Distributions of Matching Distances in Topological Data Analysis

So Mang Han, Taylor Okonek, Nikesh Yadav, Xiaojun Zheng
St. Olaf College, Northfield, Minnesota, USA

January 1, 2019

Abstract

In topological data analysis, we want to discern topological and geometric structure of data, and to understand whether or not certain features of data are significant as opposed to simply random noise. While progress has been made on statistical techniques for single-parameter persistence, the case of two-parameter persistence, which is highly desirable for real-world applications, has been less studied. This paper provides an accessible introduction to two-parameter persistent homology and presents results about matching distance between 2-D persistence modules obtained from families of point clouds. Results include observations of how differences in geometric structure of point clouds affect the matching distance between persistence modules. We offer these results as a starting point for the investigation of more complex data.

1 Introduction and Motivations

Topological data analysis (TDA) is a collection of methods used to discern the shape of data. These methods have been used in a variety of settings, including quantifying clusters, holes, and voids in astronomical data [14], image analysis [1], and studying the structures and binding of proteins [2].

Consider Figure 1 which shows a 3D image of a rabbit. Given a large collection of digital images, possibly corrupted by noise, topological signatures can be used to distinguish rabbits shown in Figure 1 from other objects [15]. It is critical that features of the rabbit are invariant to shifts, rotations and small deformations. TDA has shown promise in being able to accurately define such
features. TDA has also been used to study texture representation of images. The TDA process is especially useful for extracting information from high dimensional and noisy data to analyze, which can be challenging for geometric approaches. While statistical methods exist for determining meaningful differences between datasets, TDA has potential to expand and improve upon these current methods, drawing from abstract algebra and topological measures of distance between datasets.

The research laid out in the paper examines the topological notion of matching distance. The goal is to better understand how matching distance changes as datasets become more dissimilar, and in particular whether or not matching distance can effectively distinguish between noise and significant features of data.

1.1 Project Data

The first analysis involved simple datasets, consisting of three dots each. Changes in matching distances were examined with two points fixed and a third point moving around the xy-plane.

The second dataset consisted of two circles with radii r, and circles were sep-
arated by a distance $d$. Each point was assigned a KNN density estimator, and many data sets were generated with various values for $d$. Matching distances were then calculated between each pair of datasets in order to examine whether or not matching distances changed in any specific pattern as distance $d$ increased with the radius unchanged.

Two-parameter persistent homology was computed using RIVET, an interactive visualization software initially developed by Michael Lesnick and Matthew Wright [12]. A detailed description of RIVET and its algorithms appears in a comprehensive preprint by Lesnick and Wright [10]. Given point-cloud data, RIVET computes a 2-parameter persistence module, a type of algebraic object. RIVET then computes barcodes along linear slices of these persistence modules. Matching distances were calculated from these barcodes, using Python code written by Bryn Keller and Michael Lesnick [13].

1.2 Outline

The organization of the paper is as follows: In Section 2, we provide mathematical background related to persistence homology and matching distance. In Section 3, we describe the two data sets consisting of three dots to understand the distributions of matching distances. The discussion and the future research are provided in Section 4 and 5.

2 Mathematical Background

Persistent homology is one of the main tools used in TDA to bridge the concepts of geometry and topology, and is an adaptation of homology to point cloud data. It quantifies multi-scale topological features of data, with topological features generally referring to the connected components, holes, and voids. Here is an example of what persistence means in one-parameter persistent homology. Given a set of points sampled from some (unknown) object in a Euclidean space, consider a set of balls centered at these points with a common radius. For certain radii, this union of balls will approximate the unknown object in various ways. Persistent homology summarizes the appearance and disappearance of topological features of the union of balls as the radius increases. The radius is the threshold parameter $\epsilon$ in one-parameter persistence [7].

Previous research has used one-parameter persistence to uncover significant features of data. However, one-parameter persistence is sensitive to outliers because the threshold parameter $\epsilon$ only depends on the distance in between
points. This sensitivity can be remedied using two-parameter persistence, which works around the outlier problem by constructing a filtration based on the importance of the data as well as the scale parameter. Moreover, real-life application data often depend on more than one parameter. Using two-parameter persistence, long-lived topological properties are separated from outliers and the short-lived ones, which are considered as possibly to be topological noise. How long a topological feature lives is from where the term “persistence” is derived. We give here a brief introduction to persistent homology; more detailed surveys of the subject are found in [6, 5].

