposable if it is not indecomposable.

**Definition 23.** [8] An interval \( I \) in \( T \) is a non-empty subset of \( T \) satisfying the condition: If \( i, j \in I \) and \( i \leq k \leq j \), then \( k \in I \).
Definition 24. [8] An interval module \( k_I \) is a persistence module \( \{M_i\}_{i \in T} \) satisfying the conditions:

i) \( M_k = k \) for \( k \in I \) and \( M_k = 0 \) else.

ii) For \( k \leq l \), \( \varphi_{k,l} = \text{id}_k \) where \( k, l \in I \) and \( \varphi_{k,l} \) is the zero map otherwise.

Theorem 2.4.3. [14] Let \( k_I \) be an interval module. Then, it is indecomposable.

Proof. The set of morphisms, \( \{\phi_s\}_{s \in T} \), from \( k_I \) to itself is the endomorphism ring of \( k_I \). Let us consider \( \phi_s \) for some \( s \in I \). It is a linear map from the field \( k \) to itself. So, it sends \( x \in k \) to \( \lambda x \) for some \( \lambda \in k \). Since all diagrams are commutative, when we fix \( \phi_s \) as a multiplication by \( \lambda \in k \), it implies each \( \phi_t \) is also a multiplication by the same \( \lambda \) for all \( t \in I \). Thus, \( \text{End}(k_I) \) is isomorphic to \( k \). Assume that \( k_I \) is decomposable such that \( k_I \cong N_1 \oplus N_2 \). Let \( \pi_1 \) be the projection of \( k_I \) to the first summand of its decomposition. Clearly, \( \pi_1 \in \text{End}(k_I) \) and \( \pi_1 \circ \pi_1 = \pi_1 \). Thus, \( \pi_1 \) is idempotent in \( k \). Since idempotents are just 0 and 1 in a field, \( \pi_1 \) is the zero or identity map. If \( \pi_1 = 0 \), then it implies \( N_1 = 0 \), and this gives a contradiction. If \( \pi_1 = \text{id}_{k_I} \), then it implies \( N_2 = 0 \) and this gives a contradiction. Therefore, \( k_I \) is indecomposable. \( \square \)

Our first aim, while working with 1-parameter persistence modules, is to decompose them as the sum of interval modules provided by Equation 2.1.

Theorem 2.4.4. [10] A persistence module indexed by \( \mathbb{N} \) of finite type over \( k \) is isomorphic to the direct sum of interval modules in the form:

\[
M \cong \bigoplus_{s=1}^{n} k_{I_s}
\]

where \( I_s = [i_s, j_s) \) for \( i_s \in \mathbb{N}, j_s \in \mathbb{N} \cup \{\infty\} \).

The index set in Theorem 2.4.4 can actually be extended to \( \mathbb{R} \) with suitable finiteness conditions (for more details, see [10, Proposition 3]).

Definition 25. [8,11] Let \( M \) be a persistence module.

i) \( M \) is pointwise finite dimensional (p.f.d. for short) if \( \dim(M_i) < \infty \) for all \( i \in \mathbb{N} \).
ii) $M$ is said to be **tame** if for all $i \in \mathbb{N}$, $\dim(M_i) < \infty$.

iii) If each linear map, $\varphi_{ij}^M$ for $i < j$, in the collection of $M$ has finite rank, then $M$ is called **q-tame**.

Clearly, for a persistence module, being p.f.d. is equivalent to being tame. Furthermore, every p.f.d. persistence module is q-tame, but the converse is not true.

**Remark 2.4.1.** The relation between a p.f.d. persistence module and a persistence module of finite type is the following: Every persistence module of finite type is p.f.d. but the converse is not true.

We stated that finite type persistence modules over $k$ indexed by $\mathbb{N}$ decompose into interval modules. The following result of Botnan and Lesnick [8] generalizes the result by extending the index set from $\mathbb{N}$ to $T$ and persistence modules from finite type to p.f.d. Thus, [8, Theorem 3.4] shows that 1-parameter p.f.d. persistence modules are also interval decomposable:

**Theorem 2.4.5.** [8] Let $M$ be a p.f.d. persistence module indexed by $T$. Then, $M$ decomposes into interval modules in the following way: There exists a unique multiset $B(M)$ consisting of intervals such that

$$M \cong \bigoplus_{I \in B(M)} k_I.$$

The multiset $B(M)$ is one of our meaningful summaries which is called the **barcode** of $M$.

We can observe that if we have a p.f.d. indecomposable persistence module, then it is an interval module. Hence, being indecomposable and being an interval module are equivalent for a p.f.d. persistence module. In addition, the following theorem reveals that the multiset $B(M)$ is unique up to order.

**Theorem 2.4.6.** [12] (Krull–Remak–Schmidt–Azumaya) Suppose that a persistence module $M$ indexed by $T$ can be decomposed into interval modules in two different ways:

$$M \cong \bigoplus_{I \in L} k_I \cong \bigoplus_{I \in K} k_I.$$

Then, there is a bijection $\sigma : L \to K$ such that $I_l = I_{\sigma(l)}$ for all $l$. 

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The result of Theorem 2.4.5 is also obtained in the work of Dey and Wang [15]. They stated that the result comes from a more general concept called quiver theory and gives the result in the following form:

**Proposition 2.4.7.** [15] Any p.f.d. persistence module $M$ indexed by $T$ decomposes uniquely into interval modules:

$$M \cong \bigoplus_{j \in J} k_{(b_j, d_j)}$$

where $(b_j, d_j)$ stands for one of the intervals: $[b_j, d_j]$, $[b_j, d_j)$, $(b_j, d_j]$, $(b_j, d_j)$.

Although, a $q$-tame persistence module is not necessarily p.f.d, we have a similar result for $q$-tame persistence modules.

**Proposition 2.4.8.** [15] Any $q$-tame persistence module indexed by $T$ decomposes uniquely into interval modules.

Let us put together what we did so far. We start with a filtration indexed by $\mathbb{N}$ obtained from the initial data. Then, we apply homology functor with field coefficients to this filtration. So, we get a persistence module. If it is pointwise finite dimensional, then we see that it is decomposed into interval modules. Since our indices comes from $\mathbb{N}$, all interval modules in the decomposition are of the form $[i, j)$ which means a homology class is born at $i$-th level, and dies at $j$-th level. We usually work on this case, but the theory can be extended to the index set $T \subseteq \mathbb{R}$.

From the beginning, understanding the shape of data is our main aim. This also covers how we can make a distinction among them, and the answer is that we can examine the corresponding persistence modules. Another question arises from here: Is there any complete invariant for 1-parameter setting? First of all, an **invariant** means a function from a set of structures, such as graded modules, to some set sending isomorphic structures to the same value. Moreover, we say an invariant is **complete** if it always assigns different values to non-isomorphic structures.

In our case, the structure set is the set of p.f.d. persistence modules and we send them to their barcodes. With this construction, the barcode is a complete invariant. Thus, if barcodes of two persistence modules are not equal to each other, then we can
conclude that they are not isomorphic. Moreover, the computation of the barcode is independent from the underlying field of a persistence module.

In Theorem 2.4.5 we defined the barcode of a persistence module. The other well-known meaningful summary is the persistence diagram. Actually, a barcode and a persistence diagram are very useful to visualize the persistent homology. If we work on a p.f.d. persistence module indexed by \( \mathbb{N} \), then we can define the persistence diagram of it as follows:

**Definition 26.** [16] The \( p \)-th persistence diagram is a multiset of points in the extended real plane, \( \bar{\mathbb{R}}^2 \), and it is denoted as \( \text{Dgm}_p(M) \) for a persistence module \( M \). We draw a point at \((i, j)\) if \( \mu_{i,j}^p > 0 \). When the multiplicity increases, we make those points slightly bigger. If a class is born at \( K \), and never dies, then we draw a point at \((i, \infty)\) where the second coordinate can be putted thanks to the extension of \( \mathbb{R}^2 \). The index persistence of a class is the vertical distance of the point to the diagonal.

**Example 2.4.1.** [13] Consider the surface \( M \) in \( \mathbb{R}^3 \) given by Figure 2.2. The filtration function \( f : M \to \mathbb{R} \) is defined by a projection onto the value of \( z \)-coordinate. This is an example of a height function, and we can construct the filtration by choosing \( M_a = f^{-1}(-\infty, a] \) for all \( a \in \mathbb{R} \).

The vertical red bars correspond to the lifespans of 0-dimensional homology classes. The first homology class appears when \( M_a \) is non-empty for the first time for some
$a \in \mathbb{R}$, and it never vanishes. On the other hand, after the second homology class emerges, it merges with the former when the subspace becomes connected, and stops at that level because of the Elder Rule.

We can also understand the behaviour of 1-dimensional homology classes. When $a$ is near enough to $a_1$, $F_a$ is homeomorphic to two disjoint solid disks. Thus, we do not have any 1-dimensional class. For $a = a_i$ where $i \in \{1, 2, 3\}$, there exists a 1-cycle, $\sigma_i$, creating 1-dimensional homology class. Observe that $\sigma_3$ is filled when $a = a_4$, so the homology class born at $a_3$ dies at $a_4$. The other two cycles are never filled; indeed, they span $H_1(M)$. This process is shown by the vertical blue bars.

After finding the barcode of $M$ for 0 and 1-dimensional persistent homology, we know birth and death places of each classes. Thus, we can obtain the corresponding persistence diagrams, and show in a single diagram as in Figure 2.2 where the red and blue points represent the 0th and 1st dimensional homology classes, respectively. Moreover, the level of $a$ for which $M$ is fully obtained in the filtration gives the points having infinite lifespan.

We can find $\beta^{i,j}_p$ from persistence diagram by considering the upper, left quadrant of the point $(i, j)$. The quadrant is closed along its vertical right side since we can consider classes die at $K_{k}$ such that $j < k$, while the horizontal lower side is not included since if some class dies at $K_{j}$, then it cannot be counted for $\beta^{i,j}_p$. The number of points with their multiplicities is equal to $\beta^{i,j}_p$. Let us see this situation in the following lemma:

**Lemma 2.4.9.** [16] Let $K_0 \subseteq K_1 \subseteq \cdots \subseteq K_n$ be a filtration. For $0 \leq i \leq j \leq n$ and every dimension $p$,

$$\beta^{i,j}_p = \sum_{k \leq i} \sum_{j \leq l} \beta^{k,l}_p.$$

**Remark 2.4.2.** If we work on a p.f.d. persistence module indexed by arbitrary subset $T$ of $\mathbb{R}$, then its decomposition can consist of the intervals of the form $[b_j, d_j]$, $[b_j, d_j)$, $(b_j, d_j]$, $(b_j, d_j)$. When we pass to the persistence diagram, showing all of these four different intervals with the same point $(b_j, d_j) \in \bar{\mathbb{R}}^2$ is one of the ways. However, this implies that two non-isomorphic barcodes can have the same persistence diagram. If we want to get rid of this situation, then we insert these intervals into persistence
diagrams by attaching different tick directions depending on the form of the interval. For further details, see [12].

If we work on our classical way (i.e. p.f.d. persistence modules indexed by \( \mathbb{N} \)), then barcodes and persistence diagrams are equivalent to each other, hence the persistence diagram is also a complete invariant on them.

We have seen how to obtain a persistence module by starting from a filtration. Then, we have seen two meaningful summaries to visualize persistent homology: a barcode and a persistence diagram. Now, what are the other ways to compare two persistence modules? One of the answers is that we can define a distance between two persistence modules, and try to draw some conclusions about whether they are isomorphic or not. Furthermore, we can also classify non-isomorphic ones with respect to the distance. In this part of the thesis, we discuss two well-known distances: the bottleneck and the interleaving distances.

2.5 The Bottleneck Distance in 1-Parameter

We give the definition of the bottleneck distance by following [6]: Let us start with two p.f.d. persistence modules \( M \) and \( N \). Then, according to Theorem 2.4.5, we can write both modules as sums of interval modules constructing the barcodes \( C \) and \( D \) of \( M \) and \( N \), respectively. Thanks to the relation between a barcode and a persistence diagram, we can also see elements of the multisets \( C \) and \( D \) in their persistence diagrams. Then, we define a matching \( \mathcal{X} \) between \( C \) and \( D \) which is a bijection \( \sigma : C' \rightarrow D' \) between \( C' \subseteq C \) and \( D' \subseteq D \). Moreover, if we do not see an element of \( C \) or \( D \) in the bijection \( \sigma \), then the element is called unmatched, and we match this element with its nearest point on the diagonal, \( \{(x, x) \mid x \in \mathbb{R}\} \), of the persistence diagrams.

Define the cost \( c(I, J) \) of a matching between \( I = (a, b) \in C' \) and \( J = (c, d) \in D' \) as

\[
c(I, J) = \max(|c - a|, |d - b|).
\]

If \( I = (a, b) \) is unmatched, then define the cost of \( I \) as \( c(I) = (b - a)/2 \). We define
the cost of a matching $\mathcal{X}$, $c(\mathcal{X})$, in the following way:

$$c(\mathcal{X}) := \max \left( \sup_{(I,J) \in \mathcal{X}} c(I,J), \sup_{I \in \mathcal{C} \cup \mathcal{D} \text{ unmatched}} c(I) \right).$$

We say that $\mathcal{X}$ is an $\epsilon$-matching if $c(\mathcal{X}) \leq \epsilon$.

**Definition 27.** [8] The bottleneck distance between $\mathcal{C}$ and $\mathcal{D}$ is defined as

$$d_B(\mathcal{C}, \mathcal{D}) := \inf \{ c(\mathcal{X}) \mid \mathcal{X} \text{ is a matching between } \mathcal{C} \text{ and } \mathcal{D} \}.$$ 

Equivalently, we can define $d_B(C, D)$ as:

$$d_B(C, D) = \inf \{ \epsilon \in [0, \infty] \mid \text{there exists an } \epsilon\text{-matching between } C \text{ and } D \}.$$ 

We give the definition as the bottleneck distance between barcodes of $M$ and $N$. It is also equivalent to saying the bottleneck distance between $M$ and $N$, i.e.,

$$d_B(M, N) := d_B(C, D).$$

**Remark 2.5.1.** To find the bottleneck distance between two persistence modules, their barcodes must exist, and we satisfy this condition by working on p.f.d. persistence modules. However, this does not mean that we can find the bottleneck distance only for p.f.d. ones. For instance, the definition can be extended to q-tame persistence modules because of Proposition [2.4.8](#).

The importance of the bottleneck distance comes from the fact that it is stable under small perturbations of the filtration function or the starting set of points. That is, the perturbations cause smaller difference in terms of the bottleneck distance. Let us see the stability of $d_B$ in detail:

Let $X$ be a topological space with two filtration functions $f, g : X \to \mathbb{R}$. Then, define the corresponding persistence modules $M^f$ and $M^g$ as

$$M^f_j := H_i(f^{-1}(-\infty, j]) \quad M^g_j := H_i(g^{-1}(-\infty, j]).$$

where $j \in \mathbb{R}$ and $i \in \mathbb{N}$ is fixed. Assume that both of the persistence modules are p.f.d. so that they decompose into interval modules. Therefore, we can pass through the barcodes of them, namely $B(M^f)$ and $B(M^g)$ and see the stability feature:
Theorem 2.5.1. \cite{6} The bottleneck distance satisfies the following:

\[ d_B(B(M^f), B(M^g)) \leq ||f - g||_{\infty} \]

where \( ||f - g||_{\infty} := \sup_{x \in X} |f(x) - g(x)| \).

