THE PERSISTENT HOMOLOGY OF COMPLEXES FROM POINT DATA SETS

by

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CHAPTER 1

INTRODUCTION

The purpose of this report is to give a formal understanding of the theory of persistent homology. The persistence diagram, a concise summary of how topological features persist throughout a growing filtration of an underlying point dataset, underpins the rapidly growing field of Topological Data Analysis. Fundamental to the persistence diagram is the notion of homology. Originally introduced by Poincaré in his seminal paper Analysis Situs [21], homology groups are algebraic objects that are provably topologically invariant. We define homology groups of simplicial complexes: spaces built from the union of p-dimensional generalisations of a triangle, called simplices. However, the domain of homology theory goes beyond simplicial complexes: in 1952 Norman Steenrod and Samuel Eilenberg published the Steenrod-Eilenberg axioms [9], five axioms which give a homology theory on any system that abides by them.

A finite set X of points in $\mathbb{R}^d$ does not naturally have interesting topological properties. However, they may be indicative of the topology of some underlying space that the points are sampled from. We construct a space from the point data set using the Čech and Rips complexes. We construct the Čech complex of X, denoted $\mathcal{C}_\epsilon(X)$, by placing balls of radius $\epsilon > 0$ around each point in X, defining simplices based on the non-empty intersections of these balls. Then we can use homology groups to analyse the topology of the complex: the 0th homology counts connected components, the 1st homology counts holes, the 2nd homology counts voids, and so on [7, Section 1]. However, the simplicial complex constructed depends heavily on your choice of ϵ.

A technique to overcome this was first introduced in 1999, when Vanessa Robins introduced the notion of persistence [23]. Knowing a finite number of points in an attractor of a topological dynamical system, she wanted to computationally infer the topology of the whole attractor. Her method was to look at how a topological feature persists over an evolving complex. Consider the set of open balls in a Čech complex. As ϵ increases, any intersection of balls is preserved, but new intersections can happen. Therefore we get a chain of inclusions

$$\mathcal{C}_{\epsilon_0}(X) \subseteq \mathcal{C}_{\epsilon_1}(X) \subseteq \cdots \subseteq \mathcal{C}_{\epsilon_n}(X)$$

whenever $\epsilon_0 \leq \epsilon_1 \leq \cdots \leq \epsilon_n$. This is called a filtration. Persistence is the study of how features, known as homology classes, are born and die throughout the filtration.

In 2005 Zomorodian and Carlsson introduced the persistence module [27] by showing that the collection of homology groups of a filtration is equivalent to some finitely generated $R[\mathbb{R}]$-module. In fact, the spaces of persistence modules is in one-to-one correspondence with the space of finitely generated graded modules. Thus the structure theorem for finitely generated graded modules allows us to decompose the persistence module whenever R is a principle ideal domain. In particular, the births and deaths of homology classes give a basis of the persistence module that tell us how to decompose it. This decomposition gives birth to the persistence diagram, a multiset in the extended plane $\bar{\mathbb{R}}^2$ that corresponds to the decomposition of the persistence module.

To analyse the suitability of persistence diagrams as representations of the homology of the filtration, Cohen-Steiner, Edelsbrunner and Harer proved the Stability Theorem in 2007 [6]. Defining the *bottleneck distance* on the space of persistence diagrams, they bounded the distance between two diagrams above by the distance between two filtrations of some point set X. In 2008 Cohen-Steiner extended the Stability Theorem by using the interleaving distance between persistence modules to give an upper bound on the distance between two persistence diagrams [3]. Finally, in 2011, Lesnick showed the Converse Stability Theorem [17], proving that the opposite inequality holds and implying that there was in fact an isometry between the space of persistence modules and the space of persistence diagrams.

In this report we cover the ideas spoken of in this introduction. In Chapter 2 we introduce simplices and simplicial complexes, proving results that are fundamental to their understanding. We introduce the Čech and Rips complex, giving an efficient means of computing the Čech complex and showing that any Čech complex is contained within two Rips complexes of similar radii. In Chapter 3 we move on to homology groups. We review some necessary algebra before defining homology groups; compute the homology groups of some common surfaces; and give an algorithm to compute any homology group that takes its coefficients from a principle ideal domain. In Chapter 4 we come on to persistence, defining the persistent homology before restating it as a finitely generated $R[\mathbb{R}]$-module and finding its decomposition. We also give an efficient method to decompose the persistence module. We finish by analysing the stability of the persistence diagram, giving Cohen-Steiner et al.'s original stability result, before giving a sketch proof of the generalised Stability Theorem and proving the Converse Stability Theorem. As all datasets are finite, we work only with finite point sets X in $\mathbb{R}^d$

Although this report does not go into details about the uses of this theory, persistence diagrams of datasets are being used with great success in a large number of applications. Some examples of their use will be given in the conclusion of this report.

CHAPTER 2

COMPLEXES

2.1 Simplices

Simplices generalise the triangle to p dimensions and are the building blocks of simplicial complexes. Before defining the simplex, we introduce the notion of geometric independence.

Definition 2.1.1. *A list of points $a_0, \ldots, a_n \subseteq \mathbb{R}^d$ is geometrically independent if for any $t_0, \ldots, t_n \in \mathbb{R}$,*

$$\left(\sum_{i=0}^{n} t_i = 0 \text{ and } \sum_{i=0}^{n} t_i a_i = 0 \right) \implies t_i = 0 \ \forall \ i \in \{0, \ldots, n\}.$$

If a set of scalars $t_0, \ldots, t_n$ fulfils the left hand side of the definition then we shall refer to $\sum t_i a_i$ as a *geometric combination*. Observe that a singleton in $\mathbb{R}^d$ is geometrically independent. We shall see now that sublists of geometrically independent lists are also geometrically independent lists.

Proposition 2.1.2. *A sublist of a geometrically independent set is also geometrically independent.*

Proof. Suppose $a_0, .., a_n$ is a geometrically independent list. Let $b_0, \ldots, b_m$ be a sublist of $a_0, \ldots, a_n$. As $a_0, \ldots, a_n$ is geometrically independent, any set of real scalars $t_0, \ldots, t_n$ such that ($\sum_{i=0}^{n} t_i = 0$ and $\sum_{i=0}^{n} t_i a_i = 0$) gives that $t_i = 0 \forall i \in \{0, \ldots, n\}$. Now let t_i be such a set of real scalars. As $b_0, \ldots, b_m$ is a sublist of $a_0, \ldots, a_n$, we can consider the set

of s_i's given by

$$\begin{cases} s_i = 0, & \text{if } a_i \notin \{b_0, \ldots, b_m\}, \\ s_i = t_i, & \text{if } a_i \in \{b_0, \ldots, b_m\}. \end{cases}$$

Then the s_i's give a geometric combination, so the sublist is geometrically independent.

□

If we have a list of geometrically independent points $a_0, \ldots, a_n$ then we can construct a list of vectors by subtracting an origin, a_0, showing an equivalence to linear independence.

Proposition 2.1.3. *The list of points $a_0, \ldots, a_n$ is geometrically independent if and only if the list of vectors $a_1 - a_0, \ldots, a_n - a_0$ is linearly independent.*

Proof. Let $a_0, \ldots, a_n$ be geometrically independent. Suppose $t_0, \ldots, t_n$, are such that $\sum_{i=1}^{n} t_i(a_i - a_0) = 0$. Then by rearranging we have

$$\sum_{i=1}^{n} t_i a_i - a_0 \sum_{i=1}^{n} t_i = 0.$$

Define the coefficients $s_0, \ldots, s_n$ by

$$\begin{cases} s_i = t_i, & i > 0, \\ s_i = -\sum_{i=1}^{n} t_i, & i = 0. \end{cases}$$

Then $\sum_{i=0}^{n} s_i a_i = 0$ and $\sum_{i=0}^{n} s_i = 0$, so $s_i = 0$ for $0 \leq i \leq n$ by geometric independence. Hence $t_i = 0$ for $1 \leq i \leq n$ and $a_1 - a_0, \ldots, a_n - a_0$ is linearly independent.

Now let $a_1 - a_0, \ldots, a_n - a_0$ be linearly independent. Suppose that t_i, with $0 \leq i \leq n$, are such that $\sum_{i=0}^{n} t_i a_i = 0$ and $\sum_{i=0}^{n} t_i = 0$. Then

$$\sum_{i=0}^{n} t_i a_i - a_0 \sum_{i=0}^{n} t_i = 0 \iff \sum_{i=1}^{n} t_i(a_i - a_0) = 0,$$

so by linear independence $t_0 = \cdots = t_n = 0$. Therefore $a_0, \ldots, a_n$ are geometrically independent. □

In $\mathbb{R}^d$ some geometrically independent sets are: two distinct points, three points that

are not colinear (i.e. do not all lie on any line), four points that are not coplanar (do not all lie on any plane), and so on. There is, however, some hyperplane that a list of geometrically independent points do lie on.

Definition 2.1.4. *The n-plane spanned by the list of geometrically independent points* $a_0, \ldots, a_n$ *as*

$$P = \left\{ \sum_{i=0}^{n} t_i a_i : t_i \in \mathbb{R} \text{ for } 0 \leq i \leq n, \sum_{i=0}^{n} t_i = 1 \right\}.$$

In fact, the n-plane is the hyperplane uniquely determined by the points $a_0, \ldots, a_n$. Furthermore, it can be used to extend geometrically independent lists.

Proposition 2.1.5. *If* $a_0, \ldots, a_n$ *are geometrically independent and* $w \in \mathbb{R}^d$ *is not in the n-plane spanned by those points, then* $w, a_0, \ldots, a_n$ *is a geometrically independent list.*

Proof. Let $a_0, \ldots, a_n$ be geometrically independent and $P = \{\sum_{i=0}^{n} t_i a_i : \sum_{i=0}^{n} t_i = 1\}$ be the n-plane spanned by $a_0, \ldots, a_n$. Suppose w is a point in $\mathbb{R}^d$ such that $w \notin P$. Then consider the list of points $a_0, \ldots, a_n, a_{n+1} := w$. Let $t_0, \ldots, t_n$ be scalars such that $\sum_{i=0}^{n+1} t_i a_i = 0$ and $\sum_{i=0}^{n+1} t_i = 0$. Then since $a_0, \ldots, a_n$ are geometrically independent, we get that $t_0 = \cdots = t_n = 0$. Then since $w \notin P$, $w \neq \sum_{i=0}^{n} t_i a_i$ for any such $t_0, /dots, t_n$. Thus if $\sum_{i=0}^{n+1} t_i a_i = 0$, we must get that $t_{n+1} = 0$. Therefore $a_0, \ldots, a_n, a_{n+1}$ is a geometrically independent list. □

A space U is called an *affine subspace* if given any two points in U, the line through those two points is contained in U. Then we get the following proposition.

Proposition 2.1.6. *The n-plane is an affine subspace.*

Proof. Let P be the n-plane generated by the geometrically independent list $a_0, \ldots, a_n$, and let $x = \sum_{i=0}^{n} s_i a_i$, $y = \sum_{i=0}^{n} t_i a_i$ be points in P, so that s_i and t_i are sets of scalars. Now consider the line through x and y given by $\alpha x + (1 - \alpha)y$, with $\alpha \in [0, 1]$. Then we have that

$$\alpha x + (1 - \alpha y) = \alpha \sum_{i=0}^{n} s_i a_i + (1 - \alpha) \sum_{i=0}^{n} t_i a_i = \sum_{i=0}^{n} (\alpha s_i + (1 - \alpha) t_i)\, a_i.$$

Observe that

$$\sum_{i=0}^{n} (\alpha s_i + (1-\alpha)t_i) = \alpha \sum_{i=0}^{n} s_i + (1-\alpha) \sum_{i=0}^{n} t_i = \alpha + (1-\alpha) = 1,$$

so the line $\alpha x + (1-\alpha)y$ is contained with P, as required. □

We now define the simplex. The plural of simplex is simplices.

Definition 2.1.7. *Let $a_0, \ldots, a_n \in \mathbb{R}^n$ be a geometrically independent set. The n-simplex spanned by $a_0, \ldots, a_n$ is the set*

$$\sigma = \left\{ \sum_{i=0}^{n} t_i a_i : \sum_{i=0}^{n} t_i = 1 \text{ and } t_i \geq 0 \ \forall \ i \right\}.$$

Furthermore, if $x = \sum t_i a_i \in \sigma$ then the real scalars t_i are referred to as the barycentric coordinates.

Observe that the simplex spanned by the simplices $a_0, \ldots, a_n$ is simply the restriction of the n-plane spanned by $a_0, \ldots, a_n$ to having non-negative coefficients t_i. Therefore we can extend the barycentric coordinates to the whole n-plane by removing the restriction that they must be non-negative. Interestingly, the barycentric coordinate system was first proposed by August Möbius (who constructed the Möbius strip) in 1827 as a way to determine centres of mass. If $x \in \sigma$ and you put a weight of $t_i(x)$ at each vertex a_i, then the centre of mass of σ is then x [14].

From now on, we let $a_0, \ldots, a_n \subseteq \mathbb{R}^d$ is a geometrically independent set, $P(a_0, \ldots, a_n)$ is the n-plane generated by that set, and $\sigma(a_0, \ldots, a_n)$ is the n-simplex spanned by that set. We shall sometimes drop the arguments $(a_0, \ldots, a_n)$ from a simplex and (x) from the barycentric coordinates $t_i(x)$ when it is clear from context what the argument should be.

Proposition 2.1.8. *Let $x \in \sigma$. The barycentric coordinates $t_i(x)$ of $x \in \sigma$ are unique.*

Proof. Suppose s_i and t_i, $0 \leq i \leq n$, are two different sets of barycentric coordinates for $x \in \sigma$, where σ is spanned by geometrically independent $a_0, \ldots, a_n$. Then $x = \sum s_i a_i = \sum t_i a_i$. Then

$$0 = \sum s_i a_i - \sum t_i a_i = \sum (s_i - t_i) a_i.$$

Then since the a_i are geometrically independent, and $\sum(s_i - t_i) = \sum s_i - \sum t_i = 0$, we have that $s_i - t_i = 0$ for all i, so $s_i = t_i$ for all i. □

Example 2.1.9. *Figure 2.1 visualises some low-dimensional simplices.*

(i) A 0-simplex is a singleton.

(ii) The 1-simplex spanned by a_0, a_1 is the set of points $x = ta_0 + (1-t)a_1$ such that $0 \leq t \leq 1$. That is, the line segment between a_0 and a_1.

(iii) The 2-simplex spanned by a_0, a_1, a_2 is the triangle with vertices a_0, a_1 and a_2. To see this, let $x \in \sigma$. Let $x = 0$ if $t + 0 = 1$ and otherwise let

$$x = \sum_{i=0}^{2} t_i a_i = t_0 a_0 + (1 - t_0)\left(\frac{t_1}{1-t_0}a_1 + \frac{t_2}{1-t_0}a_2\right).$$

Then the point $s = \frac{t_1}{1-t_0}a_1 + \frac{t_2}{1-t_0}a_2$ is on the line segment between a_1 and a_2, and x is on the line segment between a_0 and s. From the diagram, we can see this generates a triangle.

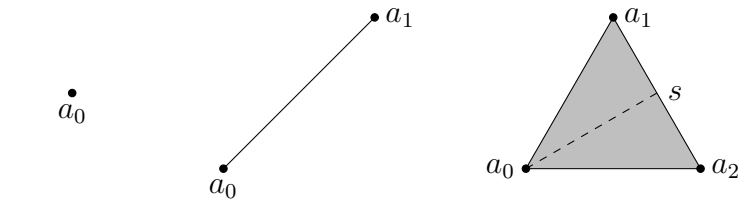


Figure 2.1

Definition 2.1.10. *A subset A of $\mathbb{R}^d$ is convex if the line segment from x to y is in A for all $x, y \in A$. The convex hull of a set A is the smallest convex set that contains the set A. It is equal to the intersection of every convex set containing A.*

Lemma 2.1.11. *If $S \subseteq \mathbb{R}^d$ is a convex set, then all non-negative linear combinations of points $a_0, \ldots, a_n \in S$ where the coefficients sum to 1 are in S.*

Proof. Let S be a convex set. We shall show by induction that if $a_0, \ldots, a_n$ are points in S, then if $x = \sum_{i=0}^{n} t_i a_i$ with each $t_i \geq 0$ and $\sum_{i=0}^{n} t_i = 1$, then $x \in S$. If $n = 0$, then a_0

is trivially a point in S by assumption. If $n = 1$, then any point x as described above lies on a line segment between a_0, a_1, so is in S by convexity.

Now suppose the inductive hypothesis is true for points $a_0, \ldots, a_k \in S$, and consider a point $a_{k+1} \in S$. Consider $x = \sum_{i=0}^{k+1} t_i a_i$ where $t_i = 0$ for $i = 0, \ldots, k+1$ and $\sum_{i=0}^{k+1} t_i = 1$. If $t_{k+1} = 1$ then $x = a_{k+1}$ which is in S, so we are done. Thus assume $0 \leq t_{k+1} < 1$. Then we can write

$$x = (1 - t_{k+1}) \sum_{i=0}^{k} \frac{t_i}{1 - t_{k+1}} a_i + t_{k+1} a_{k+1}.$$

Then $\sum_{i=0}^{k} t_i/(1 - t_{k+1}) = 1$, and each $t_i/(1 - t_{k+1})$ is non-negative, so by the inductive hypothesis $y := \sum_{i=0}^{k} \frac{t_i}{1-t_{k+1}} a_i$ is in S. Therefore x lies on the line segment between y and a_{k+1}, so x is in S by convexity, as required. □

We now prove some properties of simplices.

Theorem 2.1.12.

(i) The barycentric coordinates $t_i(x)$ are continuous functions of x.

(ii) An n-simplex σ is a compact, convex set in $\mathbb{R}^n$, which equals the intersection of all convex sets containing $a_0, \ldots, a_n$. Therefore, σ is the convex hull of the points $a_0, \ldots, a_n$.

(iii) For $n > 0$, an n-simplex σ is equal to the union of all line segments joining a_0 to the simplex spanned by $\{a_1, \ldots, a_n\}$.

(iv) An n-simplex σ is spanned by exactly one set of geometrically independent points, which are called vertices.

Proof.

(i) Consider $x \in \sigma$, so that $x = \sum_{i=0}^{n} t_i a_i$. Then by subtracting a_0 we get a linear subspace of $\mathbb{R}^n$, with a_0 as the origin and $\{a_1 - a_0, \ldots, a_n - a_0\}$. Note that this gives a basis as we obtain n linearly independent vectors by Proposition 2.1.3. Let $\hat{x}$ be the coordinates of x in the standard basis, and $\mathbf{B}$ be the matrix that changes basis from the standard basis to the basis $\{a_1 - a_0, \ldots, a_n - a_0\}$. Now, if π_i is the

natural projection onto the n^{th} element, then $t_i(x) = \pi_i \mathbf{B}\hat{x}$, which is a polynomial of the entries in x. Therefore the map from x onto its barycentric coordinates is continuous.

(ii) The simplex σ is bounded because

$$\left\| \sum_{i=0}^{n} t_i a_i \right\| \leq \max\{t_0, \ldots, t_n\} \max\{||a_0||, \ldots, ||a_n||\} \leq \max\{||a_0||, \ldots, ||a_n||\}.$$

If $f : (x_i) \mapsto \sum_i x_i$, then the standard n-simplex is equal to $f^{-1}[1]$, and so is the preimage of a closed set under a continuous map, and so is closed. Therefore σ is compact. To show that σ is convex, suppose that $(s_0, \ldots, s_n)$ and $(t_0, \ldots, t_n)$ are two distinct sets of coefficients such that $s_i, t_i > 0$ and $\sum_i s_i = 1 = \sum_i t_i$. Then a line segment between the two points in σ determined by the coefficients is given for $\lambda \in [0, 1]$ by

$$\lambda \sum_{i=0}^{n} t_i a_i + (1 - \lambda) \sum_{i=0}^{n} s_i a_i = \sum_{i=0}^{n} (\lambda t_i + (1 - \lambda) s_i) a_i.$$

Then the coefficients $r_i = \lambda t_i + (1 - \lambda) s_i$, for fixed $\lambda \in [0, 1]$, are non-negative and $\sum r_i = \lambda \sum t_i + (1 - \lambda) \sum s_i = 1$, so each point on the line segment is in σ. Therefore σ is convex.

Now suppose that S is a convex set containing $\{a_0, \ldots, a_n\}$. Let $x = \sum_i t_i a_i \in \sigma$. Then by Lemma 2.1.11 $x \in S$, so $\sigma \subseteq S$. Therefore σ is in every convex set containing $\{a_0, \ldots, a_n\}$ and thus σ is the convex hull of the points $\{a_0, \ldots, a_n\}$ as required.

(iii) Let

$$\sigma \ni x = \sum_{i=0}^{n} t_i a_i = t_0 a_0 + (1 - t_0) \sum_{i=1}^{n} \frac{t_i}{1 - t_0} a_i.$$

If $t_0 = 1$ then $x = a_0$, so we do not divide by zero in the second summation. Then

clearly $t/(1-t_0) \geq 0$, and

$$\sum_{i=1}^{n} \frac{t_i}{1-t_0} = \frac{1}{1-t_0} \sum_{i=1}^{n} t_i = \frac{1}{1-t_0}(1-t_0) = 1,$$

so that $\sum_{i=1}^{n} \frac{t_i}{1-t_0} a_i$ lies in the simplex spanned by $\{a_1, \ldots, a_n\}$, and σ is the union of all lines segments from a_0 to such points. Then as σ is convex by (ii), the result follows.

(iv) We shall show that a point $x \in \sigma$ is a vertex of σ if and only if it does not lie on an open line segment contained in σ. Note that if a point does lie on an open line segment in σ then it can be expressed as a linear combination of the endpoints of that line. Therefore it is not geometrically independent from the other points, so is not a vertex. Hence this characterisation uniquely determines the vertices of σ, i.e. uniquely determines the geometrically independent set of points that span σ.

Let $a_0, \ldots, a_n$ be a geometrically independent set of points that spans σ. Suppose that $x = \sum_{i=0}^{n} t_i a_i \in \sigma$ and $x \neq a_0, \ldots, a_n$. Then $t_i \neq 1$ for any $0 \leq i \leq n$. Therefore at least two vertices have non-zero barycentric coordinates. Without loss of generality say that t_0 and t_1 are non-zero. Choose an $\epsilon > 0$ such that $(t_0 - \epsilon, t_0 + \epsilon) \subset (0,1)$ and $(t_1 - \epsilon, t_1 + \epsilon) \subset (0,1)$ (such an ϵ will exist, as $0 < t_0, t_1 < 1$). Then for $\delta \in (-\epsilon, \epsilon)$ we have that

$$(t_0 + \delta)a_0 + (t_1 - \delta)a_1 + \sum_{i=2}^{n} t_i a_i \in \sigma.$$

That is, x lies on an open line segment contained in σ. Therefore every non-vertex point of σ lies on an open line segment in σ.

Now suppose that a vertex, say a_0, is on an open line segment contained in σ. Then there exists points $x = \sum_{i=0}^{n} t_i a_i, y = \sum_{i=0}^{n} s_i a_i$ in σ such that $a_0 = \delta x + (1-\delta)y$ for some $\delta \in (0,1)$. That is,

$$a_0 = \delta \sum_{i=0}^{n} t_i a_i + (1-\delta) \sum_{i=0}^{n} s_i a_i = \sum_{i=0}^{n} (\delta t_i + (1-\delta)s_i) a_i.$$

This is a contradiction of the geometric independence of $a_0, \ldots, a_n$, unless $t_0 = s_0 = 1$. Hence $x = y$, so that a_0 does not lie on a line segment, as required. $\square$

We now give some key definitions. As indicated in the theorem above, the *vertices* of σ are the unique points $a_0, \ldots, a_n$ that span σ, and n is the dimension of σ. A simplex spanned by some sublist of $a_0, \ldots, a_n$ is called a *face* of σ. If the face is spanned by a proper sublist of $a_0, \ldots, a_n$ then it is a *proper face*. The *face opposite* a_i is the simplex spanned by $\{a_0, \ldots, a_n\} \setminus a_i$. The *boundary* of σ, $\mathrm{Bd}\sigma$, is the union of the proper faces of σ, and the *interior* of σ is $\operatorname{Int}\sigma := \sigma \setminus \operatorname{Bd}\sigma$. We shall sometimes refer to $\operatorname{Int}\sigma$ as the *open simplex*.

Note that if $x \in \operatorname{Bd}\sigma$ then at least one of $t_i = 0$, as x is in a simplex generated by a proper sublist of $a_0, \ldots, a_n$. Therefore if $x \in \operatorname{Int}\sigma$, we must have $t_i(x) > 0$ for each i. We prove some properties of the interior and boundary of simplices.

Proposition 2.1.13. $\operatorname{Int}\sigma$ *is convex and open in* P *and* $\mathbb{R}^d$*, and the closure of* $\operatorname{Int}\sigma$ *in* $\mathbb{R}^d$ *is* σ*.*

Proof. By Theorem 2.1.12(i) the barycentric coordinates t_i are continuous functions that map P to σ. Therefore the preimage $t_i^{-1}[(0,\infty)]$ for each $0 \leq i \leq n$ is open in P. Furthermore, since $\operatorname{Int}\sigma = \{\sum_{i=0}^n t_i a_i : t_i \in (0,\infty), \sum t_i = 1\}$, we get that

$$\operatorname{Int}\sigma = \bigcap_{0 \leq i \leq n} t_i^{-1}[(0,\infty)],$$

which is a finite intersection of open sets, so is open. The proof that $\operatorname{Int}\sigma$ is open in $\mathbb{R}^d$ is similar, but replaces P with $\mathbb{R}^d$.

To show convexity, let $x = \sum t_i a_i, y = \sum s_i a_i$ be in $\operatorname{Int}\sigma$, so that each $t_i, s_i \in (0,1)$ and $\sum t_i = \sum s_i = 1$. Then let $\delta \in [0,1]$ and consider the convex combination of x, y,

$$\delta x + (1-\delta)y = \delta \sum_{i=0}^n t_i a_i + (1-\delta) \sum_{i=0}^n s_i a_i = \sum_{i=0}^n (\delta t_i + (1-\delta)s_i)a_i.$$

Now, $\delta t_i + (1-\delta)s_i > 0$ for all $0 \leq i \leq n$, and $\sum \delta t_i + (1-\delta)s_i = \delta \sum t_i + (1-\delta)\sum s_i = 1$, so the convex combination of arbritary $x, y \in \operatorname{Int}\sigma$ is contained in $\operatorname{Int}\sigma$. Therefore $\operatorname{Int}\sigma$

is convex.

We shall now show that $\overline{\operatorname{Int}\sigma} = \sigma$. Since σ is closed in $\mathbb{R}^d$, $\overline{\operatorname{Int}\sigma} \subseteq \sigma$ trivially. Now suppose that $x \in \operatorname{Bd}\sigma$. Then we construct a sequence of points contained in $\operatorname{Int}\sigma$ that converges to x. Let $x = \sum t_i a_i$ and assume without loss of generality that $t_i > 0$ for $0 \leq i \leq k$ and $t_i = 0$ for $k < i \leq n$. Then define

$$\epsilon = \frac{1}{2} \min_{0 \leq i \leq k} t_i, \text{ and let } x_m = \sum_{i=0}^{k} \left(t_i - \frac{\epsilon}{m(k+1)} \right) a_i + \sum_{i=k+1}^{n} \frac{\epsilon}{m(n-k)} a_i.$$

Now as $m \to \infty$ the second sum on the right hand side tends to zero, and the first sum tends to $\sum i = 0^k t_i a_i$. Since the first k terms are exactly the terms with non-zero coefficients, we get that $x_m \to x$ as $m \to \infty$. Thus as $x_m \in \operatorname{Int}\sigma$ for each m, x is a limit point of $\operatorname{Int}\sigma$, so is in its closure. Therefore $\sigma \subseteq \overline{\operatorname{Int}\sigma}$, so we have equality as required. □

Recall that a *ray* emanating from a point $x \in \mathbb{R}^d$ is $\mathcal{R} = \{x + tp : t > 0\}$ where p is a fixed point in $\mathbb{R}^d \setminus 0$ called the *direction*. We now show that there is a homeomorphism from any σ with the unit ball.

Theorem 2.1.14. *Let U be a bounded, convex, open set in $\mathbb{R}^d$. Let $w \in U$. Then the following hold.*

(i) Every ray emanating from w intersects $\operatorname{Bd}U = \overline{U} \setminus U$ in exactly one point.

(ii) There is a homeomorphism from $\overline{U}$ with $B^d = \{x \in \mathbb{R}^d : ||x|| \leq 1\}$, that takes $\operatorname{Bd}U$ onto $S^d = \{x \in \mathbb{R}^d : ||x|| = 1\}$.

Proof.