2.1 One-dimensional persistence

A simplex is a basic geometric element, such as a point, an edge and a triangular face. For example, a point is a 0-simplex; an edge is a 1-simplex; a triangular face is a 2-simplex. Given a set of point-cloud data, we first build a simplicial complex. A simplicial complex is a set composed of points, line segments, triangular faces, and their n-dimensional counterparts. Figure 2 shows three different simplicial complexes. For our purpose, we build a Rips complex, which we now define.

Definition 1 Given a collection of points \( \{x_\alpha\} \) in Euclidean space \( \mathbb{E}^n \), the Rips complex, \( R_\epsilon \), is the simplicial complex whose k-simplices correspond to unordered \((k+1)\)-tuples of points \( \{x_\alpha\}^k \) which are pairwise within distance \( \epsilon \).

In other words, the Rips complex depends on a scale parameter \( \epsilon \). The complex contains an edge between two points if and only if the distance between the points is less than \( \epsilon \). The complex contains a triangular face for any three points if and only if the distance between each pair of points is less than \( \epsilon \). A Rips complex is built with a fixed \( \epsilon \), but no single choice of \( \epsilon \) reveals all interesting structure of the data. Instead, we consider many values of \( \epsilon \), resulting in a filtration.
A filtration is a sequence of simplicial complexes with inclusion maps. Figure 3 illustrates a filtration; the simplicial complexes $C_i$ are connected with inclusion maps, which mean each $C_i$ is the subset of the all $C_i$ that appear after it. In this paper, we use the Rips filtration, visualized in Figure 3 and described as follows: One can imagine that each point in a point cloud dataset is at the center of a growing ball. Let $\epsilon$ be the diameter of the growing ball around each point. As $\epsilon$ increases, edges will be drawn between these growing balls once they overlap. If growing balls of three data points pairwise overlap each other, a triangular face will appear, which is the shaded area in Figure 3. As $\epsilon$ goes to infinity, points in the point cloud will all connect to become one connected component. The filtration of a dataset $C$ can be seen in Figure 3 below. Note that simplices are added, but never removed, as $\epsilon$ increases, which is the property of inclusion map.

![Figure 3: The building of a barcode from a simplicial complex. (H_0: orange line, H_1: blue line)](image)

In order to quantify the topological features of a simplicial complex, we use the mathematics of homology. Homology associates a vector space to each simplicial complex, and a linear map to each inclusion map in the filtration. Fix an index $i \in \{0, 1, 2, \ldots\}$. Then the degree $i$ homology of simplicial complex $C$, denoted $H_i(C)$, is a vector space with basis consisting of $i$-dimensional "holes" in complex $C$. Specifically, $H_0(C)$ is a vector space whose basis consists of the connected components of $C$. $H_1(C)$ has the holes of $C$ as its basis. $H_2(C)$ has the voids of $C$ as its basis, and similarly for higher dimensions. Usually, we use vector spaces over the two-element field $F_2$. For more details about homology, see [15].

The sequence of vectors spaces $H_i(C)$ and linear maps between them is defined as a persistence module, and a one-dimensional persistence module is
essentially the homology of the filtration. The structure theorem for persistence modules says a persistence module is the sum of “intervals” and each interval is a topological feature in the filtration \(^4\). A barcode is a visualization of the persistence module, which each “interval” shown as a bar.

A **barcode**, as seen at the bottom of Figure\(^3\), is an efficient way to indicate the life of topological features. The persistence of the topological features is represented by the length of the bars. Each bar represents a feature’s “persistence” over scale as \(\epsilon\) increases. The beginning and the end of the bar represent the birth and the death of the feature.

A persistence diagram is another expression of a barcode, where the points in the persistence diagram are in one-to-one correspondence with the bars in the barcode plot. The birth and death times of the barcode become the \(x\)- and \(y\)-coordinates of the persistence diagram, so the points are always located above the diagonal line. For example, a bar from \(a\) to \(b\) is plotted as a point \((a, b)\) in the persistence diagram.