Let P and Q be two finite set of points in \( \mathbb{R}^n \) having the same cardinality. Then, we construct Vietoris-Rips complexes: \( Rips(P)_\epsilon, Rips(Q)_\epsilon \) with the same \( \epsilon \in \mathbb{R} \) values. After applying homology functor, we obtain two persistence modules. With the assumption making them pointwise finite dimensional, we have the barcodes:

\[ B(H_i(Rips(P))), B(H_i(Rips(Q))) \]

where \( i \in \mathbb{N} \) is fixed, and give the stability of the bottleneck distance between them:

Theorem 2.5.2. \cite{6} For any bijection \( \sigma : P \to Q \) such that \( ||p - \sigma(p)|| \leq \epsilon \) for all \( p \in P \), we have

\[ d_B(B(H_i(Rips(P))), B(H_i(Rips(Q)))) \leq \epsilon. \]

We find the bottleneck distance between two barcodes (or equivalently persistence diagrams) of persistence modules. Instead, we can directly work on persistence modules, and look for a different distance structure.

2.6 The Interleaving Distance in 1-Parameter

We first introduce an \( \epsilon \)-interleaving between two \( \mathbb{R} \)-indexed persistence modules \( M \) and \( N \) from a categorical point of view for \( \epsilon \in [0, \infty) \).

Define a shift functor \((-)(\epsilon) : \textit{1-mod} \to \textit{1-mod}\) by

\[ M(\epsilon)_i = M_{i+\epsilon} \quad \text{and} \quad \phi_{i,j}^{M(\epsilon)} = \phi_{i+\epsilon,j+\epsilon}^{M}. \]

For a morphism \( \alpha : M \to N \), we define \( \alpha(\epsilon) : M(\epsilon) \to N(\epsilon) \) in the following way:

\[ \alpha(\epsilon)_i = \alpha_{i+\epsilon}. \]

The internal morphisms \( \phi_{i,i+\epsilon}^{M(\epsilon)} : M_i \to M_{i+\epsilon} \) form a morphism from \( M \) to \( M(\epsilon) \).

Definition 28. \cite{8,23} We say that \( M \) and \( N \) are \( \epsilon \)-interleaved if there exists morphisms

\[ \phi : M \to N(\epsilon) \quad \psi : N \to M(\epsilon) \]
such that the following diagrams commute for all $i \leq j$:

$$\begin{align*}
M_i \xrightarrow{\phi_i} M_{i+\epsilon} & \quad M_i \xrightarrow{\phi_{i+\epsilon}} M_{i+2\epsilon} \\
N_{i+\epsilon} & \quad N_{i+\epsilon} \xrightarrow{\psi_{i+\epsilon}} N_{i+2\epsilon}
\end{align*}$$

Alternatively, it can also be stated as follows: There exists an $\epsilon$-interleaving between $M$ and $N$ if there are two collections of linear maps

$$\{\phi_i : M_i \to N_{i+\epsilon}\}_{i \in \mathbb{R}}, \{\psi_i : N_i \to M_{i+\epsilon}\}_{i \in \mathbb{R}}$$

making the triangle diagrams given above and the following parallelogram diagrams commutative:

$$\begin{align*}
M_i \xrightarrow{\phi_i} M_{i+\epsilon} & \quad M_i \xrightarrow{\phi_{i+\epsilon}} M_{i+2\epsilon} \\
N_{i+\epsilon} \xrightarrow{\psi_{i+\epsilon}} N_{i+2\epsilon} & \quad N_{i+\epsilon} \xrightarrow{\psi_i} N_{i+2\epsilon}
\end{align*}$$

Indeed, $\epsilon$-interleaved relation measures how far two persistence modules from being isomorphic. The next proposition is well-known in PH and easy to see.

**Proposition 2.6.1.** $M$ and $N$ are isomorphic persistence modules if and only if they are $0$-interleaved.

The following proposition is also well-known for which we provide our proof.

**Proposition 2.6.2.** If two persistence modules $M$ and $N$ are $\epsilon$-interleaved, then they are also $\delta$-interleaved for all $\delta > \epsilon$.

**Proof.** Define two linear maps $\phi'_i : M_i \to N_{i+\delta}$, $\psi'_i : N_i \to M_{i+\delta}$ as the following compositions:

$$\begin{align*}
M_i \xrightarrow{\phi_i} N_{i+\epsilon} & \quad M_i \xrightarrow{\phi'_i} M_{i+\delta} \\
N_{i+\epsilon} \xrightarrow{\psi'_i} N_{i+\delta} & \quad N_{i+\epsilon} \xrightarrow{\psi_i} N_{i+\delta}
\end{align*}$$
With varying $i \in \mathbb{R}$, we have two morphisms $\phi' : M \to N(\delta)$, $\psi' : N \to M(\delta)$. We need to show triangle diagrams in the Definition 28 commutes. Observe that the following diagram commutes:

```
M_i \xrightarrow{\phi_i} M_{i+2\epsilon} \xrightarrow{\psi_{i+\epsilon}} M_{i+\epsilon+\delta} \xrightarrow{\psi_{i+\delta}} M_{i+2\delta}
```

This implies that

```
M_i \xrightarrow{\phi'_i} M_{i+2\delta}
```

commutes. In a similar way,

```
N_i \xrightarrow{\psi_i} N_{i+\epsilon} \xrightarrow{\phi_{i+\epsilon}} N_{i+\epsilon+\delta} \xrightarrow{\phi_{i+\delta}} N_{i+2\delta}
```

commutes. Thus,

```
N_i \xrightarrow{\psi'_i} N_{i+2\delta}
```

also commutes. Thus, $M$ and $N$ are $\delta$-interleaved.

**Definition 29.**[15] Let $M$ and $N$ be two $\mathbb{R}$-indexed persistence modules. We define their **interleaving distance** $d_I(M, N)$ as

$$d_I(M, N) := \inf \{ \epsilon \mid M \text{ and } N \text{ are } \epsilon\text{-interleaved} \}.$$  

If no such $\epsilon$ exists, then define $d_I(M, N) = \infty$. In this case, we also say they are $\infty$-interleaved.

We need to emphasize that being 0-interleaved and having interleaving distance as 0 are not the same thing. If the interleaving distance of two persistence modules, $M$
and $N$, is 0, then we cannot guarantee that they are 0-interleaved. So, $d_I(M, N) = 0$ does not imply $M$ and $N$ are isomorphic in all cases.

**Example 2.6.1.** Let $M$ and $N$ be two persistence modules such that $M_0 = \mathbb{Z}_2, M_i = 0$ for all $i \in \mathbb{R} \setminus \{0\}$ and $N_i = 0$ for all $i \in \mathbb{R}$. Then, they are not isomorphic, but $d_I(M, N) = 0$. As a second example, consider interval modules $\mathbb{I}_{(3,5)}$ and $\mathbb{I}_{[3,5)}$. Although the interleaving distance between them is 0, they are not isomorphic.

**Definition 30.** An extended pseudometric on some set $X$ is a function $d : X \times X \rightarrow [0, \infty]$ satisfying the followings:

i) $d(x, x) = 0$ for all $x \in X$.

ii) $d(x, y) = d(y, x)$ for all $x, y \in X$.

iii) $d(x, z) \leq d(x, y) + d(y, z)$ for all $x, y, z \in X$ where $d(x, y), d(y, z) < \infty$.

An extended metric is an extended pseudometric with an additional property: If $d(x, y) = 0$, then $x = y$. Moreover, the word "extended" is added since distance can be $\infty$.

Our last example implies that the interleaving distance is an extended pseudometric on persistence modules indexed by $\mathbb{R}$. On the other hand, if we work on such modules indexed by $\mathbb{N}$, and exclude classes born and died at the same time, then $d_I$ is an extended metric.

Throughout this thesis, the word "distance" always means an extended pseudometric.

The following proposition shows how the interleaving distance changes when we take direct sums of persistence modules.

**Proposition 2.6.3.** Let $M_1, M_2, N_1$ and $N_2$ be persistence modules. Then,

$$d_I(M_1 \oplus M_2, N_1 \oplus N_2) \leq \max(d_I(M_1, N_1), d_I(M_2, N_2)).$$

Moreover, for two families of persistence modules $\{M_p \mid p \in J\}$ and $\{N_p \mid p \in J\}$ where each persistence module is indexed by $\mathbb{R}$, let us take

$$M = \bigoplus_{p \in J} M_p \text{ and } N = \bigoplus_{p \in J} N_p,$$
then we have
\[ d_I(M, N) \leq \sup \{ d_I(M_p, N_p) \mid p \in J \}. \]

The interleaving distance and the bottleneck distance have different constructions, and we want to find a relation between them: Are they equal to each other? If not, can we say that one of them is always bigger than the other? These are natural questions, and to answer these questions, we need more.

**Proposition 2.6.4.** [12] Let \( I = \langle a, b \rangle, J = \langle c, d \rangle \) be two intervals and \( k_I, k_J \) be the corresponding interval modules. Then, we have
\[ d_I(k_I, k_J) \leq c(I, J) = \max( |c - a|, |d - b| ) \]
where the right hand side of the inequality comes from a matching between \( I \) and \( J \) in the process to find the bottleneck distance. We can also consider \( I \) is unmatched as another case, i.e., it is matched with its nearest point on the diagonal. Thus, we have the following analogous equality:
\[ d_I(k_I, \mathcal{O}) = c(I) = \frac{1}{2}(b - a) \]
where \( \mathcal{O} \) is the zero persistence module.

Now, we are ready to give the main result of 1-parameter persistent homology.

**Theorem 2.6.5. (The Isometry Theorem)** [22] Theorem 3.4] Let \( M \) and \( N \) be two p.f.d. persistence modules. Then,
\[ d_I(M, N) = d_B(B(M), B(N)). \]

In the literature, the inequality \( d_B(B(M), B(N)) \leq d_I(M, N) \) is called the algebraic stability theorem, and the converse inequality \( d_I(M, N) \leq d_B(B(M), B(N)) \) is said to be the converse algebraic stability theorem.

**Proof.** [12] Let us show that \( d_I(M, N) \leq d_B(B(M), B(N)) \). Since \( M \) and \( N \) are pointwise finite dimensional,
\[ M = \bigoplus_{i \in L_1} k_{I_i} \text{ and } N = \bigoplus_{j \in L_2} k_{J_j}, \]
where \( I_i \in B(M) \) and \( J_j \in B(N) \). Let \( \mathcal{X} \) be a matching between the barcodes \( B(M) \) and \( B(N) \) where its cost equals to \( \epsilon \). We have three cases:
i) If $I_i$ and $J_j$ are matched, then from Theorem 2.6.4, $d_I(k_{I_i}, k_{J_j}) \leq c(I_i, J_j) \leq \epsilon$.

ii) If $I_i$ is unmatched, then from Theorem 2.6.4, $d_I(k_{I_i}, \emptyset) = c(I_i) \leq \epsilon$. Moreover, for each unmatched interval module, add the zero persistence module $\emptyset$ to the direct sum decomposition of $N$ by adding a new index to $L_2$.

iii) If $J_j$ is unmatched, then from Theorem 2.6.4, $d_I(\emptyset, k_{J_j}) = c(J_j) \leq \epsilon$. Moreover, for each unmatched interval module, add $\emptyset$ to the direct sum decomposition of $M$ by adding a new index to $L_1$.

Therefore, index sets in the direct sums become same in terms of cardinality, call it $L$. So, after reindexing interval modules with respect to matched ones, we have

$$M = \bigoplus_{i \in L} k_{I_i} \text{ and } N = \bigoplus_{i \in L} k_{J_i}$$

where $d_I(k_{I_i}, k_{J_i}) \leq \epsilon$ for all $i \in L$. Thus, by Theorem 2.6.3, $d_I(M, N) \leq \epsilon$. Since the bottleneck distance is the infimum of $\epsilon$ values, $d_I(M, N) \leq d_B(B(M), B(N))$.

Another proof for the converse algebraic stability theorem is done by Lesnick [22]. The proof of the algebraic stability theorem is given by Chazal, Cohen-Steiner, Glisse, Guibas and Oudot [12] (also see the work of Bauer and Lesnick [3]).

We have seen that the bottleneck distance is stable, and the interleaving distance is an extended pseudometric. Since these distances are equal to each other for p.f.d. persistence modules, we conclude that they are both stable and extended pseudometrics.
CHAPTER 3

MULTIPARAMETER PERSISTENT HOMOLOGY

There is an obvious question to answer: Why do we need to construct multiparameter persistent homology? Why 1-parameter construction is not enough for us? One of the main reasons is that 1-parameter persistence is not robust to outliers. Consider finite set of points in $\mathbb{R}^n$. If we add some points as noise, then the persistent homology of the new set of points can be significantly different from the persistent homology of the former.

Let us see this situation in an example, see Figure 3.1 given by Botnan and Lesnick [8]. As demonstrated, by adding finitely many outliers, the barcode changes a lot. Before adding outliers, we can easily detect the circular shape of the data from the long bar by applying the first homology functor. However, after adding them, we cannot see such a long bar in the barcode, so we cannot determine the circular shape of the data although it still has that shape. To handle outliers in our data, we need to pass through multiparameter persistent homology by introducing new parameters such as the density parameter, that is, a function taking greater value in dense regions of the data than sparse regions of it. With the help of new parameters, we understand the shape of the data with higher density, and we can get rid of the complexity coming from outliers.

In many applications of persistent homology, one parameter is not enough to make full analysis. To extend definitions of filtration and persistence module, let us give the necessary background:

Let $P_1, P_2, \ldots, P_n$ be posets. Define the product poset $P_1 \times P_2 \times \ldots \times P_n$ as

$$(x_1, x_2, \ldots, x_n) \preceq (y_1, y_2, \ldots, y_n) \text{ if and only if } x_i \leq y_i \text{ for all } i \in \{1, 2, \ldots, n\}.$$ 

**Definition 31.** [8] An interval $I$ in a poset $P$ is a non-empty subset of $P$ satisfying
the followings:

i) If $i, j \in I$ and $i \leq k \leq j$, then $k \in I$.

ii) If $i, j \in I$, then there are $i = k_0, k_1, \ldots, k_n = j \in I$ such that $k_s$ and $k_{s+1}$ are comparable for all $s \in \{0, 1, \ldots, n\}$.

**Example 3.0.1.** Consider three subsets shown in Figure 3.2.

![Figure 3.2](image)

**Figure 3.2**: Subsets of $\mathbb{R}^2$ given in the plane with specified points and the line $L$.  

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i) $I_1$ is not an interval in $\mathbb{R}^2$ since $a, b \in I_1$ and $a \leq c \leq b$, but $c \notin I_1$. We also see this situation by the restriction of $L$ to $I_1$. It has two disconnected components implying our result.

ii) $I_2$ is an interval.

iii) $I_3$ is not an interval because although $d, e \in I_3$, there exists no elements $\{k_i\}_{i=0}^n$ of $I_3$ making second condition satisfied.

As in 1-parameter, intervals are one of our main interests. However, intervals are more complicated in multiparameter case and to obtain particular results, we sometimes consider their subsets such as rectangles:

**Definition 32.** [8] A rectangle in $T_1 \times \ldots \times T_n$ is an interval of the form $I_1 \times \ldots \times I_n$, where $I_i$ is an interval in totally ordered set $T_i$ for all $i \in \{1, \ldots, n\}$.

### 3.1 Multiparameter Filtration and Its Examples

**Definition 33.** [8] Let $\text{Top}$ be the category of topological spaces and $P$ be a poset. Then, a $P$-indexed filtration is a functor $F : P \to \text{Top}$ such that $F_x \subseteq F_y$ for all $x \leq y \in P$ where $F_x := F(x)$. If we take $P = T_1 \times T_2 \times \ldots \times T_n$ where each $T_i$ is a totally ordered set for all $i \in \{0, 1, \ldots, n\}$, then we call $F$ a multiparameter or $n$-parameter filtration.

In fact, Definition 33 is a generalization of a 1-parameter filtration (Definition 1).