(i) Let $\mathcal{R}$ be a ray emanating from w with direction p. Then since $\mathcal{R}$ is convex and open, $\mathcal{R} \cap U$ is bounded, convex, and open in $\mathcal{R}$. Therefore, $\mathcal{R} \cap U = \{w + tp : t \in [0, a)\}$, where $a \in \mathbb{R}$ is some constant. Furthermore, $\mathcal{R}$ intersects $\operatorname{Bd}U = \overline{U} \setminus U$ at $x = w + ap$. Now suppose that $\mathcal{R}$ also intersects $\operatorname{Bd}U$ at a distinct point y. Then as x will be on $\mathcal{R}$ between w and y, we have $y = w + bp$ for some $b > a$. As x, y, w lie on a line

segment, we can write $x = (1-t)w + ty$, where $t = a/b$. Rearranging, we get that

$$w = \frac{x - ty}{1 - t}.$$

Since y is on the boundary of U by assumption, we can choose a sequence of points y_n in U that converge to y. Define the sequence

$$w_n = \frac{x - ty_n}{1 - t}.$$

Then w_n converges to w, so $w_n \in U$ for all n greater than some $N \in \mathbb{N}$. We have $x = tw_n + (1-t)y_n$. Take $n > N$. Then by the convexity of U, $x \in U$. But this is a contradiction, as $x \in \overline{U} \setminus U$. Therefore $\mathcal{R}$ intersects $\operatorname{Bd} U$ at a unique point.

(ii) Without loss of generality, let $w = 0$. The map $f : \mathbb{R}^d \backslash 0 \to s^{d-1}$ given by $x \mapsto x/||x||$ is a continuous map that restricts to a bijection from $\operatorname{Bd} U$ onto S^d by *(i)*. Then since the boundary of a bounded set is compact, f is a bijective map from a compact set to a Hausdorff space, so is a homeomorphism. Let $g : S^d \to \operatorname{Bd} U$ be its inverse. Then we extend g to a bijection $G : B^d \to \overline{U}$, where B^d is the unit d-ball, by defining

$$G(x) = \begin{cases} ||g(x/||x||)||x, & x \neq 0, \\ 0, & x = 0. \end{cases}$$

Then if $x \neq 0$, G is continuous at x as it is a composition of continuous functions and there is no division by 0. If $x = 0$, then let M be a bound of $||g(x)||$ (since U is bounded, a finite M exists). Then we have that $||G(x) - G(0)|| < M\delta$ whenever $||x - 0|| < \delta$, so G is continuous at x. Therefore G is continuous everywhere, so is the required homeomorphism. □

Corollary 2.1.15. *There is a homeomorphism of a simplex σ with the unit n-ball that takes $\operatorname{Bd}\sigma$ onto S^{n-1}.*

Proof. By Proposition 2.1.13 and Theorem 2.1.12(ii), an n-simplex σ is a bounded convex open set in $\mathbb{R}^n$. □

We end this section by defining the orientation of a simplex. We will revisit this definition at the beginning of Chapter 3. Recall that a permutation of points $\rho : (x_0, \ldots, x_n) \to (\rho(x_0), \ldots, \rho(x_n))$ is defined to be *even* if the minimum number of two-element swaps required to obtain ρ is even.

Definition 2.1.16. *Let σ be the simplex spanning $a_0, \ldots, a_n$. Without loss of generality consider an ordering of σ's vertex set $(a_0, \ldots, a_n)$. Define an equivalence relation on the orderings of $a_0, \ldots, a_n$ by saying two orderings are equivalent if the permutation between them is even. When $n > 0$, this partitions the orderings of $a_0, \ldots, a_n$ into two equivalence classes. These equivalence classes are the orientations of σ. An oriented simplex is a simplex σ along with an orientation of its vertices.*

Note that if $n = 0$ then there is only one vertex, so only one orientation of σ. If $a_0, \ldots, a_n$ are geometrically independent points then we shall write

$$[a_0, \ldots, a_n]$$

to denote the simplex spanned by $a_0, \ldots, a_n$ along with the vertex ordering $(a_0, \ldots, a_n)$.

2.2 Simplicial Complexes

Definition 2.2.1. *A simplicial complex K is a collection of simplices such that the following hold.*

(i) Every face of a simplex in K is in K.

(ii) If σ, τ are non-disjoint simplices in K, then $\sigma \cap \tau$ is a face of both σ and τ.

If L is a subcollection of a simplicial complex K and every face of each simplex of L is also in L, then L is a *subcomplex* of K. The *p-skeleton* of K, denoted $K^{(p)}$, is the subcomplex containing all simplices in K of dimension p or less. The points in $K^{(0)}$ are called the *vertices* of K.

Example 2.2.2. *The diagram on the left in Figure 2.2 is a simplicial complex, as it fulfils both* (i) *and* (ii) *from the definition. However, the diagram on the right is not a simplicial complex, as the intersection of the two* 2*-simplices is a face of neither of the simplices.*

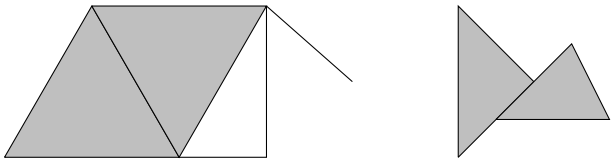


Figure 2.2

Proposition 2.2.3. *Every point* $x \in K$ *is in the interior of a unique simplex in* K*.*

Proof. Take any point x and a simplex σ that contains x. If x lies in the interior of σ then we are done, as any any higher dimensional simplex that contains x must have σ as a proper face. If x is not in the interior of σ, then x is in the boundary of σ. Consider the proper face σ' of σ that contains x. If x is in the interior of σ' then we are done, else we can recursively consider the proper face that contains x. We terminate when either x is in the interior, or when we reach a vertex. Then x is a vertex of σ, and x is the unique 0-simplex with itself as its interior. □

We now prove a proposition that gives us a different way to identify complexes.

Proposition 2.2.4. *A collection of simplices* K *is a simplicial complex if and only if the following hold.*

(i) Every face of a simplex in K *is in* K*.*

(ii) Every pair of distinct simplices of K *have disjoint interiors.*

Proof. Assume that K is a simplicial complex. Consider two simplices σ and τ in K and let $s = \sigma \cap \tau$ be their intersection. Suppose that x is in the interior of both σ and τ. If s is a proper face of σ then x would be on the boundary of σ, but $x \in \operatorname{Int} \sigma$. Therefore s is not a proper face of σ, and so $s = \sigma$. By the same argument, $s = \tau$. Therefore if x is in the interior of σ and τ then $\sigma = \tau$.

Now assume that (i) and (ii) hold. We shall show that if $\sigma \cap \tau \neq \emptyset$ then $s = \sigma'$, where σ' is the face spanned by the vertices $b_0, \ldots, b_m$ of σ that lie within τ. Since σ and τ are convex, so is $\sigma \cap \tau$. Furthermore, $\sigma \cap \tau$ contains all of $b_0, \ldots, b_m$. Therefore $\sigma' \subseteq \sigma \cap \tau$. To show the opposite inclusion, suppose that $x \in \sigma \cap \tau$. Then $x \in \operatorname{Int} s \cap \operatorname{Int} t$ for some face s of σ and some face t of τ. By (ii), we must have that $s = t$, therefore the vertices of s must lie within t, and so are a subset of $b_0, \ldots, b_m$. Therefore s is a face of σ, so $x \in \sigma'$. Therefore $\sigma' = \sigma \cap \tau$ and K is a simplicial complex. □

Let $|K|$ be the union of all $\sigma \in K$ and let each σ have the standard topology in $\mathbb{R}^d$. We let a subset A of $|K|$ be closed in $|K|$ if and only if $A \cap \sigma$ is closed for each $\sigma \in K$. This collection of sets is closed under finite union and arbitary intersection and so defines a topology on $|K|$.

Definition 2.2.5. *The space $|K|$ with the topology described above is the polytope, or underlying space, of K.*

When there is a finite number of simplices in K, the topology on $|K|$ is equivalent to the standard topology on $\mathbb{R}^d$ [18, Page 9]. This is because each simplex inherits the Euclidean topology, the open sets of which are preserved under finite intersection. We shall only consider finite complexes, so from now on we assume that any K contains a finite number of simplices. We shall show that $|K|$ has a valuable property.

Proposition 2.2.6. *$|K|$ is Hausdorff.*

Proof. Let $x, y \in |K|$ such that $x \neq y$. Since $x \neq y$ there must be at least one vertex v of $|K|$ such that $t_v(x) \neq t_v(y)$ (where $t_v(x)$ is the barycentric coordinate of x with respect to the vertex v). Choose a value $r \in \mathbb{R}$ that is between $t_v(x)$ and $t_v(y)$. Then the sets $\{x : t_v(x) < r\}$ and $\{x : t_v(x) > r\}$ are disjoint open sets, each containing one of x, y. Therefore $|K|$ is Hausdorff. □

We now prove a result that allows us to determine the continuity of functions on complexes by considering their continuity on the individual simplices of the domain complex.

Proposition 2.2.7. *A map $f : |K| \to X$ is continuous if and only if $f|_\sigma$ is continuous for every $\sigma \in |K|$.*

Proof. Suppose f is continuous. Then $f|_\sigma$ must be continuous for each $\sigma \in |K|$, as σ is a subspace of $|K|$. Now suppose that $f|_\sigma$ is continuous for every $\sigma \in K$. Let C be a closed set in X. Then $f^{-1}[C] \cap \sigma = f|_\sigma^{-1}[C]$, which is closed in $|K|$ by the definition of the topology on $|K|$. Therefore f is continuous. □

Definition 2.2.8. *If v is a vertex of K then the star of v, $\operatorname{St} v$, is the union of the interiors of all simplices of K that have v as a vertex. Its closure, $\overline{\operatorname{St}} v$, is the closed star of v.*

The closure of a finite union is equal to the finite union of the closures. Therefore the closed star of v is equal to the union of all simplices of K that have v as a vertex. Then the complement of $\operatorname{St} v$ is the union of all simplices of K that don't have v as a vertex.

Lemma 2.2.9. *(Closed) stars are path connected.*

Proof. The star of v is the union of the interior of all simplices containing v. Note that the interior of a simplex is path connected, since the interior of a simplex is convex by Lemma 2.1.10. Furthermore, the interior of any simplex is path-connected with the interior of any other simplex in $\operatorname{St} v$, as there is a path through v. Therefore a star is path connected. To check that a closed star is path connected we must only verify that the interior of a simplex is path connected with its boundary. Its boundary is the union of its proper faces, so a path is given through any vertex, connecting the interior of each simplex with its boundary. Hence the closed star is path connected. □

2.3 Review of Quotient Maps

A surjective map $f : X \to Y$ is a *quotient map* if any subset $U \subseteq Y$ is open if and only if the subset $f^{-1}[U]$ is open in X. Equivalently, a surjective map $f : X \to Y$ is a quotient map if any subset $U \subset Y$ is closed if and only if the subset $f^{-1}[U]$ is closed in X. A subset A of X is *saturated* if $A = f^{-1}[B]$ for some subset B of Y.

Lemma 2.3.1. *$f : X \to Y$ is a quotient map if and only if f is surjective, continuous, and f maps saturated open sets of X to open sets of Y.*

Proof. First suppose that f is a quotient map. Then f is continuous by the open set characterisation of continuity. Now suppose that $U \subseteq X$ is an open saturated set. Then $f[U]$ is open because $f^{-1}[f[U]] = U$ is open, where the identity of $f^{-1}\dot{f}$ is due to the surjectivity of f. Therefore f maps open saturated sets to open sets.

Now suppose that f is continuous and maps open saturated sets to open sets. Suppose $V \subseteq Y$ is open. Then by continuity so is $f^{-1}[V]$. Furthermore, if $f^{-1}[V]$ is open in X, then $f^{-1}[V]$ is an open saturated set in X and by assumption $f[f^{-1}[V]] = V$ is open in Y. Therefore f is a quotient map. □

Let $f : X \to Y$ be a continuous surjective map. Then if f is either a closed or an open map, f is a quotient map, as it will map all open/closed sets to open/closed sets. Furthermore, if X is compact and Y is Hausdorff then f is closed and thus a quotient map. We prove some properties of quotient maps.

Lemma 2.3.2.

(i) A bijective quotient map is a homeomorphism.

(ii) A composite of quotient maps is a quotient map.

(iii) If $f : X \to Y$ is a quotient map and U is a saturated subspace of X that is either open or closed in X, then the restriction $f|_U : U \to f[U]$ is a quotient map.

Proof.

(i) Let $f : X \to Y$ be a quotient map. Then since the preimage of every open set is open, f is continuous. Furthermore, $f^{-1} : Y \to X$ exists as f is bijective. Let U be an open set in X. Then $(f^{-1})^{-1}[U] = f[U]$ which is open in Y, so the preimage of an open set under f^{-1} is open. Therefore f^{-1} is continuous, and so f is a homeomorphism.

(ii) Let $f : X \to Y, g : Y \to Z$ be quotient maps. Consider $g \circ f : X \to Z$. Since f, g are quotient maps they are surjective, so $g \circ f$ is surjective. Consider an open set U in Z. Then as g is a quotient map, $g^{-1}[U]$ is open in Y. Then as f is a quotient

map, $f^{-1}[g^{-1}[U]]$ is open in X. Therefore $(g \circ f)^{-1}[U] = f^{-1}[g^{-1}[U]]$ is open, and so $g \circ f$ is a quotient map.

(iii) Let $f : X \to Y$ be a quotient space and $U \subseteq X$ an open saturated subset. Let $V \subset f[U]$. First note that because U is saturated

$$\begin{aligned} f^{-1}[V] &= \{x \in X : f(x) \in V\} \\ &= \{x \in U : f(x) \in V\} \\ &= f|_U^{-1}[V]. \end{aligned}$$

Now as $f|U$ is a restriction of a quotient map, it is certainly continuous and surjective. It remains to show that if $f|_U^{-1}[V]$ is open in U, then V is open in $f[U]$. Observe that as $f|_U^{-1}[V]$ is open in U and U is open in X by assumption, $f|_U^{-1}[V] = f^{-1}[V]$ is open in X. Since f is a quotient map V is therefore open in Y. Finally, this implies that V is open in $f[U]$, as $V \cap f[U] = V$. Therefore $f|_U$ is a quotient map. The proof for closed saturated U is the same, only with closed sets. □

We end this review by defining quotient spaces.

Definition 2.3.3. *Let X^* be a partition of the space X. Let $\pi : X \to X^*$ map each point to the part containing it. We give X^* a topology by defining $U \subseteq X^*$ to be open in X^* if and only if $\pi^{-1}[U]$ is open in X. Then π is a quotient map, and we call X^* a quotient space of X.*

2.4 Simplicial Maps

In this section we define maps between simplicial complexes. Maps between simplicial complexes are induced by maps between their vertex sets.

Proposition 2.4.1. *Let K and L be complexes and $f : K^{(0)} \to L^{(0)}$ be a map between their vertex sets. Suppose that whenever the vertices $a_0, \ldots, a_n \subseteq K$ span a simplex of K, the points $f(a_0), \ldots, f(a_n)$ are vertices of a simplex in L. Then f can be extended to a*

continuous map $g : K \to L$ given by

$$x = \sum_{i=0}^{n} t_i a_i \longmapsto \sum_{i=0}^{n} t_i f(a_i) = g(x).$$

Then g is called the simplicial map induced by the vertex map f.

Proof. Suppose $a_0, \ldots, a_n$ span a simplex $\sigma \in K$. Note that even though $f(a_0), \ldots, f(a_n)$ are not necessarily distinct, they span a simplex τ of L by definition. Let x be a point in σ and consider $g(x)$. Then if $g(x) = \sum_{i=0}^{n} t_i f(a_i) = \sum_{i=0}^{m} s_i f(a_i)$ for some $m \leq n$ and with $s_i = \sum_j t_j$ for j such that $f(a_j) = f(a_i)$. That is, we 'collect the terms' of coefficients of distinct vertices in K that are mapped to the same vertex in L. Then $\sum s_i = \sum t_i = 1$ and each $s_i \geq 0$. Therefore $g(x) \in \tau$, and so g maps σ to τ. Furthermore, consider the map from $x \to \{t_i(x)\} \to \{s_i(g(x))\} \to g(x)$. The first and third arrow are continuous by Theorem 2.1.12 (i). The second arrow is just the 'collecting terms' and so is also continuous. Therefore $x \mapsto g(x)$ is a continuous function on each $\sigma \in K$. Therefore the simplicial map $g : K \to L$ is continuous by Proposition 2.2.7. □

Proposition 2.4.2. *Let K, L be simplicial complexes. Given an injective simplicial map $f : K \to L$, $\{f[\sigma] : \sigma \in K\}$ is a subcomplex of L.*

Proof. First, observe that because f is a simplicial map, $f[\sigma]$ is a simplex in L for each $\sigma \in K$. Furthermore, as K is a complex, $f[\sigma]$ will contain all of its faces, as the faces of σ in K will map to the faces of $f[\sigma]$ in L. Since f is injective the set $\{f[\sigma] : \sigma \in K\}$ is a subset of L, and it is such that every simplex in $\{f[\sigma] : \sigma \in K\}$ contains all of its faces. Therefore $\{f[\sigma] : \sigma \in K\}$ is a subcomplex of L. □

Note that in the definition of a simplicial map the vertex map f does not necessarily have to be injective, so two vertices of a simplex in K can map to one vertex of a simplex in L. If we further have that the vertex map is a bijection, we get the following result.

Proposition 2.4.3. *Suppose $f : K^{(0)} \to L^{(0)}$ is a bijective map such that vertices $a_0, \ldots, a_n$ in K span a simplex of K if and only if the vertices $f(a_0), \ldots, f(a_n)$ span a simplex of L. Then the induced simplicial map $g : K \to L$ is a homeomorphism.*

Such a g is called a *simplicial homeomorphism* or an *isomorphism of K and L*.

Proof. Since f is a bijection, each simplex $\sigma \in K$ is mapped to a simplex $\tau \in L$ of the same dimension. To prove that g is a homeomorphism we need to show that the map $h : \tau \to \sigma$ induced by the vertex map f^{-1} is the inverse of the map g. Conside $x = \sum t_i a_i \in \sigma$. Then

$$h(g(x)) = h\left(\sum t_i f(a_i)\right) = \sum t_i f^{-1}(f(a_i)) = \sum t_i a_i = x,$$

where we use that f is a bijection to get $f^{-1}(f(a_i)) = a_i$. Therefore g^{-1} is the simplicial map induced by f^{-1}. Therefore f is a homeomorphism as it is a bijection, continuous, and its inverse is continuous. □

Let Δ^N be the *full N-complex*, which consists of the N-simplex on a geometrically independent set of N points in $\mathbb{R}^d$ (with $d > N$) along with all of its faces. We shall prove a result that states any finite simplicial complex is isomorphic to some subcomplex of Δ^N for some N.

Corollary 2.4.4. *Let K be a finite simplicial complex. Then K is isomorphic to a subcomplex of Δ^N for some N.*

Proof. Let $a_0, \ldots, a_N$ be the vertices of K. For $0 \leq i \leq N$ let $a_i = (0, \ldots, 0, 1, 0, \ldots, 0)$, where each entry is 0 apart from the ith element, which is 1. Then $a_0, \ldots, a_N$ is a set of geometrically independent points in $\mathbb{R}^d$, where $d > N$. Let Δ^N be the full N-complex over $a_0, \ldots, a_N$. Then the simplicial map induced by the vertex map $f(v_i) = a_i$ for $i = 0, \ldots, N$ is an isomorphism from K to some subcomplex of Δ^N. □

Note that if $g : K \to L$ is a simplicial map that takes a simplex $\sigma \in K$ to a simplex $\tau \in L$, then g maps some face of σ homeomorphically onto τ. To see this, consider the list of vertices of σ. If multiple vertices of σ are mapped onto a single vertex of τ, remove vertices from the list until the list of vertices of σ maps bijectively onto the vertices of τ. The remaining vertices span a face of σ, and that face maps homeomorphically onto τ by Proposition 2.4.3.

2.5 Abstract Simplicial Complexes

Definition 2.5.1. *An abstract simplicial complex $\mathcal{S}$ is a finite collection of non-empty sets such that if $A \in \mathcal{S}$, then every non-empty subset of A is in $\mathcal{S}$.*

The element A is a *simplex* in $\mathcal{S}$. The *dimension* of A is $|A| - 1$. A *face* of A is a non-empty subset of A. The *dimension* of $\mathcal{S}$ is $\max_{S \in \mathcal{S}} |S|$. The *vertex set* of $\mathcal{S}$ is the union of singletons in $\mathcal{S}$. We call a subcollection of $\mathcal{S}$ that is also an abstract complex a *subcomplex*.

Definition 2.5.2. *Let $\mathcal{S}$ and $\mathcal{T}$ be abstract complexes. We say that they are isomomorphic if there exists a bijective mapping f from the vertices of $\mathcal{S}$ to the vertices of $\mathcal{T}$ such that*

$$\{a_0, \ldots, a_n\} \in \mathcal{S} \iff \{f(a_0), \ldots, f(a_n)\} \in \mathcal{T}.$$

We can link abstract complexes to simplicial complexes. To do this, we define the *vertex scheme*.

Definition 2.5.3. *Let K be a simplicial complex with vertex set V. The vertex scheme of K, $\mathcal{K}$, is the collection of all subsets $\{a_0, \ldots, a_n\}$ of V such that $a_0, \ldots, a_n$ span a simplex in K.*

It follows from the definitions that $\mathcal{K}$ is an abstract simplicial complex. The following result shows that the vertex scheme is the most natural abstract complex to consider from some simplicial complex.

Theorem 2.5.4.

(i) Every abstract complex is isomorphic to the vertex scheme of some simplicial complex K.

(ii) If K, L are simplicial complexes, then K is isomorphic to L if and only if their vertex schemes are isomorphic as abstract simplicial complexes.

Proof. To show (i) let $n \in \mathbb{N}^+$ and $\mathbb{R}^n$ be the space with cofficients in $\mathbb{R}$ and basis $E = \{(1, 0, \ldots, 0), (0, 1, \ldots, 0), \ldots, (0, \ldots, 0, 1)\}$. That is, E is the set of n-vectors with

zeros in all positions except the i-th, for $1 \leq i \leq n$. Let Δ^n be the collection of all simplices spanned by a subset of E. Observe that if a simplex σ is in Δ^n, then all of its faces are in Δ^n, as any face of σ is spanned by some subset of E. Furthermore, if σ, τ are distinct simplices in Δ^n then they are spanned by a distinct set of points, so have distinct interiors. Therefore Δ^n is a simplicial complex.

Now let $\mathcal{S}$ be an abstract complex that has vertex set V and let $n = |V|$, so that there exists a function $f : V \to \{m \in \mathbb{N}^+ : m \leq n\}$ that is injective. Now let K be a subcomplex of Δ^J with simplices such that if $\{a_0, \ldots, a_p\}$ is an abstract simplex in $\mathcal{S}$, then the simplex spanned by $f(a_0), \ldots, f(a_p)$ is in K. Then if $a_0, \ldots, a_l$ is a face of the abstract simplex $a_0, \ldots, a_m$ in $\mathcal{S}$, then the simplex spanned by $f(a_0), \ldots, f(a_l)$ is a face of the simplex spanned by $f(a_0), \ldots, f(a_m)$ in K, so that every simplex in K contains all its faces. Furthermore, since K is a subset of Δ^n and the interiors of distinct simplices in Δ^n have empty intersection, the same is true for K. Therefore K is a simplicial complex that is a subcomplex of Δ^N, and $\mathcal{S}$ is isomorphic to the vertex scheme of K, with f the correspondence between their vertex sets.

To show (ii), observe that by (i) the vertex scheme of K is isomorphic to some abstract simplicial complex $\mathcal{S}(K)$ and the vertex scheme of L is isomorphic to some abstract simplicial complex $\mathcal{S}(L)$. Then by Proposition 2.4.3, K is isomorphic to L if and only if $\mathcal{S}(K)$ is isomorphic to $\mathcal{S}(L)$, as required. □

If $\mathcal{S}$ is isomorphic to the vertex scheme of some simplicial complex K, then we call K a *geometric realisation* of $\mathcal{S}$. Observe that by the previous theorem, any two geometric realisations of an abstract complex $\mathcal{S}$ are isomorphic. We now see some examples which demonstrate how we use abstract complexes to represent simplicial complexes.

Example 2.5.5. *Consider the complex L shown below in Figure 2.3. It has underlying space homeomorphic to the cylinder $S^1 \times [0, 1]$. There are several ways to represent this complex: firstly we can consider the complex L in the same figure. It is a complex which has a rectangle its underlying space, however we can label the vertices of L so that it is homeomorphic to K. In fact, both complexes will have vertex schemes isomorphic to the*

abstract complex $\mathcal{S}$ *whose simplices are the sets*

$$\{a, f, d\}, \{a, b, d\}, \{b, c, d\}, \{c, d, e\}, \{a, c, e\}, \{a, e, f\}$$

along with their non-empty subsets. Then by Theorem 2.5.4, the quotients of K *and* L *by the vertex identifications made in Figure 2.3 are isomorphic because their vertex schemes are both isomorphic to the abstract complex* $\mathcal{S}$*. Furthermore,* K *is a geometric realisation of* $\mathcal{S}$*.*

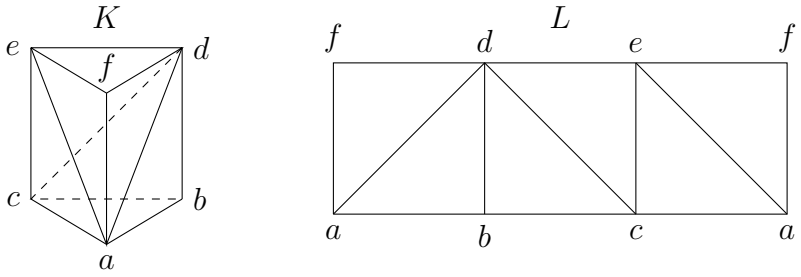


Figure 2.3

Let $f : L^{(0)} \to K^{(0)}$ be a map that takes each vertex of L to the corresponding labelled vertex of L in Figure 2.3. As we saw in the previous section, we can extend f into a simplicial map $g : |L| \to |K|$. As complexes are compact Hausdorff, the map between each complex is a quotient map, sometimes known as a 'pasting map'. The latter name is appropriate in this context: if we wanted to turn a rectangular piece of paper into a cylinder, we could fold it round and 'paste' the ends together to do so.

Definition 2.5.6. *An embedding of a topological space* X *into a topological space* Y *is an injective continuous map* $f : X \to Y$ *such that* $f : X \to f[X]$ *is a homeomorphism.*

We can use embeddings into $\mathbb{R}^3$ to help visualise our examples in a familiar space.