In one-dimensional persistence, the bottleneck distance is a metric for determining how different one data set is from another, which can be computed from two persistence diagrams. Before defining bottleneck distance, we introduce the concept of matching.

Given two persistence diagrams \(D_1\) and \(D_2\), each point in \(D_1\) can be either matched with a point in \(D_2\) or a point on the diagonal line. By convention, we use the \(L_{\infty}\) metric to obtain the distance from a point \(x = (x_1, x_2)\) to its matched point \(\eta(x) = (y_1, y_2)\):

\[
||x - \eta(x)||_{\infty} = \max(|x_1 - y_1|, |x_2 - y_2|)
\]

Let the “size” of a matching refer to the supremum of the \(L_{\infty}\) distance between matched points. Among all possible matchings, we seek a matching with the smallest size. The bottleneck distance between \(D_1\) and \(D_2\) is the size of this optimal matching, as defined below.

**Definition 2** The **bottleneck distance** between persistence diagrams \(D_1\) and \(D_2\) is

\[
d_{B}(D_1, D_2) = \inf_{\eta} \sup_{x} ||x - \eta(x)||_{\infty},
\]

where the supremum is taken over all matched points \(x\) and the infimum is taken over all matchings \(\eta\).

In other words, the bottleneck distance is calculated by determining the maximum distance between two barcodes, plotted as persistence diagrams, as in Figure\(^4\). In the figure, \(D_1\) is plotted in blue, and \(D_2\) is plotted in red. Every
point from each barcode must either be connected to a point from the other barcode, or connected to the diagonal. For example, the blue point \((a, b)\) is matched with the red point \((c, d)\), so the \(L_\infty\)-distance between these two points is \(\max(|a-c|, |b-d|)\). These connecting distances are minimized by finding the optimal matching, and the bottleneck distance is the maximum \(L_\infty\) distance in the optimal matching. This figure shows the optimal matching for the given persistence diagrams.

![Figure 4: Calculating bottleneck distance from two barcodes](image)

2.2 Two-dimensional persistence

A bifiltration is a set of simplicial complexes with inclusion maps in two directions, as in Figure 5 (left), thus extending a filtration to two dimensions. The homology of a bifiltration is a 2-dimensional persistence module, which is a set of vector spaces with linear maps in two directions, as in Figure 5 (right). In two-dimensional persistence, the matching distance is a metric for determining how different one data set is from another.

Unfortunately, there is no 2-D barcode for a 2-D persistence module due to the complicated algebraic structure of such modules [9]. Instead, we can obtain a barcode along any line with nonnegative slope by restricting the 2-D persistence module to the line, as we next explain.

Let \(M\) be a 2-D persistence module and \(\ell\) be a line in \(\mathbb{R}^2\) with non-negative slope. Then let \(M_\ell\) be the 1-D persistence module obtained by restricting \(M\) to line \(\ell\) (as in Figure 6b). To define \(M_\ell\), it suffices to give the homology vector spaces along \(\ell\) and the maps between them.

The degree \(i\) homology vector space at the intersection point of line \(\ell\) and the horizontal linear-map arrow is the same vector space as the one on its left, and the vector space at the intersection point of \(\ell\) and the vertical linear-map arrow...
Figure 5: A bifiltration (left) and the corresponding 2-D persistence module (right)

is the same as the vector space at the point below it. In Figure 6a, point A gives the same vector space as $H_0(C_{1,1})$, and point B gives the same vector space as $H_0(C_{2,1})$. The maps along the linear maps are induced by those in the 2-D module. We can then visualize the barcode of $\mathcal{M}_\ell$ by RIVET plot (as in Figure 6a).

Furthermore, we can define a distance between 2-D persistence modules by considering the bottleneck distance along all possible lines through the 2-D persistence modules. In the following definition, we use the bottleneck distance between two 1-D persistence modules, but we really mean the bottleneck distance between persistence diagrams of the modules. We ask the reader to forgive this abuse of notation.

