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Bachelor Thesis

Persistent Homology Transform

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Abstract

Understanding and analysing the shape of geometric objects is crucial in various fields, such as morphology and medical imaging. In this thesis, we introduce the persistent homology transform, a tool for analysing shapes in the three-dimensional Euclidean space. It uses persistent homology, which is a variant of homology adapted to filtrations of spaces to represent a shape as a collection of intervals. We justify this representation by showing that the mapping from shapes to their persistent homology transform is both continuous and injective. As an application, we show how the persistent homology transform can be used to distinguish the heel bones of different primate species.

Contents

1 Introduction

Comparing shapes of objects is of high interest in many fields, such as biology, medicine and computer science. This thesis introduces an approach which uses topology to compare the shape of objects.

Topology is a branch of mathematics which deals with the properties of geometric objects that are preserved under continuous deformations. Intuitively, continuous deformations of an object are the deformations that can be achieved by stretching, twisting and contracting. Tearing an object apart or gluing parts of an object together can, however, not be done in a continuous fashion. One invariant under continuous deformation is the number of n-dimensional holes. This geometric property is described by homology.

To compute the homology of a shape in an algorithmic fashion, we introduce simplicial complexes. They describe piece-wise linear spaces in a very combinatorial way. Simplicial complexes are built up by n-simplices, which are convex hulls of $(n+1)$ points which do not lie in a $(n-1)$-dimensional hyperplane. A 0-simplex for example is a point, a 1-simplex is a line, a 2-simplex is a triangle and a 3-simplex is a tetrahedron.

In this thesis, we work with an adaptation of homology called persistent homology. Intuitively, persistent homology keeps track of the changes in homology we get when adding more simplices to a simplicial complex. To describe the process of adding simplices to a simplicial complex, we introduce the notion of a filtration, which is a family of sets that is ordered by inclusion. Filtrations can be constructed in many different forms. In this thesis, we are mostly interested in the so-called sublevelset filtrations: Given a simplicial complex $M \subseteq \mathbb{R}^d$, we start by choosing an arbitrary direction $v \in S^{d-1}$. We then consider the subcomplex of M which consists of all simplices which lie beneath a height $r \in \mathbb{R}$ in this direction.

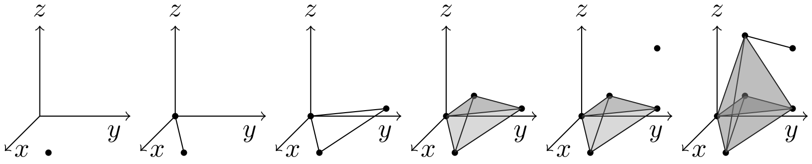


Figure 1: This sublevelset filtration corresponds to direction z. It is the family of simplicial complexes, where the simplicial complex corresponding to the parameter $r \in \mathbb{R}$ consists of the simplices below the height r in the direction of the z-axis.

We are primarily interested in the heights for which the homology changes. This means that at these heights, simplices are added and the subcomplex with these simplices has different homology than without them. The heights corresponding to changes in n-dimensional homology are displayed in a so-called persistence diagram, which is a set of points in $\mathbb{R}^2$. The x-coordinate of such a point corresponds to the height for which a homology classes is born, and the y-coordinate corresponds to the height where this homology class dies. To represent homology classes that never die, there is an additional line above the persistence diagram. We denote the n-dimensional persistence diagram of the sublevelset filtration corresponding to the direction $v \in S^{d-1}$ by $X_n(M, h_v)$.

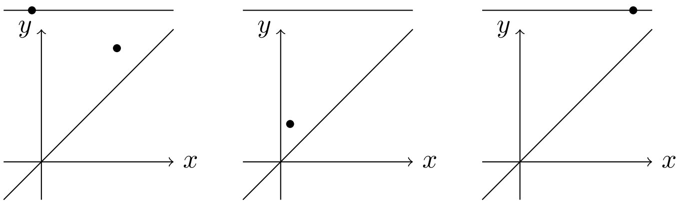


Figure 2: This persistence diagrams correspond to the filtration in Figure 1. The x-coordinate of a point in the first diagram indicates when a connected component appears and its y-coordinate indicates when this connected component disappears. Similarly, the x-coordinate of a point in the second diagram represents the time a hole appears and the y-coordinate tells when this hole disappears. Finally, the x-coordinate of the point in the third diagram stands for the time a void appears and the y-coordinate indicates when this void disappears.