Example 2.5.7. *Consider the complex* L *in Figure 2.3. By relabelling the vertices, we can produce different complexes. Consider Figure 2.4. As before, the new labelling identifies the left and right edges of* L *together, however this time it twists round. The geometric realisation of* L *is therefore the space known as the Möbius band, shown embedded in* $\mathbb{R}^3$ *as* K*.*

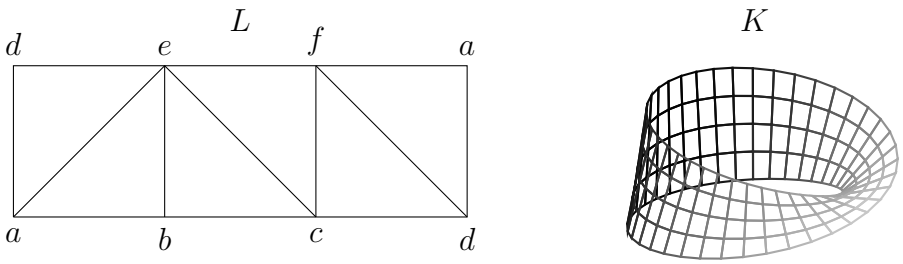


Figure 2.4

Example 2.5.8. *The torus can be defined as the quotient space obtained from a rectangle via the identifications in Figure 2.5. Following previous examples, we can then create a complex whose geometric realisation is a torus, such as K in Figure 2.6. However, we have to be careful: L in Figure 2.6 looks at first glance like a torus, but upon closer examination it is not. The vertices with label 'a' all pinch together into a single point, pulling the complex in on itself. In K the additional point on the vertical boundaries means that the complex can 'roll' into a cylindrical shape, but L cannot do that - with only one point seperating the a vertices on the vertical boundaries the corners come together in a single point, with the remaining identified points forming a sphere 'below' that point, so L has the surface of a sphere as its underlying space. In particular, imagine trying to 'roll' up L. For it to eventually become a torus, we'd require that each side ada would becomes a circle. However, because there is only the point d between each point a its more like folding the side ada in half: you get another edge. However, the points e and f are not the same, so they cannot be folded onto each other, so they bulge out after the two edges ada have been pasted together. Hence we get that L has the sphere as its underlying space.*

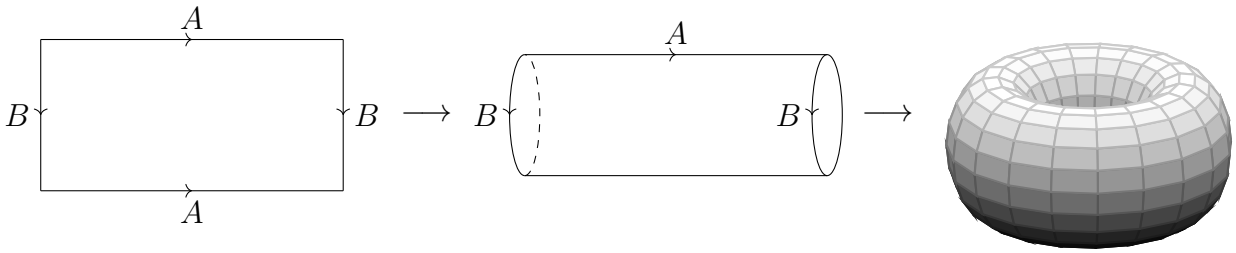


Figure 2.5

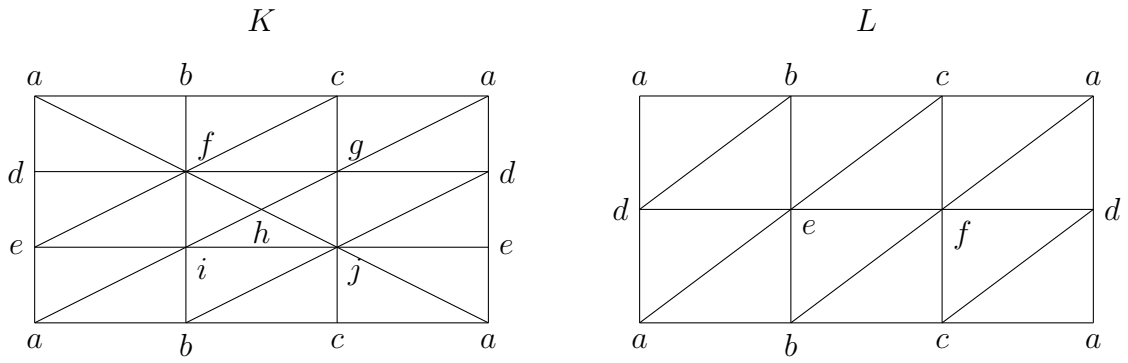


Figure 2.6

Example 2.5.9. *Consider the complex K in Figure 2.7. It is a labelling of a complex that has the Klein bottle as its underlying space. As demonstrated in Figure 2.8, is similar to the construction of the Torus, only you add a 'twist' when pasting the left and right edges together, in a way analogous to the cylinder/Möbius strip. The Klein bottle cannot be embedded into $\mathbb{R}^3$ [13, Corollary 3.46] - it passes through itself, but there is not a hole in it, therefore you require an additional dimension - but you can draw it in $\mathbb{R}^3$ as shown in Figure 2.8.*

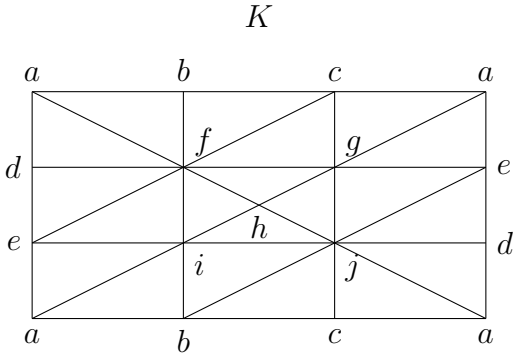


Figure 2.7

Definition 2.5.10. *Let L be a finite complex. Let f be a surjective function from the vertex set of L to a set of labels. We call f a labelling of L, and the image of f the labels. We can construct an abstract complex $\mathbb{S}$ which has the labels of L as vertices and whose simplices are the sets $\{f(a_0), \ldots, f(a_n)\}$ such that $\{a_0, \ldots, a_N\}$ span a simplex in L. Now, let K be a geometric realisation of $\mathbb{S}$. Then f yields a vertex map from $L^{(0)}$ to*

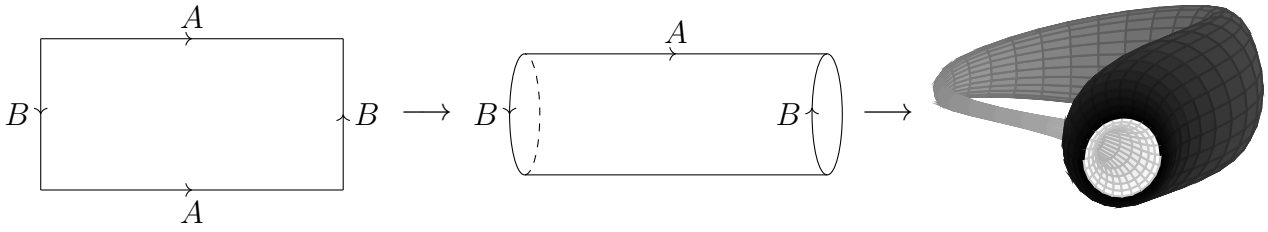


Figure 2.8

$K^{(0)}$ *that extends to a surjective simplicial map* $g : |L| \to |K|$. *We call* K *the complex derived from the labelled complex* L, *and call* g *the associated pasting map.*

Lemma 2.5.11. *The associated pasting map,* g, *is a quotient map.*

Proof. As $|L|$ is finite it is a finite union of compact subspaces σ, and so is compact. Also, by Proposition 2.2.6 $|K|$ is Hausdorff. Since g is a continuous map from a compact space to a Hausdorff space, it is a closed map. Furthermore, g is defined onto a geometric realisation of the image of a surjective map f, and is induced by the same f, g is a surjective map. Therefore g is a quotient map as required. □

Definition 2.5.12. *A subcomplex* L_0 *of a complex* L *is said to be a full subcomplex if and only if every simplex of* L *whose simplices are all in* L_0 *is also in* L_0.

Proposition 2.5.13. *Let* L *be a complex,* f *a labelling of its vertices, and* $g : |L| \to |K|$ *be the associated pasting map. Let* L_0 *be a full subcomplex of* L. *Suppose the following hold whenever* v, w *are two vertices of* L *with the same label:*

(i) The vertices v *and* w *are in* L_0, *and*

(ii) $\bar{\mathrm{St}}v$ *and* $\bar{\mathrm{St}}w$ *are disjoint.*

Then $\dim g(\sigma) = \dim \sigma$ *for all* $\sigma \in L$, *and if* $g(\sigma_1) = g(\sigma_2)$ *for distinct* σ_1, σ_2, *then* σ_1 *and* σ_2 *must be disjoint simplices belonging to* L_0.

Proof. Suppose no two vertices have the same labels. Then g is a bijection and L is homeomorphic to K. Therefore the proposition holds.

Let $\sigma \in L$. Suppose $\dim g(\sigma) < \dim \sigma$. Then g must label two vertices of σ with the same label. Call these vertices v and w. Then by assumption, $\bar{\text{St}}v$ does not intersect $\bar{\text{St}}w$. But then v and w cannot be in the same simplex, giving a contradiction. Therefore $\dim g(\sigma) = \dim \sigma$ as required.

Now suppose that σ_1, σ_2 are distinct vertices in L such that $g(\sigma_1) = g(\sigma_2)$. Then $\sigma_1, \sigma_2, g(\sigma_1)$ and $g(\sigma_2)$ all have the same dimension. Therefore there is a bijection between the vertices of σ_1 and σ_2 given by: a vertex in σ_1 corresponds to the vertex in σ_2 with the same labelling. Then by (i) each of the vertices of σ_1 and σ_2 is in L_0. Also, clearly every vertex in σ_1 is adjacent to every other vertex of σ_1, and the same for the vertices of σ_2. Therefore by (ii) σ_1 and σ_2 are disjoint simplices. Also, as each of the vertices of σ_1 and σ_2, and L_0 is a full subcomplex, σ_1 and σ_2 are in L_0. □

This proposition tells us how our complexes will collapse under a pasting map. Consider again Figure 2.6. Let K and L be our complexes from Figure 2.6, and K_0 and L_0 their respective boundaries. Then in K, the closed stars of any vertices on the boundary with the same label are disjoint, so the image of every simplex has the same dimension under the pasting map. However, this is not true for L, so we do not get the same guarantee.

2.6 Čech and Rips Complexes

To use the techniques that we are going to develop on data sets, we must be able to turn point data sets in $\mathbb{R}^d$ into complexes. In this section we shall introduce and compare two common to do exactly that.

Definition 2.6.1. *Let X be a finite set of points in $\mathbb{R}^d$ and $\epsilon > 0$ be a radius. Let $\mathcal{U}_\epsilon = \{B_{\epsilon/2}(x) : x \in X\}$ be the set of open balls (with respect to the Euclidean distance) of radius $\epsilon/2$ with centres the points of X. Then the Čech complex $\mathcal{C}_\epsilon$ of X is the abstract simplicial complex whose p-simplices correspond to non-empty intersections of $p+1$ distinct elements of $\mathcal{U}_\epsilon$.*

The Nerve Lemma [9, Theorem 5.1] states that the Čech complex captures the underlying topology of X. In particular it states that homotopy axiom holds for the space of Čech complexes: we elaborate in Section 3.3 when we have further developed the theory of homology groups. An important point is that the topology of the set $\cup\mathcal{U}_\epsilon$ depends heavily on ϵ. There is no guarantee that if X are points sampled from a space with an underlying topology that the Čech complex will capture that topology. However, as we shall see later, by varying ϵ we can get information about the topology of X at all scales.

Example 2.6.2. *In Figure 2.9 we can see the Čech complex for different ϵ. Observe that the complex grows as ϵ increases. At $\epsilon = 0$ is is just the vertices and at $\epsilon = 15$ it is the full 3-simplex.*

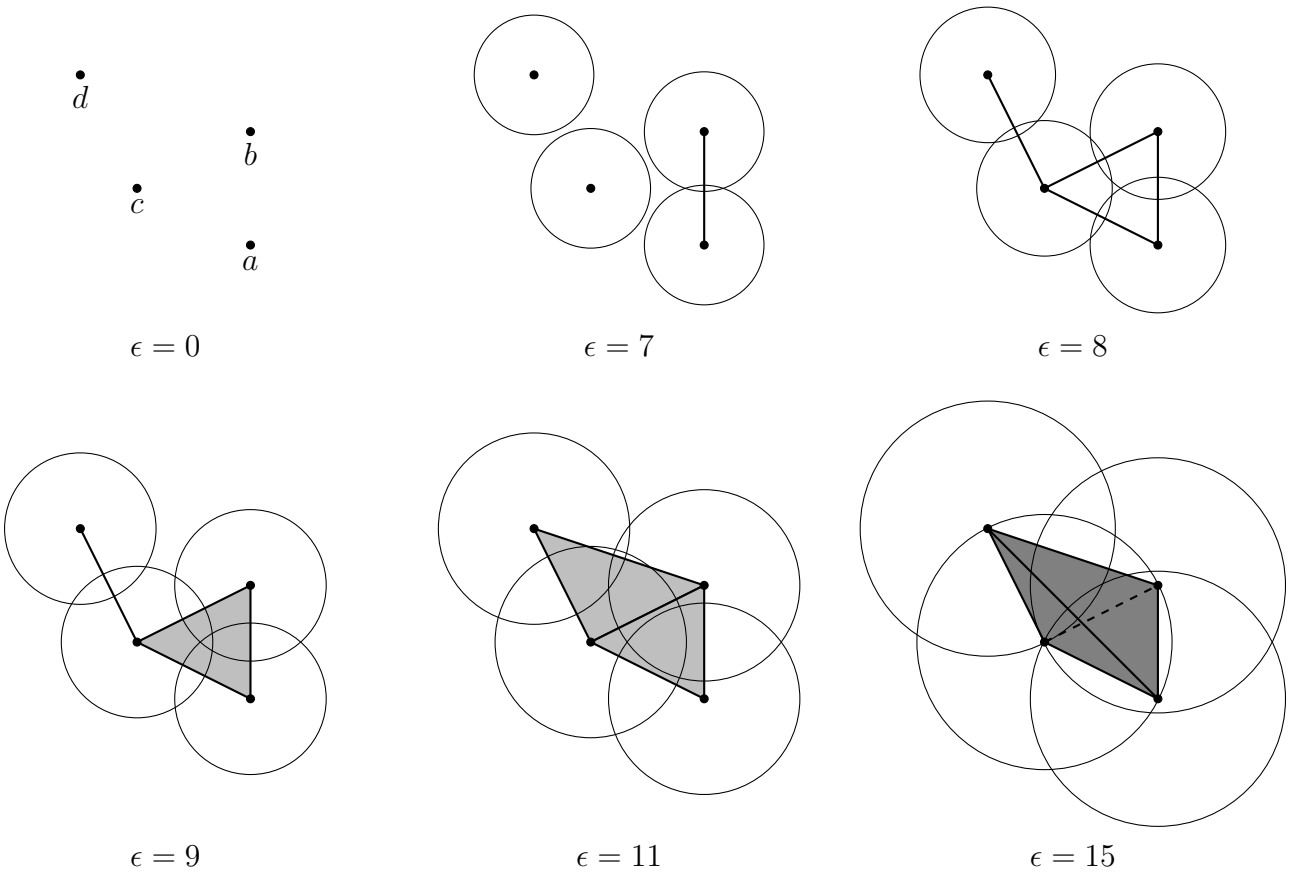


Figure 2.9

Suppose you have a set of balls centred at points $\{x_i\}$ and you wish to work out their intersections, in order to compute the Čech complex. A point y belongs to all balls centred $\{x_i\}$ if and only if $||x_i - y|| < r$ for each point x_i. If y belongs to all balls centred at $\{x_i\}$

then clearly their intersection is non-empty. Therefore if we have some set of points X, we can decide if some subset of points $x_0, \ldots, x_n \subseteq X$ generate a simplex in $\mathcal{C}_\epsilon$ based on if the points σ fit inside a ball of radius $\epsilon/2$. Let the *miniball* of σ, $\text{mb}(a_0, \ldots, a_n)$, be the smallest closed ball that contains $a_0, \ldots, a_n$. Then based on our reasoning, we know that

$$\sigma \in \mathcal{C}_\epsilon \iff (\text{the radius of } \text{mb}(a_0, \ldots, a_n)) < \epsilon/2.$$

Therefore to efficiently compute whether simplices are included in $\mathcal{C}_\epsilon$ we need to be calculate the smallest enclosing ball of some collection of points in $\mathbb{R}^d$. Fortunately, Welzl published an efficient algorithm in 1991 that does exactly that [26].

Suppose P is a collection of points in $\mathbb{R}^d$ for some fixed $d \in \mathbb{N}^+$. Let $\text{mb}(P)$ be the smallest open ball that contains all points of P. By convention we shall let $\text{mb}(\emptyset) = \emptyset$ and $\text{mb}(\{x\}) = \{x\}$ for $x \in \mathbb{R}^d$.

Proposition 2.6.3. *$mb(P)$ is unique.*

Proof. Suppose B_1 and B_2 are two smallest enclosing balls of P. Let $z_1, z_2 \in \mathbb{R}^d$ be their centres respectively, and let r be the radius of both balls (if one had smaller radius, then they would not both be smallest enclosing balls). As $P \subset B_1$ and $P \subset B_2$, we must have $P \subset B_1 \cap B_2$. Therefore the two balls have non-empty intersection. Consider Figure 2.10. Let $z = (z_1 + z_2)/2$ be the midpoint between z_1 and z_2. We calculate the radius of the smallest ball containing $B_1 \cap B_2$ using Pythagoras on the triangle in Figure 2.10. That radius is $r' = \sqrt{r^2 - a^2}$, where $a = ||z_1 - z_2||/2$. Then $B_1 \cap B_2$ is contained within the closed ball of radius r' and and centre z. We cannot have $r' < r$, else B_1 and B_2 are not smallest enclosing balls. Therefore we must have $a = 0$, which is true when

$$||z_1 - z_2||/2 = 0 \iff z_1 = z_2,$$

so $B_1 = B_2$. Therefore any smallest enclosing ball is unique, as required. □

Proposition 2.6.4. *A collection of $n + 1$ points uniquely determines the boundary of an n-ball in $\mathbb{R}^n$.*

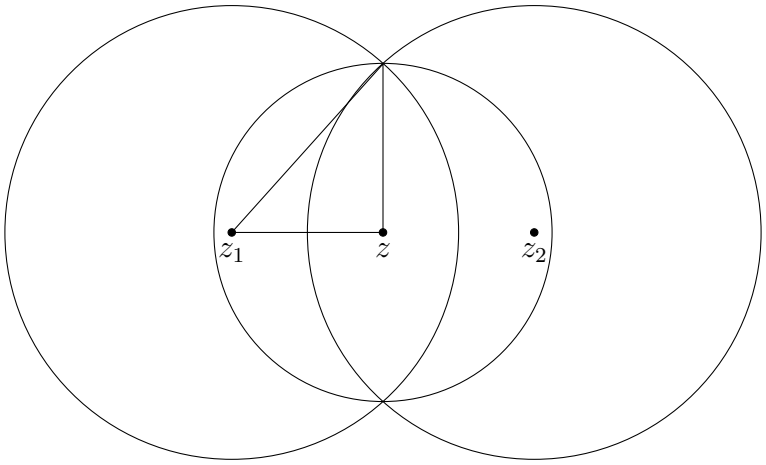


Figure 2.10

Proof. Suppose that $\{a_0, \ldots, a_n\}$ are not co-spherical points in $\mathbb{R}^n$. Consider the hyperplanes that are given by the perpendiular bisectors of the points a_n and a_i for $0 \leq i \leq n-1$. Each of these perpendicular bisectors is an $n-1$-plane. Since none of the points are co-spherical, no two planes will be perpendicular. Therefore every plane will intersect. Each time a plane intersects another the dimension of the intersection is reduced by one, so the intersection of every perpendicular bisector is a point (we have n planes). This point defines the centre of the ball. In particular, as each perpendicular bisector is unique, the intersection of every perpendicular bisector is unique, so the centre of the ball is unique. By our method of solving the centre, each point $a_0, \ldots, a_n$ is the same distance from the centre: this distance is our radius.

Specifically, each perpendicular bisector is of the form $(a_{n+1} - a_i) \cdot (x_i - p_i) = 0$. The collection of these equations for each $0 \leq i \leq n-1$ is a linear system which solves to give the unique centre of our ball. Since we've reasoned this centre must exist and be unique, the system of linear equations can be solved uniquely. We can then calculate the radius by finding the distance from the centre to any point, uniquely determining our ball. □

We now describe an algorithm to compute the miniball of a set of points P. By Proposition 2.6.4 we need at most $d+1$ points on the boundary of the ball to determine $\mathrm{mb}(P)$, so there must exist a subset $S \subseteq P$ on the boundary of $\mathrm{mb}(P)$ such that $\mathrm{mb}(P) = \mathrm{mb}(S)$, where $|S| \leq d+1$. This means that if a point $x \notin S$, then $\mathrm{mb}(P \setminus \{x\}) = \mathrm{mb}(P)$.

In other words, if $\mathrm{mb}(P \setminus \{x\}) \neq \mathrm{mb}(P)$, then x is on the boundary of $\mathrm{mb}(P)$. This notion will form the basis of our algorithm to compute $\mathrm{mb}(P)$, shown in Algorithm 1.

Suppose you want to compute the miniball containing $P = \{p_1, \ldots, p_n\}$. Start with $\emptyset$ and incrementally add points from P, computing the miniball each time. Suppose $B = \mathrm{mb}(\{p_1, \ldots, p_i\})$. If $p_{i+1} \in B$ then we can retain B and move onto p_{i+2}. If $p_{i+1} \notin B$ then we know that $p_{i+1} \in \mathrm{Bd}\,\mathrm{mb}(\{p_1, \ldots, p_{i+1}\})$. We shall define an algorithm B_MiniBall(A,p), which computes the smallest ball containing $A = \{p_1, \ldots, p_i\}$, with $p = p_{i+1}$ on its boundary. With this in mind, we define the algorithm MiniBall(P).

Algorithm 1 MiniBall Algorithm

```
1: function MiniBall(P)
2:     if P = ∅ then
3:         B := ∅
4:     else
5:         choose p ∈ P
6:         B := MiniBall(P \ {p})
7:         if p ∉ B then
8:             B = B_MiniBall(P \ {p}, p)
9:     return B
```

We now prove a lemma that justifies defining an algorithm B_MiniBall and helps us to determine it. For brevity we shall sometimes refer to B_MiniBall as b_mb. With the assumption that b_mb exists, we shall denote the miniball containing P and with R on its boundary as b_mb(P, R). We prove some properties of b_mb, then use that to inform how we construct the algorithm.

Lemma 2.6.5. *Let P, R be finite sets of points in $\mathbb{R}^d$ with $P \neq \emptyset$, and let $x \in P$. Then*

(i) If there exists a ball containing P with R on its boundary then b_mb(P, R) *is unique.*

(ii) If $x \notin$ b_mb$(P \setminus \{x\}, R)$*, then x is on the boundary of* b_mb(P, R)*. In particular,* b_mb$(P, R) =$ b_mb$(P \setminus \{x\}, R \cup \{x\})$.

(iii) If b_mb(P, R) *exists, then there is a set of at most* $\max(0, d + 1 - |R|)$ *points in P such that* b_mb$(P, R) =$ b_mb(S, R).

Proof. First note that a closed ball with center $z \in \mathbb{R}^d$ and radius $r > 0$ is $B_r(z) = \{x \in \mathbb{R}^d : f(x) < 0\}$, where f is the function of B defined to be $f(x) = ||x - z||^2 - r^2$.

Furthermore, the boundary of $B_r(z)$ is the $(d-1)-$sphere consisting of points $x \in \mathbb{R}^d$ such that $f(x) = 0$. If f, g are two functions of balls B, C that have non-empty intersection, then we define the convex combination of B and C by $\{x \in \mathbb{R}^d : \lambda f(x) + (1-\lambda)g(x) < 0\}$ for each $\lambda \in [0,1]$. In particular, suppose that B and C have radii r, s and centres z_1, z_2 respectively. Then

$$\begin{aligned}
\lambda f(x) + (1-\lambda)g(x) &= \lambda||x - z_1||^2 - \lambda r^2 + (1-\lambda)||x - z_2|| - (1-\lambda)(s^2) \\
&= ||x - (\lambda z_1 + (1-\lambda)z_2||^2 - \lambda r^2 - (1-\lambda)s^2 \\
&\quad + \lambda(1-\lambda)(||z_1||^2 + ||z_2||^2 - 2\langle z_1, z_2\rangle) \\
&= ||x - (\lambda z_1 + (1-\lambda)z_2||^2 - (\lambda r^2 + (1-\lambda)s^2 - \lambda(1-\lambda)||z_1 - z_2||^2)
\end{aligned}$$

Therefore the convex combination of B and C for $\lambda \in [0,1]$ is the ball with centre $\lambda z_1 + (1-\lambda)z_2$ and radius $(\lambda r^2 + (1-\lambda)s^2 - \lambda(1-\lambda)||z_1 - z_2||^2)^{1/2}$, denoted B_λ. Now assume B and C have non-empty intersection. Note if $x \in \mathbb{R}^d$ is in the intersection of B and C, then $f(x) < 0$ and $g(x) < 0$, which implies that for $\lambda \in [0,1]$, $\lambda f(x) + (1-\lambda)g(x) < 0$, so $B \cap C \subseteq B_\lambda$. Furthermore, if x is on the boundary of both B and C, then $f(x) = 0$ and $g(x) = 0$, so $\lambda f(x) + (1-\lambda)g(x) = 0$, meaning that x is on the boundary of B_λ, i.e. $\operatorname{Bd} B \cap \operatorname{Bd} C \subseteq \operatorname{Bd} B_\lambda$.

(i) Consider the set of radius/centre pairs that give open balls containing P with R on their boundaries. This is the set $T = \{(r, z) : P \subseteq B_r(z), R \subseteq \operatorname{Bd} B_r(z)\}$. Then since $r \geq 0$ the radii are bounded below, so $r := \inf_{(r,z)\in T} r$ exists and is at least 0. Therefore there exists an open ball that has radius r. Suppose that B_0, B_1 are distinct balls, each with radius r whilst containing P and having R on their boundaries. Then consider their convex combination with $\lambda = 1/2$. The convex combination $B_{1/2}$ contains P and has R on its boundary as $P \in B_0 \cap B_1$ and $R \in \operatorname{Bd} B_0 \cap \operatorname{Bd} B_1$, but by our calculation of the radius of B_λ above, $B_{1/2}$ has radius $(r^2 - ||z_1 - z_2||/4)^{1/2}$. This is less than r as $z_1 \neq z_2$, a contradiction.

(ii) Assume that $x \notin B_0 = \text{B\_MB}(P \setminus \{x\}, R)$, and x does not lie on the boundary of $B_1 = \text{B\_MB}(P, R)$. As the convex combination of B_0 and B_1, given by B_λ,

continuously deforms B_0 into B_1 as λ goes from 0 to 1, there must be a value $\lambda' < 1$ for which p is on the boundary of $B_{\lambda'}$. Then the ball $B_{\lambda'}$ contains P, has x and R on its boundary, and has a smaller radius than B_0 or B_1. This is a contradiction, as B_0 and B_1 were assumed to be miniballs. Therefore x must be on the boundary of B_1.

(iii) Assume that $\text{B\_MB}(R, R)$ exists. Firstly, if $|R| > d + 1$ then the points R must be geometrically dependent, as they are are in $\mathbb{R}^d$. Then there cannot be a unique ball with the points R on its boundary. Hence we may assume $|R| < d + 1$. In the algorithm B_MB is only called when we are adding an additional point to the boundary, therefore all points in R must lie on the boundary and we can further assume that $|R| < d$. By (ii) we know that if S are the points of P that lie on the boundary of $\text{B\_MB}(P, R)$, then $\text{B\_MB}(P, R) = \text{B\_MB}(S, R)$. Now, if the points in $P \cup R$ are not geometrically dependent or co-spherical, that is, all lie on the boundary of some $(d-1)$-sphere, then we are done, as we need exactly $(d+1) - |R|$ extra points to uniquely define the ball.

If some of the points are co-spherical, then we can permute the points by a negligible amount that does not move the point out of the miniball, but ensures that no points are co-spherical. Suppose $p_1, \ldots, p_{d+2}$ are cospherical. Then we wish to move one of the points by a small amount so that it is not cospherical to any other points. Consider the collection of tuples of points $r_1, \ldots, r_{d+1}$ that are cospherical. Then each of these tuples determines a unique sphere which is nowhere dense. We do not want to move a point, say p_1 without loss of generality, into any of these uniquely determined spheres, as we would create a new set of $d + 2$ cospherical points. The finite union of the nowhere dense uniquely determined spheres is also nowhere dense. Therefore we can move p_1 by a small amount without making it cospherical to anything else. Then we are once again done, as we need exactly $(d + 1) - |R|$ extra points to uniquely define the ball as before. □

Observe that the set R is not in general unique. There could be different sets, each of size at most $d + 1$, that determine the miniball.

We can use the properties shown in Lemma 2.6.3 to determine our algorithm B_MB, which we now describe. First, if $P = \emptyset$ then the boundary points R must determine the ball, so we can compute it directly. Similarly, if $R = |d + 1|$ then we can compute the algorithm directly. The way B_MB is called from MiniBall guarantees that if $R = |d+1|$ then all points P will be inside the ball with R the points on the boundary. If $P \neq \emptyset$ then choose a random $x \in P$ and compute $B = \text{B\_MiniBall}(P \setminus \{x\}, R)$. If $x \in B$, then $\text{B\_MiniBall}(P, R) = B$, otherwise $\text{B\_MiniBall}(P, R) = \text{B\_MiniBall}(P \setminus \{x\}, R \cup \{x\})$, as it must therefore be on the boundary. This algorithm is expressed formally in Algorithm 2.

Algorithm 2 MiniBall Boundary Algorithm

```
1: function B_MiniBall(P)
2:     if (P = ∅) or (|R| = d + 1) then
3:         B := B_MiniBall(∅, R)
4:     else
5:         choose random p ∈ P
6:         B := B_MiniBall(P \ {p}, R)
7:         if (B defined) and (p ∉ B) then
8:             B = B_MiniBall(P \ {p}, R ∪ {p})
9:     return B
```

A disadvantage of the Čech complex is that we must check every subcollection of X for inclusion as a simplex when computing the complex. Instead of checking all subcollections, which quickly gets computationally intensive, we can simplify our construction of complexes by just considering pairs of points in X. This simplified technique was discovered independently by Vietoris, who used it to study metric spaces [25], and Rips, whose techniques were bought to prominence after Grobov used them to study hyperbolic groups [11]. As such, it is sometimes referred to as the *Vietoris-Rips complex*, although we shall call it the *Rips complex*.

Definition 2.6.6. *Let X be a finite set of points in $\mathbb{R}^n$ and $\epsilon > 0$ be a radius. Then the Rips complex $\mathcal{R}_\epsilon$ of X is the abstract simplicial complex whose k-simplices correspond to unordered $(k+1)$-tuples of points that are pairwise at most Euclidean distance ϵ from each other.*

However, the Rips complex does not have the same guarantee as the Čech complex:

it does not necessarily capture the underlying topology of the space. One example of this is seen in Figure 2.11. To justify the use of Rips complexes we shall prove a Theorem that states two Rips complexes of varying radii contain a Čech complex. This means that although the Rips complex may not fully capture the homology, it will be close to a Čech complex that does. The question of which complex to use ultimately comes down to choosing computational efficiency or accuracy. We prove two powerful results, Radon's Theorem and Helly's Theorem, in order to show the complex inclusion.