**Definition 3** The matching distance, $d_M$, between two 2-D persistence modules $\mathcal{M}$ and $\mathcal{N}$ is the supremum of the bottleneck distances between the persistence diagrams on corresponding lines of non-negative slope, $\ell$, in the two modules. Precisely,

$$d_M = \sup_{\ell} \{d_B(\mathcal{M}_\ell, \mathcal{N}_\ell), \text{weight}(\text{slope}(\ell))\},$$

where the supremum is over all lines of nonnegative slope and $\text{weight}(m) = \frac{1}{\sqrt{1+q^2}}$, where $q = \max \left(m, \frac{1}{m}\right)$.

1The size of a persistence module is determined by the coordinates of the lower left and the upper right corners, which $\delta x$ is the range of the second parameter, and the $\delta y$ is the range of the
Calculating matching distance based on weighted bottleneck distance (RIVET Plot)

A weight is assigned to each line, which depends on the slope. The line with slope 1 gets the highest weight and the weight is smaller for the lines that are more horizontal or vertical. The weight is chosen such that if the interleaving distance between two persistence modules is 1, then the weighted bottleneck distance between the slices is at most 1 [9, 8].

Imagine that one wants to determine how dissimilar two datasets are from each other using two-dimensional persistence. RIVET computes a 2-parameter persistence module from each data set. We choose to visualize these modules with codensity on the x-axis and distance on the y-axis. Codensity is used to quantify how close a data point is from other data points, and it is the opposite of density. A data point that is close to the other points in the data set will be assigned a low codensity, and a data that is far from other points will be assigned a high codensity. Along the x-axis, the points with the low codensity in the data set will first appear. As the codensity increases, more points will be added.

Figure 6a is a RIVET visualization for $H_0$ computed from the bifiltration shown

Figure 6: 2-D persistence barcodes visualization
The green dots represent the birth of the connected components, and the red dots represent the death of the connected components. The size of the dots tells the number of births or deaths at the given codensity and distance. For example, the green dot on the lower left shows that two components appear at codensity 1 with the distance 0. As the distance increases, these two components are connected to each other, so one component disappears at the red-dot position. The shaded area tells the number of connected components at these various co-densities and distances. The grayscale shading indicates the dimension of the homology vector spaces (i.e., the number of connected components) for all codensity and distance pairs. Darker shades indicate higher dimension of homology. In the plot, the color of the shaded area becomes lighter above the red dot at codensity 1, indicating a single connected component.

The blue line in Figure 6a is a sample line \( \ell \) of nonegative slope, and the purple segments represent the barcode of \( M_\ell \). The barcodes shown on the plot are at angle around 45 degrees with the offset around 1, where the angle is the one between the blue line and the x-axis, and the offset is the perpendicular distance from the origin to the blue line. The angle and the offset can be changed in RIVET to get a collection of barcodes from different lines.

As described above, each pair of barcodes for two data sets determines a bottleneck distance. In two-dimensional persistence, the pair of barcodes are the ones with the same angle and offset. We approximate the matching distance using a large number of angles and offsets, and the matching distance between two data sets is the maximum, weighted bottleneck distance across all angles and offsets used in the RIVET calculation, as in Figure 6a. Thus, matching distance is a notion of distance between 2-D persistence modules, and is the most easily computed distance given current technology. For our purpose in this paper, matching distance is considered as the distance between two pointcloud data sets.

## 3 Data analysis

### 3.1 Three-point Example

In order to understand distributions of matching distances between point clouds with many observations, it is first useful to understand more simple cases. Using data sets with three points, matching distances were calculated between many pairs of data sets. Every data set consisted of two of the same points (labeled A and B in Figure 7), and a third additional point somewhere in the \( xy \)-plane. Figures 7a and 7b show two examples of these data sets, and Figure
Figure 7 shows $C_i$ used in this study. Since $A$ and $C_i$ are always the closest pair of points, we assigned to these points a codensity of 1, and then we assigned the codensity of 2 to $B$.