We then introduce the persistent homology transform, which represents simplicial complexes as families of persistence diagrams. In particular, the persistent homology transform of a simplicial complex M is defined to be the map which takes a direction and assigns the persistence diagrams of its corresponding sublevelset filtration to it:

$$\mathrm{PHT}(M) : S^{d-1} \to \mathcal{D}^d, v \mapsto (X_0(M, h_v), X_1(M, h_v), \ldots, X_{d-1}(M, h_v)).$$

Using the bottleneck stability theorem, we can prove that the persistent homology transform is continuous with respect to the Wasserstein distance and the bottleneck distance. These distances are metrics on the set of persistence diagrams, denoted by dist_p and dist_∞. Furthermore, we consider the following map:

$$\mathcal{M}_3^* \to (S^2 \to \mathcal{D}^3), M \mapsto \mathrm{PHT}(M).$$

Here, $\mathcal{M}_3^*$ denotes the set of all 3-dimensional simplicial complexes which only use as many vertices as needed. We show that this map, which takes a simplicial complex and maps it to its persistent homology transform, is injective. Following from this two facts, the persistent homology transform can indeed be used to represent simplicial complexes and thus their shapes. Hence, we can compare simplicial complexes by measuring distances between the families of persistence diagrams which we get from their persistent homology transforms.

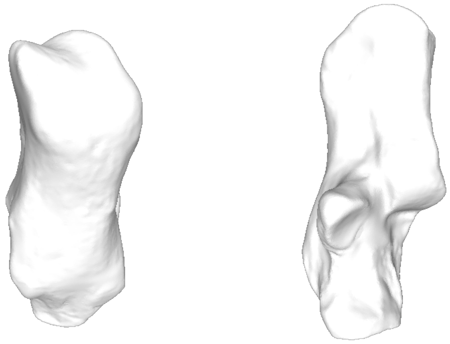


Figure 3: Scan of a heel bone, viewed from the front and the back. (Source [5])

In the last section, we demonstrate how one can use the persistent homology transform to classify heel bones of the following primates: Adapiforms (Adp), Cercopithecoids (Cerc), Hominoids (Hm), Omomyiforms (Om), Parapithecids (Pp), Platyrrhines (Plat) and Strepsirrhines (Str) [5]. Bones are often visualised as meshes due to our modern scanning technologies, such as computerized tomography scans. These meshes are then converted to simplicial complexes. To compare the simplicial complexes $M_1, \ldots, M_k$ constructed from the scans of the heel bones, they must be aligned, scaled evenly and rotated properly. Then, one can compute the persistent homology transform of the simplicial complexes for a selection of evenly distributed directions $v_1, \ldots, v_l \in S^2$. These can be pairwise compared using the following metric:

$$\mathrm{dist}^*_{\mathcal{M}_d}(M_i, M_j) = \frac{1}{k} \sum_{n=1}^{d} \sum_{m=1}^{l} \mathrm{dist}_1(X_n(M_i, h_{v_m}), X_n(M_j, h_{v_m})).$$

Finally, plotting the heel bones according to these distances helps to visualise this analysis. We can see that the points corresponding to the same species form clusters. Thus, it is possible to distinguish different species of primates by analysing the shape of their heel bones.

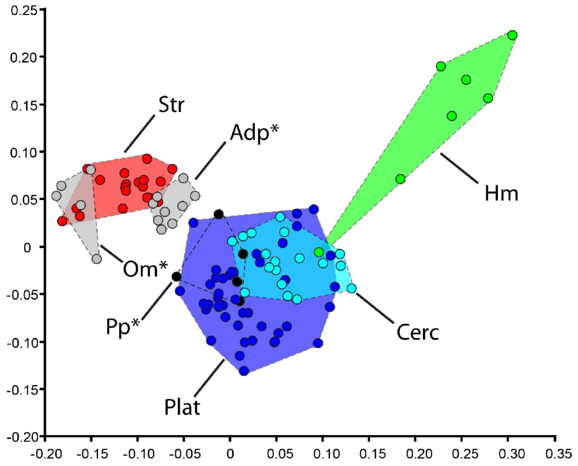


Figure 4: Phenetic clustering of phylogenetic groups of primate heel bones. (Source [5])

2 Homology

This chapter introduces simple combinatorial objects called simplicial complexes and a topological invariant called homology. Homology is a feature of a space or shape that counts the number of generalized holes of geometric objects. This chapter is mainly based on the article "Topological pattern recognition for point cloud data" [1].