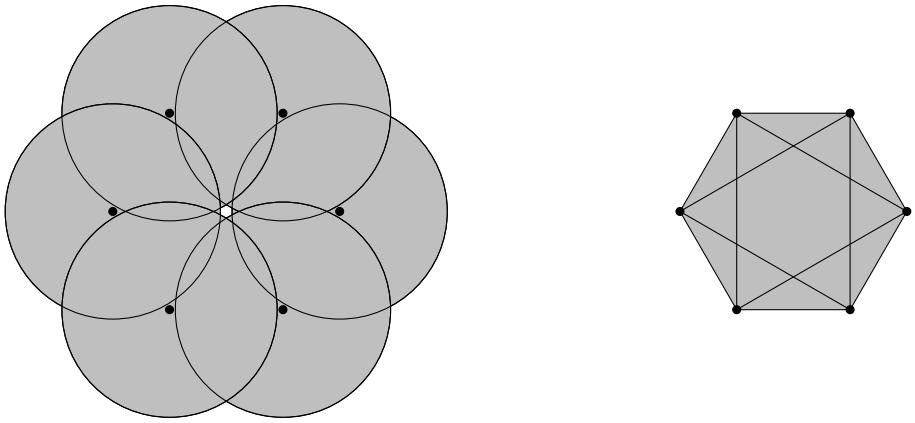


Figure 2.11: The left diagram shows the Čech open balls of radius ϵ, $\epsilon > 0$, on six equidistant points on the circumference of the unit ball. The right diagram shows the Rips complex with the same radius on the same set of points. The Čech complex is isomorphic to the boundary of a ball, whereas the Rips complex is isomorphic to a ball.

Theorem 2.6.7 (Radon's Theorem)**.** *If A is a finite collection of $d+2$ points in $\mathbb{R}^d$, then A can be partitioned into two disjoint sets whose convex hulls intersect.*

Proof. Let $A = \{x_1, \ldots, x_{d+2}\} \subset \mathbb{R}^d$, and let $t_1, \ldots, t_{d+2}$ be a set of coefficients in $\mathbb{R}$, not all of which are zero, such that

$$\sum_{i=1}^{d+2} t_i x_i = 0 \text{ and } \sum_{i=1}^{d+2} t_i = 0.$$

Such a set of coefficients exists because we have one more equation than unknown, so we can solve by substitution to find each t_i. Let P be the set of coefficients that are strictly postiive, and let N be the set of coefficients that are zero or less. Then P and N is the required partition.

Indeed, observe that by construction we have $\alpha = \sum_{p\in P} t_p = -\sum_{n\in N} t_n$ and let

$$z = \sum_{p\in P} \frac{t_p}{\alpha} x_p = \sum_{n\in N} \frac{-t_n}{\alpha} x_n.$$

Then in both expressions for z the sum of coefficients equals one, and all coefficients are non-negative by the properties of P and N. Hence the two expressions for z are both convex combinations, so that z lies in the convex hull of both P and N. Therefore P and N give a partition of the points with intersecting convex hulls, as required. □

Theorem 2.6.8 (Helly's Theorem)**.** *If $\mathcal{U}$ is a finite collection of $k > d+1$ convex sets in $\mathbb{R}^d$, and each subcollection $\mathcal{V} \subset \mathcal{U}$ of size $d+1$ is such that $\cap\mathcal{V} \neq \emptyset$, then $\cap\mathcal{U} \neq \emptyset$.*

Proof. We proceed by induction on k. Suppose $k = d+2$ and $\mathcal{U} = \{X_1, \ldots, X_k\}$. Then by assumption we have that for each $j \in \{1, \ldots, k\}$, there exists an $x_j \in \mathbb{R}^d$ such that

$$x_j \in \bigcap_{\substack{1\leq j\leq k \\ j\neq i}} X_i.$$

Now let $A = \{x_1, \ldots, x_k\}$, so that each x_j is in each X_i, except for maybe $i = j$. Then by Radon's Theorem we can partition A into two sets A_1, A_2 such that there is at least one point in the intersection of their convex hulls. Call that point z. Let $j \in \{1, \ldots, k\}$ be fixed. Then we shall show that $z \in X_j$, so that z is in the intersection of $\mathcal{U}$, as required. Now we have either $x_j \in A_1$ or $x_j \in A_2$. If $x_j \in A_1$, then $x_j \notin A_2$, so $A_2 \subseteq X_j$, as every other element of A is within X_j by construction. Then since X_j is convex by assumption and A_2 is contained within X_j, we have that the convex hull of A_2 is contained within X_j. Therefore $z \in X_j$. If $x \in A_2$ we can use the same argument, permuting A_2 and A_1, to show again that $z \in X_j$. Therefore z is in each X_j in $\mathcal{U}$, so $\cap\mathcal{U}$ is non-empty.

Now suppose that the statement holds for $l \geq d+2$ and consider $l+1$. Suppose $\mathcal{U} = \{X_1, \ldots, X_l, X_{l+1}\}$ such that every subcollection of $d+1$ sets has non-empty intersection. Replace X_l and X_{l+1} with the set $X_l \cap X_{l+1}$, so $U' = \{X_1, \ldots, X_{l-1}, X_l \cap X_{l+1}\}$ still has the property that every subcollection of size $d+1$ has non-empty intersection. But the size of U' is l, so the inductive hypothesis applies. Therefore $\cap U' \neq \emptyset$. Then $\cap U' \neq \emptyset$ implies

that $\cap U \neq \emptyset$, as U' differs only by elements that are in the intersection of subcollections. Therefore the theorem holds by induction. □

The following theorem is due to de Silva and Ghrist [24]. They proved it as part of their application of persistent homology to working out the coverage of sensor networks.

Theorem 2.6.9. *Let X be a finite set of points in $\mathbb{R}^d$. Then we have the inclusions*

$$\mathcal{R}_\epsilon(X) \subset \mathcal{C}_{\epsilon'}(X) \subset \mathcal{R}_{\epsilon'}(X) \text{ whenever } \frac{\epsilon'}{\epsilon} \geq \sqrt{\frac{2d}{d+1}}.$$

Proof. First, observe that if the points $a_0, \ldots, a_n$ are the vertices of a simplex in $\mathcal{C}_{\epsilon'}$ then the balls of radius $\epsilon'/2$ have a common intersection, so certainly each pair a_i, a_j are within ϵ' distance of each other. Therefore $\mathcal{C}_{\epsilon'}(X) \subset \mathcal{R}_{\epsilon'}(X)$.

Therefore it remains to show the first inclusion. Consider $k+1$ points that span a k-simplex $\sigma \in \mathcal{R}_\epsilon$. These points are pairwise separated by distance at most ϵ. To show that $\sigma \in \mathcal{C}_{\epsilon'}$, we must show that the the balls of radius $\epsilon'/2$ centred on those points have a common intersection.

First consider a set of $d'+1$ points $\{x_0, \ldots, x_{d'}\} \subset \mathbb{R}^d$, with $d' < d$. Let $f : \mathbb{R}^d \to \mathbb{R}$ be given by

$$f(y) = \max_{0 \leq i \leq d'} ||x_i - y||,$$

where $||\cdot||$ is the Euclidean distance in $\mathbb{R}^d$. This function is continuous (as both max and $||\cdot||$ are continuous) and $f(y) \to \infty$ as $||y|| \to \infty$. We shall show that f has a global minimum. Since $f(y) \to \infty$ as $||y|| \to \infty$, there exists a $K > 0$ that may depend on an $M > 0$ such that $f(y) \geq K$ whenever $||y|| > M$. Then we can consider f as a continuous function on $[0, M]^d$, a closed bounded interval. Therefore f attains a minimum on $[0, M]^d$. Now, let M be large enough so that K is greater than the minimum attained on $[0, M]^d$. Then that minimum is a global minimum, call it $f(y_0)$.

If $||x_i - y_0|| = f(y_0)$ then define x_i to be a *critical vertex*. Let $I = \{x_i : ||x_i - y_0|| < f(y_0)\} \subseteq \{x_0, \ldots, x_d\}$ be the set of non-critical vertices. Now let $g_{x_i} : [0, \infty) \to \mathbb{R}$ be given by $g_{x_i} : \lambda \mapsto \max_{i \in I} ||x_i - (y_0 + \lambda v)||$.

Consider $x_i \in I$. Now by the continuity of f and because we are considering non-critical vertices, there exists an $r > 0$ such that $g(\lambda) < f(y_0)$ for all $\lambda \in [0, r)$. Therefore $||x_i - (y_0 + \lambda v)|| \leq g(\lambda) < f(y_0)$. That is, the non-critical vertices remain non-critical even when subtracting λv.

Now consider the critical vertices. Suppose for a contradiction there exists a vector v such that $v \cdot (x_i - y_0) > 0$ for each critical vertex x_i. Then for all $\lambda > 0$,

$$\begin{aligned} ||x_i - y_0||^2 &= ||x_i - (y_0 + \lambda v)||^2 + 2\lambda v \cdot (x_i - y_0) + \lambda^2 ||v^2|| \\ &> ||x_i - (y_0 + \lambda v)||^2. \end{aligned}$$

Then for $0 < \lambda < r$, we would get $f(y_0 + \lambda v) < f(y_0)$, which contradicts minimality. Note that such a vector v would give a hyperplane $v \cdot (p - y_0) = 0$, which does not separate any of the x_i's, as $v \cdot (x_i - y_0) > 0$ for each i. Therefore y_0 cannot be separated from any x_i by a hyperplane, so is in the convex hull of the points x_i by the Seperating Hyperplane Theorem [1, Section 2.5.1]. So we have that y_0 is equal to a convex combination $y_0 = \sum_{i=0}^{d''} a_i x_i$ for some $d'' \leq d'$, where each $a_i > 0$ and $\sum a_i = 1$. Relabel the a_i's and x_i's so that a_0 is the largest coefficient. Now define $\hat{x}_i = x_i - y_0$, and subtract y_0 from our previous expression to get that

$$\sum_{i=0}^{d''} a_i \hat{x}_i = 0, \text{ so } \hat{x}_0 = \sum_{i=1}^{d''} \frac{a_i}{a_0} \hat{x}_i.$$

Furthermore, since x_0 is a critical vertex we get that $f(y_0) = ||x_0 - y_0|| = ||(\hat{x}_0 + y_0) - y_0|| = ||\hat{x}_0||$. Then we have that

$$-f(y_0)^2 = -||\hat{x}_0||^2 = \sum_{i=1}^{d''} \frac{a_i}{a_0} \hat{x_0} \cdot \hat{x}_i.$$

Now, at least one of the terms in the final sum must be such that $(a_i/a_0)\hat{x}_0 \cdot \hat{x}_i \leq -f(y_0)^2/d''$. Then since $a_0 > a_j$ for all $j \neq 0$ and $d'' < d$ we get that

$$\hat{x}_0 \cdot \hat{x}_i \leq \frac{a_i}{a_0} \hat{x}_0 \cdot \hat{x}_i \leq \frac{-f(y_0)^2}{d''} \leq \frac{-f(y_0)^2}{d} \implies \frac{f(y_0)^2}{d} \leq -\hat{x}_0 \cdot \hat{x}_i.$$

Since x_i are critical points, we know that $f(y_0)^2 = ||\hat{x}_0||^2 = ||\hat{x}_i||^2$. Putting this all together we get that

$$\begin{aligned} f(y_0)^2\left(1+\frac{2}{d}+1\right) &= f(y_0)^2 + 2\frac{f(y_0)^2}{d} + f(y_0)^2 \\ &\leq ||\hat{x}_0||^2 - 2\hat{x}_0\hat{x}_i + ||\hat{x}_i||^2 \\ &= ||\hat{x}_0 - \hat{x}_i||^2 \\ &= ||x_0 - x_i||^2 \\ &\leq \epsilon^2. \end{aligned}$$

Therefore it follows that

$$f(y_0) \leq \sqrt{\frac{\epsilon^2 d}{2(d+1)}} = \frac{\epsilon}{2}\sqrt{\frac{2d}{d+1}} = \frac{\epsilon'}{2}$$

and so each of the given $d+1$ points is within distance $\epsilon'/2$ of y_0. Hence the $(\epsilon'/2)$-balls centred at the given points all intersect at y_0, as required.

If the set of points is larger than $d+1$ then the collection of balls centred at the points is a finite collection of convex sets of size strictly greater than $d+1$. By the previous part of the proof, each subcollection of these balls of size $d+1$ has a non-empty intersection. Therefore by Helly's Theorem, the full collection of balls has a non-empty intersection.

We have shown that if a set of points span a simplex in $\mathcal{R}_\epsilon(X)$, then they also span a simplex in $\mathcal{C}_{\epsilon'}(X)$, so $\mathcal{R}_\epsilon(X) \subset \mathcal{C}_{\epsilon'}(X)$ as required.

□

CHAPTER 3

HOMOLOGY GROUPS

3.1 Review of Free Abelian Groups

We shall use this section to review some results concerning free groups.

Recall that a group is called *abelian* if all of its elements commute. A map between two groups, $f : G \to H$, is a *homomorphism* if for all $g, h \in G$, $f(gh) = f(g)f(h)$. If f is a homomorphism then we define the *kernel*, *image*, and *cokernel* of f respectively by

$$\ker f = f^{-1}(0),\ \mathrm{Im} f = f[G],\ \text{and cok } f = H/f[G].$$

We call f a *monomorphism* if and only if $\ker f = 0$ and an *epimorphism* if and only if cok $f = 0$. If f is an epimorphism then $G/\ker f \cong H$.

Definition 3.1.1. *We call an abelian group G free if there exists a family of elements $\{g_\alpha\}_{\alpha \in I}$ such that each $g_\alpha \in G$ and every $g \in G$ can be written uniquely as a finite sum*

$$g = \sum_{\alpha \in J} n_\alpha g_\alpha,$$

where J is a finite subset of I and each $n_\alpha \in \mathbb{Z} \setminus \{0\}$. The family $\{g_\alpha\}$ is the basis of G.

Note that the basis of a free group is not uniquely determined. Uniqueness of the finite sum implies that each g_α has infinite order. If Definition 3.1.1 holds except for uniqueness then we say $\{g_\alpha\}$ *generates* G. If $\{g_\alpha\}$ is finite then we say that G is *finitely generated*.

If G is a free group with a basis consisting of n elements, then every basis of G has n elements. We define the *rank* of G to be n. An important property of free groups is the *universal property* [10, Theorem 6.7], that we show below.

Theorem 3.1.2 (The Universal Property)**.** *Suppose G is a free Abelian group with basis $X = \{g_\alpha\}_{\alpha \in I}$. Let $\eta : X \to G$ be the inclusion map. Then for every mapping f from X into a group H, there is a unique homomorphism $\varphi : G \to H$. The universal property is shown in the commutative diagram below.*

$$\begin{array}{ccc} X & \xrightarrow{\eta} & G \\ & \searrow^{f} & \downarrow{\scriptstyle \varphi} \\ & & H \end{array}$$

Proof. Let X be the basis of a free Abelian group G. Let η the inclusion map from X to G. Suppose f is a homomorphism from G to some group H. If $g \in G$, then g can be uniquely written as some finite sum $g = \sum_{\alpha \in J} n_\alpha g_\alpha$ with J some finite subset of the indexing set. Then since g is uniquely written we can write ψ uniquely as

$$\psi(g) = \psi\left(\sum_{\alpha \in J} n_\alpha g_\alpha\right) := \sum_{\alpha \in J} n_\alpha f(g_\alpha).$$

Therefore ψ is a unique map given by the above. We must also verify that ψ is a homomorphism. Suppose $g = \sum_{\alpha \in J} n_\alpha g_\alpha$ and $h = \sum_{\alpha \in K} m_\alpha g_\alpha$ are elements in G, where J, K are finite subsets of the indexing set I. Then we can write $g + h$ as

$$g + h = \sum_{\alpha \in J \cup K} (n_\alpha + m_\alpha) g_\alpha,$$

where we take n_α or m_α as zero if $\alpha \notin J$ or $\alpha \notin K$ respectively. Then we have that

$$\psi(g + h) = \sum_{\alpha \in J \cup K} (n_\alpha + m_\alpha) f(g_\alpha) = \sum_{\alpha \in J} n_\alpha f(g_\alpha) + \sum_{\alpha \in K} m_\alpha f(g_\alpha) = \psi(g) + \psi(h),$$

so that ψ is indeed a group homomorphism. □

Definition 3.1.3. *An element f of an abelian group G has finite order if $ng = 0$ for some $n \in \mathbb{N}^+$. The minimal such n is called the order of g and denoted $o(g) = n$. The*

set of all elements of finite order, T, is a subset of G called the torsion subgroup. If T is the trivial group we call G torsion-free.

Proposition 3.1.4. *T is a subgroup of G.*

Proof. Suppose g, h are elements of T. By the subgroup criterion it suffices to show that $gh^{-1} \in T$. Suppose $\mathrm{o}(g) = n$ and $\mathrm{o}(h) = m$, where n and m are finite natural numbers by hypothesis. Then $\mathrm{o}(h^{-1}) = m$, so $\mathrm{o}(gh^{-1}) = \mathrm{lcm}(m, n)$ which is finite. Therefore $gh^{-1} \in T$ as required. □

Proposition 3.1.5. *Every free abelian group is torsion-free.*

Proof. Let G be a free abelian group with basis $\{g_\alpha\}_{\alpha \in I}$. Suppose $g = \sum_{\alpha \in J} n_\alpha g_\alpha$ is a non-zero element of G that has finite order, where J is a finite subset of I. Then there exists some $\lambda \in \mathbb{N}^+$ such that $\lambda g = 0$. Then we must have that $\sum_{\alpha \in J} \lambda n_\alpha g_\alpha = 0$ for each $\alpha \in J$. Therefore $\lambda = 0$, so there is no such element g and G is torsion-free. □

3.2 Homology Groups

Recall that an oriented simplex $\sigma = [v_0, .., v_n]$ is the simplex spanning the points $v_0, .., v_n$ with the orientation $(v_0, \ldots, v_n)$. If σ is an oriented simplex then we will denote the same simplex with the opposite orientation as σ'. If a p-dimensional simplex has an orientation, then we can induce an orientation on its proper faces. For example, if a 2-simplex has an orientation with the vertex ordering (a_0, a_2, a_1) then we can induce the vertex orderings (a_0, a_2), (a_2, a_1) and (a_1, a_0) onto its 1-simplices.

Example 3.2.1. *Figure 3.1 shows some examples of oriented simplices.*

Definition 3.2.2. *Let K be a simplicial complex. A p-chain on K is a function c from the set of all oriented p-simplices in K to a group G such that the following hold.*

(i) $c(\sigma) = -c(\sigma')$.

(ii) $c(\sigma) = 0$ *for all but finitely many oriented p-simplices.*

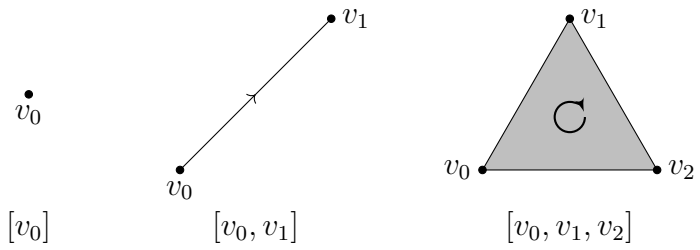


Figure 3.1

We can define addition on two p-chains in K by adding their values. The set of every oriented p-chains of K with the addition we just described forms a group, $C_p(K)$, called the group of oriented p-chains of K.

For the remainder of this Chapter we shall set $G = \mathbb{Z}$. In computational applications, the group $\mathbb{Z}_2$ is most commonly used. Sometimes G is taken to be $\mathbb{Q}$; in this case the existence of multiplicative inverses allows for some interesting properties.

Let σ be an oriented simplex in K and σ' be σ with the opposite orientation. Then the *elementary chain* c associated with σ is the function defined as

$$\begin{cases} c(\sigma) = 1, \\ c(\sigma') = -1, \\ \sigma(\tau) = 0, \end{cases}$$

where τ is any other simplex in K. By an abuse of notation, we let σ denote the elementary chain associated with σ. With this notation we get that $\sigma = -\sigma'$. From context it should be clear whether σ refers to a simplex, an oriented simplex, or the elementary chain.

Proposition 3.2.3. *$C_p(K)$ is free abelian. Orient the p-simplices of K arbitrarily, then the elementary chains associated with each oriented p-simplex in K form a basis of $C_p(K)$.*

Proof. Arbitrarily order each of the p-simplices of K. Then every p-chain can be written as a finite linear combination in the form

$$c = \sum n_i \sigma_i,$$

where σ_i is the elementary chain associated with each oriented $\sigma_i \in K$. Then c assigns the value n_i to σ_i and $-n_i$ to the simplex with opposite orientation to σ_i. It assigns 0 to all simplices not appearing in the (finite) linear combination. In this way, any p-chain on the p-simplices of K can be written as a sum of elementary chains. Therefore the elementary chains of the ordered simplices represents a basis of $C_p(K)$, as required. □

Corollary 3.2.4. *Let f be a map from the oriented p-simplices of K to an abelian group G such that $f(-\sigma) = -f(\sigma)$ for all oriented σ in $|K|$, so that f preserves the notion of the orientation over the mapping. Then f extends to a unique homomorphism from $C_P(K)$ to G.*

Proof. This follows from the universal property of free abelian groups. Note that we must also check that $f(-\sigma) = -f(\sigma)$ because we have oriented the simplices arbitrarily: if the map preserves this property then it respects our orientation of the simplices. □

Definition 3.2.5. *We define the boundary operator*

$$\delta_p : C_p(K) \to C_{p-1}(K)$$

for $p > 0$ by defining it on the oriented p-simplices of σ, then using the above corollary to extend it to the full p-chain group. Let $\sigma = [v_0, \ldots, v_p]$ be an oriented simplex of K with $n > 0$. Then we define

$$\delta_p \sigma = \delta_p [v_0, \ldots, v_p] = \sum_{i=0}^{p} [v_0, \ldots, \hat{v}_i, \ldots, v_p],$$

where $\hat{v}_i$ indicates that the ith vertex is removed from the list of vertices that the simplex spans. Specifically, $[v_0, \ldots, \hat{v}_i, \ldots, v_p]$ is the simplex generated by $\{v_0, \ldots, v_p\} \setminus v_i$.

Proposition 3.2.6. *The boundary operator δ_p, for $p > 0$, extends to a homomorphism $C_p(K) \to C_{p-1}(K)$.*

Proof. Note that $C_{p-1}(K)$ is an abelian group by Proposition 3.2.3, so by Corollary 3.2.4 we need only check that $\delta_p(-\sigma) = -\delta_p(\sigma)$. Suppose $\sigma = [v_0, \ldots, v_j, v_{j+1}, \ldots, v_p]$, then

without loss of generality $\sigma' = [v_0, \ldots, v_{j+1}, v_j, \ldots, v_p]$. We shall compare the expressions for $\delta_p\sigma$ and $\delta_p\sigma'$.

When $i \neq j$ and $i \neq j+1$ the ith terms in $\delta_p\sigma$ and $\delta_p\sigma'$ are identical except they differ by a sign. For the terms when $i = j$ and $i = j+1$ we get the expressions

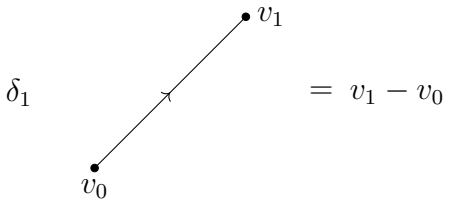
$$(-1)^j[\ldots, v_{j-1}, \hat{v_j}, v_{j+1}, v_{j+2}, \ldots] + (-1)^{j+1}[\ldots, v_{j-1}, v_j, \hat{v_{j+1}}, v_{j+2}, \ldots]$$

$$(-1)^j[\ldots, v_{j-1}, \hat{v_{j+1}}, v_j, v_{j+2}, \ldots] + (-1)^{j+1}[\ldots, v_{j-1}, v_{j+1}, \hat{v_j}, v_{j+2}, \ldots] \ .$$

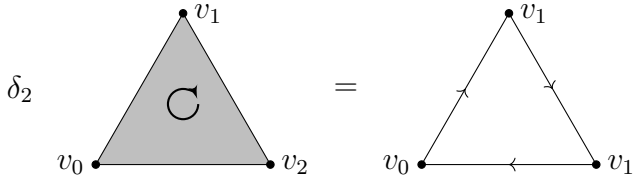
Comparing these two terms we can see that they also differ by a sign. Therefore $\delta_p(-\sigma) = -\delta_p(\sigma)$ as required. □

We give some examples of the boundary operator acting on simplices.

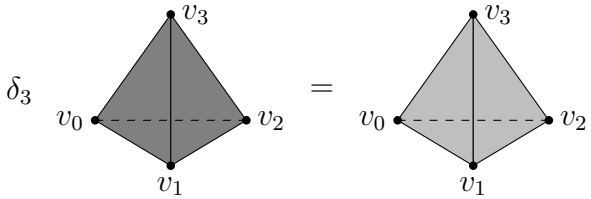
Example 3.2.7. *(i) For a 1-simplex we get* $\delta_1[v_0, v_1] = v_1 - v_0$.



(ii) For a 2-simplex we get $\delta_2[v_0, v_1, v_2] = [v_1, v_2] - [v_0, v_2] + [v_0, v_1]$.



(iii) For a 3-simplex we get $\delta_3[v_0, v_1, v_2, v_3] = [v_1, v_2, v_3] - [v_0, v_2, v_3] + [v_0, v_1, v_3] - [v_0, v_1, v_2]$.



Observe that $\delta_0\delta_1[v_0, v1] = \delta_0(v_1 - v_0) = 0$, and

$$\delta_1\delta_2[v_0, v_1, v_2] = \delta_1([v_1, v_2] - [v_0, v_2] + [v_0, v_1]) = (v_2 - v_1) - (v_2 - v_0) + (v_1 - v_0) = 0.$$

Through a similar calculation you can see that $\delta_2\delta_3[v_0, v_1, v_2, v_3] = 0$. This is indicative of a general property, which we prove below.

Lemma 3.2.8. $\delta_{p-1} \circ \delta_p = 0$.

Proof. We have that

$$\begin{aligned}
\delta_{p-1}\delta_p[v_0, \ldots, v_p] &= \delta_{p-1} \sum_{i=0}^{p} (-1)^i [v_0, \ldots, \hat{v}_i, \ldots, v_p] \\
&= \sum_{i=0}^{p} (-1)^i \delta_{p-1}[v_0, \ldots, \hat{v}_i, \ldots, v_p] \\
&= \sum_{j<i} (-1)^i (-1)^j [\ldots, \hat{v}_j, \ldots, \hat{v}_i, \ldots] + \sum_{i<j} (-1)^i (-1)^{j-1} [\ldots, \hat{v}_i, \ldots, \hat{v}_j, \ldots].
\end{aligned}$$

The two sums in the final line cancel each other by matching terms with opposite signs, giving $\delta_{p-1} \circ \delta_p = 0$, as required. □

Definition 3.2.9. *We now define two important groups that we use to define the homology group.*

(i) The kernel of $\delta_p : C_p(K) \to C_{p-1}(K)$ is called the group of p-cycles, denoted $Z_p(K)$.

(ii) The image of $\delta_{p+1} : C_{p+1}(K) \to C_p(K)$ is called the group of p-boundaries, denoted $B_p(K)$.

The cycle group is denoted Z_p due to the German "Zyklus". Note that by Lemma 3.2.8 the boundary of a $p+1$ chain is a p-cycle. Therefore $B_P(K) \subseteq Z_p(K)$. Therefore we can define the homology group as follows.

Definition 3.2.10. *The pth homology group of K is the group*

$$H_p(K) = Z_p(K)/B_p(K).$$

We refer to as a conjugacy class in the homology group as a *homology class.*

Definition 3.2.11. *The pth Betti number is the rank of H_p.*

In fact, the 0th Betti number counts the number of connected components in the complex, the 1st Betti number counts the number of holes, and the 2nd Betti number counts the number of voids [7, Section 1]. Here a hole is the space contained in the boundary of a 2-simplex, and a void is the space contained in the boundary of a 3-simplex.