We computed the 2-D persistence modules for each data set, and the matching distance between each pair of persistence modules. Let $x_1$ be the $x$-coordinate of $C_1$, and $x_2$ be the $x$-coordinate of $C_2$. Let $y_1$ be the $y$-coordinate of $C_1$, and $y_2$ be the $y$-coordinate of $C_2$. Figures 8 and 9 display the changes in matching distances with different combinations of $x_i$ for both data sets. The $x$-axis represents $x_2$, and the color of each curve represents $x_1$. Specifically, $x_1$ ranges from 0, colored in dark green, to 3.3, colored in brown. Figure 8 shows the trend when $y_1$ for both data sets are 3, and Figure 9 shows the trend when $y_1$ for both data sets are 10.

As shown in Figure 8, when $y_1$ and $y_2$ are small, there is a relatively linear
Figure 8: Distribution of matching distance when $y_1 = 3$ and $y_2 = 3$

Figure 9: Distribution of matching distance when $y_1 = 10$ and $y_2 = 10$
increase in matching distances as the \( x_1 \) increases with \( x_2 \) fixed. Before the linear trends appear, some of the curves display a nonlinear segment for small values of \( x_2 \). It was found that these curves had \( x_2 \) smaller than 1, which is the \( x \)-coordinate for \( A \).

Figure 9 displays the trends in matching distances when \( y_1 \) and \( y_2 \) are large. It is clear that the linear trend in matching distances disappears in these cases, as the matching distance appears to increase faster as \( x_1 \) increases.

We noticed that a prominent feature in Figure 9 is that the matching distance goes back to 0 sometime, and we now explain why this happens.

**Proposition 1** Suppose \( A \) and \( B \) are points on the \( xy \)-plane with Euclidean distance between them \( d > 0 \). Now suppose there are two points \( C_1 \) and \( C_2 \), both distance \( r < d \) away from \( A \), with the distance between \( C_i \) and \( B \) as \( h > d \). Then, if two point clouds are constructed with points \( A, B, C_1, \) and \( A, B, C_2 \) respectively, the two point clouds will have a matching distance of \( 0 \). (See Figure 10)

![Figure 10](image.png)

**Figure 10:** A graphical representation of the cases the Proposition applies to. (The orange part is where \( C_i \) lives in.)

**Proof:** Since the distance between points \( C_1, C_2 \) and \( A \) is smaller than the distance between the \( C_i \)'s and \( B \), a codensity of 1 is assigned to \( C_1, C_2 \), and \( A \). Point \( B \) is assigned a codensity of 2. In the point clouds constructed from these three points, we have a bifiltration as shown in Figure 11 (Right).
We now explain the construction of the bifiltration.

**Codensity 1:** When the scale parameter \( \epsilon = 0 \), only \( C_1 \) and \( A \) appear, so we have two isolated points. As \( \epsilon \) increases to \( r \), \( C_1 \) and \( A \) will connect to form an edge when \( \epsilon = r \). The simplicial complex will remain unchanged even though \( \epsilon \) increases beyond \( r \).

**Codensity 2:** When the scale parameter \( \epsilon = 0 \), all points \( A, B, C_1 \) in the point cloud appear, so we have three isolated points. As \( \epsilon \) increases to \( r \), \( C_1 \) and \( A \) will form an edge. This results in one connected component and two isolated points. Thus, there is only one edge between \( C_1 \) and \( A \). As \( \epsilon \) increases to \( d \), \( B \) will connect to \( A \). Since \( C_1 \) remains connected to \( A \), only edges exist in simplicial complex, and all points are connected to each other. Since all points are connected, \( H_0 \) homology doesn’t change as \( \epsilon \) increases beyond \( d \).

Similarly, we have the exact same bifiltration for the point cloud consisting of \( A, B, C_2 \), so we get the topologically equivalent bifiltrations for the two data sets. Then the 2-D persistence modules are the same, and the barcodes are the same. Thus, the matching distance between the two point clouds is 0.

According to the proposition above, it would be easy to compute the probability of having matching distance of 0 if \( C_1 \) and \( C_2 \) are randomly selected on circle \( O_A \) and circle \( O_B \) in Figure 10. The following corollary gives such a
probabilistic interpretation of the proposition; we leave the proof to the reader.