2.1 Simplicial complexes

First, we introduce the notion of simplicial complexes, as we can approximate most geometric objects by them. A simplicial complex consists of so-called simplices, which are glued together in a certain fashion. This simplices are defined to be points, lines, triangles, tetrahedrons and n-dimensional generalisations of them. To see how such a generalisation looks like, we observe that the complex hull of three points only forms a triangle, if they are not lying on the same line. Similarly, the convex hull of four points forms a tetrahedron, if the points do not lie on a plane. Therefore, it is reasonable to define simplices to be the convex hull of m points in general position, where being in general positions means that the convex hull is of dimension $m-1$. Formally, points in general position are defined in the following way.

Definition 2.1 (general position). *A set of m points $x_1, \dots, x_m \in \mathbb{R}^d$ are in* ***general position****, if there is no $m-2$-dimensional subspace of $\mathbb{R}^d$ which contains the set $\{x_1, \dots, x_m\}$.*

Note that a subset of a set of points in general position is in general position too. With that, we can now define simplices formally.

Definition 2.2 (simplex).

1. *For points $x_1, \dots x_m \in \mathbb{R}^d$ in general position, the convex hull of the subset $S = \{x_1, \dots, x_m\}$ is called* ***simplex*** *spanned by S and is denoted by $\sigma(S)$.*
2. *For an integer $n \in \mathbb{N}$, a simplex is called* ***n-dimensional****, if it contains exactly $n+1$ vertices.*
3. *The points $x_1, \dots, x_m$ are called* ***vertices*** *of $\sigma(S)$.*
4. *For all non-empty subsets $T \subseteq S$, the simplex $\sigma(T)$ is called* ***face*** *of $\sigma(S)$.*

Example 2.3. *Let $x_1 = (0,0)$, $x_2 = (0,2)$ and $x_3 = (1,0)$ be three points in two dimensional Euclidean space. Note that x_1, x_2 and x_3 are in general position, since they do not lie on a line. Hence, the complex hull $\sigma = \sigma(\{x_1, x_2, x_3\})$ is a 2-dimensional simplex, which is of the form of a triangle. The points x_1, x_2 and x_3 are vertices of σ and $\{x_1\}$, $\{x_1\}$ and $\{x_1\}$ are faces of σ. Furthermore, the line between the points x_1 and x_2 corresponds to the convex hull of the set $\{x_1, x_2\}$ and is thus a face of σ. Similarly, the other two boundary lines of the triangle are faces too. Finally, we note that a simplex spanned by three points is indeed a triangle, as a direct consequence of the definition of general position.*

As we already mentioned, we now want to glue simplices together. To get an idea of what we mean by gluing together simplices, we consider a convex quadrilateral. Then, its 4 boundary edges together with a diagonal form two triangles which share an edge. This, however, means that by gluing an edge of a triangle to an edge of the same length of another triangle, we can create a quadrilateral. Therefore, it is reasonable to glue together simplices which share a face. This leads to the following definition:

Definition 2.4 (simplicial complex). *A* ***simplicial complex*** $M \subseteq \mathbb{R}^d$ *is a finite collection of simplices satisfying the following conditions:*

1. *For every simplex* $\sigma \in M$*, all its faces* $\tau \subseteq \sigma$ *are also contained in* M*.*
2. *For any two simplices* $\sigma, \tau \in M$*, its intersection* $\sigma \cap \tau$ *is either empty or a face of both* σ *and* τ*.*

A simplicial complex M *is called finite, if it consists of finitely many simplices.*

Intuitively, the first condition assures that for every simplex in the simplicial complex, its boundary is also contained in the simplicial complex. The second condition prevents that two simplices in a simplicial complex intersect anywhere else then on their boundaries.