**Example 3.1.1.** For a topological space $K$, we consider the sublevel set filtration $S(f) : P \to \text{Top}$ via a not necessarily continuous function $f : K \to P$ defined as $S(f)_p := \{k \in K \mid f(k) \leq p\}$. For instance, the diagram of the 2-parameter sublevel set filtration $S(f) : \mathbb{N} \times \mathbb{N} \to \text{Top}$ can be seen as follows:

$$
\begin{array}{cccc}
\vdots & \vdots & \vdots \\
F_{0,2} & \hookrightarrow & F_{1,2} & \hookrightarrow & F_{2,2} & \hookrightarrow & \ldots \\
\uparrow & & \uparrow & & \uparrow & & \uparrow \\
F_{0,1} & \hookrightarrow & F_{1,1} & \hookrightarrow & F_{2,1} & \hookrightarrow & \ldots \\
\uparrow & & \uparrow & & \uparrow & & \uparrow \\
F_{0,0} & \hookrightarrow & F_{1,0} & \hookrightarrow & F_{2,0} & \hookrightarrow & \ldots \\
\end{array}
$$
Figure 3.3: Degree-Rips bifiltration where degree parameter is 4, 3, 1 from left to right, [8].

It’s time to see a few constructions for bifiltrations where number of parameters is 2, and $(X, d_X)$ is a finite metric space.

**Example 3.1.2.** [8] Let us give the **degree-Rips bifiltration**, $DRips(X)$. We have two parameters: $\epsilon$ is a scale parameter, and $d$ is a degree parameter. $DRips(X)_{d,\epsilon}$ is a maximal subcomplex of $Rips(X)_\epsilon$ only including vertices have degree at least $d - 1$ in the 1-skeleton of $Rips(X)_\epsilon$. For an illustration, see Figure 3.3.

**Example 3.1.3.** [8,23] Let $f : X \to \mathbb{R}$ be a function. The **sublevel-Rips bifiltration** obtained from $f$ is the function $Rips_{sub}(f) : \mathbb{R} \times [0, \infty) \to \text{Simp}$ defined as

$$Rips_{sub}(f)_{a, \epsilon} := Rips(f^{-1}(-\infty, a])_\epsilon,$$

where $a \in \mathbb{R}$ is the parameter changing the data set of points with the inverse image of $f$, and $\epsilon \in [0, \infty)$ is the scale parameter of the Vietoris-Rips complex. In addition, $\text{Simp}$ shows the category of simplicial complexes.

Similarly, the **superlevel-Rips bifiltration** obtained from $f$ is the function $Rips_{super}(f) : \mathbb{R}^{op} \times [0, \infty) \to \text{Simp}$ defined as

$$Rips_{super}(f)_{a, \epsilon} := Rips(f^{-1}[a, \infty))_\epsilon.$$
The crucial part of the above filtrations is the choice of \( f \). For instance, we can choose \( f \) as \( f_r : X \to \mathbb{R} \) defined by

\[
f_r(x) = \left| \{ y \in X \mid d_X(x, y) \leq r \} \right|,
\]

where \( r > 0 \) is fixed. Moreover, \( f_r \) is a density function, and in general, the superlevel-Rips bifiltration obtained from a density function is called a **density-Rips bifiltration**.

**Remark 3.1.1.** Choosing a different \( r > 0 \) in the construction of \( f_r \) can change function values. This dependency on \( r \) can lead to deficiencies in the usage of the density-Rips bifiltration. On the other hand, the degree-Rips bifiltration does not have such a dependency. In addition, we can define the degree-Rips bifiltration by using \( f_r \), but this time \( r \) is not fixed, and it equals to the scale parameter, \( \epsilon \), of Vietoris-Rips complex.

For another example, define \( f : X \to \mathbb{R}^+ \cup \{0\} \) by

\[
f(x) = \frac{1}{|X|} \sum_{y \in X} d_X(x, y),
\]

where \(|X|\) is the number of the elements of \( X \). Thus, \( f \) gives the average distance of \( x \) to the points of \( X \). It is said to be an eccentricity function, and we call the superlevel-Rips bifiltration obtained from \( f \) as the **eccentricity-Rips bifiltration**.

Instead of using sublevel or superlevel filtrations, we can take the inverse image of the function on finite intervals. By this way, we can define a trifiltration. To do that, start with the set \( I = \{(a, b) \mid a \leq b\} \) where \( a, b \in \mathbb{R} \). So, \( I \) can be seen as a poset with the poset relation induced by \( \mathbb{R}^{op} \times \mathbb{R} \).

**Example 3.1.4.** [8] Let \( f : X \to \mathbb{R} \) be a function. The **interval-Rips trifiltration** \( \text{Rips}(f)_{(a,b),\epsilon} : I \times [0, \infty) \to \text{Simp} \) is defined as

\[
\text{Rips}(f)_{(a,b),\epsilon} := \text{Rips}(f^{-1}[a, b])_\epsilon.
\]

**Example 3.1.5.** [23] We have another bifiltration method called the **multi-cover bifiltration** defined as follows: Let \( X \subseteq \mathbb{R}^n \) be finite, and \( \text{Cov}(X) : \mathbb{N}^{op} \times \mathbb{R} \to \text{Top} \) be

\[
\text{Cov}(X)_{k,\epsilon} = \{ y \in \mathbb{R}^n \mid \exists k \text{ points } \{ x_i \}_{i=1}^k \in X \text{ such that } \| y - x_i \| \leq \epsilon, \forall i \in T \},
\]

where \( T = \{1, \ldots, k\} \).
Before our last example for a multiparameter filtration, let us define the barycentric subdivision of a simplicial complex $K$. Then its barycentric subdivision, denoted by $\text{bary}(K)$, is an abstract simplicial complex whose $(k-1)$-simplices are of the form $\{\sigma_1, \sigma_2, \ldots, \sigma_k\}$ where each $\sigma_i$ is a simplex of $K$ such that $\sigma_i \subset \sigma_{i+1}$ for all $i \in \{1, 2, \ldots, k-1\}$. Observe that we are taking simplices of $K$ as vertices of $\text{bary}(K)$.

**Example 3.1.6.** [8] For $m \in \mathbb{N}^+$, define $S(K)_m$ as the maximal subcomplex of $\text{bary}(K)$ such that vertices of $S(K)_m$ are only the simplices of $K$ with dimension at least $m-1$. With varying $m$, corresponding subcomplexes give a $(\mathbb{N}^+)^{\text{op}}$ filtration in 1-variable.

To construct the subdivision-Rips bifiltration, start with $X$. Consider the Vietoris-Rips complexes with scale parameter $\epsilon$. For each $\text{Rips}(X)_\epsilon$, pass through its barycentric subdivision. Then, include the second parameter $m$ assigning subcomplexes of $\text{bary}(\text{Rips}(X)_\epsilon)$. So, we obtain the **subdivision-Rips bifiltration** given as

$$\text{bary}(X)_{\epsilon,m} : [0, \infty) \times (\mathbb{N}^+)^{\text{op}} \to \text{Simp}.$$

### 3.2 Multiparameter Persistence Module

**Definition 34.** [8] Let $\text{Vect}$ be the category of $k$-vector spaces where morphisms correspond to linear maps. For $(P, \leq)$ a poset, a $P$-indexed persistence module is a functor $M : P \to \text{Vect}$. Define $M_i := M(i)$. For $i \leq j$, $\varphi_{i,j}^M$ denotes the linear map $M_i \to M_j$. If we take $P = T_1 \times T_2 \times \ldots \times T_n$ where each $T_i$ is a totally ordered
set for all \( i \in \{0, 1, \ldots, n\} \), then we call \( M \) a **multiparameter** or an **\( n \)-parameter persistence module**. Furthermore, they form a category shown by **\( n \)-mod** where morphisms are taken as natural transformations.

In 1-parameter case, we defined persistence module as a collection of \( R \)-modules where \( R \) is a ring. Then, we took \( R = \mathbb{k} \) to obtain results, and we had \( \mathbb{k} \)-vector spaces in the collection of a persistence module like in this situation. In fact, if we take \( n = 1 \) in Definition 34, then it becomes the same definition in 1-parameter case in which we choose \( R = \mathbb{k} \).

**Example 3.2.1.** If we apply homology functor to the filtration obtained in the Example 3.1.1 then we obtain the persistence module \( M : \mathbb{N} \times \mathbb{N} \rightarrow \text{Vect} \) with the following commutative diagram:

\[
\begin{array}{ccc}
   & & \\
   & \uparrow & \\
M_0,2 & \rightarrow & M_1,2 \rightarrow & M_2,2 \rightarrow & \ldots \\
   & \uparrow & \\
   & \uparrow & \\
M_0,1 & \rightarrow & M_1,1 \rightarrow & M_2,1 \rightarrow & \ldots \\
   & \uparrow & \\
M_0,0 & \rightarrow & M_1,0 \rightarrow & M_2,0 \rightarrow & \ldots \\
\end{array}
\]

So, the pipeline of multiparameter persistent homology is the same as 1-parameter case. After starting with a multiparameter filtration, we apply homology functor and we obtain corresponding multiparameter persistence module.

We directly extend definitions of graded rings and modules introduced in \([15]\) and \([16]\) to \( n \)-parameter setting by taking \( T = T_1 \times T_2 \times \ldots \times T_n \) where each \( T_i \) is a totally ordered set.

For the present, we take \( T = \mathbb{N}^n \) or \( \mathbb{Z}^n \). Linear maps of a persistence module \( M \), namely \( \varphi^M_{i,j}, \, i \leq j \in T \), can be seen as a map

\[
x^{j-i} = x_1^{j_1-i_1}x_2^{j_2-i_2}\ldots x_n^{j_n-i_n} : M_i \rightarrow M_j.
\]
These maps give the structure of a graded module:

\[ M \cong \bigoplus_{i \in T} M_i \text{ over } k[x_1, \ldots, x_n]. \]

Conversely, starting with a graded module over \( k[x_1, \ldots, x_n] \) gives us an \( n \)-parameter persistence module. In fact, we have equivalence between their categories, and restricting persistence modules to finite type (with its obvious extension to the multiparameter case) yields the following:

**Theorem 3.2.1.** \([9]\) The category of persistence modules over \( k \) of finite type indexed by \( T \) and the category of finitely generated \( T \)-graded modules over \( k[x_1, \ldots, x_n] \) are equivalent categories.

In 1-parameter persistent homology, we have seen that if we take a finitely generated graded module over \( k[x] \), then it decomposes uniquely by the Structure Theorem given in 2.4.2. What allows us to use it is that \( k[x] \) is a PID. However, in \( n \)-parameter case, we take such a module over \( k[x_1, \ldots, x_n] \), and since \( k[x_1, \ldots, x_n], n \geq 2 \), is no more a PID, we cannot use the Structure Theorem. To see why \( k[x_1, \ldots, x_n], n \geq 2 \), is not a PID, consider the ideal generated by \( x_1 \) and \( x_2 \): we cannot write it by a single generator.

Let \( T = \mathbb{R}^n \), and \( P^n \) be a ring analogue of \( k[x_1, \ldots, x_n] \) such that powers of indeterminates come from the set \([0, \infty)\). For \( i = (i_1, \ldots, i_n) \in [0, \infty)^n \), \( x^i \) denotes \( x_1^{i_1} \cdots x_n^{i_n} \in P^n \). Then, \( P^n \) is an \( \mathbb{R}^n \)-graded ring, and there exists an equivalence between categories of \( n \)-parameter persistence modules indexed by \( \mathbb{R}^n \) and \( \mathbb{R}^n \)-graded modules over \( P^n \), \([22]\).

The next step is to decide how to decompose our persistence module. We cannot use the Structure Theorem due to the reason we have mentioned above. On the other hand, we can still decompose p.f.d. persistence modules:

**Theorem 3.2.2.** \([8, \text{Theorem 4.2}]\) For a poset \( P \) and a p.f.d. \( n \)-parameter persistence module \( M : P \rightarrow \text{Vect} \),

(i) \( M \) is written as a direct sum of indecomposables \( \{M^\lambda\}_{\lambda \in \Lambda} \) so that

\[ M \cong \bigoplus_{\lambda \in \Lambda} M^\lambda. \]
Suppose that \( M \) is separated into indecomposables in two different ways:

\[
M \cong \bigoplus_{\lambda \in \Lambda} M^\lambda \cong \bigoplus_{\gamma \in \Gamma} M^\gamma.
\]

Then, there is a bijection \( \sigma : \Lambda \to \Gamma \) such that \( M^\lambda \cong M^{\sigma(\lambda)} \) for all \( \lambda \in \Lambda \).

Remark 3.2.1. The proof of Theorem 3.2.2 has huge background, but Botnan and Crawley-Boevey proved the first part of the theorem in their article [7] in the recent past. The second part is coming from the Azumaya–Krull–Remak–Schmidt Theorem, [1].

In \( n \)-parameter case where \( n \geq 2 \), the main problem is that we do not know the exact list of isomorphism classes of indecomposables, and this makes everything very complex. In 1-parameter case, those indecomposables are just interval modules and the set of intervals is called the barcode.

Moreover, the related question is: If we define the barcode on multiparameter p.f.d. persistence modules as a set of indecomposable components of them obtained by Theorem 3.2.2 (i), does it fulfill all the properties satisfying by the barcode of a 1-parameter persistence module?

Definition 35. [8] Let \( B \) be a multiset of subsets of \( P \). Then, we say \( B \) is a good barcode of the persistence module \( M \) if

\[
\text{rank}(M_i \to M_j) = \left| \{S \in B \mid i, j \in S \} \right|
\]

for all \( i, j \in P \).

Observe that every barcode coming from p.f.d. 1-parameter persistence modules is automatically a good barcode. However, if we start with a p.f.d. \( n \)-parameter persistence module \( M \), then there is not always a good barcode of \( M \). Let us see this by the following example.

Example 3.2.2. [8] Start with the bifiltration shown in Figure 3.5. If we apply \( H_1(\mathcal{I}; \mathbb{Z}_2) \), then the corresponding persistence module \( M \) can be seen by the following diagram:
Clearly, this persistence module is p.f.d. and let us show that it cannot have a good barcode.

Say $B$ is a good barcode of it. Observe the followings:

i) $\text{rank } (M_{(0,1)} \rightarrow M_{(2,1)}) = 1$, so there is $I \in B$ such that $(0, 1), (2, 1) \in I$.

ii) $\text{rank } (M_{(0,1)} \rightarrow M_{(1,2)}) = 1$, so there is $J \in B$ such that $(0, 1), (1, 2) \in J$.

iii) $\text{rank } (M_{(1,0)} \rightarrow M_{(2,1)}) = 1$, so there is $K \in B$ such that $(1, 0), (2, 1) \in K$.

Since $\text{dim}(M_{(0,1)}) = 1$, we have $I = J$, and since $\text{dim}(M_{(2,1)}) = 1$, this makes $I = K$. Thus, $I = J = K$. This implies that $(1, 0), (1, 2) \in I$. However,

$$\text{rank}(M_{(1,0)} \rightarrow M_{(1,2)}) = 0.$$ 

So, this gives a contradiction. Therefore, $M$ does not have a good barcode.

Hence, extending the barcode to p.f.d. multiparameter persistence modules by keeping all of its properties is not the case. Furthermore, as we mentioned earlier, working
on indecomposables without knowing what they are exactly does not allow us to go further. Thus, unlike 1-parameter case, the barcode is not a complete invariant among multiparameter p.f.d. persistence modules, for details see [9].

On the other hand, we can restrict ourselves to interval-decomposable persistence modules to know the list of indecomposables.

In multiparameter setting, the definition of an interval module is same as in 1-parameter case given in Definition 24. Moreover, interval modules are indecomposable in multiparameter persistence, and a proof of this is the direct extension of the proof given for Theorem 2.4.3.