**Corollary 1** Suppose \( A \) and \( B \) are points on the \( xy \)-plane with distance between them \( d > 0 \). Let \( O_A \) be a circle of radius \( r < d \) centered at \( A \), and \( O_B \) a circle of radius \( r < d \) centered at \( B \). Now suppose there are two points \( C_1 \) and \( C_2 \), which are randomly selected on the two circles. Then, if two point clouds are constructed with points \( A, B, C_1, \) and \( A, B, C_2 \) respectively, the two point clouds will have a matching distance of 0 with probability of 
\[
\left( \frac{360 - (2 \cos^{-1} \left( \frac{r}{d} \right))}{360} \right)^2
\]
(degrees are used here).

Then the theorem below gives a \( n \)-dot generalization of the three-dot example. In this example, \( n \) points on the \( xy\)-plane form a regular polygon with euclidian distance between them \( d > 0 \), with another moving point in each data set.

**Theorem 1** Suppose \( A_1, A_2, \ldots, A_n \) are points on the \( xy \)-plane forming the vertices of a regular polygon with euclidian distance between consecutive points \( d > 0 \). Now suppose there are two points \( C_1 \) and \( C_2 \), both distance \( r > 0 \) (also \( r < d \)) away from the \( A_i \) that they are closest to, with the distance away from all other \( A_i \)'s greater than \( d \). Then, if two point clouds are constructed with points \( A_1, A_2, \ldots, A_n, C_1, \) and \( A_1, A_2, \ldots, A_n, C_2 \) respectively, the two point clouds will have a matching distance of 0.

**Proof:** Similar to the proof for the proposition above, each point will be assigned to either codensity 1 or 2. Since the distance between points \( C_1, C_2 \) and the respective \( A_i \)'s that they are closest to is smaller than the distance between the \( C_i \)'s and all other \( A_i \)'s, a codensity of 1 is assigned to \( C_1, C_2 \), and the respective \( A_i \)'s that they are closest to (note that they could both be closest to the same \( A_i \)). All other \( A_i \)'s are assigned a codensity of 2. In the point clouds consisting of these points, we have a bifiltration for both codensity 1 and codensity 2.

In the bifiltration for codensity 1, only \( C_1 \) and the \( A_i \) that it is closest to appear, so the proof follows the same steps as the one for proposition.

In the bifiltration for codensity 2, all points in the point cloud appear (all \( A_i \)'s and \( C_1 \)). As \( \epsilon \) increases to \( r \), \( C_1 \) and the \( A_i \) it is closest to will form an edge, but no other edges will form between any points. As \( \epsilon \) increases to \( d \), all \( A_i \)'s will connect to their \( A_i \) neighbors, forming edges around the regular polygon that they form.

Similarly, we have the exact same bifiltration for the point cloud consisting of \( C_2, A_i \)'s. Followed by the same reasonings in the proof for proposition, the matching distance between the two point clouds is 0.

\[ \blacksquare \]
3.2 Two-circle example

The data sets explored in two-circle example consisted of two circles each, with radii \( r \) and separated by a distance \( d \). Two hundred points were selected randomly from a uniform distribution on a circle, and each point was assigned a codensity estimator defined as the distance to the 20th nearest neighbor. An example of these data sets can be seen in Figure 12.

![Figure 12: Example of circle dataset (\( r = 1, d = 1 \))](image)

Many data sets were generated with various values for \( d \). Specifically, we chose \( d \in \{0, 0.5, 1, \ldots, 30\} \). Let \( d_1 \) be the separated distance \( d \) for dataset 1, and \( d_2 \) be the separated distance \( d \) for dataset 2, with \( d_2 > d_1 \). Datasets were hypothesized to be further apart if \( d_2 - d_1 \) was large.

Figure 13 displays the changes in matching distance as \( d_2 - d_1 \) increases with 4 \( d_2 \) representatives. In this example, the radii \( r \) for all data sets are 3. The range for \( d_1 \) is from 0.5 to 29.5, and the range for \( d_2 \) is from 1 to 30. The 4 samples of \( d_2 \) are 10, 15, 22 and 28. The shape of the data points represents \( d_2 \).