Example 3.2.12. *Consider the complex K in Figure 3.2 that has the boundary of a square as its underlying space. The 1-chains of K are formal sums of the form $\sum_{i=1}^{4} n_i e_i$, so $C_1(K)$ is a free abelian group of rank 4 with basis $\{e_1, e_2, e_3, e_4\}$. To calculate the cycle group we find the kernel of $\delta_1 c$, where $c \in C_1(K)$. Let $c = \sum_{i=1}^{4} n_i e_i \in C_1(K)$. Then*

$$\begin{aligned}
\delta_1 c &= \delta_1(n_1 e_1 + n_2 e_2 + n_3 e_3 + n_4 e_4) \\
&= \delta_1(n_1[v_0, v_1] + n_2[v_1, v_2] + n_3[v_2, v_3] + n_4[v_3, v_0]) \\
&= n_1\delta_1[v_0, v_1] + n_2\delta_1[v_1, v_2] + n_3\delta_1[v_2, v_3] + n_4\delta_1[v_3, v_0] \\
&= n_1(v_1 - v_0) + n_2(v_2 - v_1) + n_3(v_3 - v_2) + n_4(v_0 - v_3) \\
&= (n_4 - n_1)v_0 + (n_1 - n_2)v_1 + (n_2 - n_3)v_2 + (n_3 - n_4)v_3.
\end{aligned}$$

Therefore we get $c \in \ker \delta_1 \iff \delta_1 c = 0 \iff n_1 = n_2 = n_3 = n_4$. So the cycle group of K is given by all chains of the form $n\sum_{i=1}^{4} e_i$, so $Z_1(K)$ is a free abelian group of rank 1 with basis $\{e_1 + e_2 + e_3 + e_4\}$. Since there are no 2-simplices in K, $B_1(K)$ is trivial, so we conclude that

$$H_1(K) = Z_1(K) \cong \mathbb{Z}.$$

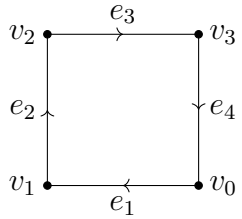


Figure 3.2

Example 3.2.13. *Now consider the complex L in Figure 3.3 that has a square as its underlying space. The 1-chains are formal sums of the form $\sum_{i=1}^{5} n_i e_i$, so $C_1(K)$ is a free abelian group of rank 5. Again, we calculate $\delta_1 c$ to find the cycles of L.*

$$\begin{aligned}\delta_1 c &= n_1\delta_1[v_0,v_1] + n_2\delta_1[v_1,v_2] + n_3\delta_1[v_2,v_3] + n_4\delta_1[v_3,v_0] + n_5\delta_1[v_3,v_1] \\ &= n_1(v_1 - v_0) + n_2(v_2 - v_1) + n_3(v_3 - v_2) + n_4(v_0 - v_3) + n_5(v_1 - v_3) \\ &= (n_4 - n_1)v_0 + (n_1 - n_2 + n_5)v_1 + (n_2 - n_3)v_2 + (n_3 - n_4 - n_5)v_3.\end{aligned}$$

Therefore c is a cycle if and only if $n_1 = n_4$, $n_2 = n_3$, and $n_5 = n_1 - n_2$. We can determine n_3, n_4, n_5 by assigning values to n_1 and n_2, so $Z_1(L)$ is a free abelian group of rank 2. To find a basis of Z_1, we let $(n_1, n_2) = (1, 0)$, which determines that $(n_3, n_4, n_5) = (0, 1, 1)$, so $e_1 + e_4 + e_5$ is one basis element of Z_1. Letting $(n_1, n_2) = (0, 1)$ we determine that $(n_3, n_4, n_5) = (1, 0, -1)$, so the second basis element is $e_2 + e_3 - e_5$. Note that $e_1 + e_4 + e_5 = \delta_2\sigma_2$ and $e_2 + e_3 - e_5 = \delta_2\sigma_1$, so both basis elements of $Z_1(L)$ are in $B_1(L)$. Therefore

$$H_1(L) = Z_1(L)/B_1(L) = 0,$$

where 0 denotes the trivial group $\{0\}$.

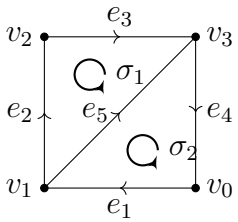


Figure 3.3

Although direct computation of the cycle and boundary groups gives us a better idea of what is happening, it is possible in some cases to use proven properties of a complex to find the homology groups H_p directly. We shall see this in the Section 3.4, where we find the homology of some common surfaces. To enable us to do this we introduce some more nomenclature. We say that a chain c is *carried by* a subcomplex L of K if c has

value 0 on every simplex not in L. If two p-chains c and c' differ by a boundary, that is if $c - c' = \delta_{p+1}d$ for some $d \in C_{p+1}$, then we say that c and c' are *homologous*. If $c = \delta_{p+1}d$ then we say that c *bounds* or is *homologous to zero*.

Example 3.2.14. *Consider the complex M that has a square as its underlying space shown on the left in Figure 3.4. Rather than compute the 1-cycles, consider a 1-chain c. Let a be the value of c on e_1 (recall that a 1-chain is a function that gives a value on 1-simplices). Then we can define the chain*

$$c_1 = c + \delta_2(a\sigma_1).$$

This chain has value 0 on the oriented simplex e_2. By modifying the chain by a boundary, we have pushed it off e_2. The chain now has value 0 on e_2. We can push c_1 off e_2 in a similar manner. Let $c_2 = c_1 + \delta_2(b\sigma_2)$, where b is the value of c_2 on e_2. Then c_2 has value 0 on the oriented simplex e_2. Since e_1 does not appear in the expansion of $\delta_2\sigma_2$ it does not change the value of c_1 on e_1, so c_2 also equals 0 on e_1. Finally, we push c_2 off e_3 by defining $c_3 = c_2 + \delta_2(d\sigma_3)$, where d is the value of c_2 on e_3. Then the value of c_3 on e_3 is 0, and since $\delta_2(\sigma_3)$ does not involve either e_1 or e_2, the value of c_3 is still 0 on both e_1 and e_2. Therefore we have pushed c off e_1, e_2, and e_3.

Therefore we have proved that any 1-chain c is homologous to a chain c_3 that is carried by the subcomplex of M shown on the right in Figure 3.4. Observe that we cannot push the chain off e_4 - there are no more higher dimensional simplices that we can use to alter the chain by a boundary.

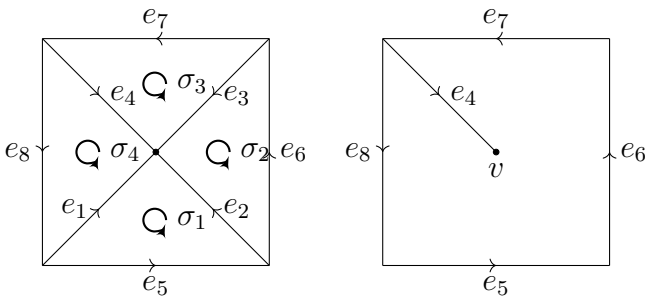


Figure 3.4

3.3 Invariance of Homology Groups

In order to know that homology groups are reasonable objects to describe the underlying topology of a complex, we give an overview of the invariance of homology groups. In 1952 Eilenberg and Steenrod published 'Foundations of Algebraic Topology', giving an axiomatic approach to homology theory. Their fifth axiom of a homology was the Homotopy Axiom [9, Page 11], which helps to justify homology groups as natural objects to describe topological spaces. To define this we need a small amount of supporting theory. Proving the space of simplicial complexes satisfies this axiom is beyond the scope of this project, but we shall give an overview of the theory.

Definition 3.3.1. *Let X and Y be topological spaces and $f, g : X \to Y$ be continuous functions. Then f is homotopic to g if there is a continuous function $H : X \times [0,1] \to Y$ such that for all $x \in X$,*

$$H(x,0) = f(x) \text{ and } H(x,1) = g(x).$$

Then H is called a homotopy between f and g.

If topological equivalence is defined as a continuous deformation between two spaces, then homotopic equivalence is a continuous deformation between two maps. We can then use this homotopy to induce a homomorphism between pairs of homology groups.

Definition 3.3.2. *Suppose $f : K \to L$ is a map between simplicial complexes. Then for each dimension p, the homomorphism induced by f is given a function*

$$f_{*,p} : H_p(K) \to H_p(L).$$

When referring to the induced homomorphism, we shall sometimes drop the p from $f_{*,p}$ if it clear from context which dimension we refer to.

The Eilenberg-Steenrod axioms are given in terms of categories in order to extend the domain of homology theory to any category that abides by the five axioms.

Axiom 1 (Homotopy Axiom). *Let X and Y be categories and f, g be homotopies between K and L. Then for each dimension $p \in \mathbb{N}_0$, the induced homomorphisms $f_*, g_* : H_p(K) \to H_p(L)$ coincide.*

To formally check that the category of simplicial complexes with their homology groups give a homology by the Eilenberg-Steenrod axioms, each one must be verified. For this section, we're only interested in the Homotopy Axiom. Given that homology theory was originally introduced to study simplicial complexes [21], it comes as no surprise that the axioms do indeed hold.

Theorem 3.3.4. *The homotopy axiom holds for the space of simplicial complexes.*

As stated, we omit the proof of this theorem. However, the interested reader can find the details of the proof, along with an axiomatic description of the homology groups from a categorical point of view, in Eilenberg and Steenrod's textbook [9, Page 162]. Now assuming that the homotopy axiom is true, we can answer our question about the suitability of homology groups for studying topological properties.

Theorem 3.3.5. *A homeomorphism $f : |K| \to |L|$ induces isomorphisms $f_* : H_p(K) \to H_p(L)$ for each $p \in \mathbb{N}_0$.*

Proof. The homeomorphism implies homotopic equivalence, so f induces a homomorphism of the homology groups. Since f is a homeomorphism, $f \cdot f^{-1} = \mathrm{id}$. Then since f_* is an induced homomorphism, $(f \cdot f^{-1})_* = f_* \cdot (f^{-1})_* = \mathrm{id}$. Similarly, $(f^{-1} \cdot f)_* = \mathrm{id}$. Therefore f_* has an inverse given by $(f_*)^{-1} = (f^{-1})_*$, Therefore the induced homomorphisms are isomorphisms. □

This theorem states that if two simplicial complexes are homeomorphic, then the homology groups they generate are isomorphic. This invariance justifies using homology groups to study topological properties. Note that any isomorphic homology groups will have equal Betti numbers, implying that Betti numbers are also invariant for homeomorphic simplicial complexes.

3.4 Homology Groups of Surfaces

In this section we shall compute the homology groups of the torus and the Klein bottle. We shall use a technique that relies on the proposition below.

Proposition 3.4.1. *Let L be the complex with a rectangle as its underlying space, shown in Figure 3.5. Let* $\operatorname{Bd} L$ *be the complex with the boundary of the rectangle as its space. Orient every* 2*-simplex of L counterclockwise and orient the* 1*-simplices arbitrarily. Then*

(i) Every 1*-cycle of L is homologous to a* 1*-cycle carried by* $\operatorname{Bd} L$*.*

(ii) If d is a 2*-chain of L and δd is carried by* $\operatorname{Bd} L$*, then d is a multiple of the chain* $\sum_i \sigma_i$*.*

L

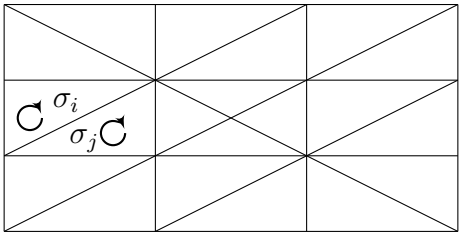


Figure 3.5

Proof. To show *(i)* we can use the same technique we used in Example 3.2.13. If c is a 1-cycle of L, then we can add the boundary of an appropriate 2-simplex to get c_1, a homologous chain carried by the subcomplex K_1 in Figure 3.6. Then c_1 is homologous to a chain c_2 that is carried by the subcomplex K_2 in Figure 3.6. Finally note that if c was in fact a 1-cycle, then c_2 would also be a cycle, as it only differs from c by boundaries. If c_2 has non-zero coefficients on one or more of the vertices $a_1, \ldots, a_5$ then it could not be a cycle, and so c_2 must be carried by $\operatorname{Bd} L$.

To show *(ii)*, observe that if σ_i and σ_j share an edge e, then δd must have value 0 on e (if they share an edge, that edge cannot be on $\operatorname{Bd} L$, and δd is carried by $\operatorname{Bd} L$). Therefore d must have the same value on σ_i as σ_j. As σ_i, σ_j were arbitary, d must have

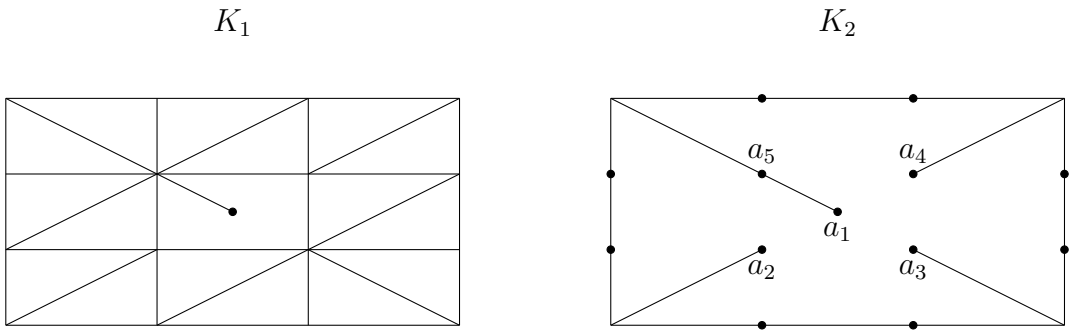


Figure 3.6

the same value on every oriented 2-simplex. Therefore d must be a multiple of the chain $\sum \sigma_i$, as required. □

Theorem 3.4.2. *Let T denote the complex represented by the labelled rectangle L with underlying space the torus, shown in Figure 3.7. Then*

$$H_1(T) \cong \mathbb{Z} \oplus \mathbb{Z} \text{ and } H_2(T) \cong \mathbb{Z}.$$

Orient each 2-simplex of L counterclockwise and use the induced orientation for the 1-simplices. Let $\gamma = \sum_i \sigma_i$ where each σ_i is a 2-simplex in L. Let

$$w_1 = [a, b] + [b, c] + [c, a],$$
$$z_1 = [a, d] + [d, e] + [e, a].$$

Then γ generates $H_2(T)$ and w_1 and z_1 generate $H_1(T)$.

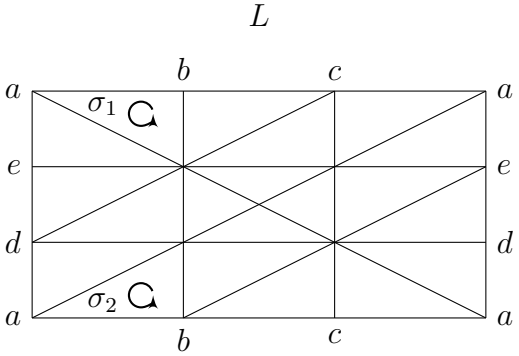


Figure 3.7

Proof. Let $g : |L| \to |T|$ be the pasting map and define $A = g(|\operatorname{Bd} L|)$. In fact, A is homeomorphic to a space that is the union of two circles with a single point in the intersection. This space is called the *wedge of two circles* and is shown in Figure 3.8. Orient the 1-simplices of T arbitrarily. Since g only identifies vertices in $\operatorname{Bd} L$, we can use the proof of Proposition 3.4.1 to get the same results about our space T, namely that the following properties hold:

(i) Every 1-cycle of T is homologous to a 1-cycle carried by A.

(ii) If d is a 2-chain of T and δd is carried by A, then d is a multiple of the chain γ.

For the complex T we can also prove the following two properties:

(iii) Let c be a 1-cycle of T that is carried by A. Then $c = nw_1 + mz_1$ for some $n, m \in \mathbb{Z}$.

(iv) $\delta\gamma = 0$.

To prove (iii) observe that the space A is the complex shown in Figure 3.8. Any 1-cycle is clearly a sum of the boundaries of the two 2-simplices, hence the result. To show (iv) first observe that $\delta\gamma$ has value 0 on any 1-simplex of T not in A, as it must be the boundary of a boundary. Direct computation on each of the 1-simplices of L present in A show that $\delta\gamma$ also equals 0 on each of the 1-simplices contained in A. One example of the direct computation is for the chain $[a, b]$. By consulting Figure 3.7 we can see that $\delta\sigma_1 = [a, b] + \dots$ and $\delta\sigma_2 = -[a, b] + \dots$ are the only times that $[a, b]$ appears in a boundary of a 2-simplex in L. Therefore

$$\delta\gamma = \delta \sum \sigma_i = \sum \delta\sigma_i$$

has value $[a, b] - [a, b] = 0$ on $[a, b]$. Similar calculations for each of the other 1-simplices present in A prove (iv).

We use the results proven so far to find the homology groups of T. Combining (i) and (iii) we can see that every 1-cycle of T is homologous to a 1-cycle carried by A, which in turn must be of the form $c = nw_1 + mz_1$. To find the first homology group we are

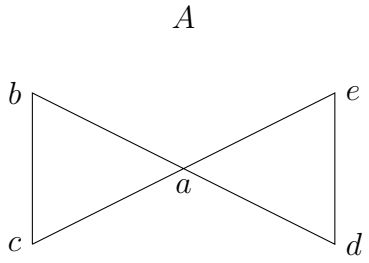


Figure 3.8

interested in the cycles that bound: if $c = \delta d$ for some d, then (ii) tells us that d is a multiple of γ, and since $\delta\gamma = 0$ by (iv) we have that $c = \delta d = 0$. Therefore the first boundary group is trivial, and as the first cycle group is free Abelian of rank 2 by (iii), we get that

$$H_1(T) \cong \mathbb{Z} \oplus \mathbb{Z},$$

with basis $\{w_1, z_1\}$.

To compute $H_2(T)$, observe that any 2-chain of T must be a multiple of γ. Every such 2-chain is in fact a cycle, as there are no 3-simplices. Therefore

$$H_1(T) \cong \mathbb{Z},$$

with basis γ. □

Theorem 3.4.3. *Let S denote the complex represented by the labelled rectangle L with underlying space the Klein bottle, shown in Figure 3.9. Then*

$$H_1(S) \cong \mathbb{Z} \oplus \mathbb{Z}/2 \text{ and } H_2(S) = 0.$$

The torsion element of $H_1(S)$ is represented by the chain z_1, and a basis for the group $H_1(S)$ modulo torsion is w_1, where

$$w_1 = [a, b] + [b, c] + [c, a],$$
$$z_1 = [a, d] + [d, e] + [e, a].$$

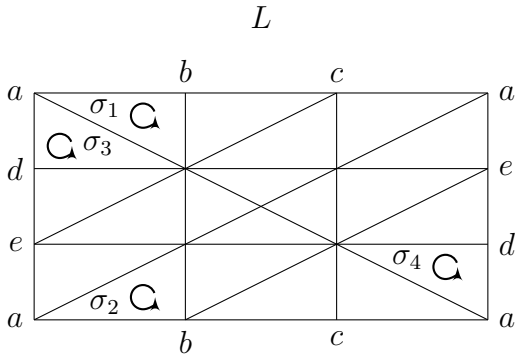


Figure 3.9

Proof. Let $g : |L| \to |S|$ be the pasting map and define $A = g(|\operatorname{Bd} L|)$ as before. Orient the 2-simplices of S counter-clockwise and let $\gamma = \sum_i \sigma_i$ where each σ_i is a 2-simplex in L. Orient the 1-simplices of S arbitrarily. Both (i) and (ii) from the previous proof hold, as none of the changed identifications on L are involved. Since A is still the wedge of two circles, (iii) from the previous proof also still holds. In fact, only (iv) differs from the previous proof. In particular, we have that

(iv) $\delta\gamma = 2z_1$.

This is shown by direct computation. Similar to last time, we shall only compute the chain $[a, b]$ as an example. Consulting Figure 3.9 we see that $\delta\sigma_1 = -[a, b] + \dots$ and $\delta\sigma_2 = [a, b] + \dots$ are the only times that $[a, b]$ appears in the boundary of a 2-simplex, so $[a, b]$ has coefficient 0 in the expression for $\delta\gamma$. Similarly, we can see that $\delta\sigma_3 = [a, d] + \dots$ and $\delta\sigma_4 = [a, d] + \dots$ are the only times that $[a, d]$ appears in a boundary of a 2-simplex, so $[a, d]$ has coefficient 2 in the expression for $\delta\gamma$. Similar calculations yield the result that $\delta\gamma = 2z_1$ as required.

Using these facts together, we can compute the homology groups of S. Combining (i) and (iii) we can see that every 1-cycle of S is homologous to a cycle of the form $c = nw_1 + mz_1$. If $c = \delta d$ for some d, then (ii) tells us that $d = p\gamma$ for some $p \in \mathbb{Z}$, so $\delta d = 2pz_1$ by (iv). Therefore $nw_1 + mz_1$ bounds if and only if m is even and n is zero. Therefore

$$H_1(S) \cong \mathbb{Z} \oplus \mathbb{Z}/2.$$

The cycle z_1 represents the torsion element and w_1 generates the infinite cyclic group $H_1(S)/T_1(S)$.

To compute $H_2(S)$, observe (ii) states that any 2-cycle of S must be in the form $p\gamma$. Since $\delta\gamma \neq 0$ by (iv), γ is not a cycle, so we get that

$$H_2(S) = 0. \quad \square$$

3.5 Computing Homology Groups

In the previous section we computed the homology groups of the torus and the Klein bottle. However, we relied on some specific properties to calculate those groups by hand. In this section we'll show that it is always possible to algorithmically compute homology groups, and give the algorithm that allows us to do so.

Let K be a complex, and $C_p(K)$ and $C_{p-1}(K)$ be its pth and $(p-1)$th chain groups, with bases $e_1, \ldots, e_n$ and $f_1, \ldots, f_m$ respectively. Then the boundary operator can be completely determined by how it acts on the basis elements $e_1, .., e_n$. With this in mind, we construct the matrix of δ_p.

Definition 3.5.1. *Let K be a simplicial complex, and C_p and C_{p-1} be the chain groups of K with bases $e_1, \ldots, e_n$ and $f_1, \ldots, f_m$ respectively. Then for the boundary operator $\delta_p : C_p \to C_{p-1}$ we have*

$$\delta_p(e_j) = \sum_{i=1}^{m} \lambda_{ij} f_i$$

for each $1 \leq j \leq n$. Then the matrix of δ_p is given by

$$M(\delta_p) = (\lambda_{ij})_{1 \leq i \leq n, 1 \leq j \leq m}.$$

The setup of this matrix is shown explicitly in Table 3.1.

Note that the entries of $M(\delta_p)$ are from the integers, as the chain groups take coefficients from the integers. We shall sometimes denote $M(\delta_p)$ as M_p.

We can perform elementary row and column operations on M_p. So that it continues

$M(\delta_p)$	e_1	$\dots$	e_n
f_1	λ_{11}	$\dots$	λ_{1n}
$\vdots$	$\vdots$	$\ddots$	$\vdots$
f_m	λ_{m1}	$\dots$	λ_{mn}

Table 3.1

to represent the boundary operator, we must update the basis entries e_i and f_j as we perform these operations. This can be done as follows.

Theorem 3.5.2. *Elementary row and column operations require updating the corresponding basis element as indicated in Table 3.2 to preserve the matrix of the boundary operator.*

Row/Column Operations	Domain/Codomain Basis Operation
Swap R_i and R_j	Swap f_i and f_j
$R_j \mapsto \alpha R_j$	$f_j \mapsto \alpha^{-1} f_j$
$R_j \mapsto R_j + \alpha R_k$	$f_k \mapsto f_k - \alpha f_j$
Swap C_i and C_j	Swap e_i and e_j
$C_i \mapsto \alpha C_i$	$e_i \mapsto \alpha e_i$
$C_i \mapsto C_i + \alpha C_j$	$e_i \mapsto e_i + \alpha e_j$

Table 3.2

Proof. It is obvious that swapping rows or columns corresponds to swapping the relevant basis element. Similarly, as each column operation only affects elements in the domain, we update the basis elements in the expected way. Now let $[\delta_p(e_j)]_{f_i}$ denote the f_i term in the basis expansion of $\delta_p(e_j)$. Then we require that $[\delta_p(e_j)]_{f_i} = \lambda_{ij} f_j$ is preserved as we update $\lambda_{ij} \mapsto \alpha\lambda_{ij}$. Therefore we must also update the codomain basis element. We update the basis element f_i to $\alpha^{-1} f_i$, then

$$[\delta_p(e_j)]_{\alpha^{-1} f_i} = (\alpha\lambda_{ij})(\alpha^{-1} f_i) = \lambda_{ij} f_i$$

as required.

Now, consider the rows j, k and each column e_i. Let $\lambda_{i,j}, \lambda_{i,k}$ be the initial matrix elements and f_j, f_k be the initial codomain basis elements. Then we update our expansion $\delta_p e_i = \dots + \lambda_{i,j} f_j + \lambda_{i,k} f_k + \dots$ by $\lambda_{i,j} \mapsto \lambda_{i,j} + \alpha\lambda_{i,k}$ and the corresponding basis update $f_k \mapsto f_k - \alpha f_j$. We must verify that the expression for δ_p remains the same.

$$\begin{aligned}\delta_p e_i &= \cdots + \lambda_{i,j} f_i + \lambda_{i,k} f_k + \dots \\ &= \cdots + (\lambda_{i,j} + \alpha\lambda_{i,k}) f_i + \lambda_{i,k}(f_k - \alpha f_i) + \dots \\ &= \lambda_{i,j} f_i + \alpha\lambda_{i,k} f_i - \alpha\lambda_{i,k} f_i + \lambda_{i,k} f_k + \dots \\ &= \cdots + \lambda_{i,j} f_i + \lambda_{i,k} f_k + \dots .\end{aligned}$$

Note in the expression above we update the rows and basis elements in the second line, then show it is equivalent to the first line. Therefore we preserve the boundary operator, and we are done. □

Definition 3.5.3. *A matrix is in Smith normal form if it is in the form*

$$\left[\begin{array}{ccc|ccc} a_1 & & & & & \\ & \ddots & & & & \\ & & a_n & & & \\ \hline & & & 0 & & \\ & & & & \ddots & \\ & & & & & 0 \end{array}\right]$$

where $a_1 | \dots | a_n$.

We shall now give the key algorithm of this section, the *reduction algorithm*. It reduces any matrix with elements from $\mathbb{Z}$ to Smith normal form.

Theorem 3.5.4. *Any matrix with entries* $\mathbb{Z}$ *can be reduced to Smith normal form.*

Proof. Let A be an $m \times n$ matrix with entries from $\mathbb{Z}$. We shall demonstrate how to reduce the matrix to Smith normal form using elementary row and column operations.

The first stage of the reduction is to reduce A to a matrix C of the form

$$C = \left[\begin{array}{c|ccc} a_1 & 0 & \dots & 0 \\ \hline 0 & & & \\ \vdots & & \hat{C} & \\ 0 & & & \end{array}\right],$$

where a_1 divides every element of $\hat{C}$. Refer to this matrix structure as $(*)$. We shall give a finite list of elementary operations that, given A, either describe a matrix of the form $(*)$, or give a matrix $B = (b_{i,j})$ such that $b_{1,1} < a_{1,1}$ (call this condition $(\dagger)$) in which case we repeat the operations again. This repetition must eventually terminate, otherwise the degree of the $(1,1)$st element will create an infinitely strictly decreasing and non-negative sequence, which is a contradiction. We now describe the list of operations.

If A is the zero matrix, then we have the form $(*)$, so suppose A has a non-zero element. By exchanging rows and columns we can put this in the position $(1,1)$, so we may assume $a_{1,1} \neq 0$. Then we consider three cases.

Case 1: There is an entry in the first row $a_{1,j}$ such that $a_{1,1} \nmid a_{1,j}$.
Then by the division algorithm for $\mathbb{Z}$ there exists $q, r \in \mathbb{Z}$ such that $a_{1,j} = qa_{1,1} + r$ where $0 \leq r < a_{1,1}$. Subtract the first column from the jth column q times and swap the 1st and jth column, putting r in position $(1,1)$ and achieving $(\dagger)$.

Case 2: There is an entry in the first column $a_{i,1}$ such that $a_{1,1} \nmid a_{i,1}$.
Then follow the same procedure as in case 1, only using columns instead of rows, to achieve $(\dagger)$.

Case 3: $a_{1,1}$ divides every entry in the first row and the first column.
In this case we can subtract multiples of the first column from the other columns to achieve zeros in the first column, except for position $(1,1)$. Similarly, we can subtract multiples of the first row from other rows to achieve zeros in the first row, except again

for position $(1,1)$. Then we reach a matrix of the form

$$D = \left[\begin{array}{c|ccc} a_{1,1} & 0 & \dots & 0 \\ \hline 0 & & & \\ \vdots & & \hat{D} & \\ 0 & & & \end{array}\right].$$

If $a_{1,1}$ divides every entry of $\hat{D}$ then we are done. If it doesn't then there is an entry $a_{i,j}$ such that $a_{1,1} \nmid a_{i,j}$. Then we can add row i to the first row and return to case 1.

Thus by repeating this process we eventually reach a matrix of the form $(*)$ after a finite number of steps. By repeating this process with the sub-matrix $\hat{C}$, we zero out more non-diagonal elements each time, leaving a diagonal element that divides the next sub-matrix. Note that any elementary operation we may perform on $\hat{C}$ does not affect the first row and column, so we can repeat the process without disrupting previously cleared rows/columns. Further, since the element $a_{1,1}$ divides all of $\hat{C}$, and elementary operations on $\hat{C}$ are just swapping rows/columns or adding scalar multiples of rows/columns, we have that any elementary operation on $\hat{C}$ retains the property that $a_{1,1}$ divides every element in $\hat{C}$. Therefore by repeating this process we end up with a matrix in Smith normal form. □

In Theorem 4.1.14 we use this algorithm again for principle ideal domains. Since it is a vital part of the computation of homology groups, we state it in full here, then give an overview of the modifications required for the proof of Theorem 4.1.14.