**Definition 36.** [8] A persistence module $M$ indexed by $P$ is said to be **interval decomposable** if there exists a multiset $B(M)$ of intervals in $P$ such that

$$M \cong \bigoplus_{I \in B(M)} k_I.$$

Here, we define $B(M)$ as the **barcode** of $M$.

**Definition 37.** [4] Let $M$ be an interval decomposable persistence module indexed by $T = T_1 \times \ldots \times T_n$ where each $T_i$ is totally ordered set for all $i \in \{1, \ldots, n\}$. If all $I \in B(M)$ are rectangles in $T$, then we call $M$ **rectangle decomposable**.

By definitions, rectangle decomposable modules forms a subset of interval decomposable modules. Sometimes, we restrict persistence modules into one of these two types of modules.

Now, let us see an important kind of persistence modules. For $P$ be a poset and $a \in P$, $Q^a$ is a persistence module given by

$$Q^a_x = \begin{cases} k & \text{if } a \leq x, \\ 0 & \text{otherwise.} \end{cases}$$

$$Q^a_{x,y} = \begin{cases} \text{id}_k & \text{if } a \leq x, \\ 0 & \text{otherwise.} \end{cases}$$

**Example 3.2.3.** Consider $Q^{1,0}$ where all maps between $k$’s are identity and $P = \mathbb{N}^2$. 41
Definition 38. [22] A persistence module $F$ is called free if there exists a multiset $A$ of elements of $P$ such that

$$F \cong \bigoplus_{a \in A} Q^a.$$ 

Definition 39. [23] A presentation of a persistence module $M$ is a morphism $f : F_1 \to F_0$ of free persistence modules such that $F_0 / \text{im}(f) \cong M$. If $F_1$ and $F_0$ are finitely generated, then $M$ is called finitely presented.

From [23, Proposition 6.40], we can see that $F_0$ and $F_1$ are generated by the set of generators, and the set of elements generating all relations of $M$, respectively. Thus, it is enough to show these sets have finite cardinality to call a persistence module finitely presented.
CHAPTER 4

METRICS AND STABILITY

We have seen that the barcode does not have an extension to p.f.d. multiparameter persistence modules. Instead, Carlsson and Zomorodian proposed the rank invariant for multiparameter setting \[9\].

**Definition 40.** \[9\] The rank invariant of \( M \) denoted as \( \rho_M \) is defined by

\[
\rho_M(i, j) := \text{rank} \left( \varphi^M_{i,j} \right)
\]

for every \( i \leq j \in \mathbb{R}^n \).

In the literature, the rank invariant is also called persistent Betti numbers, which are already defined for the 1-parameter case in the Definition\[6\].

The rank invariant draws the attention because it is easy to compute and equivalent to the barcode in 1-parameter case implying that the rank invariant is complete in 1-parameter setting. However, its extension to multiparameter case is no more a complete invariant, and this can be seen by the following example:

**Example 4.0.1.** \[24\] Consider the persistence modules:

\[
\begin{array}{cccccccccc}
M & \xrightarrow{id} & \xrightarrow{\begin{pmatrix} 1 & 0 \end{pmatrix}^T} & \xrightarrow{id^2} & \cdots & & & & & \ \\
0 & \xrightarrow{id} & \xrightarrow{\begin{pmatrix} 0 & 1 \end{pmatrix}^T} & \xrightarrow{id^2} & \cdots & & & & & \ \\
\end{array}
\]

\[
\begin{array}{cccccccccc}
N & \xrightarrow{id} & \xrightarrow{\begin{pmatrix} 1 & 0 \end{pmatrix}^T} & \xrightarrow{id^2} & \cdots & & & & & \ \\
0 & \xrightarrow{id} & \xrightarrow{\begin{pmatrix} 0 & 1 \end{pmatrix}^T} & \xrightarrow{id^2} & \cdots & & & & & \ \\
\end{array}
\]

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While $M$ is the free module with two generators at $(1, 0)$ and $(0, 1)$, that is,

$$M \cong \mathbb{Q}^{1,0} \oplus \mathbb{Q}^{0,1},$$

$N$ has another generator at $(1, 1)$, and the homology classes of $N$ at $(1, 0)$ and $(0, 1)$ generates a single class at $(1, 1)$ as a result of the relation $\langle (1, 0) - (0, 1) \rangle$.

Observe that ranks of the following maps

$$M_{(1,0)} \oplus M_{(0,1)} \to M_{(1,1)}, \quad N_{(1,0)} \oplus N_{(0,1)} \to N_{(1,1)}$$

$$(x, y) \to (x, y), \quad (x, y) \to (x, 0)$$

are 2 and 1, respectively. Therefore, $M$ and $N$ are not isomorphic to each other. Alternatively, if we write $M$ and $N$ as a direct sum of indecomposables, then we can see that there is no bijection giving isomorphisms between corresponding components. Hence, they are not isomorphic by Theorem 3.2.2. On the other hand, ranks of all linear maps, $\varphi_{i,j}^M$ and $\varphi_{i,j}^N$ for $i \leq j$, are equal to each other. This implies that although $M$ and $N$ are not isomorphic, they have the same rank invariant. Therefore, the rank invariant is not complete in multiparameter persistent homology.

All in all, prominent candidates, namely the barcode and the rank invariant, are not complete. Furthermore, there is no known complete invariant for multiparameter persistent homology. Therefore, the duty of understanding whether two persistence modules are isomorphic or not belongs to distances. We extend the familiar ones to $n$-parameter case, and define another one: the matching distance.

### 4.1 The Interleaving Distance

In this subsection, we extend the definition of the interleaving distance to the multiparameter persistent homology. However, we first give the definition of an $\epsilon$-interleaving between two functors $F, G : \mathbb{R}^n \to C$ where $C$ is an arbitrary category. Let $C^{\mathbb{R}^n}$ denote the category of functors from $\mathbb{R}^n$ to $C$.

For $\epsilon \in [0, \infty)$, we define the shift functor as

$$(-)(\bar{\epsilon}) : C^{\mathbb{R}^n} \to C^{\mathbb{R}^n}$$
by
\[ F(\vec{\epsilon})_i = F_{i+\vec{\epsilon}} \text{ and } \varphi_{i,j}^{F(\vec{\epsilon})} = \varphi_{i+\vec{\epsilon},j+\vec{\epsilon}} \]
where \( \vec{\epsilon} = (\epsilon, \ldots, \epsilon) \in \mathbb{R}^n \), and \( \varphi_{i,j}^{F} : F_i \to F_j \) denotes the corresponding morphism of \( i \leq j \) in \( C \) for the functor \( F : \mathbb{R}^n \to C \).

For a natural transformation \( N : F \to G \), we define \( N(\vec{\epsilon}) : F(\vec{\epsilon}) \to G(\vec{\epsilon}) \) in the following way: \( N(\vec{\epsilon})_i = N_{i+\vec{\epsilon}} \). Moreover, the internal morphisms \( \varphi_{i,i+\vec{\epsilon}}^{F} : F_i \to F_{i+\vec{\epsilon}} \) form a natural transformation from \( F \) to \( F(\vec{\epsilon}) \).

**Definition 41.** [8] For \( \epsilon \in [0, \infty) \), two functors \( F, G : \mathbb{R}^n \to C \) are said to be \( \epsilon \)-interleaved if there exist morphisms
\[ \phi : F \to G(\vec{\epsilon}) \quad \psi : F \to G(\vec{\epsilon}) \]
satisfying
\[ F_i \xrightarrow{\varphi_{i,i+2\vec{\epsilon}}^{F}} F_{i+2\vec{\epsilon}} \xrightarrow{\phi_{i+\vec{\epsilon}}} G_{i+\vec{\epsilon}} \quad \psi_{i+\vec{\epsilon}} \]
\[ F_i \xrightarrow{\psi_{i+\vec{\epsilon}}} G_{i+\vec{\epsilon}} \xrightarrow{\phi_{i+\vec{\epsilon}}} G_{i+2\vec{\epsilon}} \]
\[ F_i \xrightarrow{\psi_{i+\vec{\epsilon}}} G_{i+\vec{\epsilon}} \xrightarrow{\phi_{i+\vec{\epsilon}}} G_{i+2\vec{\epsilon}} \]

**Definition 42.** [8] Let \( F \) and \( G \) be two functors from \( \mathbb{R}^n \) to \( C \). We define their interleaving distance \( d_I(F, G) \) as
\[ d_I(F, G) := \inf \{ \epsilon \mid F \text{ and } G \text{ are } \epsilon \text{-interleaved} \} \]
If no such \( \epsilon \) exists, then we set \( d_I(F, G) = \infty \).

In the above construction, if we specify \( C = \text{Top} \), then functors become \( \mathbb{R}^n \)-indexed filtrations, and we can obtain \( d_I \) between such filtrations. Similarly, taking \( C \) as \( \text{Vect} \) causes functors to be \( \mathbb{R}^n \)-indexed persistence modules and enables us to extend \( d_I \) to multiparameter setting.

Like in 1-parameter case, two multiparameter persistence modules are said to be isomorphic persistence modules if and only if they are 0-interleaved. Moreover, if two \( n \)-parameter persistence modules are \( \epsilon \)-interleaved, then they are also \( \delta \)-interleaved for all \( \delta > \epsilon \). The proof of it is just the extension of the proof of Proposition 2.6.2.

Recall that, for 1-parameter case, we state that both the bottleneck distance and the interleaving distance are stable.

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For multiparameter case, let us first give a general definition of what we mean by a stable distance: Let $X$ be any topological space with two functions $f, g : X \to \mathbb{R}^n$ defined on it. We can obtain persistence modules $M^f$ and $M^g$ via maps $f$ and $g$ as homology of sublevel set filtrations $S(f)$ and $S(g)$ respectively, that is,

$$
M^f_j := H_i(S(f)_j) \quad M^g_j := H_i(S(g)_j)
$$

where $j \in \mathbb{R}^n$ and $i \in \mathbb{N}$ is fixed. In addition, consider $\mathbb{R}^n$ with the max norm given as

$$
||r||_\infty = \max_i |r_i|
$$

where $r = (r_1, \ldots, r_n) \in \mathbb{R}^n$. After these constructions, we are ready to define the notion of a stable distance:

**Definition 43.** [22] Let $d$ be a distance (i.e., extended pseudometric) on multiparameter persistence modules. We say that $d$ is $i$-stable if it satisfies the following inequality:

$$
d(M^f, M^g) \leq \sup_{x \in X} ||f(x) - g(x)||_\infty,
$$

where $M^f$ and $M^g$ are defined as above. Moreover, $d$ is called stable if it is $i$-stable for all $i \geq 0$.

**Theorem 4.1.1.** [22] The interleaving distance $d_I$ is stable.

**Proof.** Let $\sup_{x \in X} ||f(x) - g(x)||_\infty = \epsilon$. Then, we have $S(f)_j \subseteq S(g)_{j+\epsilon}$ and $S(g)_j \subseteq S(f)_{j+\epsilon}$. These inclusion maps give an $\epsilon$-interleaving between $S(f)$ and $S(g)$. Applying homology functor to these filtrations brings out an $\epsilon$-interleaving between $H_i(S(f))$ and $H_i(S(g))$ which follows from the naturality of the homology functor. Therefore, $M^f$ and $M^g$ are $\epsilon$-interleaved. Hence,

$$
d_I(M^f, M^g) \leq \epsilon = \sup_{x \in X} ||f(x) - g(x)||_\infty.
$$

Thus, small perturbations of functions lead to small changes in the corresponding persistence modules in terms of the interleaving distance. In fact, we also look for a stable pseudometric to be as sensitive as perturbations of functions. This quest reveals the universality property:
Definition 44. [22] For \( i \geq 0 \), a pseudometric \( d \) on \( n\text{-mod} \) is called \( i\)-universal if it is \( i\)-stable and for any \( i\)-stable pseudometric \( d' \) on \( n\text{-mod} \), we have \( d'(M, N) \leq d(M, N) \) for all \( n\)-parameter persistence modules \( M \) and \( N \) obtained from \( i\)-th homology of sublevel set filtrations.

Moreover, \( d \) is called universal if it is stable and for any stable pseudometric \( d' \) on \( n\text{-mod} \), we have \( d'(M, N) \leq d(M, N) \) for all \( n\)-parameter persistence modules \( M \) and \( N \) obtained from \( i\)-th homology of sublevel set filtrations for some \( i \geq 0 \).

Now, suppose we have two \( n\)-parameter persistence modules \( M \) and \( N \). Recall that to define the interleaving distance between \( M \) and \( N \), these modules are not necessarily coming from two filtering functions defined on a single topological space. So, if we want to define stability for a more general setup, that is, for arbitrary persistence modules, we need a result guaranteeing the existence of such functions and a topological space. The following theorem solves this problem when the modules are over a prime field, that is, \( \mathbb{Q} \) or \( \mathbb{Z}_p \) where \( p \) is prime:

**Proposition 4.1.2.** [22, Proposition 5.8] Let \( k \) be a prime field, and \( M \) and \( N \) be \( \epsilon\)-interleaved \( n\)-parameter persistence modules whose underlying field is \( k \). Then, for any \( i \geq 1 \), there exist a CW-complex \( X \) and continuous functions \( f, g : X \to \mathbb{R}^n \) such that

\[
M \cong H_i(S(f)), \quad N \cong H_i(S(g)), \quad \sup_{x \in X} \|f(x) - g(x)\|_{\infty} = \epsilon.
\]

Therefore, a persistence module over a prime field can be obtained from the \( i\)-th homology of a sublevel set filtration up to isomorphism for all \( i \geq 1 \). This implies that we can write the statement of Definition 44 for arbitrary persistence modules over a prime field except for the definiton of \( 0\)-universal.

**Theorem 4.1.3.** [22, Theorem 5.5] For a prime field \( k \) and \( i \geq 1 \), \( d_i \) is \( i\)-universal.

**Proof.** Let \( M \) and \( N \) be \( n\)-parameter persistence modules such that \( d_i(M, N) = \epsilon \). Then, for any \( \delta > 0 \), there is an \((\epsilon + \delta)\)-interleaving between them. So, by Proposition 4.1.2, there exists a CW complex \( X \) and continuous functions \( f, g : X \to \mathbb{R}^n \) such that \( M \cong H_i(S(f)), \quad N \cong H_i(S(g)), \quad \sup_{x \in X} \|f(x) - g(x)\|_{\infty} = \epsilon + \delta \). Let us take
any \(i\)-stable pseudometric \(d\) on \(n\text{-mod}\) where \(i \geq 1\), then by Definition 43,

\[
d(M, N) \leq \sup_{x \in X} \|f(x) - g(x)\|_\infty = \epsilon + \delta \text{ for all } \delta > 0.
\]

Thus, we have

\[
d(M, N) \leq \epsilon = d_I(M, N).
\]

In addition, we need to consider the case with \(d_I(M, N) = \infty\). Then, trivially \(d(M, N) \leq \infty = d_I(M, N)\).

\textbf{Corollary 4.1.4.} \cite{22} Corollary 5.6] For a prime field \(k\), \(d_I\) is universal.

\textbf{Proof.} We have already showed \(d_I\) is stable. Let \(d\) be a stable pseudometric on \(n\)-parameter persistence modules. So, it is also 1-stable. Since \(d_I\) is 1-universal, we have \(d(M, N) \leq d_I(M, N)\) for all \(n\)-parameter persistence modules. \(\square\)

However, universality of \(d_I\) over a non-prime field have not showed yet. Proving or disproving it is an open problem.

Being \(\epsilon\)-interleaved and having the interleaving distance as \(\epsilon\) are different. We cannot guarantee that two persistence modules are \(\epsilon\)-interleaved when the interleaving distance between them is \(\epsilon\). In fact, for finitely presented ones, they are equivalent:

\textbf{Theorem 4.1.5.} (The Closure Theorem) \cite{22} Theorem 6.1] If \(M\) and \(N\) are two finitely presented \(\mathbb{R}^n\)-indexed persistence modules and \(d_I(M, N) = \epsilon\), then \(M\) and \(N\) are \(\epsilon\)-interleaved.