Figure 13 (left) shows the trend when \( d_2 \) is smaller than 21. As \( d_2 - d_1 \) increases, the matching distance of the pairs of data sets increases till some point and then remains unchanged. Before the constant part of each shape, there are three linearly increasing segments and a jump after each of the first two segments. There is almost no difference between the first two increasing segments when \( d_2 \) changes. However, the constant part is higher when \( d_2 \) is larger, which means matching distance becomes larger as \( d_2 \) increases with \( d_2 - d_1 \) unchanged.

When \( d_2 \) in a pair is larger or equal to 21 as shown in Figure 13 (right), the matching distance of that pair follows almost the same trend as Figure 13 (left). However, there are only two linearly increasing segments before the constant part. Also, when \( d_2 \) is 22, the first segment looks random without a clear trend. Interestingly, the constant part is higher when \( d_2 \) is lower this time, which is
exactly the opposite as shown in Figure 13 (left).

Figure 13: Distribution of matching distance for two-circle example

In order to understand why we have the segments, the jumps between each segment and the near-constant part, we looked at the RIVET plots of each pair of the data sets to get some insights from them. Also, we compared the barcodes along the line which produces matching distance, and determined which bar gives us matching distance.

Figure 14 is an example of the RIVET comparison, and the matching distance between these two persistence modules is plotted as the starting point of the first increasing segment of $d_2 = 10$ on Figure 13 (left). The optimal line that produces matching distance has angle $= 85.7^\circ$ and offset $= -0.35$. By counting the number of bars in the persistence module or the number of dots in the persistence diagram, we can see that there are only 4 dots in the first persistence diagram, but 6 in the second one. We compared the persistence diagrams in each pair of data sets to understand matching distance.

In order to understand Figure 13 better, the two-circle example deserves further investigation. We would like to understand the following questions:

1. Why do we get the segments, the jumps, and the near-constant part in the distribution of matching distances plot about the circle data?

2. Why is the near-constant part slightly declining as $d_2 - d_1$ increases?

3. Why is the near-constant value increase with $d_2$, but then decrease when $d_2$ gets sufficiently large? In our experiments, this maximum occurs when $d_2 = 21$. What determines this maximum value?
We now have some insights about the near-constant part in the distribution of matching distances plot. We looked at the persistence diagrams for the pair of circle with $d_1 = 5$ and circle with $d_2 = 10$, and the pair of circle with $d_1 = 0.5$ and circle with $d_2 = 10$. The matching distance of these two pairs are respectively the starting point and the ending point of the near-constant part as $d_2$ is 10. Since the lines which give the matching distance for both pairs have the same angle, so the persistence diagrams for circle 20 are the same for both cases. We found that circle 20 only has one finite bar along that line, which corresponds to a finite point in the persistence diagram. For circle 1 and circle 10, they have either one or two finite points on the persistence diagrams. Among all the possible matchings of the points, the best matching always consists the match between the finite point for circle 20 and a point on the diagonal line, and that gives the maximum distance for the optimal matching. Thus, no
matter how $d_1$ changes, as long as the angle of the line which gives matching distance remains unchanged, and the maximum distance of the optimal matching is always the distance between the finite point for circle 20 and a point on the diagonal line, the matching distance would always be near-constant.

We conclude with several other observation related to this study.

**First Homology** We did the analysis for the matching distance of $H_1$ in two-circle example. However, the data sets used in this experiment are slightly different. Many data sets were generated with various values for $r$ and a fixed separated distance of 3. Specifically, we chose $r \in \{0.2, 0.4, 0.6, \ldots, 6\}$. Let $r_1$ be the radii of the circles $r$ for dataset 1, and $r_2$ be the radii of the circles $r$ for dataset 2, with $r_2 > r_1$.

We got similar results as in $H_0$. In the distribution of the matching distances plot of $H_1$, as $r_2 - r_1$ gets larger, the matching distance first increases, and then becomes near-constant. Also, the near-constant part is slightly declining as $r_2 - r_1$ increases.

**Robustness to noise** We introduced some noise in the original data sets, and the way we did that was to add some error to the 20% or 40% of the data points. We found that the distribution of the matching distance for noisy data shares almost the same features as for the original data sets. Thus, we can still distinguish the noisy data with different separated distance for $H_0$ and different radii for $H_1$. This confirms that two-parameter persistent homology is robust against outliers, which is one of the primary motivations for this study.