Corollary 3.5.5. *The matrix of the boundary operator, M_p, with domain and codomain bases $e_1, \dots, e_n$ and $f_1, \dots, f_n$ respectively, has a corresponding matrix $\tilde{M}_p$ that is in Smith normal form, along with updated bases for the domain and codomain, denoted $\tilde{e}_1, \dots, \tilde{e}_n$ and $\tilde{f}_1, \dots, \tilde{f}_m$. The matrix $\tilde{M}_p$ represents the boundary operator on the updated bases.*

Proof. Let M_p be the matrix of the boundary operator. Then by Theorem 3.5.4 we can reduce it to Smith normal form using just elementary row and column operations, and

by Theorem 3.5.2 we can update the basis elements for each elementary row and column operation in a way that preserves the matrix representation. □

Once we have reduced the matrix M_p to Smith normal form, we can use it to find the bases for Z_p and B_{p-1}, and thus the pth homology group and Betti numbers [28, Equation 7.3].

Theorem 3.5.6. *If $\tilde{M}_p$ is in Smith normal form as below, then*

(i) $\tilde{e}_{l_p+1}, \ldots, \tilde{e}_n$ is a basis for Z_p.

(ii) $a_1\tilde{f}_1, \ldots, a_{l_p}\tilde{f}_{l_p}$ is a basis for B_{p-1}.

$\tilde{M}_p$	$\tilde{e}_1$	$\ldots$	$\tilde{e}_{l_p}$	$\tilde{e}_{l_p+1}$	$\ldots$	$\tilde{e}_{n_p}$
$\tilde{f}_1$	a_1					
$\vdots$		$\ddots$				
$\tilde{f}_{l_p}$			a_{l_p}			
$\tilde{f}_{l_p+1}$				0		
$\vdots$					$\ddots$	
$\tilde{f}_{m_p}$						0

Proof. Let c_p be a general p-chain. Then

$$c_p = \sum_{i=1}^{n} t_i \tilde{e}_i \text{ and } \delta_p c_p = \sum_{i=1}^{l_p} t_i a_i \tilde{f}_i.$$

Observe that each $a_i \neq 0$ as $\tilde{M}_p$ is in Smith normal form. Therefore c_p is a cycle if it is in the kernel of δ_p: c_p is a cycle if and only if $t_i = 0$ for each $1 \leq i \leq l_p$. Therefore (i) holds. To show (ii), observe that any $p-1$ boundary is of the form $\delta_p c_p$. Therefore any boundary is in the free group with basis $a_1\tilde{f}_1, \ldots, a_{l_p}\tilde{f}_{l_p}$, as required. □

Therefore by computing the Smith normal form of the matrix representing the boundary operator for each dimension of a complex K, we can get the basis of each cycle and boundary group, and therefore compute the homology groups of K. If we only want the

Betti numbers for each dimension p, then by the following corollary we don't even need to keep track of the bases when computing Smith normal form.

Corollary 3.5.7. *The Betti number of H_p, $\beta_p = \text{rank}(H_p)$, is given by $\beta_p = n_p - l_p - l_{p+1}$.*

Proof. Observe that $\beta_p = \text{rank}(H_p) = \text{rank}(Z_p/B_p) = \text{rank}(Z_p) - \text{rank}(B_p)$. By Theorem 3.5.6 we know that $\tilde{e}_{l_{p+1}}, \ldots, \tilde{e}_{n_p}$ is a basis for Z_p, so $\text{rank}(Z_p) = n_p - l_p$. Also by Theorem 3.5.6, a basis for B_p is given by the elements from M_{p+1}: $a_1\tilde{f}_1, \ldots, a_{l_p}\tilde{f}_{l_{p+1}}$, so $\text{rank}(B_p) = l_{p+1}$. Therefore $\text{rank}(B_p) = l_{p+1}$. Combining these results we get that

$$\beta_p = \text{rank}(Z_p) - \text{rank}(B_p) = n_p - l_p - l_{p+1}.$$

□

CHAPTER 4

PERSISTENCE

4.1 Graded Modules

Definition 4.1.1. *A ring is a set R with binary operations addition $+$ and multiplication $\cdot$ satisfying the following axioms.*

(i) *R is an abelian group under $+$.*

(ii) *R is a monoid under multiplication (i.e. $\cdot$ is associative and there exists a multiplicative identity 1).*

(iii) *Multiplication is distributive with respect to addition.*

If there is a multiplicative identity then we say R is a *ring with identity.* If $\cdot$ commutes, then we R is a *commutative ring.* If $r, s \in R \setminus \{0\}$ and $r \cdot s = 0$ then r and s are called *zero divisors.* If R has no zero divisors then we call R an *integral domain.* A ring such that every element has a multiplicative inverse is called a *division ring.* If $S \subseteq R$ is also a ring with $+$ and $\cdot$, then S is a *subring* of R. If I is a subring of R such that for any $s \in I$, $r \in R$, we have $s \cdot r \in I$, then I is an *ideal* of R. If I is a proper subset of R, then I is a *proper ideal.* One particular type of ideal is particularly important.

Definition 4.1.2. *Let R be a commutative ring with identity. Then an ideal generated by a subset $S \subseteq R$ is the subring*

$$\langle S \rangle = \left\{ \sum_{i=0}^{k} r_i s_i : r_i \in R, s_i \in S \right\}.$$

In particular, if S is a single element s, then $\langle s \rangle$ is the principle ideal generated by s.

Definition 4.1.3. *If R is an integral domain such that every proper ideal can be generated with a single element then we call R a principle ideal domain, often shortened to PID.*

Note a ring does not require the existence of multiplicative inverses. In fact, if every non-zero element of F has a multiplicative inverse then the ring is a *field*.

Suppose from now on that R is a non-zero commutative ring with 1.

Definition 4.1.4. *A module M over a ring R is an abelian group M along with a binary operation $\cdot : R \times M \to M$ such that for $r, s \in R$ and $m, n \in M$ the following hold.*

(i) $0 \cdot m = 0$ *and* $1 \cdot m = 1$.

(ii) $r \cdot (s \cdot m) = (r \cdot s) \cdot m$ *and* $(r + s) \cdot m = r \cdot m + s \cdot m$.

(iii) $r \cdot (m + n) = r \cdot m + r \cdot n$.

If N is a subgroup of M and for any $r \in R$ and $n \in N$ we have $r \cdot n \in N$, then N is a *submodule* of M and we write $N \leq M$. It is the *trivial submodule* if $N = 0_M$ and it is a *proper submodule* if N is a proper subgroup of M.

Definition 4.1.5. *A module M over R is finitely generated if there exists $m_1, \ldots, m_n \in M$ such that*

$$M = \left\{ \sum_{i=1}^{n} r_i m_i : r_i \in R \right\}.$$

In this case, we call $\{m_1, \ldots, m_n\}$ a generating set of M. The smallest generating set is called the basis. If n is the size of the basis then we write $\operatorname{rank}(M) = n$.

Note that the number of basis elements for a module is only invariant in some cases. Since we've taken R to be a commutative ring we get that M has an invariant basis number [22, Theorems 1,2].

Definition 4.1.6. *Let M, N be modules over a ring R. Then the direct sum $M \oplus N$ is the module with the set $M \times N$ and operation defined elementwise. Specifically, if $(m, n), (m', n') \in M \oplus N$ and $r \in R$ then $(m, n) + r(m', n') = (m + rm', n + rn')$. Then $M \oplus N$ is a module over R.*

Definition 4.1.7. *A ring R is graded over a monoid $(G, +)$ if we can decompose the ring into a direct sum $R = \oplus_{g \in G} R_g$, where each R_g is a subgroup of $(R, +)$ and for every $g, h \in G$, $R_g R_h \subseteq R_{g+h}$.*

A module M is graded over a graded ring R if we can decompose the module into a direct sum $M = \oplus_{g \in G} M_g$, where each M_g is a subgroup of G and $r \in R_g$, $m \in M_h$ implies that $r \cdot m \in M_{g+h}$.

An element from a single R_g or M_g are called *homogeneous* and are said to have *degree* g, so that $\deg x = g$ if $x \in R_g$ for rings or $x \in M_g$ for modules. We shall consider gradings over $\mathbb{R}$. Other commonly used gradings are $\mathbb{N}$ and $[0, \infty)$.

Example 4.1.8. *The monoid ring $R[\mathbb{R}] = \sum_i r_i t^i$, with $r_i \in R$ and $i \in \mathbb{R}$, is a graded ring over $\mathbb{R}$ with the standard grading. In particular, rt^i has degree i, where $r \in R$ and $i \in \mathbb{R}$. Indeed, for $r, s \in R$ and $i, j \in \mathbb{R}$, we have that $\deg rt^i = i$ and $\deg st^j = j$, so $\deg(rt^i)(st^j) = \deg(rs)t^{i+j} = i + j$, as required.*

Definition 4.1.9. *Recall that a matrix is in Smith normal form if it is in the form*

$$\left[\begin{array}{ccc|ccc} a_1 & & & & & \\ & \ddots & & & & \\ & & a_n & & & \\ \hline & & & 0 & & \\ & & & & \ddots & \\ & & & & & 0 \end{array}\right]$$

where $a_1 | \ldots | a_n$.

Definition 4.1.10. *A Euclidean function on a ring R is a function $\deg : R \setminus \{0\} \to \mathbb{N}_0$ such that if $a, b \in R$ with b non-zero, then there exists $q, r \in R$ such that $a = qb + r$, with either $r = 0$ or $\deg(r) < \deg(b)$. A Euclidean domain is an integral domain R that can support at least one Euclidean function.*

Proposition 4.1.11. *In a Euclidean domain R, any two elements have a highest common factor (HCF).*

Proof. As R is a Euclidean domain, there exists a Euclidean function that can be used to find a division with remainder $a = qb + r$, as described above. We can utilise this division with remainder in the extended Euclidean algorithm [12, Page 63] to generate a highest common factor of any two elements. □

Theorem 4.1.12. *Every Euclidean domain is a PID.*

Proof. Let R be a Euclidean domain and I an ideal of R. Let n be the minimal degree of an element in I, and b the element in I such that $\deg(b) = n$. We shall show that I is generated by b.

Let a be an element of $I \setminus \{b\}$. Since R is a Euclidean domain and $\deg(a) \geq \deg(b)$, there exists some elements $q, r \in R$ such that $a = qb + r$ where either $r = 0$ or $\deg(r) < \deg(b)$. Furthermore, since $r = a - bq$ and $a, b \in I$, we have $r \in I$. Therefore if $r \neq 0$ then $\deg(r) < \deg(b)$, a contradiction. So $r = 0$ and $a = bq$, implying that $a \in \langle b \rangle$, as required. □

Theorem 4.1.13. *The graded monoid ring $R[\mathbb{R}]$ is a Euclidean domain, and therefore a principle ideal domain.*

Proof. For $\sum r_i t^i \in R[\mathbb{R}]$, let $\deg(\sum r_i t^i) := \max\{i : r_i \neq 0\}$. This is a Euclidean function for $R[\mathbb{R}]$ (that also coincides with the definition of the degree of a polynomial and the grading of $R[\mathbb{R}]$). Then $R[\mathbb{R}]$ is a Euclidean domain, and hence by Theorem 4.2.12 a principle ideal domain. □

Any matrix with entries from a principle ideal domain can be reduced to Smith normal form [12, Page 109]. However, it is sufficient for the matrix to have entries from a Euclidean domain, and since we have shown that $R[\mathbb{R}]$ is a Euclidean domain, we shall state the case for a PID, as it coincides with the reduction algorithm we gave in Theorem 3.5.4.

Theorem 4.1.14. *Any matrix with entries from a Euclidean domain can be reduced to Smith normal form.*

Proof. The proof is identical to the proof of Theorem 3.5.4, with one modification to allow for matrix entries from a Euclidean domain R instead of from $\mathbb{Z}$. Every time the proof of Theorem 3.5.4 compares the size of two elements, $a < b$, we now use the Euclidean function associated with R, making the comparison $\deg a < \deg b$. □

Theorem 4.1.15 (Structure Theorem for Finitely Generated Modules)**.** *Let M be a finitely generated module over a PID R. Them M decomposes into the form*

$$M \cong R/a_1 \oplus \cdots \oplus R/a_m \oplus R^t,$$

where $a_1|a_2|\ldots|a_m$ and $t \geq 0$.

Proof. Let $\{m_1, \ldots, m_n\}$ be a generating set for M. Define the module homomorphism $\phi : R^n \to M$ by $(r_1, \ldots, r_n) \mapsto \sum r_i m_i$. Let $K = \ker \phi$ (note that here R^n denotes $R \times \cdots \times R$ n times. Then ϕ is a surjective map, so by the first isomorphism theorem for modules, $M \cong R^n/K$.

Note any element of M is of the form $\sum r_i m_i$. Since K is a submodule, any element of K must also be of the form $\sum r_i m_i$. However, there may be some elements of the generating set for M that are not needed in the expression of any element of K. Remove those elements and we are left with a generating set $\{k_1, \ldots, k_l\}$ for K, where each $k_i \in R^n$. Define A as the matrix that has rows $k_1, \ldots, k_l$. Then by Theorem 4.1.14, we can reduce A to Smith normal form $\tilde{A}$. Suppose $\tilde{A}$ has diagonal elements $a_1, \ldots, a_m$ followed by $t := n-m$ zero columns. To construct the Smith normal form of A we only use elementary row and column operations: swapping rows or columns, or adding one row or column to the scalar multiple of another row or column respectively. Therefore the rows of $\tilde{A}$ still generate K.

Now consider the surjective module homomorphism $R^n \to R/a_1 \oplus \cdots \oplus R/a_m \oplus R^t$, given by $(r_1, \ldots, r_n) \mapsto (r_1 + a_1, \ldots, r_m + a_m, r_{m+1}, \ldots, r_n)$. Since K is also the kernel of this homomorphism, by the isomorphism theorem we get that $R/a_1 \oplus \cdots \oplus R/a_m \oplus R^t \cong R^n/K$.

The result follows immediately on combining our two congruences of R^n/K. □

Corollary 4.1.16 (Structure Theorem for Finitely Generated Graded Modules)**.** *Every graded module M over a graded PID R with grading over a monoid G decomposes uniquely into the form*

$$\left(\bigoplus_{j=1}^{m} \Sigma^{\gamma_j} R/a_j\right) \oplus \left(\bigoplus_{i=1}^{n} \Sigma^{\alpha_i} R\right),$$

where $a_j \in R$ are homogeneous elements such that $a_1|a_2|\ldots|a_m$, $\alpha_i, \gamma_j \in G$, and Σ^α represents an α-shift upwards in grading.

Proof. The proof only differs from Theorem 4.1.15 when we take into account the grading. Each row in the Smith normal form of A corresponds to a generating element of the image of the module homomorphism. The shift Σ^α is the degree of that element. □

4.2 Persistent Homology

In this section we introduce persistent homology. This is a mathematical construction that allows us to consider how homology classes 'persist' throughout a filtration of complexes and, along with the Ćech or Rips complex, enables us to consider the homology of a point data set at all scales.

Definition 4.2.1. *The chain complex of K, denoted C_*, is the collection of chain groups $C_p = C_p(K)$ with the boundary operator δ connecting each chain group, as shown below.*

$$\cdots \to C_{p+1}(K) \xrightarrow{\delta_{p+1}} C_p(K) \xrightarrow{\delta_p} C_{p-1}(K) \to \ldots.$$

Definition 4.2.2. *A filtration is the collection $\mathcal{F} = \{K_i\}_{i\in\mathbb{R}}$, where each $K_i \subseteq K_j$ if $i \leq j$, so we get the chain of inclusions*

$$\emptyset = K_{i_0} \subseteq K_{i_1} \subseteq K_{i_2} \subseteq \ldots, \text{whenever } i_0 \leq i_1 \leq i_2 \leq \ldots.$$

Example 4.2.3. *The Čech or Rips complex of a point data set gives a filtration of complexes as you increase the parameter ϵ. Recall our example of a Čech complex for different ϵ, shown again in Figure 4.1. Then defining $K_i = \mathcal{C}_i(X)$, we get the filtration*

$K_0 \subset K_7 \subset \cdots \subset K_{15}$. *Call this filtration $\mathcal{F}$; we shall use it as the basis for an example that runs throughout this chapter.*

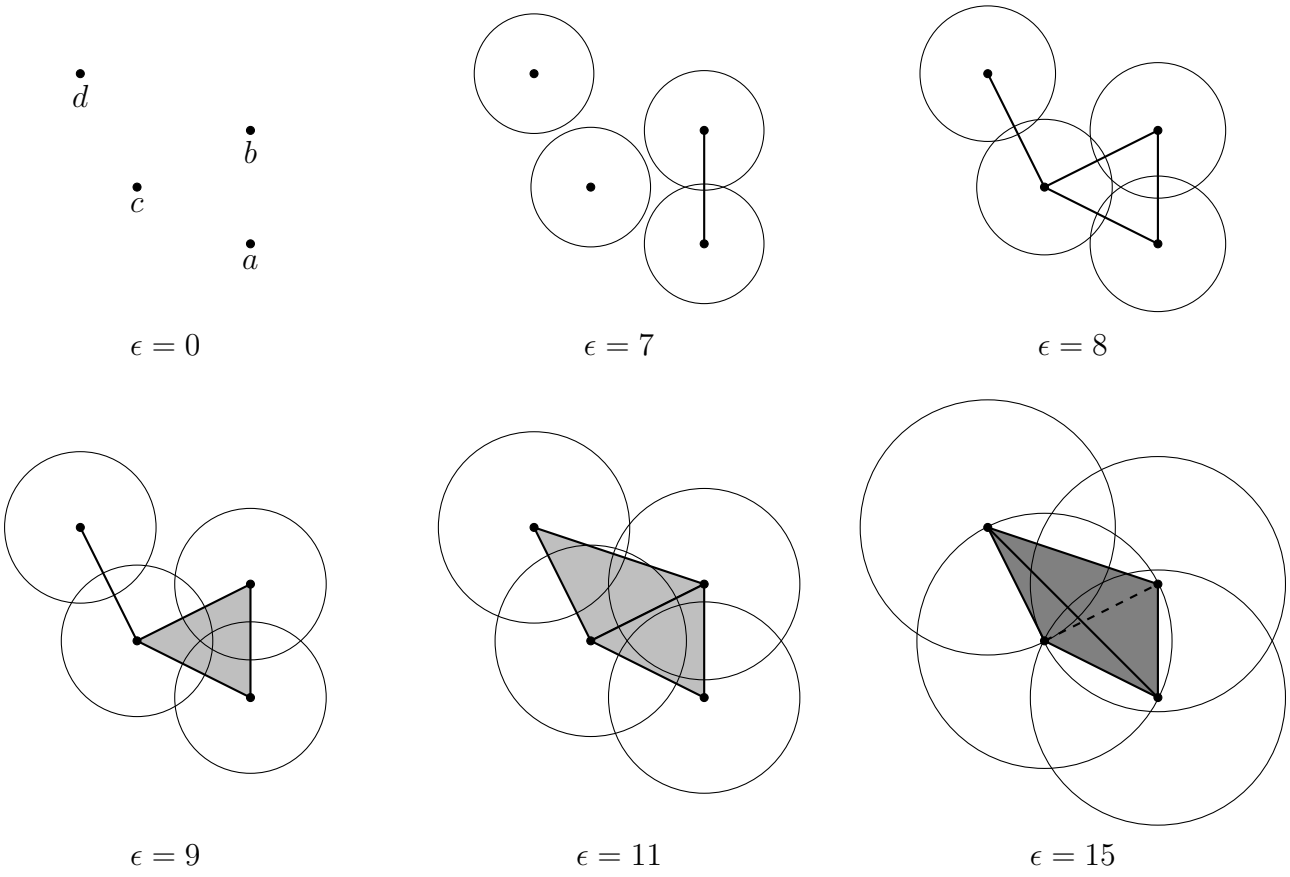


Figure 4.1

The filtration then gives a natural degree function for R, where a simplex σ in minimal K_i has degree i. Since $K_i \subseteq K_{i+\epsilon}$ for $\epsilon > 0$, if σ is in K_i then σ is also in $K_{i+\epsilon}$. We define a function t^ϵ, $\epsilon > 0$, that 'shifts' σ: it increases the grading of σ by ϵ, so if $\sigma \in K_i$, then $t^\epsilon\sigma$ is the same simplex in $K_{i+\epsilon}$. Note that this map is well defined as any σ in K_i is in all subsequent K_j, where $i \leq j$.

Example 4.2.4. *Consider the filtration introduced in Example 4.2.3. Then we grade each of the complexes as shown in Table 4.1, based on where each simplex σ enters the complex. Note that we drop the square brackets from our simplex notation: where we previously would have written $[a, b, c]$ we shall now simply write abc.*

We can define a chain complex for each complex in the filtration by letting $C_*(K_i) =$

σ	a	b	c	d	ab	ac	bc	cd	abc	bd	bcd	ad	abd	acd	$abcd$
Grade	0	0	0	0	7	8	8	8	9	11	11	15	15	15	15

Table 4.1

C_*^i. Then we can connect these chain complexes with the homomorphism Σ induced by t. Thus Σ^ϵ shifts a homology class in $H(K_i)$ to $H(K_{i+\epsilon})$.

Definition 4.2.5. *The persistence complex $P(\mathcal{F})$ is a collection of chain complexes C_*^i connected with the map $\Sigma^\epsilon : C_*^i \to C_*^{i+\epsilon}$. Consider the chain complex indexed by $\mathbb{N}_0 \subseteq \mathbb{R}$, connected by Σ^1. Then we get*

$$C_*^0 \xrightarrow{\Sigma^1} C_*^1 \xrightarrow{\Sigma^1} C_*^2 \xrightarrow{\Sigma^1} \dots.$$

We can expand the chain complexes in the diagram above to see how each individual chain group is connected to the other. Remember that we are only viewing the complexes that correspond to elements of $\mathbb{N}_0$: these are actually graded over $\mathbb{R}$.

$$\begin{array}{ccccccc}
\vdots & & \vdots & & \vdots & & \\
\downarrow{\scriptstyle \delta_3} & & \downarrow{\scriptstyle \delta_3} & & \downarrow{\scriptstyle \delta_3} & & \\
C_2^0 & \xrightarrow{\Sigma} & C_2^1 & \xrightarrow{\Sigma} & C_2^2 & \xrightarrow{\Sigma} & \dots \\
\downarrow{\scriptstyle \delta_2} & & \downarrow{\scriptstyle \delta_2} & & \downarrow{\scriptstyle \delta_2} & & \\
C_1^0 & \xrightarrow{\Sigma} & C_1^1 & \xrightarrow{\Sigma} & C_1^2 & \xrightarrow{\Sigma} & \dots \\
\downarrow{\scriptstyle \delta_1} & & \downarrow{\scriptstyle \delta_1} & & \downarrow{\scriptstyle \delta_1} & & \\
C_0^0 & \xrightarrow{\Sigma} & C_0^1 & \xrightarrow{\Sigma} & C_0^2 & \xrightarrow{\Sigma} & \dots
\end{array}$$

We are interested in how the homology groups evolve over the persistence complex. Define $H_p^i = H_p(K_i)$ for each p and i. For each $i < j$ we have an inclusion map $\Sigma^{j-i} : K_i \to K_j$. Therefore using Definition 3.3.2 we induce a homomorphism $f_p^{i,j} : H_p(K_i) \to H_p(K_j)$ for each dimension p. This gives a collection of homology groups, each connected with the induced homomorphism. Hence for each dimension p and filtration $\mathcal{F}$ we have the *persistence module* $H_p(\mathcal{F})$, shown below.

$$H_p(K_0) \to H_p(K_1) \to H_p(K_2) \to \dots.$$

Again, we only view the homology groups indexed by $\mathbb{N}_0$ to keep our diagrams clear: each of these are indexed by $\mathbb{R}$.

Definition 4.2.6. *The pth persistent homology groups of K_i to K_j is the group*

$$H_p^{i,j} = Z_p^i/(B_p^j \cap Z_p^i).$$

Equivalently, they are the images of the relevant induced homomorphism described above:

$$H_p^{i,j} = \mathrm{Im} f_p^{i,j}.$$

The pth persistent Betti numbers are defined as $\beta_p^{i,j} = \mathrm{rank} H_p^{i,j}$.

Observe that since both B_p^j and Z_p^i are subgroups of C_p^j, their intersection is also a group, and so the quotient is well defined. Recall that a conjugacy class of a homology group is sometimes called a homology class. The map $f_p^{i,j}$ takes the homology classes in $H_p(K_i)$ into the corresponding homology classes of $H_p(K_j)$, but only if they are still present in j. This performs the same role as the pth homology group from K_i to K_j: it is the collection of homology classes that have persisted from $H(K_i)$ into $H(K_j)$. That is why we get the equivalence in our defintion. The pth persistent homology group $H_k^{i,j}$ tells us which p-homology classes have *persisted* from i to j. In particular, we can describe the birth and death of homology classes in our filtration.

Definition 4.2.7. *Let γ be a homology class in H_p^i. Then γ is born at K_i if $\gamma \in H_p^i$ but $\gamma \notin H_p^{i-1,i}$. Furthermore, if γ is born at i then it dies at j if it merges with an older conjugacy class at j, that is if $f_p^{i,j-1}(\gamma) \notin H_p^{i-1,j-1}$ but $f_p^{i,j}(\gamma) \in H_p^{i-1,j}$. If γ is born at K_i and dies entering K_j, then $j - i$ is the persistence of γ.*

Intuitively, any conjugacy class γ is the result of simplicial structures that first appear appear in a minimal K_i. This is the 'birth' of the homology class. Now, as K_i evolves into K_j throughout the filtration, the simplicial structure becomes a boundary in some minimal K_j, so that γ ceases to be a part of the homology group in K_j. Then we say that degree j is the *death* of the simplex, as it ceases to contribute to the homology group. So

every homology has a *birth/death pair* (i, j) with $i, j \in \bar{\mathbb{R}} = \mathbb{R} \cup \{\infty\}$. Capturing how the homology classes *persist* through the evolving filtration is the main idea behind persistent homology. We say that γ dies when it merges with an older class because of the Elder rule, a rule that describes how conjugacy classes die.

Definition 4.2.8. *The Elder rule states that if paths are merging, then the older path continues and the younger path comes to an end.*

For homology classes, this means we let the younger homology class die and the older homology class survive when merging two classes. In this situation, the younger class is the homology class with the smaller birth value. In fact, the Elder rule is the natural way to merge paths: it is the only rule that produces unique path decompositions for sufficiently nice function classes [8, Page 150]. An example of the Elder rule is shown in Figure 4.2.

4.3 The Persistence Module

In the previous section we used the inclusion maps $\Sigma^{j-i} : K_i \to K_j$ for each $i < j$ to induce a homorphism $f_p^{i,j} : H_p(K_i) \to H_p(K_j)$ for each dimension p. This homomorphism allows us to define the persistence module.

Definition 4.3.1. *For each dimension p the pth persistence module is the collection $H_p(\mathcal{F})$, linked by the induced homomorphisms. It is shown here for some $\epsilon > 0$:*

$$H_p(K_0) \xrightarrow{f_p^{0,\epsilon}} H_p(K_\epsilon) \xrightarrow{f_p^{\epsilon,2\epsilon}} H_p(K_{2\epsilon}) \xrightarrow{f_p^{2\epsilon,3\epsilon}} \dots.$$

Now, suppose that each homology group H_p^i takes coefficients from a principle ideal domain R. Then we let t^i be a map that moves the degree of elements by i, for $i \in \mathbb{R}$. Then we can associate each homology group H_p^i with Rt^i. Therefore the whole persistence module is a graded module over $R[\mathbb{R}]$ with the standard grading. In particular, we define

$$H_p(\mathcal{F}) = \bigoplus_{i \in \mathbb{R}} H_p(K_i).$$

Then the $R[\mathbb{R}]$-action is given by

(i) scalar multiplication on H_p^i with elements of R, and

(ii) $t^\epsilon H_p^i \to H_p^{i+\epsilon}$ shifting the grading of elements.

Note that the grading of any element is then equivalent to its birth time. If a homology class comes into the module at time i, then it enters as a subset of Rt^i, and therefore has degree i in $H_p(\mathcal{F})$. Therefore the persistence module $H_p(\mathcal{F})$ is an $R[\mathbb{R}]$-module.

Corollary 4.3.2. *The persistence module decomposes into the form*

$$\left(\bigoplus_{i\in S} \Sigma^{\alpha_i} R[\mathbb{R}]\right) \oplus \left(\bigoplus_{j\in T} \Sigma^{\beta_j} R[\mathbb{R}]/t^{n_j}\right),$$

where S and T are finite subsets of $\mathbb{R}$, n_j are such that $n_j | n_{j+1}$, and $\alpha_i, \beta_j \in \mathbb{N}_0$.

Proof. By Theorem 4.1.13, $R[\mathbb{R}]$ is a principle ideal domain. Therefore the result follows from Corollary 4.1.16 (the Structure Theorem for finitely generated graded modules). □

We can parametrise this decomposition as follows.