The interleaving distance is an extended pseudometric in the multiparameter persistent homology. However, if we work on finitely-presented \(\mathbb{R}^n\)-indexed ones, then having \(d_I\) of two such modules as 0 implies that they are 0-interleaved by the Closure Theorem. Hence, they are isomorphic. So, we have the following corollary:

\textbf{Corollary 4.1.6.} \cite{22} \(d_I\) is an extended metric on finitely presented \(\mathbb{R}^n\)-indexed persistence modules.
4.2 The Bottleneck Distance

When we define the bottleneck distance for multiparameter persistence modules, we need to examine all matchings between indecomposable summands as in the 1-parameter case. However, while working with objects of $n$-mod, decomposing a given module into known indecomposable summands is a big problem even the module is known to be p.f.d.

Hence, we restrict our attention to interval decomposable persistence modules, and define the bottleneck distance on them.

Let $M$ and $N$ be two $n$-parameter interval decomposable persistence modules indexed by $\mathbb{R}^n$, and let $C$ and $D$ be the barcodes of $M$ and $N$, respectively, that is

$$M \cong \bigoplus_{I \in C} k_I \quad \text{and} \quad N \cong \bigoplus_{J \in D} k_J.$$ 

We define a matching between $C$ and $D$ as a bijection $\sigma : C' \to D'$ where $C' \subseteq C$ and $D' \subseteq D$. Moreover, if we do not see an element of $C$ or $D$ in the bijection $\sigma$, then the element is unmatched.

**Definition 45.** With the above construction, we say a matching is an $\epsilon$-matching if it satisfies the following conditions:

i) for all $I \in C'$, $k_I$ and $k_{\sigma(I)}$ are $\epsilon$-interleaved.

ii) for all unmatched $I \in C$, $k_I$ is $\epsilon$-interleaved with the zero module.

iii) for all unmatched $J \in D$, $k_J$ is $\epsilon$-interleaved with the zero module.

Observe that if we have an $\epsilon$-matching, then all pairs in the above construction are $\epsilon$-interleaved with each other. So, they are all $\delta$-interleaved for all $\delta > \epsilon$. This implies that we have a $\delta$-matching as well.

**Definition 46.** The bottleneck distance between $C$ and $D$ is defined as

$$d_B(C, D) := \inf \{ \epsilon \mid \text{there is an } \epsilon\text{-matching between } C \text{ and } D \}.$$ 

If no such $\epsilon$ exists, then $d_B(C, D) = \infty.$
Note that this definition of the bottleneck distance for multiparameter persistence modules is consistent with the 1-parameter case. To see this, let us first suppose that elements of the barcodes that we consider are of the form \([a, b)\) for some \(a, b \in \mathbb{R}\). For an arbitrary persistence module \(M\), we define \(M'\) so that

\[
\text{if } M \cong \bigoplus_{(a_i, b_i) \in C} \mathbb{I}_{(a_i, b_i)}, \text{ then } M' \cong \bigoplus_{(a_i, b_i) \in C'} \mathbb{I}_{(a_i, b_i)}.
\]

Observe that \(d_B(M, M') = 0\). Similarly, define \(N'\) for another persistence module \(N\). Then, by transitivity of the bottleneck distance, we have

\[
d_B(M, N) = d_B(M', N').
\]

This implies that the consistency argument can be proved by working on the barcodes we have supposed, that is, it does not matter whether we include the endpoints or not.

It is enough to show that the cost of a matching between \(C\) and \(D\) is smaller than or equal to \(\epsilon\) if and only if there exists an \(\epsilon\)-matching between \(C\) and \(D\) as in Definition 45. First, start with a matching \(\mathcal{X}\) between \(C\) and \(D\) such that \(c(\mathcal{X}) \leq \epsilon\). So, there exists a bijection \(\sigma : C' \rightarrow D'\) where \(C' \subseteq C\) and \(D' \subseteq D\). Let \(I \in C'\) and \(\sigma(I) = J\).

Thus, \(c(I, J) \leq \epsilon\). From the Proposition 2.6.4, we have

i) \(d_I(\mathbb{I}_I, \mathbb{I}_J) \leq c(I, J) \leq \epsilon\), so \(\mathbb{I}_I\) and \(\mathbb{I}_J\) are \(\epsilon\)-interleaved since both interval modules are finitely presented.

ii) \(d_I(\mathbb{I}_{L_1}, \emptyset) = c(L_1) \leq \epsilon\) where \(L_1 \in C \setminus C'\). So, \(\mathbb{I}_{L_1}\) is \(\epsilon\)-interleaved with the zero module.

iii) \(d_I(\mathbb{I}_{L_2}, \emptyset) = c(L_2) \leq \epsilon\) where \(L_2 \in D \setminus D'\). So, \(\mathbb{I}_{L_2}\) is \(\epsilon\)-interleaved with the zero module.

Hence, the matching \(\mathcal{X}\) is an \(\epsilon\)-matching.

Conversely, let us start with an \(\epsilon\)-matching. Say \(I = [a, b)\) and \(J = [c, d)\) are matched with each other. Consider them as two interval modules \(\mathbb{I}_I\) and \(\mathbb{I}_J\). Then, they are \(\epsilon\)-interleaved. To create the desired matching, we examine some cases. As a first one, if both intervals does not include any subinterval of the form \([t, t + 2\epsilon]\) for an arbitrary \(t \in \mathbb{R}\), then we can classify them as unmatched, and obtain a matching with cost at most \(\epsilon\).
In any other case, one of the intervals include such a subinterval. We claim that when they match with each other, we obtain $c(I, J) \leq \epsilon$. Assume that

$$c(I, J) = \max\{|c - a|, |d - b|\} > \epsilon.$$

Our aim is to get a contradiction by using the $\epsilon$-interleaving between $\mathbb{k}_I$ and $\mathbb{k}_J$. Let us suppose that $c(I, J) = |c - a| > \epsilon$ and without loss of generality, $c > a$. So, $c > a + \epsilon$. Let $[t, t + 2\epsilon] \subseteq [a, b)$ for some $t \in \mathbb{R}$. Then, we have the following non-commutative diagram

$$\begin{align*}
(k_I)_a &= \mathbb{k} \\
(k_I)_a + 2\epsilon &= \mathbb{k} \\
(k_I)_a + \epsilon &= 0 \\
\end{align*}$$

and this contradicts with the $\epsilon$-interleaving between modules. Thus, $c(I, J) \leq \epsilon$.

Let $[t, t + 2\epsilon] \nsubseteq [a, b)$ for any $t \in \mathbb{R}$ and $[s, s + 2\epsilon] \subseteq [c, d)$ for some $s \in \mathbb{R}$. Then, the following diagram does not commute

$$\begin{align*}
(k_I)_e &= \mathbb{k} \\
(k_I)_e + \epsilon &= 0 \\
(k_I)_e + 2\epsilon &= \mathbb{k} \\
\end{align*}$$

and this also contradicts with the $\epsilon$-interleaving. Hence, $c(I, J) \leq \epsilon$.

Similar arguments show that if $c(I, J) = |d - b| > \epsilon$ where at least one of $I$ or $J$ include a closed subinterval of length $2\epsilon$, then we get a contradiction as before. Thus, $c(I, J) \leq \epsilon$, and we obtain a matching with cost $\leq \epsilon$ in each case.

In addition, say $L = [a, b)$ is matched with the zero module. Then, $\mathbb{k}_L$ is $\epsilon$-interleaved with the zero persistence module. So, $\frac{b-a}{2} \leq \epsilon$, and this implies that $c(L) \leq \epsilon$. If we combine all of this, and write in a single matching $\mathcal{X}$, then $c(\mathcal{X}) \leq \epsilon$. So, both constructions for the bottleneck distance in 1-parameter are equivalent to each other.

Moreover, if we have an $\epsilon$-matching between the barcodes $\mathcal{C}$ and $\mathcal{D}$, then we can construct an $\epsilon$-interleaving between the corresponding interval decomposable persistence modules. Therefore, we always have the following statement:

$$d_I(M, N) \leq d_B(\mathcal{C}, \mathcal{D}).$$
To see this, start with an $\epsilon$-matching. Let

$$M \cong \bigoplus_{I \in C} \mathbb{k}_I \text{ and } N \cong \bigoplus_{J \in D} \mathbb{k}_J.$$ 

If $\mathbb{k}_I$ and $\mathbb{k}_J$ are matched with each other, then they are $\epsilon$-interleaved with morphisms $\phi_I : \mathbb{k}_I \to \mathbb{k}_J(\epsilon)$ and $\psi_I : \mathbb{k}_J \to \mathbb{k}_I(\epsilon)$. Furthermore, if $\mathbb{k}_L$ is matched with the zero module for $L \in C \setminus C'$ (resp. $D \setminus D'$), then there exist two morphisms $\phi_L : \mathbb{k}_L \to \mathbb{0}$ and $\psi_L : \mathbb{0} \to \mathbb{k}_L(\epsilon)$ (resp. $\phi_L : \mathbb{0} \to \mathbb{k}_L(\epsilon)$ and $\psi_L : \mathbb{k}_L \to \mathbb{0}$) giving an $\epsilon$-interleaving. In this case, we just add the zero module to the direct sum of $N$ (resp. $M$). So, this makes no change in persistence modules up to isomorphism. Also, corresponding $C$ and $D$ become the same in cardinality after adding new elements with empty support coming from the zero modules. Then, we can write a bijection $\beta : C \to D$ so that $\mathbb{k}_I$ and $\mathbb{k}_J := \mathbb{k}_{\beta(I)}$ are $\epsilon$-interleaved.

Observe that for $M \cong \bigoplus_{I \in C} \mathbb{k}_I$, we have

$$M(\epsilon) \cong \left( \bigoplus_{I \in C} \mathbb{k}_I \right)(\epsilon) = \bigoplus_{I \in C} \mathbb{k}_I(\epsilon) \text{ since } M(\epsilon)_i = M_{i+\epsilon} \cong \left( \bigoplus_{I \in C} \mathbb{k}_I \right)_{i+\epsilon} = \bigoplus_{I \in C} (\mathbb{k}_I)_{i+\epsilon} \text{ where } i \in \mathbb{R}^n.$$ 

Similarly, we have

$$N(\epsilon) \cong \left( \bigoplus_{J \in D} \mathbb{k}_J \right)(\epsilon) = \bigoplus_{J \in D} \mathbb{k}_J(\epsilon).$$

Define two maps $\phi : M \to N(\epsilon) \cong \bigoplus_{J \in D} \mathbb{k}_J(\epsilon)$ and $\psi : N \to M(\epsilon) \cong \bigoplus_{I \in C} \mathbb{k}_I(\epsilon)$ by

$$\phi\left( \bigoplus_{I \in C} (\mathbb{k}_I)_i \right) := \bigoplus_{I \in C} \phi_I\left( (\mathbb{k}_I)_i \right) \text{ and } \psi\left( \bigoplus_{J \in D} (\mathbb{k}_J)_i \right) := \bigoplus_{I \in C} \psi_I\left( (\mathbb{k}_{\beta(I)})_i \right)$$

where $i \in \mathbb{R}^n$. Since each $\phi_I$ and $\psi_I$ are morphisms making all diagrams in Definition 41 commute, $\phi$ and $\psi$ give an $\epsilon$-interleaving between $M$ and $N$.

We have seen that in the 1-parameter case, $d_I = d_B$ via Theorem 2.6.5. So, we can directly ask that are they also equal to each other in the multiparameter setting? Actually, we have already showed $d_I(M, N) \leq d_B(C, D)$ by the explanation given in the previous paragraph. So, it is all about whether the converse is true or not. The answer is no, and it can be seen by the following counterexample given by Bjerkevik, [4, Example 5.1]:

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Figure 4.1: Intervals where $I_1$ and $I_2$ are outer light purple squares, $I_3$ is the inner purple square and $J$ is the red one, [4].

Let $M = \mathbb{k}_{I_1} \oplus \mathbb{k}_{I_2} \oplus \mathbb{k}_{I_3}$ and $N = \mathbb{k}_J$ where

\[
I_1 = (-3, 1) \times (-1, 3), \quad I_2 = (-1, 3) \times (-3, 1), \\
I_3 = (-1, 1) \times (-1, 1), \quad J = (-2, 2) \times (-2, 2),
\]

and intervals can be seen in Figure 4.1.

So, $\mathcal{C} = B(M) = \{I_1, I_2, I_3\}$ and $\mathcal{D} = B(N) = \{J\}$. Consider all possible matchings between barcodes.

Matching 1: $I_1$ is matched with $J$, $I_2$ and $I_3$ are unmatched.

Matching 2: $I_2$ is matched with $J$, $I_1$ and $I_3$ are unmatched.

Matching 3: $I_3$ is matched with $J$, $I_1$ and $I_2$ are unmatched.

Matching 4: $I_1, I_2, I_3$ and $J$ are unmatched.

In any case, at least one of $I_1$ or $I_2$ is unmatched. So, they are matched with the zero module. Without loss of generality, consider the interleavings between $\mathbb{k}_{I_1}$ and $\mathbb{0}$.

The morphisms

\[
\phi : \mathbb{k}_{I_1} \to \mathbb{0}(\vec{e}) \quad \psi : \mathbb{0} \to \mathbb{k}_{I_1}(\vec{e})
\]

are the zero maps where $\vec{e} = (\epsilon, \epsilon)$. Then, we just need to examine triangle diagrams.

Take $\epsilon = 2$, then the internal morphisms of $\mathbb{k}_{I_1}$:

\[
\varphi_{p,p+(4,4)}^{k_{I_1}} : \mathbb{k}_{(I_1)_p} \to \mathbb{k}_{(I_1)_{p+(4,4)}}
\]

53
is just the zero map since at least one of $k(I_1)_p$ and $k(I_2)_{p+(4,4)}$ is the zero vector space for $I_1 = (-3, 1) \times (-1, 3)$. So, we have one of the following cases:

In any case, our diagram commutes. Since we are taking $\phi_p = 0 = \psi_p$ for all $p \in \mathbb{R}^2$, the other triangle diagram also commutes. Thus, $k_{I_1}$ and $\mathbb{0}$ are $2$-interleaved.

**Claim 1:** $k_{I_1}$ and $\mathbb{0}$ are not $(2 - \delta)$-interleaved for all $\delta \in \mathbb{R}$ such that $0 < \delta \leq 2$.

Let $p = (-3 + \delta, -1 + \delta)$. So, $p \in I_1 \Rightarrow (k_{I_1})_p = k$. Moreover,

$$p + 2\vec{e} = (-3 + \delta, -1 + \delta) + 2(2 - \delta, 2 - \delta) = (1 - \delta, 3 - \delta).$$

Thus, $p + 2\vec{e} \in I_1 \Rightarrow (k_{I_1})_{p+2\vec{e}} = k$. So, we have the following triangle diagram:

This diagram does not commute since the horizontal map is the identity map, but composition of other two maps is just the zero map. This shows that our claim is true. Thus, $k_{I_1}$ and $\mathbb{0}$ are $\epsilon$-interleaved only for all $\epsilon \geq 2$. The same is true for $k_{I_2}$. Since all of four matchings include $I_1$ or $I_2$ as unmatched, they cannot be an $\epsilon$-matching for any $\epsilon < 2$.

Furthermore, with a similar argument, we can see that $k_{I_3}$ is $1$-interleaved with the zero persistence module.

Now, let us try to find interleavings between $k_{I_i}$ and $k_J$ where $i \in \{1, 2, 3\}$.