**Grid-size** When we calculate matching distance, one of the arguments in the function is called grid-size, which represents the number of angles or offsets. For example, if the grid-size is 20, 20 angles and 20 offsets will be generated to form 400 combinations of lines, which will be used to calculate bottleneck distance along each line. During the calculating process, we found that the matching distances between each pair of data sets are almost the same when we set grid-size as 20 or 50. Thus, matching distances are quite stable even though we used fewer lines, and it would help us to save much time and memory.
4 Discussion and Future Research

These findings, though for very specific cases, suggest that there are non-trivial cases in which datasets may be considered topologically the same. They also lead to further questions regarding how to quantify when two things are close. In regards to this research’s original motivation, it will be difficult to quantify how far apart datasets are from one another using matching distance. Furthermore, this research provides a step towards a deeper understanding of what matching distance truly says about point cloud datasets.

In this research, we only used the lines with positive slope in 2-D persistence, because otherwise we would have difficulty assigning maps within 1-D linear maps. Taking the lines with negative slope would possibly yield more information, but might involve a zigzag persistence, see [3] for more information.

Apart from the open questions mentioned in Section 3.2 about circle data, this research will be extended in the future to the analysis of real-world data. One example of such data is Simple English Wikipedia Articles, where each article is converted into a 200-dimensional vector using a semantic algorithm. Matching distance will be used to determine whether or not there is a meaningful difference between a subset of the article vectors and a random point cloud dataset.

Acknowledgements

We would like to thank Professor Matthew Wright and Professor Matthew Richey for their guidance in this project. In addition we are grateful for the Collaborative Undergraduate Research and Inquiry (CURI) program for the generous support of undergraduate research at St. Olaf College. This work was supported by NSF DMS-1606967 and NSF DMS-1045015.

References

[1] A. Asaad and S. Jassim, Topological data analysis for image tampering detection, in International Workshop on Digital Watermarking, Springer, 2017, pp. 136–146.
[2] Z. Cang, L. Mu, K. Wu, K. Opron, K. Xia, and G.-W. Wei, A topological approach for protein classification, Computational and Mathematical Biophysics, 3 (2015).
[3] G. Carlsson and V. de Silva, Zigzag persistence, Foundations of Computational Mathematics, 10 (2010), pp. 367–405.
[4] F. Chazal, W. Crawley-Boevey, and V. De Silva, The observable structure of persistence modules, ArXiv e-prints, (2014).

[5] H. Edelsbrunner and J. Harer, Persistent homology - a survey, Contemporary Mathematics, 453 (2008), pp. 257–282.

[6] R. Ghrist, Barcodes: The persistent topology of data, Bulletin of the American Mathematical Society, 45 (2008), pp. 61–75.

[7] V. Kovacev-Nikolic, P. Bubenik, D. Nikolić, and G. Heo, Using persistent homology and dynamical distances to analyze protein binding, Statistical Applications in Genetics and Molecular Biology, 15 (2016), pp. 19–38.

[8] C. Landi, The rank invariant stability via interleavings, ArXiv e-prints, (2014).

[9] M. Lesnick, The theory of the interleaving distance on multidimensional persistence modules, Foundations of Computational Mathematics, 15 (2015), pp. 613–650.

[10] M. Lesnick and M. Wright, Interactive Visualization of 2-D Persistence Modules, ArXiv e-prints, (2015).

[11] J. A. Perea and G. Carlsson, A klein-bottle-based dictionary for texture representation, International journal of computer vision, 107 (2014), pp. 75–97.

[12] RIVET: The rank invariant visualization and exploration tool. http://rivet.online 2015-2018.

[13] Rivet-Python: Python api for rivet. https://github.com/rivetTDA/rivet-python 2018.

[14] P. Rosen, B. Wang, A. Seth, B. Mills, A. Ginsburg, J. Kamenetzky, J. Kern, and C. R. Johnson, Using contour trees in the analysis and visualization of radio astronomy data cubes, ArXiv e-prints, (2017).

[15] L. Wasserman, Topological data analysis, Annual Review of Statistics and Its Application, 5 (2018), pp. 501–532.