Definition 4.3.3. *A $\mathcal{P}$-interval is an ordered pair (i, j) such that $i < j \in \bar{\mathbb{R}}$.*

Proposition 4.3.4. *Every persistence module is generated by a set of $\mathcal{P}$-intervals.*

Proof. Let (i, j) be a $\mathcal{P}$-interval and define

$$Q(i,j) = \begin{cases} \Sigma^i R[\mathbb{R}]/t^{j-i}, & j \neq \infty, \\ \Sigma^i R[\mathbb{R}], & j = \infty. \end{cases}$$

Then for a set of $\mathcal{P}$-intervals, $\mathcal{S} = \{(i_1, j_1), \ldots, (i_n, j_n)\}$, define

$$Q(\mathcal{S}) = \bigoplus_{k=1}^{n} Q(i_k, j_k).$$

This defines a correspondence between persistence modules and sets of $\mathcal{P}$-intervals. □

We call such a set $\mathcal{S}$ a *basis of the persistence module*. In fact, if we have a persistence module then we can show that its basis is exactly the $\mathcal{P}$-intervals given by the life/death pairs of all its homology classes.

Theorem 4.3.5. *The birth/death pairs of a persistence module's homology classes are a basis of the persistence module.*

Proof. Let (i, j) be a $\mathcal{P}$-interval in the basis of a persistence module. Then $Q(i, j)$ contributes a homology class that is born at time i and merges into another homology class at time j. This is precisely the definition of a birth/death pair. □

This is a powerful result: the persistence module, a construction that encompasses the homology classes of the entire filtration, is described entirely by the birth/death pairs of its homology classes. We then use the birth/death pairs to construct the *persistence diagram*, a diagram that by the previous theorem fully represents the persistent homology of a filtration. A multiset is a set that allows for multiple identical elements in it. The multiplicity of an element in a multiset is how many times it appears in the multiset. Recall that the extended real plane is $\bar{\mathbb{R}}^2 = (\mathbb{R} \cup \{\pm\infty\})^2$.

Definition 4.3.6. *The pth persistence diagram of a filtration $\mathcal{F}$ is a multiset $\{(i_\alpha, j_\alpha) : \alpha \in I\}$ for some finite index set I, in the extended plane $\bar{\mathbb{R}}^2$. The horizontal axis corresponds to birth times and the vertical axis corresponds to death times of homology classes. Therefore each point $(i, j) \in \bar{\mathbb{R}}^2$ corresponds to a summand $Q(i, j)$ in the decomposition of the persistence module.*

Note that we require the persistence diagram to be in the extended real plane so that we can plot homology classes that never merge, represented by the $\mathcal{P}$-interval (i, ∞). The persistence diagram is a multiset because two homology classes could have the same birth and death times. In the next chapter we look at the stability of the persistence diagram, to evaluate the suitability of using it to represent the persistence module. To better visualise multisets, we also define the persistence barcode.

Definition 4.3.7. *A persistence barcode is a plot in the plane with time on the horizontal axis and the homology classes on the vertical axis. We plot the persistence of a homology*

class via an interval in the persistence barcode that corresponds to the interval (i, j)*. An example of a persistence barcode is shown in Figure 4.2.*

The barcode also contains all the information of the persistence module, as it visualises each point (i, j). On top of this, we can easily see the Betti number of the homology group at time k by seeing how many homology classes the vertical line at time k intersects.

An important observation is that with the restrictions we've placed on our filtrations, the persistence diagram is always well defined. In particular, our filtrations comprise of finite complexes (as they are built from finite datasets), and they the homology groups are over PIDs, so can the persistence module can always be decomposed. Therefore we can always compute a persistence diagram from our complexes.

4.4 Computing the Persistence Module

In this section we shall present an algorithm that computes the persistence module. Specifically, it computes the $\mathcal{P}$-intervals that generate the persistence module of a filtration $\mathcal{F}$ for each dimension p. Therefore this algorithm can be used to find the persistence diagrams of a filtration. This algorithm uses the properties of the persistence module to simplify the reduction algorithm, and was first introduced in its general form by Zomorodian and Carlsson [27, Section 4.2].

Recall the chain complex $C_p(\mathcal{F})$. If each C_p^i has coefficients from a principle ideal domain R then we can associate it with the monoid ring $R[\mathbb{R}]$ with the usual grading by letting each C_p^i be associated with Rt^i. Since each C_p has a grading associated with it, each basis element must be homogeneous.

We construct the matrix of $\delta_p : C_p \to C_{p-1}$ as in Definition 3.5.1. We call a basis homogeneous if each basis element is homogeneous. If C_p has homogeneous basis $e_1, \ldots, e_n$ and C_{p-1} has homogeneous basis $f_1, \ldots, f_m$, then we have

$$\delta_p(e_j) = \sum_{i=1}^{m} \lambda_{i,j} f_i, \text{ so that } M(\delta_p) = (\lambda_{i,j})_{1 \leq i \leq n, 1 \leq j \leq m}.$$

The matrix of a map between graded rings must preserve the grading. Therefore, the matrix M_p will be such that for all i, j

$$\deg f_j + deg\lambda_{i,j} = \deg e_i.$$

Call this property the *homogeneous property.*

The standard bases of the domain and codomain of δ_p given by the oriented p and $p-1$ simplices of $\mathcal{F}$ are homogeneous by the definition of the grading. Our goal is to calculate the matrices for δ_p, denoted M_p, relative to some homogeneous bases for C_p and Z_{p-1} for each dimension p. We can do this inductively. As a base case, consider $p = 0$. Then $\delta_0 \equiv 0$, so that $Z_0 = C_0$ and we can use the standard basis for C_0 to get δ_1.

Example 4.4.1. *We continue our running example by constructing the matrix of δ_1 for our filtration. As said, for δ_0 we can use the standard basis for C_0 when finding δ_1. The matrix for δ_1 is shown below. As expected, the homogeneous property holds for the matrix. As each simplex a, b, c, c has grade 0 in the filtration, our basis for C_0 is also sorted in descending grade order.*

M_1	ab	ac	bc	cd	bd	ad
a	$-t^7$	$-t^8$				$-t^{15}$
b	t^7		$-t^8$		$-t^{11}$	
c		t^8	t^8	$-t^8$		
d				t^8	t^{11}	t^{15}

Assume that we know M_p relative to the standard basis $e_1, \ldots, e_n$ of C_p and some homogeneous basis $f_1, \ldots, f_m$ of Z_{p-1}. Order the rows and basis elements of Z_{p-1} in decreasing degree order (highest degree basis element in the first row, lowest degree basis element in the last row). The reason for this will become clear in the proof of Proposition 4.4.2. Now use elementary column operations to transform M_p into column echelon form, notated $\tilde{M}_p$. An example of column echelon form is shown below: the boxed elements are

referred to as *pivots*.

$$\begin{bmatrix} \boxed{*} & 0 & 0 & 0 & 0 & 0 \\ * & \boxed{*} & 0 & 0 & 0 & 0 \\ * & * & \boxed{*} & 0 & 0 & 0 \\ * & * & * & 0 & 0 & 0 \end{bmatrix}$$

To reach column echelon form we only need the two column operations and the associated basis operations, shown in Table 4.2 and proven in Theorem 3.5.2.

	Column Operations	Domain Basis Operation
1	Swap C_i and C_j	Swap e_i and e_j
2	$C_i \mapsto C_i + \alpha C_j$	$e_i \mapsto e_i + \alpha e_j$

Table 4.2

Proposition 4.4.2. *When using operations (1) and (2) to update a matrix element $\lambda_{i,k}$ to zero, each basis element remains homogeneous.*

Proof. The result is obvious for operation (1). For (2), consider the operation $C_i \mapsto C_i + \alpha C_j$, for each row k. Let our matrix elements be $(\lambda_{i,j})_{i,j}$ and the domain and codomain bases be $e_1, .., e_n$ and $f_1, .., f_m$ respectively. We are adding $\alpha\lambda_{i,k}$ to $\lambda_{i,j}$ so that the sum is zero. Since they sum to zero, $\alpha\lambda_{i,k}$ must be of the same grade as $\lambda_{i,j}$. Since $\deg f_j$ is unchanged by this operation, the homogeneous property implies that $\deg \alpha e_j = \deg e_i$. Therefore the basis elements remain homogeneous, as required. □

To reduce to column echelon form using these operations, proceed as follows. In the first row, choose a non-zero element of lowest degree to be the pivot element. If no elements are non-zero, move on to the next row. Use operation (2) to zero out that row, and use operation (1) to make the pivot column the first column. Repeat for the next row, terminating when we run out of non-zero columns. By Proposition 4.4.2 the basis of the domain is still homogeneous. In fact, the next proposition shows that column echelon form provides sufficient information to decompose the persistence module. We do not need to continue to transform the matrix into Smith normal form.

Example 4.4.3. *Using this technique we reduce the matrix of M_1 in our running example into column echelon form, updating the domain basis as we go. Doing so, we arrive*

at the following matrix, where $z_1 = ac - tab - bc$, $z_2 = bd - t^3bc - t^3cd$ *and* $z_3 = ad - t^8ab - t^7bc - t^7cd$. *The pivot elements are boxed.*

$\tilde{M}_1$	$-ab$	z_1	$-bc$	$-cd$	z_2	z_3
a	$\boxed{t^7}$					
b	$-t^7$		$\boxed{t^8}$			
c			t^8	$\boxed{t^8}$		
d				$-t^8$		

Proposition 4.4.4. *The pivots in column echelon form,* $\tilde{M}_p = (\lambda_{i,j})$ *are the same as the diagonal elements in Smith normal form. Furthermore, the degree of the basis elements on pivot rows is the same in both forms.*

Proof. We sorted the rows so that the degree of the basis elements $f_1, \ldots, f_m$ are decreasing. Furthermore, each column operation does not change the codomain basis, so they are unchanged when in column echelon form. For a fixed column j, $\deg e_j$ is constant, call it c. Then by the homogeneous property, $\deg \lambda_{i,j} = c - \deg f_i$, so the degree of the matrix elements are monotonically increasing down the column. Thus we can use row operations, that do not affect the pivot elements or the degree of the corresponding codomain basis element, to eliminate non-zero elements beneath the pivot. Finally, we can swap rows and columns to put the updated matrix into Smith normal form. □

Therefore we can read the degree of the basis elements and non-zero matrix entries in Smith normal form directly from the column echelon form. This information is exactly what we need to use Corollary 4.3.2 to decompose the $(p-1)$th persistence module.

Corollary 4.4.5. *Let* $\tilde{M}_p = (\lambda_{i,j})$ *be the matrix of* δ_p *in column echelon form, with respect to bases* $e_1, \ldots, e_n$ *and* $f_1, \ldots, f_m$ *for* C_p *and* Z_{p-1} *respectively. If row* i *has pivot* $\lambda_{i,j} = t^n$, $n \in \mathbb{R}$, *then it contributes* $\Sigma^{\deg f_i}\mathbb{K}[t]/t^n$ *to the decomposition of* H_{p-1}. *Otherwise, it contributes* $\Sigma^{\deg f_i}\mathbb{K}[t]$ *to the decomposition of* $H_{p-1}(\mathcal{F})$.

Proof. By Proposition 4.4.2 the degree of each basis element and the pivot element are the same as the degree of the basis elements and non-zero entries in the Smith normal of the matrix of δ_p. Therefore by Corollary 4.3.2 a row with $\lambda_{i,j} = t^n$ as the pivot element will

begin contributing a homology class at $\deg f_j$. This class will merge into another homology class n grades later. Therefore this contributes $Q(\deg f_j, \deg f_j + n)$ to the decomposition of $H_{p-1}(\mathcal{F})$. If row i does not have a pivot, then the homology class will not merge into another homology class, so does not die. Therefore this contributes $Q(\deg f_j, \infty)$ to the decomposition of $H_{p-1}(\mathcal{F})$. □

The $\mathcal{P}$-intervals $(\deg f_i, \deg f_i + n)$ and $(\deg f_i, \infty)$ give the birth/death pairs of the homology classes by Theorem 4.3.5. They can be used both as a basis of the $(p-1)$th persistence module and to plot the $(p-1)$th persistence diagram or barcode for $\mathcal{F}$.

Example 4.4.6. *We continue our example by decomposing $H_0(\mathcal{F})$ using our matrix for δ_1. Each row has a basis element with degree 0. The first row has pivot t^7, so contributes $Q(0,7)$. The second and third row have pivots t^8, so each contributes $Q(0,8)$. Finally the fourth row has no pivot, so contributes $Q(0,\infty)$. Therefore we can decompose the 0th homology group as*

$$H_0(\mathcal{F}) = R[\mathbb{R}]/t^7 \oplus R[\mathbb{R}]/t^8 \oplus R[\mathbb{R}]/t^8 \oplus R[\mathbb{R}].$$

The points in the persistence diagram of $H_0(\mathcal{F})$ are therefore $(0,7), (0,8), (0,8)$ and $(0,\infty)$. To view the multiset properly, we view it as a persistence barcode in Figure 4.2. The dashed arrows downwards represent the Elder rule, described in Definition 4.2.8.

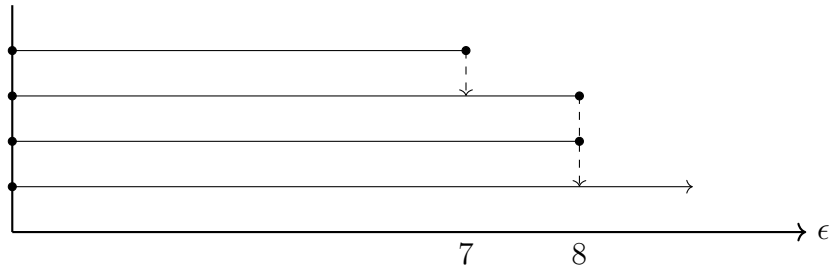


Figure 4.2: The persistence barcode of $H_0(\mathcal{F})$. The dashed lines show the homomology classes merging according to the Elder rule.

Now, as the Betti number of H_0 represents the number of connected components, we can read it off the persistence barcode to verify our computation. At $\epsilon = 0$ we have four disconnected points and the slice of the persistence barcode at $\epsilon = 0$ has four homology

classes. At $\epsilon = 7$ this drops to three points, which corresponds to the simplex ab connecting the points a and b and the homology classes generated by a and b merging. Similarly at $\epsilon = 8$ the Betti number drops to indicate one connected component, which then persists to ∞. This is the time in the filtration that everything becomes connected, so our barcode lines up with our visualisation of the filtration.

Now, we have used our assumed representation of M_p to decompose the $(p-1)$th homology group. In order to complete our induction, we must use it to find the matrix representation of δ_{p+1}. Suppose we know M_{p+1} relative to the standard bases for C_{p+1} and C_p. Recall that Lemma 3.2.8 shows $\delta_p \delta_{p+1} = 0$. Therefore we must have that $M_p M_{p+1} = 0$. As we reduce M_p to column echelon form, we get a list of column operations. Our approach is to define corresponding row operations to apply to M_{p+1}. If we apply both sets of operations (column operations to M_p and the corresponding row operations to M_{p+1}), then we preserve the property that $M_p M_{p+1} = 0$. Therefore at the end of the operations, the zero columns we have created in M_p must correspond to zero rows in M_{p+1}. Furthermore, the homogeneous basis that we have found for Z_p on the domain of M_p has also been made the homogeneous basis of the codomain of M_{p+1}.

Proposition 4.4.7. *To represent δ_{p+1} relative to the standard basis for C_{p+1} and the previously computed basis for Z_p, write M_{p+1} relative to the standard bases and delete rows that correspond to pivot columns in $\tilde{M}_p$.*

Proof. Let M_{p+1} be the matrix of δ_{p+1} and M_p be the matrix of δ_p, both relative to the standard bases. Suppose $\tilde{M}_p$ is the column echelon form of M_p, along with its updated basis for Z_k. Each column operation on M_p is either of the form (1) or (2) from Table 4.2. We get the corresponding row operation from the column operations as follows. The column operation $C_i \mapsto \alpha C_i$ corresponds to the row operation $R_i \mapsto \alpha R_i$. Similarly, the column operation $C_i \mapsto C_i + \alpha C_j$ corresponds to $R_i \mapsto R_i + \alpha R_j$. Apply the column operations to M_p and the corresponding row operations to M_{p+1}, as discussed in the paragraph above.

Now, since column j is a pivot row in M_p, it will be a row of zeros in M_{p+1}. This is because the non-pivot rows correspond to zeroed out columns. Because the property

$M_pM_{p+1} = 0$ is preserved as we apply our column and row operations, we must get that zero columns in M_p correspond to non-zero rows in M_{p+1}, and vice versa. Therefore we may delete the rows in M_{p+1} that correspond to pivot columns in M_p to obtain the matrix $\tilde{M}_{p+1}$. As discussed in the preceding paragraph, the codomain basis has also been updated by the corresponding row operations, so we may update the corresponding rows with the homogeneous basis for Z_p we found by computing the column echelon form of M_p. □

Therefore we have obtained the next matrix in our induction, $\tilde{M}_{p+1}$, so we have described an algorithm that can decompose each of the pth persistence modules.

Example 4.4.8. *Continuing with our running example, we use Proposition 4.4.7 to calculate the matrix of δ_2 using our homogeneous basis z_1, z_2, z_3 for Z_1 and the column echelon form $\tilde{M}_1$. First we construct the matrix M_2 using the standard basis for the codomain. Note that we order the codomain basis elements by decreasing grading. We then remove the columns that correspond to the pivot rows in $\tilde{M}_1$ and replace the codomain elements with the homogeneous basis elements z_1, z_2, z_3, again in descending grade order, to obtain the matrix M_2' that is the matrix for δ_2 with respect to the basis z_1, z_2, z_3 we found earlier.*

M_2	abc	bcd	abd	acd
ad			-1	-1
bd		-1	t^4	
cd		t^3		t^7
bc	t	t^3		
ac	$-t$			t^7
ab	t^2		t^8	

M_2'	abc	bcd	abd	acd
z_3			-1	-1
z_2		-1	t^4	
z_1	$-t$			t^7

Letting $w_1 = acd - abd - t^4bcd + t^6abc$, we put our matrix M_2' into column echelon form to obtain $\tilde{M}_2$, so that we can read off the decomposition of $H_1(\mathcal{F})$.

$\tilde{M}_2$	$-abc$	$-bcd$	$-abd$	w_1
z_3			1	
z_2		1	$-t$	
z_1	t			

The first and second rows have 1 as their pivot. This means that the homology class is born and dies at the same time. Therefore these rows contribute nothing to the persistence

module. Thus only the third row contributes to the persistence module. The element z_1 *has degree* 8 *and the pivot element has degree* 1*, so*

$$H_2 \cong \Sigma^8 R[\mathbb{R}]/t.$$

This lines up with what we'd expect, as there is a single hole in our filtration that is born at $\epsilon = 8$ *and dies when it becomes the boundary of* abc *at* $\epsilon = 9$*. The persistence diagram is therefore the point* $(8, 9)$ *and the persistence barcode is shown in Figure 4.3.*

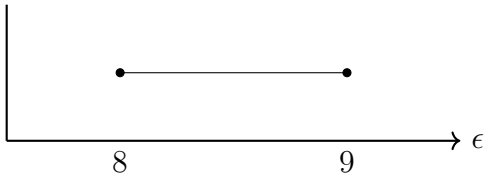


Figure 4.3: The persistence barcode of $H_1(\mathcal{F})$

Finally, we can construct the matrix of M_3 *and once again use Proposition 4.4.7 to get the matrix* M_3' *of* δ_3 *relative to* w_1*. We then reduce the matrix to column echelon form to obtain* $\tilde{M}_3$*.*

M_3	$abcd$
acd	-1
abd	1
bcd	t^4
abc	$-t^6$

M_3'	$abcd$
w_1	-1

$\tilde{M}_3$	$-abcd$
w_1	1

Now we have $\tilde{M}_3$ *we can read off the* 2*nd persistence module. In this case, it is just the zero persistence module. The filtration* $\mathcal{F}$ *never has any voids, so this is what we would expect. Furthermore, there are no higher dimensional simplices, so every higher order persistence module is also* 0*. Therefore we have fully computed* $H_p(\mathcal{F})$ *for each dimension* p*.*

CHAPTER 5

STABILITY

5.1 Bottleneck Distance

In this chapter we shall prove that persistence diagrams are a stable representation of the homology groups. In particular, we define distances on the space of persistence diagrams and the space of persistence modules, then bound how far apart persistence diagrams can be in terms of how far apart their respective persistence modules are. This implies a 'stability' of persistence diagrams: if the persistence modules are close together then their diagrams must be close together as well.

The bottleneck distance is a natural way to measure the distance between two persistence diagrams. Recall from Definition 4.3.6 that a persistence diagram is a multiset of points in the extended plane $\bar{\mathbb{R}}^2 = (\mathbb{R} \cup \{\pm\infty\})^2$. For finite complexes, persistence diagrams must have a finite number of points above the diagonal as they only have a finite number of homology classes. We refer to the points above the diagonal as *non-diagonal points*. We shall define a distance between persistence diagrams based on matching the non-diagonal points of two persistence diagrams. To deal with the case where two persistence diagrams have a different number of non-diagonal points, we add points of infinite multiplicity at (i, i) for every $i \in \mathbb{R}$.

Recall that the d_∞ metric in $\mathbb{R}^2$ is given by $d_\infty((i,j),(k,l)) = \max\{|i-k|, |j-l|\}$. We

extend this metric to the extended plane by defining

$$d_\infty((-\infty, j), (-\infty, l)) = |j - l|,$$
$$d_\infty((i, +\infty), (k, +\infty)) = |i - k|, \text{and}$$
$$d_\infty((-\infty, +\infty), (-\infty, +\infty)) = 0.$$

If one or more of the coordinates are $\pm\infty$ but they are on a different 'edge' of the extended plane then we define the distance between the points as ∞. We are now in our position to define the distance we will consider between two persistence diagrams.

Definition 5.1.1. *Let X, Y be two persistence diagrams. Consider bijections $\eta : X \to Y$. Then the bottleneck distance between X and Y is given by*

$$d_b(X, Y) = \min_{\eta: X \to Y} \sup_{x \in X} d(x, \eta(x))_\infty.$$

Note that a bijection between multisets can be described as a bijection between sets by giving any point with multiplicity greater than one unique labels. For example, if (i, j) has multiplicity 2 then you turn remove the multiplicity by labelling the elements $(i, j)_1$ and $(i, j)_2$. The bottleneck distance works by matching the points between the persistence diagrams X and Y via the bijection η, finding the supremum of the distance between pairs of points, then taking the infimum over all bijections η. If $\eta : X \to Y$ is a bijection such that $\sup_{x \in X} d(x, \eta(x))_\infty < \epsilon$ for some $\epsilon \geq 0$, then we say that η gives an *ϵ-matching.* We can represent matched points in X and Y by $(x, \eta(x)) \in X \times Y$. If a point in the persistence diagram has been matched with a diagonal point, then the minimal matching will match the point with the point on the diagonal that is perpendicular to it, so that it contributes the smallest distance between a point and the diagonal. A non-diagonal point that is matched to a point on the diagonal can be referred to as *unmatched.*

Sometimes the definition of the bottleneck distance takes the infininum over all bijections η. We define the bottleneck distance by taking the minimum over η, which for

the finite case is equivalent to the infinum [4, Section 4.3]. Observe that the minimum is attained. In particular, the infinite diagonal points are almost all matched to a point in the same position, so they contribute 0 to the distance. The remaining diagonal points are attached to unmatched points, which then contribute the minimum distance between the point and the diagonal. Finally, the remaining finite number of non-diagonal points can be matched to another non-diagonal point, each contributing a finite amount. Therefore a bijection exists that allows the minimum distance possible to be attained.

Proposition 5.1.2. *The bottleneck distance d_b is a metric on the space of persistence diagrams.*

Proof. Let X, Y and Z be persistence diagrams. If the bottleneck distance between X and Y is 0, then every point of X corresponds to a point in the same position in Y. Therefore the two persistence diagrams are the same. Any bijection η has a bijective inverse that matches up the points identically. Therefore the symmetry of d_b holds. Finally, we must show the triangle inequality. Suppose that $d_b(X, Y) = \epsilon_1$ and $d_b(Y, Z) = \epsilon_2$, so there is a bijection from X to Y that gives an ϵ_1-matching and a bijection from Y to Z that gives an ϵ_2-matching.

We shall show that there is an $\epsilon := \epsilon_1 + \epsilon_2$ matching between X and Z. If $(x, z) \in X \times Y$, then

$$d_\infty(x, z) \leq d_\infty(x, y) + d_\infty(y, z) \leq \epsilon_1 + \epsilon_2 = \epsilon,$$

where the first inequality is because d_∞ is a metric, and the second inequality is because X, Y have an ϵ_1-matching and Y, Z have an ϵ_2-matching. Therefore an arbitrary pair of points in $X \times Z$ are at most ϵ apart. Taking the minimum over all possible pairs of points, we get that $d_b(X, Z) \leq \epsilon = d_b(X, Y) + d_b(Y, Z)$, as required. □

5.2 Filtration Stability

For our first consideration of stability, we shall define a method to turn a complex K into a filtration based on a function that maps K to the real numbers. We can then

consider the stability of the persistence diagrams under different maps. This was one of the first methods used to evaluate the stability of persistence diagrams, developed by Cohen-Steiner et al. [6]. It is, however, limited; it can only evaluate the stability of different filtrations based on one underlying complex.

Let K be a simplicial complex and let $f : K \to \mathbb{R}$ be a monotonic function, where monotonic on a complex means that f is non-decreasing along increasing chains of faces. In particular, $f(\sigma) \leq f(\tau)$ whenever σ is a face of τ. Let the *sublevel set* be given by $K(a) = f^{-1}[(\infty, a]]$ for each $a \in \mathbb{R}$. Then the monotonocity of f means that $K(a)$ is a subcomplex of $K(b)$ whenever $a < b$. Therefore for any $a_1 < \cdots < a_n$, $K(a_1) \subseteq \cdots \subseteq K(a_n)$ is a filtration.

Definition 5.2.1. *Let K be a simplicial complex and let $f : K \to \mathbb{R}$ be monotonic. Then $a \in \mathbb{R}$ is a critical value of f if a_i is a minimal value such that $K(a)$ is not equal to $K(a - \epsilon)$ for every $\epsilon > 0$.*

That is, a is a critical value of f if it is a value at which the sublevel set changes. We can use this to define the filtration admitted by a function f.

Definition 5.2.2. *Let K be a simplicial complex and let $f : K \to \mathbb{R}$ be monotonic. Then the filtration admitted by f is*

$$\emptyset = K_{a_0} \subseteq K_{a_1} \subseteq \cdots \subseteq K_{a_n} = K,$$

where $K_{a_i} = K(a_i)$, with each a_i a critical value such that $a_i < a_{i+1}$ for each i.

Note that if the number of simplices in K is m and n is the number of critical values, then $n \leq m$, as there cannot be more critical values than the number of simplices. In particular, a critical value corresponds to a new simplex being added to the sublevel set. Next, if we have two distinct functions on K giving two distinct filtrations, we define a way to deform one filtration to the other.

Definition 5.2.3. *Let $f, g : K \to \mathbb{R}$ be monotonic functions on a simplicial complex K.*

Then the straight-line homotopy is the function $F : K \times [0,1] \to \mathbb{R}$ *given by*

$$F(\sigma, t) = (1-t)f(\sigma) + tg(\sigma).$$

Denote $F(\sigma, t) = f_t(\sigma)$.

As the name indicates, the straight line homotopy is an example of a homotopy, defined in Definition 3.3.1.

Proposition 5.2.4. $f_t(\sigma)$ *is monotonic for each* $t \in [0,1]$.

Proof. Let $t \in [0,1]$. If σ is a face of τ, then $f(\sigma) \leq f(\tau)$ and $g(\sigma) \leq g(\tau)$. Therefore $f_t(\sigma) = (1-t)f(\sigma) + tg(\sigma) \leq (1-t)f(\tau) + tg(\tau) = f_t(\tau)$. □

Therefore f_t admits a filtration of K. As usual, we construct a persistence module for this filtration by calculating the homology group for each complex in the filtration and connecting them by the homomorphism induced by the inclusion map.

Let K be a complex and $f, g : K \to \mathbb{R}$ be monotonic functions on K. Then f and g each admit a filtration of K. Let f_t be the straight line homotopy between the two functions. Let $X = \mathrm{Dgm}_p(f)$ and $Y = \mathrm{Dgm}_p(g)$ be the pth persistence diagrams of the filtrations admitted by f and g respectively. Then we can bound the bottleneck distance between those diagrams by the L_∞ distance between f and g. In particular, we get the filtration stability result below. Recall the L_∞ distance between two functions is given by $d_\infty(f,g) = \max_{\sigma \in K} |f(\sigma) - g(\sigma)|$.

Theorem 5.2.5 (Filtration Stability)**.** *Let* K *be a complex and* $f, g : K \to \mathbb{R}$ *be monotonic functions on* K*. Then we can bound the bottleneck distance by*

$$d_b(X, Y) \leq d_\infty(f - g).$$

Proof. Let $f_t : K \to \mathbb{R}$ be the straight line homotopy of f and g. By Proposition 5.2.4, f_t admits a filtration for each $t \in [0,1]$, so we can compute a persistence diagram for each dimension p and each $t \in [0,1]$. Fix the dimension p. Recall that a persistence diagram

is a multiset in $\bar{\mathbb{R}}^2$. By considering $\bar{\mathbb{R}}^2 \times [0,1]$ we construct a 3d visualisation of how the persistence diagram evolves as t goes from 0 to 1. Denote the persistence diagram of the filtration generated by f_t by X_t. Now, each non-diagonal point in any 'layer' X_t is of the form $x(t) = (f_t(\sigma), f_t(\tau), t)$, where $\sigma, \tau \in K$. The simplex σ is responsible for adding, at time $f_t(\sigma)$ a new homology class. That same homology class dies when we add τ at time $f_t(\tau)$.