**Claim 2:** $k_{I_i}$ and $k_J$ are $2$-interleaved for all $i \in \{1, 2, 3\}$.

In any case, if we take $\phi : k_{I_i} \rightarrow k_J(2)$ and $\psi : k_J \rightarrow k_{I_i}(2)$ as zero morphisms, then they are trivial natural transformations. For triangle diagrams, since composition of
above morphisms is zero, we just need to show horizontal maps are always zero. This is true since
\[ \varphi_{p,p+2(2,2)} = \varphi_{p,p+(4,4)} : k_K \to k_{K+p(4,4)} = 0 \]
for all \( K \in \{ I_1, I_2, I_3, J \} \). Therefore, all triangle diagrams also commutes.

Hence, \( k_{I_i} \) and \( k_J \) are 2-interleaved for all \( i \in \{ 1, 2, 3 \} \). So, all of 4 matchings between barcodes are 2-matching. Since we showed that they cannot be an \( \epsilon \)-matching for \( \epsilon < 2 \), \( d_B(C,D) = 2 \).

In the next step, we try to find \( d_I(M,N) \) by investigating following interleavings:

**Claim 3:** None of \( k_{I_i} \) for \( i \in \{ 1, 2, 3 \} \) is not \((1-\delta)\)-interleaved with \( k_J \) for any \( 0 < \delta \leq 1 \).

Let us work on \( k_{I_1} \). Consider \( p = (-3+\delta,1+\delta) \) with the following diagram:

Then, \( p = (-3+\delta,1+\delta) \in I_1 \Rightarrow (k_{I_1})_p = k \). Moreover,
\[ p + (1-\delta) = (-3+\delta,1+\delta) + (1-\delta,1-\delta) = (-2,2) \notin J \Rightarrow (k_J)(-2,2) = 0. \]
\[ p+2(1-\delta) = (-3+\delta,1+\delta)+(2-2\delta,2-2\delta) = (-1-\delta,3-\delta) \in I_1 \Rightarrow (k_{I_1})(-1-\delta,3-\delta) = k. \]

So, the diagram becomes:

\[ \begin{array}{c}
\downarrow \quad \text{id} \\
0 \\
\end{array} \]

and it does not commute. Hence, \( k_{I_1} \) is not \((1-\delta)\)-interleaved with \( k_J \) for any \( 0 < \delta \leq 1 \). The same situation for \( k_{I_2} \) and \( k_{I_3} \) can be seen in a similar way.

**Claim 4:** \( k_{I_1} \) and \( k_J \) are 1-interleaved.

Define morphisms \( \phi_{I_1} : k_{I_1} \to k_J(1) \) and \( \psi_{I_1} : k_J \to k_{I_1}(1) \) as follows:
If $i \in I_1$ and $i + (1, 1) \in J$, then let $\phi_i^{I_1} = \text{id}$ where $i \in \mathbb{R}^2$. If at least one of $i$ or $i + (1, 1)$ is not an element of the corresponding interval, then let $\phi_i^{I_1}$ be the zero map. Similarly, if $j \in J$ and $j + (1, 1) \in I_1$, then let $\psi_j^{I_1} = \text{id}$ where $j \in \mathbb{R}^2$. If at least one of $j$ or $j + (1, 1)$ is not an element of the corresponding interval, then let $\psi_j^{I_1}$ be the zero map.

Then, let us show triangle diagrams commute:

\[
\begin{array}{c}
(\mathbb{k}_{I_1})_i \\
| \downarrow \phi_i^{I_1} \quad \downarrow \psi_i^{I_1}| \\
(k_{J})_{i+(1,1)} \\
| \downarrow \phi_{i+(1,1)} |
\end{array}
\]

As a first case, let $i, i + (2, 2) \in I_1$, $i + (1, 1) \in J$. So, our diagonal maps are in the form: $\mathbb{k} \to \mathbb{k}$ defined as the identity map. So, the corresponding diagram:

\[
\begin{array}{c}
\mathbb{k} \\
| \downarrow \text{id} |
\end{array}
\]

commutes.

The only case where we do not have commutativity happens if $i, i + (2, 2) \in I_1$, $i + (1, 1) \notin J$. We have

\[
\begin{array}{c}
\mathbb{k} \\
| \downarrow 0 |
\end{array}
\]

and it is clearly non-commutative. Observe that if both $i$ and $i + (2, 2)$ is an element of $I_1$, then $i \in (-3, -1) \times (-1, 1)$. This implies that $i + (1, 1) \in J$. However, we have already assumed that $i + (1, 1) \notin J$. So, this case cannot happen. Thus, we have commutative diagrams in all cases. For other triangle diagrams, the situation is similar. So, $\mathbb{k}_{I_1}$ and $\mathbb{k}_{J}$ are 1-interleaved. Since we know they are not $\epsilon$-interleaved for all $\epsilon < 1$, $d_I(\mathbb{k}_{I_1}, \mathbb{k}_{J}) = 1$.

In addition, we can define morphisms $\phi^{I_2}$, $\psi^{I_2}$ for $\mathbb{k}_{I_2}$ and $\phi^{I_3}$, $\psi^{I_3}$ for $\mathbb{k}_{I_3}$ in a similar
way. It can be shown
\[ d_I(k_{I_2}, k_J) = 1 = d_I(k_{I_3}, k_J) \]
with the same idea.

In the next step, we try to find two morphisms
\[ \phi : M \to N(1) \quad \text{and} \quad \psi : N \to M(1) \]
showing \( M \) and \( N \) are 1-interleaved. As a first idea, we can try to define \( \phi \) by using the following diagram:

\[
\begin{array}{ccc}
k_{I_1} \oplus k_{I_2} \oplus & k_{I_3} \downarrow \pi_{I_1} & \\
& \phi & \\
& k_{J_1} \rightarrow k_{J_1} & \phi_{I_1} \rightarrow k_{J_1}(1) \\
\end{array}
\]

where \( \pi_{I_1} \) is the projection of \( M \) onto the first component. Let \( \phi = \phi_{I_1} \circ \pi_{I_1} \), so \( \phi_{p} = \phi_{I_1} \circ \pi_{I_1} \). Take \( p = (-0.9, -2.9) \in I_2 \), then \( p + (1, 1) \in J \) and \( p + (2, 2) \in I_2 \). Indeed, the diagram

\[
\begin{array}{ccc}
M_p & \rightarrow & M_{p+(2,2)} \\
\downarrow & = & \downarrow \\
N_{p+(1,1)} & \rightarrow & k \oplus k \oplus k \\
& \phi_p & \phi_{p+(1,1)}
\end{array}
\]

However, \( \pi_{I_1} = 0 \) since \( p \notin I_1 \Rightarrow (k_{I_1})_p = 0 \). So, \( \phi = \phi_{I_1} \circ \pi_{I_1} = \phi_{I_1} \circ 0 = 0 \). Thus, the diagram cannot commute. Hence, this way of defining \( \phi \) does not make \( M \) and \( N \) 1-interleaved.

Now, try another way. In any situation, we have one of the followings:

i) \( p \in I_1 \cap I_2 \):

Observe that \( I_1 \cap I_2 = I_3 \). Thus, \( p \in I_1 \cap I_2 \Rightarrow M_p = k \oplus k \oplus k \). Also, \( p + (1, 1) \in J \Rightarrow N_{p}(1) = k \). Define \( \phi_p : k \oplus k \oplus k \to k \) by \( \phi_p = \phi_{I_1} \circ \pi_{I_1} \).

ii) \( p \in I_1 \setminus I_2 \):

Define \( \phi_p : k \oplus 0 \oplus 0 \to N_p(1) \) by \( \phi_p = \phi_{I_1} \circ \pi_{I_1} \).

So, the function \( \phi \) on the cases i) and ii) is defined in the same way.
iii) $p \in I_2 \setminus I_1$:

Define $\phi_p : 0 \oplus k \oplus 0 \to N_p(1)$ by $\phi_p = \phi_p^{I_2} \circ \pi_p^{I_2}$.

iv) $p \notin I_1 \cup I_2$:

Define $\phi_p = 0$.

For the reverse function, we define $\psi : N \to M(1)$ by

$$
\psi : N = \mathbb{K}_J \to M(1) = \mathbb{K}_{I_1}(1) \oplus \mathbb{K}_{I_2}(1) \oplus \mathbb{K}_{I_3}(1)
$$

$$(\mathbb{K}_J)_p \to (\psi_{I_1}((\mathbb{K}_J)_p), \psi_{I_2}((\mathbb{K}_J)_p), \psi_{I_3}((\mathbb{K}_J)_p)) \text{ where } p \in \mathbb{R}^2.
$$

With the above construction of $\phi : M \to N(1)$ and $\psi : N \to M(1)$, all diagrams are commutative. Thus, $M$ and $N$ are 1-interleaved.

**Claim 5:** $M$ and $N$ are not $\epsilon$-interleaved for $\epsilon < 1$.

Let us assume there exists such an interleaving. So, we have following morphisms $\phi : M \to N(\epsilon)$ and $\psi : N \to M(\epsilon)$. Moreover, we can define $\phi^{I_i}$ and $\psi^{I_i}$ as functions commuting following diagrams:

\[
\begin{array}{ccc}
\mathbb{K}_{I_i} & \xrightarrow{f_i} & \mathbb{K}_J \\
\phi_i & \downarrow & \psi_i \\
\mathbb{K}_{I_1} \oplus \mathbb{K}_{I_2} \oplus \mathbb{K}_{I_3} & \xrightarrow{\phi} & \mathbb{K}_J(\epsilon)
\end{array}
\]

where $f_i$ is the inclusion map onto the $i$-th component of $M$.

However, $\phi^{I_i}$ and $\psi^{I_i}$ show that $\mathbb{K}_{I_i}$ and $\mathbb{K}_J$ are $\epsilon$-interleaved for some $\epsilon < 1$ by the following arguments:

$\phi^{I_i}$ and $\psi^{I_i}$ are well-defined morphisms. This implies that parallelogram diagrams are commutative. Moreover,

\[
\begin{array}{cccc}
(\mathbb{K}_{I_1})_p & \xrightarrow{f_i^{I_1}} & M_p & \xrightarrow{\varphi_{p,p+2\epsilon}} & M_{p+2\epsilon} & \xrightarrow{\pi_{p+2\epsilon}} & (\mathbb{K}_{I_1})_{p+2\epsilon} \\
\phi_i^{I_1} & \downarrow & \phi_p & \downarrow & \psi_{p+\epsilon} & \downarrow & \psi_{I_1}^{I_1} \\
(\mathbb{K}_J)_{p+\epsilon} & \xrightarrow{\psi_{p+\epsilon}} & (\mathbb{K}_J)_{p+\epsilon} & \xrightarrow{\psi_{p+\epsilon}} & (\mathbb{K}_J)_{p+\epsilon}
\end{array}
\]
and

\[
\begin{array}{cccc}
(k,I)_p & \phi_{p-\epsilon} & \psi_{p-\epsilon} & (k,I)_{p-\epsilon} \\
(\mathbb{k},J)_p & \phi_{p-\epsilon} & \psi_p & (k,J)_{p+\epsilon} \\
(k,I)_{p+\epsilon} & \phi_{p+\epsilon} & \psi_{p+\epsilon} & (k,I)_{p+2\epsilon} \\
(\mathbb{k},J)_{p+2\epsilon} & \phi_{p+2\epsilon} & \psi_{p+2\epsilon} & (k,J)_{p+2\epsilon} \\
\end{array}
\]

commutes, and this contradicts with Claim 3 whose correctness is already shown. So, we get a contradiction. Thus, \( M \) and \( N \) are not \( \epsilon \)-interleaved for \( \epsilon < 1 \). Thus, \( d_I(M, N) = 1 \). Hence, we obtained

\[
d_B(C, D) = 2 \neq 1 = d_I(M, N).
\]

So, the bottleneck distance and the interleaving distance are not equal to each other in the multiparameter persistent homology.

Moreover, let us choose \( \mathbb{k} \) as a prime field. We know \( d_I \) is universal over such a field. Let us assume that \( d_B \) is stable, then by definition of universality, we have \( d_B(B(L_1), B(L_2)) \leq d_I(L_1, L_2) \) for all persistence modules \( L_1 \) and \( L_2 \). However, we have obtained that \( d_I(M, N) = 1 < 2 = d_B(C, D) \), and this contradicts with our assumption. Therefore, the bottleneck distance is not stable in multiparameter setting.

Since \( d_I \leq d_B \), the bottleneck distance cannot be smaller than the interleaving distance. So, we can ask that can we bound the bottleneck distance from above by using the interleaving distance? The answer comes from the following theorem for the case of rectangle decomposable persistence modules:

**Theorem 4.2.1.** [4, Theorem 4.3] Let \( M \) and \( N \) be rectangle decomposable persistence modules indexed by \( \mathbb{R}^n \). If \( M \) and \( N \) are \( \epsilon \)-interleaved, then there exists a \((2n-1)\epsilon\)-matching between their barcodes, \( B(M) \) and \( B(N) \). Thus,

\[
d_B(B(M), B(N)) \leq (2n-1)d_I(M, N).
\]

In our example, \( M = \bigoplus_{i=1}^{3} (k,I)_i \) and \( N = (k,J) \) are rectangle decomposable persistence modules indexed by \( \mathbb{R}^2 \), and they satisfy Theorem 4.2.1, but with respect to this example, upper bound is not optimal. However, Bjerkevik show this bound is optimal for \( n = 2 \), and give another example satisfying the bound: for details, see [4 Example 5.2].
Lastly, both of these distances have negative sides in practice. The bottleneck distance
is not stable, so it is unsuitable to use, and as our previous example shows, even if
we work on interval decomposable bipersistence modules, finding the interleaving
distance between them is so hard. Therefore, we are searching for a stable distance
which is easier to compute compared to the interleaving distance.

4.3 The Matching Distance

Computing distances in multiparameter are more difficult than the case of 1-parameter.
As an idea, we can restrict $n$-parameter persistence modules to 1-parameter ones.
Therefore, we can use our knowledge and methods in 1-parameter such as taking ad-
vantage of easy computability of the bottleneck distance. Informally, we make this
restriction by intersecting $n$-parameter persistence modules with lines which we will
define in the next definition.

Again, we take $\mathbb{R}^n$ with the max norm:

$$||r||_\infty = \max_i |r_i|$$

where $r = (r_1, \ldots, r_n) \in \mathbb{R}^n$.

**Definition 47.** [20] Let $L$ be a line in $\mathbb{R}^n$ with a direction vector $\vec{m} = (m_1, \ldots, m_n)$
whose coordinates take value in $\mathbb{R}$. So, the equation of the line is $L : u = tm + b$ where
t $\in \mathbb{R}$, and $b = (b_1, \ldots, b_n) \in \mathbb{R}^n$ is an arbitrary point on the line. If $\vec{m} \in (0, \infty)^n$,
then the line $L : u = tm + b$ is called an **admissible line**.

Let $M$ be an $n$-parameter persistence module. We can obtain a 1-parameter persis-
tence module, denoted by $M_L$, by restricting $M$ to an admissible line $L$ so that

$$(M_L)_i := M_u$$

where $u = im + b, i \in \mathbb{R}$. Moreover, for $i \leq j \in \mathbb{R}, \varphi_{i,j}^{M_L} := \varphi_{u,v}^M$ where $u = im + b$
and $v = jm + b$.

**Remark 4.3.1.** We do not count lines with direction vector having a negative coor-
dinate as admissible lines. The reason is that if we restrict $n$-parameter persistence
module to one of such a line, points of the intersection of the persistence module and
the line are not comparable with each other. Thus, we cannot define linear maps, \( \varphi_{i,j}^{ML} \) where \( i \leq j \), of the persistence module.

**Definition 48.** \([20]\) The matching distance \( d_{\text{match}} \) on rank invariants of \( q \)-tame persistence modules \( M \) and \( N \) is defined as follows:

\[
d_{\text{match}}(M, N) := d_{\text{match}}(\rho_M, \rho_N) := \sup_L m_L \cdot d_B(B(M_L), B(N_L))
\]

where \( m_L = \min_{i=1, \ldots, n} \{ m_i \} \) for a direction vector \( \vec{m} = (m_1, \ldots, m_n) \in (0, \infty)^n \), and \( L \) varies in the set of admissible lines.

Note that \( M_L \) and \( N_L \) are restrictions of \( q \)-tame persistence modules \( M \) and \( N \). Hence, \( M_L \) and \( N_L \) are 1-parameter \( q \)-tame persistence modules. So, by Proposition 2.4.8, we can guarantee that barcodes of \( M_L \) and \( N_L \) exist. Thus, we can compute the matching distance between \( M \) and \( N \) by the above argument.

Recall that if a direction vector of a line \( L \) has at least one coordinate as 0, then we don’t call this line as admissible because \( m_L = 0 \) for this line. So, when we multiply the bottleneck distance with \( m_L \) in the process of finding the matching distance, numbers coming from there are just zero. Thus, they do not have any effect on the computation.

Moreover, the size of the set of admissible lines causes problems in the computation of the matching distance. So, we look for a smaller set where the result of \( d_{\text{match}} \) remains same. We observe that each line in the set of admissible lines is represented by infinitely many different parametrizations. Hence, it is meaningful to try to parameterize the set of admissible lines uniquely in terms of the parameters \( \vec{m} \) and \( b \), provided that the computation gives the same number for different parametrizations of the same line. To achieve this, we first restrict the set of admissible lines by taking direction vectors \( \vec{m} \) as unit vectors with respect to the max norm. That is, we require \( \vec{m} \in (0, 1]^n \) because for different direction vectors, we can obtain the same line. As an example, consider the following three lines with direction vectors

\[
\vec{m}_1 = (1/2, \ldots, 1/2), \quad \vec{m}_2 = (1, \ldots, 1), \quad \vec{m}_3 = (2, \ldots, 2)
\]

and take \( b = 0 \) in each one. Then, they all give the same line.
This situation also happens for $b \in \mathbb{R}^n$. For instance, let $n = 2$ and take three lines with the same direction vector $\vec{m} = (1, 1)$ and $b = (0, 0), (1, 1), (2, 2)$, respectively.

Then, we have the same line for all of them. In addition, if we take

$$L_1 : t(1, 1) + (1/2, -1/2) \quad \text{and} \quad L_2 : t(1, 1) + (1/4, -3/4),$$

we observe that $L_1 = L_2$. Hence, we need to restrict values of $b$ under a condition, and letting $b = (b_1, \ldots, b_n) \in \mathbb{R}^n$ so that $\sum_{i=1}^n b_i = 0$ is promising.

After these restrictions, let $\Lambda$ be the set of lines $L : u = tm + b$ where $\vec{m} \in (0, 1]^n$ is a unit vector in $\mathbb{R}^n$ with respect to the max norm, and $\sum_{i=1}^n b_i = 0$.

**Proposition 4.3.1.** Every admissible line has a representative in the set $\Lambda$.

**Proof.** Let $L : u = tm + b$ be an admissible line where $m \notin (0, 1]^n$ and $\sum_{i=1}^n b_i \neq 0$. Define

$$m' := \frac{m}{||m||_\infty}.$$ 

Observe that $m' \in (0, 1]^n$, $||m'||_\infty = 1$ and the line $u = sm' + b$ is same as $L$ since

$$sm' + b = \frac{s}{||m||_\infty}||m||_\infty \cdot \left( \frac{m}{||m||_\infty} \right) + b = \frac{s}{||m||_\infty}m + b.$$ 

So, we obtain direction vector of the line as we want. Now, consider the hyperplane $x_1 + \ldots + x_n = 0$ in $\mathbb{R}^n$. Normal vector of this hyperplane is $\vec{n} = (1, \ldots, 1) \in \mathbb{R}^n$ and $\vec{n} \cdot \vec{m}' \neq 0$. Thus, $\vec{m}'$ is not parallel to the hyperplane. In addition, dimensions of the hyperplane $(n - 1)$ and the line (1) are complement of $n$. This implies that the hyperplane and the line $u = sm' + b$ intersect with each other. Therefore, there exists $b' = (b'_1, \ldots, b'_n) \in L$ such that $\sum_{i=1}^n b'_i = 0$. Thus, we rewrite $L$ as $u = sm' + b'$. □

**Proposition 4.3.2.** Every line in the set $\Lambda$ is uniquely determined by $\vec{m}$ and $b$.

**Proof.** Let $L_1 : tm + b$ and $L_2 : th + d$ be equal lines in $\Lambda$. Then, their direction vectors are parallel. So, let $h = cm$ for some $c \in \mathbb{R}$. Since $\vec{m}$ and $\vec{h}$ are unit vectors, there exists $i, j \in \{1, \ldots, n\}$ such that $m_i = 1$ and $h_j = 1$. So, $h_i = c \cdot 1 = c$ and we also have $1 = h_j = cm_j$. Moreover, we know that $c = h_i \in (0, 1]$. Suppose that $c \neq 1$, then $1 = cm_j$ implies that $m_j > 1$, but this contradicts with the fact $m_j \in (0, 1]$. Thus, $c = 1$, and $h = m$. 

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Therefore, $L_1 : tm + b$ and $L_2 : tm + d$. Then, let $t_1m + b = t_2m + d$ for some $t_1, t_2 \in \mathbb{R}$. So, $(t_1 - t_2)m = d - b$. If we consider each coordinate, we have

$$(t_1 - t_2)m_i = d_i - b_i$$

$$\Rightarrow \sum_{i=1}^{n} (t_1 - t_2)m_i = \sum_{i=1}^{n} d_i - b_i$$

$$\Rightarrow (t_1 - t_2)\sum_{i=1}^{n} m_i = \sum_{i=1}^{n} d_i - \sum_{i=1}^{n} b_i$$

$$\Rightarrow (t_1 - t_2)\sum_{i=1}^{n} m_i = 0.$$ 

Since $m_i > 0$ for all $i \in \{1, \ldots, n\}$, $t_1 - t_2 = 0$. Thus, $t_1 = t_2$ and $t_1m + b = t_1m + d$ implies that $b = d$. So, by choosing $\bar{m}$ and $b$, we decide lines in the set $\Lambda$ uniquely.

Since we uniquely obtain lines in $\Lambda$, we take a line $L$ only once in the computation of the bottleneck distance. However, we can ask whether the computation of $m_L.d_B(M_L, N_L)$ is always same for different parametrizations of an admissible line $L$. If we change constant $b$, it creates the same shifting in 1-parameter persistence modules $M_L$ and $N_L$, so the bottleneck distance does not change. Let us see this situation in practice: Say

$L_1 : u = t(m_1, m_2, \ldots) + (x_1, x_2, \ldots)$ and $L_2 : u = t(m_1, m_2, \ldots) + (y_1, y_2, \ldots)$

are two different parametrizations of the same line $L$. Assume that when we compute the bottleneck distance between barcodes of $M_{L_1}$ and $N_{L_1}$, the interval modules $[a_1, c_1)$ and $[b_1, d_1)$ are matched with each other. Consider the corresponding interval modules of $[a_1, c_1)$ and $[b_1, d_1)$ in the decompositions of $M_{L_2}$ and $N_{L_2}$, respectively: $[a_2, c_2)$ and $[b_2, d_2)$. So, we have

$$a_1(m_1, m_2, \ldots) + (x_1, x_2, \ldots) = a_2(m_1, m_2, \ldots) + (y_1, y_2, \ldots)$$

$$b_1(m_1, m_2, \ldots) + (x_1, x_2, \ldots) = b_2(m_1, m_2, \ldots) + (y_1, y_2, \ldots)$$

$$\Rightarrow (x_1 - y_1, x_2 - y_2, \ldots) = (a_2 - a_1)(m_1, m_2, \ldots)$$

$$= (b_2 - b_1)(m_1, m_2, \ldots)$$

$$\Rightarrow a_2 - a_1 = b_2 - b_1$$

$$\Rightarrow b_1 - a_1 = b_2 - a_2.$$ 

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Similarly,
\[ d_1 - c_1 = d_2 - c_2. \]

Costs coming from the matchings of pairs are equal to each other:
\[
\max\{|b_1 - a_1|, |d_1 - c_1|\} = \max\{|b_2 - a_2|, |d_2 - c_2|\}.
\]

In a similar way, if \([a_1, c_1]\) is matched with the zero module, then we obtain the following relation with the corresponding interval module \([a_2, c_2]\):
\[
c_1 - a_1 = c_2 - a_2 \Rightarrow c\left(\frac{a}{K}, \frac{c}{k}\right) = \frac{c_1 - a_1}{2} = \frac{c_2 - a_2}{2} = c\left(\frac{a}{k}, \frac{c}{k}\right).
\]

Hence, costs are again equal to each other. This implies that \(d_B\) gives the same number although we change the parametrization of the line with respect to \(b\).

Moreover, let us investigate what happens to \(d_B\) if we take a \(k\)-multiple of the direction vector where \(k > 0\): Say
\[
L_1 : u = t(m_1, m_2, \ldots) + (x_1, x_2, \ldots) \text{ and } L_2 : u = t(km_1, km_2, \ldots) + (x_1, x_2, \ldots)
\]
are two different parametrizations of the same line \(L\). If \([a, c]\) and \([b, d]\) are matched in some matching between \(M_{L_1}\) and \(N_{L_1}\), then
\[
\left[\begin{array}{cc}
a & c \\
\frac{a}{K} & \frac{c}{k}
\end{array}\right] \text{ and } \left[\begin{array}{cc}
b & d \\
\frac{b}{K} & \frac{d}{k}
\end{array}\right]
\]
are matched with each other in the corresponding matching between \(M_{L_2}\) and \(N_{L_2}\).

Thus, we have the following relation between costs:
\[
c\left(\frac{a}{k}, \frac{c}{k}\right) = \max\{|b - a|, |d - c|\} \\
= k \cdot \max\left\{\left|\frac{b - a}{k}\right|, \left|\frac{d - c}{k}\right|\right\}
\]

Similarly, if an interval module is matched with the zero module, its cost is divided by \(k\) in the case of \(L_2\). Therefore, the corresponding bottleneck distance is divided by \(k\), but \(m_L\) is multiplied by \(k\), so we have the same result for \(m_L, d_B\). Thus, matching distance does not be affected from different parametrizations of the same admissible line.

Remark 4.3.2. As a result of above parts, the matching distance between \(M\) and \(N\) can be found by only considering lines from \(\Lambda\). From now on, \(L\) always varies in \(\Lambda\) when we compute \(d_{\text{match}}\).
Furthermore, the matching distance is an extended pseudometric. To see why it is not an extended metric, we examine the following example:

**Example 4.3.1.** In Figure 4.2, we have two 2-parameter interval decomposable persistence modules

\[ M \cong M_1 \oplus M_2 \text{ and } N \cong N_1 \oplus N_2. \]

We claim first that they are not isomorphic. To see this, assume otherwise. Then, by Theorem 3.2.2 (ii), there is a bijection between index sets \{1, 2\} giving isomorphisms between the corresponding modules. Thus, \( N_1 \) is isomorphic to either \( M_1 \) or \( M_2 \).

To see that neither is possible, consider the linear maps

\[ (N_1)_{(0,1)} \to (N_1)_{(1,1)} \text{ and } (N_1)_{(1,0)} \to (N_1)_{(1,1)}. \]

These are by definition just the identity maps from the field \( \mathbb{k} \) to itself. However,

\[ (M_1)_{(0,1)} = 0 \to (M_2)_{(1,1)} = \mathbb{k} \text{ and } (M_2)_{(1,0)} = 0 \to (M_2)_{(1,1)} = \mathbb{k} \text{ are zero maps.} \]

Hence, none of the modules \( M_1 \) and \( M_2 \) have both maps as identity. So, \( N_1 \) is not isomorphic to any of \( M_1 \) and \( M_2 \). This gives a contradiction. Thus, \( M \) and \( N \) are not isomorphic.

On the other hand, if we restrict \( M \) and \( N \) to lines \( L \in \Lambda \), then it can be seen from Figure 4.2 that corresponding 1-parameter persistence modules \( M_L \) and \( N_L \) are equal to each other. Thus, we have

\[ d_B(B(M_L), B(N_L)) = 0 \text{ for all } L \in \Lambda. \]
So, we have

\[ d_{\text{match}}(M, N) = 0. \]

This implies that \( d_{\text{match}} \) is not an extended metric.

Moreover, we can also make an inference about the interleaving distance. To achieve this, let us first observe that both of \( M \) and \( N \) are finitely presented. Let \( 1^{(i,j)} \) show the multiplicative identity of \( k \) at the grade \( (i, j) \in \mathbb{R}^2 \).

\( M_1 \) is generated by \( 1^{(1,0)} \), and the relations are generated by \( 1^{(1,5)} \) and \( 1^{(5,0)} \). Hence, taking \( F_1 = Q^{(1,5)} \oplus Q^{(5,0)} \), and \( F_0 = Q^{(1,0)} \) in Definition \( 39 \) makes \( M_1 \) finitely presented. In the other ones, we just state the generators of \( F_0 \) and \( F_1 \):

i) For \( M_2 \), \( 1^{(0,1)} \) generates \( F_0 \), and \( 1^{(0,5)}, 1^{(5,1)} \) generate \( F_1 \).

ii) For \( N_1 \), \( 1^{(1,0)}, 1^{(0,1)} \) generate \( F_0 \), and \( 1^{(0,5)}, 1^{(5,0)}, 1^{(1,1)} \) generate \( F_1 \).

iii) For \( N_2 \), \( 1^{(1,1)} \) generates \( F_0 \), and \( 1^{(1,5)}, 1^{(5,1)} \) generate \( F_1 \).

So, all of them are finitely presented. This implies that direct sums \( M \) and \( N \) are also finitely presented. Now, let us assume that \( d_I(M, N) = 0 \). Then, since they are also finitely presented, there exists a 0-interleaving between \( M \) and \( N \) by the Closure Theorem. However, being 0-interleaved means that these modules are isomorphic to each other, and we have observed that they are not. Therefore, our assumption is wrong. Thus, \( d_I(M, N) > 0 = d_{\text{match}}(M, N) \).

The matching distance shows up as a computable surrogate of other distances. Recently, the exact computation of the matching distance gets attention in the theory of multiparameter persistence modules, [19] and [2]. Researchers mainly work on 2-parameter persistence modules because visualizing them is rather easy and results in 2-parameter are more likely to be generalized. Kerber et. al. showed that the computation of the matching distance can be done in polynomial time [19]. Later, Brooks et. al. restricted the set of lines \( \Lambda \) to some set which is enough to consider to find the matching distance [2]. Moreover, they have provided both geometric interpretation and easy implementation.
In the next step, we want to understand whether the matching distance is stable or not. We examine this obscurity with the help of the interleaving distance.

**Lemma 4.3.3.** [20] If $M$ and $N$ are $\epsilon$-interleaved, then $M_L$ and $N_L$ are $\left(\frac{\epsilon}{m_L}\right)$-interleaved.