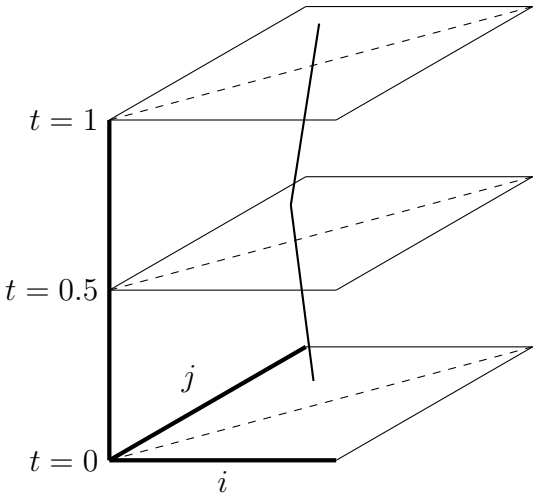


Figure 5.1: An example of a vine

Since our complex K is finite, there are a finite number of indices t_i when our vine could change path, merge into another path, or merge into the diagonal. Each of these cases can happen as the simplices σ, τ change position in the filtration due to the evolving f_t. Denote the times where such events occur as $t_0, \ldots, t_n$. Then the path taken by every point $x(t)$ in the persistence diagrams between $t_i < t < t_{i+1}$ is continuous, as the straight line homotopy is a continuous deformation. The continuous path followed by the point $x(t)$ is referred to as a vine. An example of a vine can be seen in Figure 5.1. Our method is to differentiate $x(t)$ with respect to t, maximising to find the maximum possible gradient of any vine. Since t goes from 0 to 1, the maximum gradient is the same as the maximum distance any two points in the persistence diagrams X_0 and X_1 can be apart. The maximum distance between any two points in X_0 and X_1 is exactly the maximum distance between two matched points in any bijection $\eta : X_0 \to X_1$. Therefore an upper bound on the bottleneck distance is given by this maximum distance. Note that although

$x(t)$ is not differentiable everywhere, we can differentiate $x(t)$ on any interval (t_i, t_{i+1}). This still gives us an upper bound, as we can find the maximum gradient on any (t_i, t_{i+1}), then extrapolate as if the vine was differentiable on $(0, 1)$. We calculate the gradient at differentiable points t as

$$\begin{aligned} x(t) &= (f_t(\sigma), f_t(\tau), t) \\ &= (1-t)(f(\sigma), f(\tau), 0) + t(g(\sigma), g(\tau), 1) \\ \implies \frac{\delta x}{\delta t} &= (g(\sigma) - f(\sigma), g(\tau) - f(\tau), 1). \end{aligned}$$

Now, to maximise the gradient, we want to maximise $f(\sigma) - g(\sigma)$ for some $\sigma \in K$. Therefore $d_\infty(f, g)$ is an upper bound for the gradient, and thus also an upper bound for $d_b(X_0, X_1)$, □

5.3 The Stability Theorem

In this section we develop the theory to state the more general version of the Filtration Stability Theorem. Instead of considering filtrations generated by the sublevel sets of some monotonic function, we go 'down a layer' to consider the persistence modules themselves. To do this we must develop a distance between two persistence modules. The main notion we use is 'interleaving' two modules. To do this we define a family of maps between modules that commute under certain conditions. We use this to define a distance that allows us to restate our stability theorem.

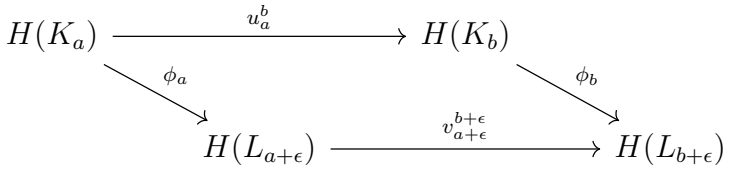
Let $\mathcal{F} = \{K_\alpha\}_{\alpha \in R}$ and $\mathcal{G} = \{L_\alpha\}_{\alpha \in R}$ be two filtrations of simplicial complexes graded over $\mathbb{R}$. Let $\mathbb{U}$ and $\mathbb{V}$ be their persistence modules respectively, so that $\mathbb{U} = \{H(K_\alpha)\}_{\alpha \in R}$ and $\mathbb{V} = \{H(L_\alpha)\}_{\alpha \in R}$, where each family is joined by the homomorphisms induced by the inclusion map. Denote these homomorphisms $u_\alpha^\beta : H(K_\alpha) \to H(K_\beta)$ and $v_\alpha^\beta : H(L_\alpha) \to H(L_\beta)$ respectively, where $\alpha < \beta$. Take our persistence modules over a principle ideal domain R so that every persistence module can be decomposed by Corollary 4.3.2.

Definition 5.3.1. *Let $\epsilon \in \mathbb{R}$. Then a homomorphism of degree $\epsilon > 0$ is a collection Φ of*

linear maps

$$\{\phi_a : H(K_a) \to H(L_{a+\epsilon})\}_{a\in R},$$

such that $l^{b+\epsilon}_{a+\epsilon} \cdot \phi_a = \phi_b \cdot u^b_a$ *for all* $a \leq b$. *We denote the set of all degree* ϵ *homomorphisms between* $\mathbb{U}$ *and* $\mathbb{V}$ *as* $\mathrm{Hom}^\epsilon(\mathbb{U}, \mathbb{V})$. *Equivalently, the collection of maps* Φ *is a homomorphism of degree* ϵ *if the following diagram commutes for all* $a \in \mathbb{R}$ *and* $a < b \in \mathbb{R}$.



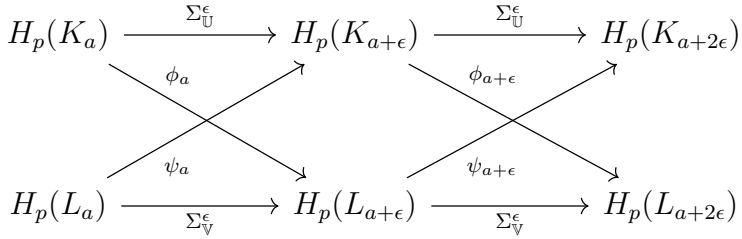
Note that our shift map $\Sigma^n_{\mathbb{U}} : H(K_\alpha) \to H(K_{\alpha+n})$, defined in Corollary 4.1.16, is in the set $\mathrm{Hom}^\epsilon(\mathbb{U}, \mathbb{U})$.

We now define the interleaving of two persistence modules.

Definition 5.3.2. *Two persistence modules* $\mathbb{U}$ *and* $\mathbb{V}$ *are said to be* ϵ*-interleaved if there are maps*

$$\Phi \in \mathrm{Hom}^\epsilon(\mathbb{U}, \mathbb{V}), \Psi \in \mathrm{Hom}^\epsilon(\mathbb{V}, \mathbb{U})$$

such that $\Psi\Phi = \Sigma^{2\epsilon}_{\mathbb{U}}$ *and* $\Phi\Psi = \Sigma^{2\epsilon}_{\mathbb{V}}$. *Equivalently, two persistence modules are interleaved if the following diagram commutes for all* $a \in \mathbb{R}$.



We define a distance between persistence modules based on the smallest possible interleaving between the two modules.

Definition 5.3.3. *The interleaving distance between two persistence modules is given by*

$$d_i(\mathbb{U}, \mathbb{V}) = \inf\{\epsilon : \mathbb{U}, \mathbb{V} \textit{ are } \epsilon\textit{-interleaved}\},$$

or $d_i(\mathbb{U}, \mathbb{V}) = \infty$ *if there is no* ϵ*-interleaving between* $\mathbb{U}$ *and* $\mathbb{V}$.

Proposition 5.3.4. *The interleaving distance defines a pseudometric on the space of persistence modules.*

Proof. An ϵ-interleaving between $\mathbb{U}$ and $\mathbb{V}$ is also an ϵ-interleaving between $\mathbb{V}$ and $\mathbb{U}$. To show the triangle inequality, suppose there is an ϵ_1-interleaving between $\mathbb{U}$ and $\mathbb{V}$ with interleaving maps Φ_1 and Ψ_1, and an ϵ_2-interleaving between $\mathbb{V}$ and $\mathbb{W}$ with interleaving maps Φ_2 and Ψ_2. Then we compose the interleaving maps to construct an $(\epsilon_1 + \epsilon_2)$-interleaving. In particular, we get

$$\mathbb{U} \xrightarrow{\Phi_1} \mathbb{V} \xrightarrow{\Phi_2} \mathbb{W}$$
$$\mathbb{U} \xleftarrow{\Psi_1} \mathbb{V} \xleftarrow{\Psi_2} \mathbb{W}.$$

Then define $\Phi = \Phi_2 \cdot \Phi_1 : \mathbb{U} \to \mathbb{W}$ and $\Psi = \Psi_1 \cdot \Psi_2 : \mathbb{W} \to \mathbb{L}$. Then by the definition of an $(\epsilon_1 + \epsilon_2)$-interleaving we require that $\Phi\Psi = \Sigma_{\mathbb{W}}^{2(\epsilon_1+\epsilon_2)}$ and $\Psi\Phi = \Sigma_{\mathbb{U}}^{2(\epsilon_1+\epsilon_2)}$. We can verify this as follows:

$$\Phi\Psi = \Phi_2\Phi_1\Psi_1\Psi_2 = \Phi_2\Sigma_{\mathbb{V}}^{2\epsilon_1}\Psi_2 = \Sigma_{\mathbb{W}}^{2(\epsilon_1+\epsilon_2)},$$
$$\Psi\Phi = \Psi_1\Psi_2\Phi_2\Phi_1 = \Psi_1\Sigma_{\mathbb{V}}^{2\epsilon_2}\Phi_1 = \Sigma_{\mathbb{U}}^{2(\epsilon_1+\epsilon_2)},$$

so we get a $(\epsilon_1 + \epsilon_2)$-interleaving, and the triangle inequality holds. □

The distance d_i is only a pseudometric and not a full metric because $d_i(\mathbb{U}, \mathbb{V}) = 0$ does not imply that $\mathbb{U} = \mathbb{V}$. This is due to the infinum in the definition of the matrix. Specifically, persistence modules that are not equal can approach a 0-interleaving without such an interleaving actually existing. For an example of this, consider the persistence modules $Q(i, j)$ and $Q[i, j]$, where we're using the definition of $Q(i, j)$ given in Proposition 4.3.4. Then these two persistence modules approach a 0-interleaving, but they are not identical as they differ at the points i and j.

We can now restate our stability property using the interleaving distance to measure the distance between two persistence modules with different underlying complexes. We give a sketch proof of the Stability Theorem. The full details of the proof can be found

in [4, Sections 4.6,4.7].

Theorem 5.3.5 (Stability Theorem)**.** *If* $\mathbb{U}$ *and* $\mathbb{V}$ *are persistence modules then*

$$d_b(\mathrm{Dgm}(\mathbb{U}), \mathrm{Dgm}(\mathbb{V})) \leq d_i(\mathbb{U}, \mathbb{V}).$$

Sketch Proof. This is equivalent to showing that whenever $\mathbb{U}$ and $\mathbb{V}$ are persistence modules that are ϵ-interleaved, there exists an ϵ-matching between $\mathrm{Dgm}(\mathbb{U})$ and $\mathrm{Dgm}(\mathbb{V})$. This statement is a special case of a stability theorem for a specific type of measure. In particular, an r-measure is a measure μ that maps the set of all rectangles $[a, b] \times [c, d]$ in a subset of the plane to $\mathbb{N} \cup \{\infty\}$. The r-measure of a persistence module $\mathbb{V}$ is defined on a rectangle $R = [a, b] \times [c, d]$ by

$$\mu_{\mathbb{V}}(R) = \begin{cases} 1 & [b, c] \subseteq (i, j) \subseteq (a, d), \\ 0 & \text{otherwise,} \end{cases}$$

where $Q(i, j)$ is a summand in the decomposition of $\mathbb{V}$.

The Interpolation Lemma [4, Lemma 3.4] states that if $\mathbb{U}$ and $\mathbb{V}$ are ϵ-interleaved persistence modules, then there exists a 1-parameter family of persistence modules $\{\mathbb{U}_x : x \in [0, \delta]\}$ with $\mathbb{U}_0 = \mathbb{U}$ and $\mathbb{U}_\delta = \mathbb{V}$ such that $\mathbb{U}_x$ and $\mathbb{U}_y$ are ϵ-interleaved for all $x, y \in [0, \delta]$.

If $R = [a, b] \times [c, d]$ is a rectangle in the plane, the ϵ-thickening of R is $R^\epsilon = [a - \epsilon, b + \epsilon] \times [c - \epsilon, d + \epsilon]$. Then the Stability Theorem for finite r-measures [4, Theorem 4.25] states that if $\{\mu_x : x \in [0, \epsilon]\}$ is a 1-parameter family of finite r-measures on an open set $\mathcal{D} \subseteq \mathbb{R}^2$, then if for all $x, y \in [0, \delta]$ we have that $\mu_x(R) \leq \mu_y(R^{|y-x|})$ holds for every rectangle whose $|y-x|$-thickening is contained in $\mathcal{D}$, then there exists an ϵ-matching between the diagrams representing μ_x and μ_y contained in $\mathcal{D}$.

Now, suppose $\mathbb{U}$ and $\mathbb{V}$ are ϵ-interleaved persistence modules. Then the Interpolation Lemma implies there exists a 1-parameter family of persistence modules such that $\mathbb{U}_x$ and $\mathbb{U}_y$ are ϵ-interleaved for all $x, y \in [0, \delta]$. We then link this 1-parameter family to the 1-parameter family of r-measures and, after proving the requisite conditions, the

Stability Theorem for finite r-measures implies that there exists an ϵ matching between the persistence diagrams of $\mathbb{U}$ and $\mathbb{V}$. Taking the infinum of ϵ gives the Stability Theorem. $\square$

5.4 The Isometry Theorem

In the previous section we showed the Stability Theorem. This gave an upper bound for the bottleneck distance between two persistence diagrams by the interleaving distance between their underlying persistence modules. This theorem was highly praised for demonstrating the stability of persistence diagrams upon its publication. Later, the Converse Stability Theorem was proven [17], which states that

$$d_b(\mathrm{Dgm}(\mathbb{U}), \mathrm{Dgm}(\mathbb{V})) \geq d_i(\mathbb{U}, \mathbb{V}).$$

In this section we shall prove the Converse Stability Theorem, then deduce that the relationship between persistence diagrams and persistence modules is in fact an isometry. Much of the work here was simplified and published by de Silva et al. [4].

Proposition 5.4.1. *Let $\{\mathbb{U}_j : i \in J\}$ and $\{\mathbb{V}_j : j \in J\}$ be two families of persistence modules indexed by the same set J. Let*

$$\mathbb{U} = \bigoplus_{j \in J} \mathbb{U}_j, \mathbb{V} = \bigoplus_{j \in J} \mathbb{V}_j.$$

Then

$$d_i(\mathbb{U}, \mathbb{V}) \leq \sup_{j \in J} \{d_i(\mathbb{U}_j, \mathbb{V}_j)\}.$$

Proof. Suppose that $\mathbb{U}_j$ and $\mathbb{V}_j$ are ϵ-interleaved with the interleaving maps Φ_j and Ψ_j for each $j \in J$. Then an ϵ-interleaving of $\mathbb{U}$ and $\mathbb{V}$ is given by the interleaving maps $\Phi := \bigoplus_{j \in J} \Phi_j$ and $\Psi := \bigoplus_{j \in J} \Psi_j$. Therefore an upper bound for every $d_i(\mathbb{U}_j, \mathbb{V}_j)$ represents the smallest possible ϵ-interleaving for one pair $\mathbb{U}_j$ and $\mathbb{V}_j$. Hence this is an upper bound for $d_i(\mathbb{U}, \mathbb{V})$. This holds true for the least upper bound over all j. Therefore it holds true for sup. $\square$

Recall the definition of $Q(i,j)$ from Proposition 4.3.4. Since any persistence module we consider can be decomposed into a sum with summands of the form $Q(i,j)$ by Proposition 4.3.4, we proceed by considering the interleaving distance of two persistence modules $Q(i,j)$. Since each (i,j) corresponds to a point in the persistence diagram by Theorem 4.3.5, we can use this to relate the interleaving distance to points matched by the bijection η in the bottleneck distance. Firstly, if a point (i,j) in the persistence diagram is matched to a non-diagonal point (j,l), then we can bound it by the d_∞ norm.

Proposition 5.4.2. *Let (i,j) and (k,l) be $\mathcal{P}$-intervals and let $\mathbb{U} = Q(i,j)$ and $\mathbb{V} = Q(k,l)$. Denote $\mathbb{U}_t$ and $\mathbb{V}_t$ as the persistence modules $\mathbb{U}$ and $\mathbb{V}$ at time t. Then*

$$d_i(\mathbb{U},\mathbb{V}) \leq d_\infty((i,j),(k,l)) = \max\{|i-k|,|j-l|\}.$$

Proof. Suppose that i,j,k,l are all finite. Suppose that

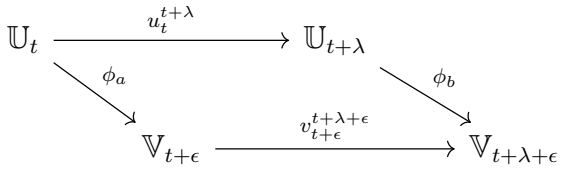
$$\epsilon > \max(|i-k|,|j-l|).$$

Observe that by our definition of $Q(i,j)$, for any $t \in \mathbb{R}$ the homology group at t will be either the principle ideal domain R or the zero homology group, denoted 0. We define two families of maps

$$\Phi : \{\phi_t : \mathbb{U}_t \to \mathbb{U}_{t+\epsilon}\}_{t\in\mathbb{R}},$$
$$\Psi : \{\psi_t : \mathbb{V}_t \to \mathbb{V}_{t+\epsilon}\}_{t\in\mathbb{R}},$$

by letting each map ϕ_t, ψ_t be equal to id_R if both its domain and codomain are R, and the zero map otherwise.

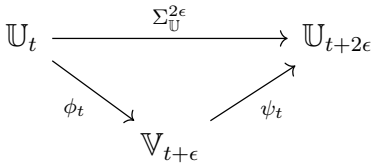
We must show two properties of our families of maps. Firstly that they actually define module homomorphisms of degree ϵ, and secondly that they define interleaving maps. Checking that they are module homomorphisms of degree ϵ is equivalent to verifying that the following diagram commutes for all $t \in \mathbb{R}$ and for all $\lambda > 0$.



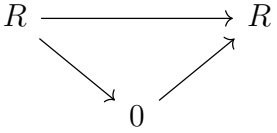
Consider each possible configuration of the four groups, where each 'vertex' of the diagram is either R or 0. Because our map is either the R identity map or the zero map, we know immediately that each diagram commutes apart from the two configurations below.

Fix t, ϵ and (i, j). If the first diagram occurs, then by the top left vertex we get that $i < t$ and by the bottom left vertex we get that $t + \epsilon \leq k$. (Observe that this condition is forced, as the bottom right vertex is R, implying that $t + \epsilon < k < t + \lambda + \epsilon < l$.) This implies that $\epsilon \leq k - i$, which is a contradiction, as $\epsilon > |i - k|$ by our choice of ϵ. Similarly, if the second diagram occurs, then by the top right vertex $j \leq t + \lambda$ and by the bottom right vertex $t + \epsilon + \lambda \leq l$. This implies that $\epsilon > l - j$. Again, this is a contradiction by our choice of ϵ. Therefore neither bad configuration occurs, and our families of maps Φ and Ψ define homomorphisms of degree ϵ.

Now to give an ϵ-interleaving, we must show that $\Psi\Phi = \Sigma_{\mathbb{U}}^{2\epsilon}$ and $\Phi\Psi = \Sigma_{\mathbb{V}}^{2\epsilon}$. To show the former, we must show that the diagram



commutes for all $t \in \mathbb{R}$. Again, each configuration can be clearly seen to commute, except for the configuration below.



If such a configuration were to exist, then the top row implies that $i \leq t$ and $t + 2\epsilon \leq j$. By our definition of ϵ we know that $\epsilon > |i - k|$ and $\epsilon > |j - l|$. Combining this information

with our other two inequalities, we can conclude that

$$k \leq \epsilon + i \leq \epsilon + t \leq j - \epsilon \leq l.$$

That is, $k \leq t + \epsilon \leq l$, and so the bottom 0 in our commutative diagram is in fact forced to be R, in which case the diagram commutes. This proves that $\Psi\Phi = \Sigma_{\mathbb{U}}^{2\epsilon}$. The case $\Phi\Psi = \Sigma_{\mathbb{V}}^{2\epsilon}$ follows by symmetry.

We have considered the case when i, j, k, l are all finite. The cases where j or l are ∞ follow easily. Therefore we have shown that there is an ϵ-interleaving between $\mathbb{U}$ and $\mathbb{V}$ whenever $\epsilon > d_\infty((i,j),(k,l))$. Taking the smallest such δ gives the required result. □

Now we consider the case when the point (i, j) in the persistence diagram is paired with one of the infinitely many points we added to the diagonal. Since a point on the diagonal has the same birth/death pair, it corresponds to the zero persistence module 0 in the decomposition of a persistence module. Incidentally, this is why we can add infinitely many diagonal points to the persistence diagram without affecting the persistence module.

Proposition 5.4.3. *Let (i, j) be a $\mathcal{P}$-interval and let $\mathbb{U} = Q(i, j)$. If 0 is the zero persistence module, then*

$$d_i(\mathbb{U}, 0) = \frac{1}{2}(j - i).$$

Proof. Let $\epsilon \geq 0$. We need to find an ϵ-interleaving between $\mathbb{U}$ and 0. Since 0 is either the domain or codomain of every interleaving map, we must take the families Φ and Ψ as the zero maps. Clearly these maps are ϵ-homomorphisms, as for any $t \in \mathbb{R}$ each ϕ_t and ψ_t is the zero map, so commutes with with the induced homomorphisms u, v.

Now, to be an ϵ-interleaving we require that $\Psi\Phi = \Sigma_{\mathbb{U}}^{2\epsilon}$ and $\Phi\Psi = \Sigma_0^{2\epsilon}$. The latter clearly holds true, as the composition of two zero maps will be the zero map, which is equal to $\Sigma_0^{2\epsilon}$. To check the former, we require that $\Sigma_{\mathbb{U}}^{2\epsilon}$ is equal to the zero map. The values k when $\mathbb{U}_k = R$ are exactly $i < k < j$. Therefore to guarantee that $\Sigma_{\mathbb{U}}^{2\epsilon}$ is equal to the zero map, the 2ϵ shift must be guaranteed to shift any point in (i, j) to be greater

than j. Therefore the first equation holds true exactly when

$$i + 2\epsilon > j \iff \epsilon > \frac{1}{2}(j - i).$$

Taking the infinum gives the required result. □

Theorem 5.4.4 (Converse Stability Theorem)**.** *Let* $\mathbb{U}$ *and* $\mathbb{V}$ *be persistence diagrams. Then*

$$d_b(\mathrm{Dgm}(\mathbb{U}), \mathrm{Dgm}(\mathbb{V})) \geq d_i(\mathbb{U}, \mathbb{V}).$$

Proof. Let η denote a ϵ-matching between the persistence diagrams $\mathrm{Dgm}(\mathbb{U})$ and $\mathrm{Dgm}(\mathbb{V})$. By Proposition 4.3.4 $\mathbb{U}$ and $\mathbb{V}$ can be decomposed into intervals $Q(i, j)$. Denoting Q-intervals by either $\mathbb{U}_m$ or $\mathbb{V}_m$, we decompose $\mathbb{U}$ and $\mathbb{V}$ into the forms

$$\mathbb{U} = \bigoplus_{m \in M} \mathbb{U}_m, \mathbb{V} = \bigoplus_{m \in M} \mathbb{V}_m$$

for some finite indexing set M, so that each pair (U_m, V_m) corresponds to either

(i) a pair of Q-intervals $Q(i, j)$ and $Q(k, l)$ so that the points $(i, j) \in \mathrm{Dgm}(\mathbb{U}_m)$ and $(k, l) \in \mathrm{Dgm}(\mathbb{V}_m)$ are matched under η, or

(ii) one Q-interval $Q(i, j)$, so that the non-diagonal point (i, j) in either $\mathrm{Dgm}(\mathbb{U}_m)$ or $\mathrm{Dgm}(\mathbb{V}_m)$ is matched with a diagonal point in the other persistence diagram.

By Proposition 5.4.1, the interleaving distance $d_i(\mathbb{U}, \mathbb{V})$ is at most the supremum of the interleaving distance between each $(\mathbb{U}_m, \mathbb{V}_m)$. We can evaluate this distance for each case using our previous results.

In the first case, Proposition 5.4.2 combined with our ϵ-matching η gives that

$$d_i(\mathbb{U}_m, \mathbb{V}_m) < d_\infty((i, j), (k, l)) < \epsilon,$$

where the second matching follows by Pythagoras' Theorem. In particular, $|i - k|^2 + |j - l|^2 < \epsilon^2$ by our ϵ-matching. Therefore $|i - k| < \epsilon$ and $|j - l| < \epsilon$. In the second case,

Proposition 5.4.3 and our ϵ-matching η tells us that

$$d_i(\mathbb{U}_m, 0) = d_i(0, \mathbb{V}) = \frac{1}{2}(j - i) \leq \epsilon,$$

where the last inequality follows because we know the point (i, j) is matched to the diagonal and has minimum distance $\frac{1}{2}(j-i)$ to the diagonal. Furthermore, every matched point is at most ϵ distance away by η. Therefore $d_i(\mathbb{U}_m, \mathbb{V}_m) \leq \epsilon$ for every $m \in M$. Therefore the result follows from Proposition 5.4.1. □

Recall an isometry is a map that preserves distances. Therefore the process of computing the persistence diagram from the persistence module is an isometry between the space of persistence diagrams and the space of persistence modules.

Theorem 5.4.5 (The Isometry Theorem)**.** *Let* $\mathbb{U}$ *and* $\mathbb{V}$ *be persistence modules. Then*

$$d_b(\mathrm{Dgm}(\mathbb{U}), \mathrm{Dgm}(\mathbb{V})) = d_i(\mathbb{U}, \mathbb{V}).$$

Proof. The result follows upon combining the Stability Theorem and the Converse Stability Theorem. □

CHAPTER 6

CONCLUSION

In this report we have described the process of constructing a filtration of simplicial complexes from a point data set in $\mathbb{R}^d$ then computing its decomposed pth persistence modules and persistence diagrams. For a finite complex with homology groups that take coefficients from principle ideal domains, we have shown that the persistence module can always be decomposed, implying that the persistence diagram is always well defined. We've further shown that their is an isometry between the space of persistence diagrams and the space of persistence modules, justifying its use as a representation of the persistent homology classes of the underlying filtration.

With a strong theoretical backing to justify its use, the persistence diagram is being utilised to great effect in a broad range of applications. In 2010 persistence diagrams were used to discover a subgroup of breast cancer that has an excellent survival rate [19]. Persistence based clustering is being used at the University of Birmingham to achieve the state of the art in analysing biological nano-structures [20]. Persistent homology is also being used in materials science to determine trigger sites for macroscopic properties in the reduction of iron ore sinters [16].

Much work is also being put into incorporating information about persistence into deep learning methods. The persistence diagram concisely provides a large amount of information about the topology of an underlying dataset, but it is unsuitable to be immediately integrated into most statistical and deep learning workflows. Its dimensions depend on the dataset, it can have multiple points in the same locations, and some of

its points may be at infinity. Many approaches to overcoming this problem have been put forward. An input layer for neural networks that processes topological signatures has achieved state of the art results in learning social network graphs [15]. A different technique that transforms persistence diagrams into finite dimensional vectors called persistence images enables integration of persistence information into any machine learning or statistical workflow that accepts vectors as inputs [5]. Another approach that is having much success is the persistence landscape, which represents a persistence diagram as a set of Lipschitz functions in a Banach space. The persistence landscape is provably stable and can be easily integrated into common machine learning and statistical techniques [2].

As well as finding many applications both as an analytic tool and as a tool in deep learning, the theory of persistence diagrams continues to be developed. In this report we have considered persistence modules over principle ideal domains with filtrations grown from finite data sets. This gives a number of nice conditions that makes our work easier. Our complexes will always be finite and our persistence modules will always be decomposable into a finite number of summands. Generally in homology theory and the study of persistence, these conditions are rarely true. A persistence module is called *q-tame* if the rank of every persistent homology group is finite. Note that this is trivially true for finite complexes, as there is a finite number of homology classes in the persistence module. Persistence modules that are q-tame are widely considered to be the most natural, and most of the properties that we show are also true for q-tame modules [4].

When Robins first introduced the notion of persistent homology in 1999, it would have been hard to comprehend the amount of data the world now produces every day. Her persistent homology, however, has given rise to a technique that concisely describes the homology of data sets of arbitrary size, producing state of the art results in data analysis across a significant number of fields and sparking a rigorous study of persistence in homology theory.

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