**Proof.** In the proof, we use the following notation:

\[
M(u) := M_u \\
\phi(u + \vec{\epsilon}) := \phi_{u+\vec{\epsilon}}; \\
\varphi^M(u, u + 2\vec{\epsilon}) := \varphi^{M,u,u+2\vec{\epsilon}}.
\]

Since $M$ and $N$ are $\epsilon$-interleaved, there exist two morphisms $\phi : M \to N(\vec{\epsilon})$ and $\psi : N \to M(\vec{\epsilon})$ such that

\[
\psi(u + \vec{\epsilon}) \circ \phi(u) = \varphi^M(u, u + 2\vec{\epsilon}),
\]

and

\[
\phi(u + \vec{\epsilon}) \circ \psi(u) = \varphi^N(u, u + 2\vec{\epsilon})
\]

where $u \in \mathbb{R}^n$, so that triangle diagrams commute. Our aim is to show the existence of two morphisms $\phi_L : M_L \to N_L(\frac{\epsilon}{m_L})$ and $\psi_L : N_L \to M_L(\frac{\epsilon}{m_L})$ such that

\[
\psi_L \left( s + \frac{\epsilon}{m_L} \right) \circ \phi_L(s) = \varphi^{M_L} \left( s + 2 \frac{\epsilon}{m_L} \right)
\]

and

\[
\phi_L \left( s + \frac{\epsilon}{m_L} \right) \circ \psi_L(s) = \varphi^{N_L} \left( s + 2 \frac{\epsilon}{m_L} \right)
\]

where $s \in \mathbb{R}$.

Consider an arbitrary $s \in \mathbb{R}$ with points $u(s) = sm + b$, $u'(s) = \left( s + \frac{\epsilon}{m_L} \right) m + b$ and $u''(s) = \left( s + 2 \frac{\epsilon}{m_L} \right) m + b$ on $L$. Consider each coordinate:

\[
u(s) = (sm_1 + b_1, \ldots, sm_n + b_n) \\
u'(s) = \left( \left( s + \frac{\epsilon}{m_L} \right) m_1 + b_1, \ldots, \left( s + \frac{\epsilon}{m_L} \right) m_n + b_n \right) \\
= u(s) + \frac{\epsilon}{m_L} (m_1, \ldots, m_n) \\
\geq u(s) + \vec{\epsilon}
\]
since \( m_L = \min_{i=1,...,n} \{m_i\} \).

Let us define \( \phi_L : M_L \to N_L \left( \frac{\epsilon}{m_L} \right) \) and \( \psi_L : N_L \to M_L \left( \frac{\epsilon}{m_L} \right) \) by

\[
\phi_L(s) = \phi(u' - \bar{\epsilon}) \circ \varphi^M(u, u' - \bar{\epsilon}) \quad \text{and} \quad \psi_L(s) = \psi(u' - \bar{\epsilon}) \circ \varphi^N(u, u' - \bar{\epsilon})
\]

where \( M_L(s) = M(u) \) and \( N_L(s) = N(u) \).

Since \( u(s) \leq u'(s) - \bar{\epsilon} \) for all \( s \in \mathbb{R} \), \( u \leq u' - \bar{\epsilon} \). Hence, linear maps \( \varphi^M(u, u' - \bar{\epsilon}) \) and \( \varphi^N(u, u' - \bar{\epsilon}) \) are well-defined. Therefore, \( \phi_L \) and \( \psi_L \) are well-defined morphisms.

Notice that \( \psi_L(s) \) is defined from \( N_L(s) = N(u) \) to \( M_L \left( s + \frac{\epsilon}{m_L} \right) = M(u') \). Also, we have \( \varphi^M(u + \bar{\epsilon}, u') \circ \psi(u) \) from \( N(u) \) to \( M(u') \) and this gives the following equality:

\[
\psi_L(s) = \varphi^M(u + \bar{\epsilon}, u') \circ \psi(u)
\]

by the following commutative diagram coming from definition of morphisms:

\[
\begin{array}{ccc}
M(u + \bar{\epsilon}) & \longrightarrow & M(u') \\
\downarrow & & \downarrow \\
N(u) & \longrightarrow & N(u' - \bar{\epsilon})
\end{array}
\]

Consider

\[
\psi_L \left( s + \frac{\epsilon}{m_L} \right) \circ \phi_L(s) = \varphi^M(u' + \bar{\epsilon}, u'' \circ \psi(u') \circ \phi(u' - \bar{\epsilon}) \circ \varphi^M(u, u' - \bar{\epsilon}).
\]

Since \( \varphi^M(u' - \bar{\epsilon}, u' + \epsilon) = \psi(u') \circ \phi(u' - \bar{\epsilon}),

\[
\psi_L \left( s + \frac{\epsilon}{m_L} \right) \circ \phi_L(s) = \varphi^M(u' + \bar{\epsilon}, u'' \circ \varphi^M(u' - \bar{\epsilon}, u' + \epsilon) \circ \varphi^M(u, u' - \bar{\epsilon})
\]

\[
= \varphi^M(u, u' + \bar{\epsilon}) \circ \varphi^M(u, u' - \bar{\epsilon})
\]

\[
= \varphi^M \left( s, s + 2 \frac{\epsilon}{m_L} \right).
\]

Similarly, \( \phi_L(s) \) is defined from \( M_L(s) = M(u) \) to \( N_L \left( s + \frac{\epsilon}{m_L} \right) = N(u') \). So, we can write \( \phi_L(s) \) as

\[
\phi_L(s) = \varphi^N(u + \bar{\epsilon}, u') \circ \phi(u).
\]

Consider

\[
\phi_L \left( s + \frac{\epsilon}{m_L} \right) \circ \psi_L(s) = \varphi^N(u' + \bar{\epsilon}, u'') \circ \phi(u') \circ \psi(u' - \bar{\epsilon}) \circ \varphi^N(u, u' - \bar{\epsilon}).
\]
Since $\varphi^N(u' - \bar{\epsilon}, u' + \epsilon) = \phi(u') \circ \psi(u' - \bar{\epsilon}),$

$$\phi_L \left( s + \frac{\epsilon}{m_L} \right) \circ \psi_L(s) = \varphi^N(u' + \bar{\epsilon}, u' + \epsilon) \circ \varphi^N(u', u' + \bar{\epsilon}) = \varphi^N(u, u' + \bar{\epsilon}) = \varphi^M_L \left( s, s + 2\frac{\epsilon}{m_L} \right).$$

Thus, triangle diagrams commute. Therefore, $M_L$ and $N_L$ are $\left(\frac{\epsilon}{m_L}\right)$-interleaved.

\[ \square \]

**Theorem 4.3.4.** [20] For arbitrary p.f.d. persistence modules $M$ and $N$, we have

$$d_{\text{match}}(M, N) \leq d_I(M, N).$$

**Proof.** Let $L \in \Lambda$. By Lemma 4.3.3 if $M$ and $N$ are $\epsilon$-interleaved, then $M_L$ and $N_L$ are $\left(\frac{\epsilon}{m_L}\right)$-interleaved. Thus,

$$m_L.d_I(M_L, N_L) \leq d_I(M, N).$$

Since $M$ and $N$ are pointwise finite dimensional, so are $M_L$ and $N_L$. Thus, from the Isometry Theorem in 1-parameter, $d_I(M_L, N_L) = d_B(B(M_L), B(N_L)).$ So,

$$d_{\text{match}}(M, N) = \sup_L m_L.d_B(B(M_L), B(N_L)) \leq d_I(M, N).$$

\[ \square \]

So, the matching distance between p.f.d. persistence modules is a lower bound for a stable distance, namely the interleaving distance. Thus, it satisfies the comparison in Definition 43 where $M^f$ and $M^g$ need to be p.f.d. Hence, the matching distance defined between $\mathbb{R}^n$ indexed p.f.d. persistence modules is also stable.

We want to point out that computing the matching distance is not straightforward since we need to take infinitely many lines into account. On the other hand, if we know the interleaving distance between two persistence modules, finding the matching distance can be easier in some cases.

**Example 4.3.2.** Recall Figure 4.1 where we have two persistence modules

$$M = \mathbb{k}_{I_1} \oplus \mathbb{k}_{I_2} \oplus \mathbb{k}_{I_3} \text{ and } N = \mathbb{k}_J.$$
We have already seen that \( d_I(M, N) = 1 \). To calculate the matching distance, we consider the line \( L_1 : u = t(1, 1) \) where \( t \in \mathbb{R} \). Then, \( m_{L_1} = 1 \) and

\[
M_{L_1} = \mathbb{I}_{(-1,1)} \oplus \mathbb{I}_{(-1,1)} \oplus \mathbb{I}_{(-1,1)} \quad \text{and} \quad N_{L_1} = \mathbb{I}_{(-2,2)}.
\]

Therefore, we have the following induced barcodes

\[
B(M_{L_1}) = (-1, 1) \oplus (-1, 1) \oplus (-1, 1) \quad \text{and} \quad B(N_{L_1}) = (-2, 2).
\]

We find the bottleneck distance by following the construction given in Subsection 2.5. We have 4 matchings between \( B(M_{L_1}) \) and \( B(N_{L_1}) \). Three of them are exactly the same: one copy of \((-1, 1)\) is matched with \((-2, 2)\) and the other copies are left unmatched. Hence, we find their cost as

\[
\max\{c((-1, 1), (-2, 2)), c((-1, 1))\} = \max\{1, 1\} = 1.
\]

In the last matching, all of the intervals are unmatched. Thus, its cost is

\[
\max\{c((-1, 1)), c((-2, 2))\} = \max\{1, 2\} = 2.
\]

Hence, the bottleneck distance is equal to

\[
d_B(B(M_{L_1}), B(N_{L_1})) = \min\{1, 2\} = 1.
\]

Observe that, this implies

\[
1 = m_{L_1} d_B(B(M_{L_1}), B(N_{L_1})) \leq \sup_L m_L d_B(B(M_L), B(N_L))
\]

\[
= d_{\text{match}}(M, N)
\]

\[
\leq d_I(M, N) = 1.
\]

Thus, we have \( d_{\text{match}}(M, N) = 1 \).

In the above example, note first that the interleaving distance is an upper bound for the matching distance since we start with p.f.d. persistence modules. Moreover, the computation of the matching distance on the line \( L_1 \) realizes this upper bound. Since the matching distance is calculated as the supremum through all admissible lines, we can immediately conclude that the matching distance between \( M \) and \( N \) is 1. However, this method is impractical because calculating \( d_I \) is much more difficult.

We may expect to catch the matching distance by considering only lines with slope 1, but the next example shows that, unlike the previous one, it is not sufficient to find the matching distance.
Example 4.3.3. Let $M$ and $N$ be 2-parameter rectangle decomposable persistence modules given as

$$M = M_1 \oplus M_2 = k_{R_1} \oplus k_{R_2} \quad \text{and} \quad N = N_1 \oplus N_2 = k_{R_3} \oplus k_{R_4}$$

where

$$R_1 = [0, 7) \times [0, 7), \quad R_2 = [0, 7) \times [4, 11),$$

$$R_3 = [0, 7) \times [0, 11), \quad R_4 = [0, 7) \times [4, 7).$$

According to Figure 4.3 observe that for the lines $L : y = x + p$ where $p \leq 0$ or $p \geq 4$, restrictions of $M$ and $N$ to such lines are equal, that is, $M_L = N_L$. Hence, $d_B(B(M_L), B(N_L)) = 0$. So, the matching distance coming from such lines is just 0.

On the other hand, if we consider the lines $L : y = x + p$ where $0 < p < 4$, they are uniquely parametrized as

$$L : t(1, 1) + \left( -\frac{p}{2}, \frac{p}{2} \right), \quad t \in \mathbb{R}$$

so that $L \in \Lambda$. Let us consider barcodes of restrictions of $M$ and $N$ to such lines.

$$B(M_L) = B((M_1)_L) \oplus B((M_2)_L) = \left[ \frac{p}{2}, 7 - \frac{p}{2} \right] \oplus \left[ 4 - \frac{p}{2}, 7 + \frac{p}{2} \right],$$

$$B(N_L) = B((N_1)_L) \oplus B((N_2)_L) = \left[ \frac{p}{2}, 7 + \frac{p}{2} \right] \oplus \left[ 4 - \frac{p}{2}, 7 - \frac{p}{2} \right].$$

In all of these lines, $m_L = 1$. So, to analyze effects of these lines on the matching distance, we only consider the corresponding bottleneck distances. Now, consider all the matchings:
σ₁: \((M_i)_L\) is matched with \((N_i)_L\) for \(i = 1, 2\). Then, \(c(σ_1) = p\).

σ₂: \((M_1)_L\) is matched with \((N_2)_L\) and \((M_2)_L\) is matched with \((N_1)_L\). Then, \(c(σ_2) = 4 - p\).

σ₃: \((M_1)_L\) is matched with \((N_1)_L\), \((M_2)_L\) and \((N_2)_L\) is unmatched. Then,
\[
c(σ_3) = \begin{cases} 
3 + p & \text{if } p \leq 3, \\
p & \text{if } p > 3.
\end{cases}
\]

σ₄: \((M_1)_L\) is matched with \((N_2)_L\), \((M_2)_L\) and \((N_1)_L\) is unmatched. Then,
\[
c(σ_4) = \begin{cases} 
4 - p & \text{if } p \leq \frac{1}{2}, \\
\frac{7}{2} & \text{if } p > \frac{1}{2}.
\end{cases}
\]

σ₅: \((M_2)_L\) is matched with \((N_1)_L\), \((M_1)_L\) and \((N_2)_L\) is unmatched. Then,
\[
c(σ_5) = \begin{cases} 
4 - p & \text{if } p \leq 1, \\
\frac{7 - p}{2} & \text{if } p > 1.
\end{cases}
\]

σ₆: \((M_2)_L\) is matched with \((N_2)_L\), \((M_1)_L\) and \((N_1)_L\) is unmatched. Then,
\[
c(σ_6) = \begin{cases} 
\frac{7}{2} & \text{if } p \leq \frac{7}{2}, \\
p & \text{if } p > \frac{7}{2}.
\end{cases}
\]

σ₇: They are all unmatched. Then, \(c(σ_7) = \frac{7}{2}\).

Remember that we take infimum of all matchings to find the bottleneck distance. If \(p < 2\), then minimum of costs of all the matchings is equal to \(p\) happening in \(σ_1\). This implies that \(d_B\) is smaller than 2 for the case \(p < 2\). If \(p > 2\), then \(4 - p\) coming from \(σ_2\) is the minimum of costs of all matchings. Therefore, \(d_B\) is also smaller than 2 for the case \(p > 2\). Lastly, we consider all matchings when \(p = 2\) and see that the corresponding bottleneck distance is 2 which is the biggest one among them.

On the other hand, consider the line \(L'\) passing through \((0, 0)\) and \((7, 11)\). Its equation is \(y = \frac{11}{7}x\). So, the parametrization of it making \(L'\) an element of \(Λ\) is
\[
L' : t\left(\frac{7}{11}, 1\right), \ t \in \mathbb{R}.
\]
Thus, we have

\[ B(M_{L'}) = B((M_1)_{L'}) \oplus B((M_2)_{L'}) = [0, 7) \oplus [4, 11), \]

\[ B(N_{L'}) = B((N_1)_{L'}) \oplus B((N_2)_{L'}) = [0, 11) \oplus [4, 7). \]

By analyzing all matchings, we see that \( d_B(B(M_{L'}), B(N_{L'})) = 4 \). Since \( m_{L'} = \frac{7}{11} \), we have

\[ m_{L'} \cdot d_B(B(M_{L'}), B(N_{L'})) = \frac{7}{11} \cdot 4 \]

\[ > 1.2 = m_L \cdot d_B(B(M_L), B(N_L)) \]

where \( L : y = x + 2 \). Since we take supremum in the computation of the matching distance, it cannot happen by a restriction of a line with slope 1 in this example. We also want to remark that at this point all we can say is that \( d_{\text{match}}(M, N) \geq \frac{28}{11} \).

When the lines are in \( \mathbb{R}^2 \), we work on the representations coming from \( \Lambda \) instead of the equations of the form: \( y = mx + c \) where \( m, c \in \mathbb{R} \). The reason is that the first way can be easily extended to \( n \)-parameter case where \( n \geq 3 \).
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