We note that every simplex of a simplicial complex is uniquely given by its set of vertices. This motivates the following definition.

Definition 2.5 (abstract simplicial complex). *An* ***abstract simplicial complex*** *is a tuple* $M = (V, \Sigma)$ *consisting of a set of* ***vertices*** V *and a set of* ***simplices*** $\Sigma \subseteq \mathcal{P}(V) \setminus \{\emptyset\}$*, such that* $\forall \sigma \in \Sigma : \forall \tau \in \mathcal{P}(V) \setminus \{\emptyset\}$:

$$\emptyset \neq \tau \subseteq \sigma \implies \tau \in \Sigma.$$

M *is called finite, if* V *is a finite set.*

Remark. Let $\{x_1, \ldots, x_m\} \in \Sigma$ be a simplex of an abstract simplicial complex (V, Σ). Then, we denote this simplex by $x_1 x_2 \ldots x_m$.

We see that the vertex sets of the simplices of a simplicial complex form an abstract simplicial complex.

Example 2.6. *Let* $a = (0,1)$*,* $b = (0,0)$*,* $c = (1,0)$*,* $d = (-1,0)$ *and* $e = (1,1)$ *be five points in* $\mathbb{R}^2$*. Consider the following three subsets of* $\mathcal{P}(\{a,b,c,d,e\})$*:*

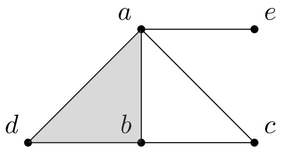
$$M = \{a, b, c, d, e, ab, ac, ad, ae, bc, bd, abd\}$$

$$N = \{a, b, c, d, ac, ad, ae, bc, bd, abd\}$$

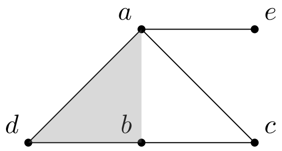
$$O = \{a, b, c, d, e, ab, ac, ad, bc, bd, be, abd\}$$

This three sets correspond to the following shapes in $\mathbb{R}^2$*:*

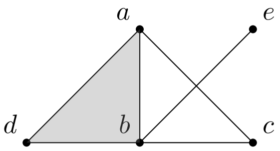
Drawing of M:



Drawing of N:



Drawing of O:



Since M fulfils both conditions of Definition 2.4, it is a simplicial complex. N, on the other hand, is not a simplicial complex, since N contains the simplex abd, but not the face ab of abd. Thus, N does not fulfil the first condition of Definition 2.4. Finally, the two simplices ac and bc of O intersect in the point $(\frac{1}{2}, \frac{1}{2})$, which itself is no simplex. As the second condition is not satisfied, O is not a simplicial complex.

Definition 2.7. *For an integer $d \in \mathbb{N}$,*

$$\mathcal{M}_d := \{M \subseteq \mathbb{R}^d \mid M \text{ is a simplicial complex}\}$$

denotes the set of all finite simplicial complexes in $\mathbb{R}^d$.

Let $M \in \mathcal{M}_d$ be an arbitrary d-dimensional simplicial complex. We define the star and the link of a simplex σ of M as in [3].

Definition 2.8 (star and link).

1. *The* ***star*** *of $\sigma \in M$ is the set*

$$\mathrm{St}(\sigma) := \{\tau \in M \mid \sigma \subseteq \tau\}.$$

2. *The* ***closed star*** *of $\sigma \in M$ is the set*

$$\overline{\mathrm{St}(\sigma)} := \bigcup_{\tau \in \mathrm{St}(\sigma)} \{\upsilon \in M \mid \upsilon \subseteq \tau\}.$$

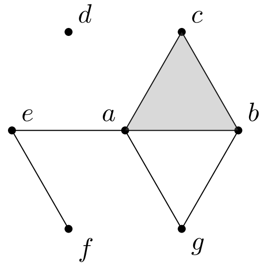
3. *The* ***link*** *of $\sigma \in M$ is the set*

$$\mathrm{Lk}(\sigma) := \{\tau \in \overline{\mathrm{St}(\sigma)} \mid \sigma \cap \tau = \emptyset\}.$$

Remark. In general, $\mathrm{St}(\sigma)$ is not a simplicial complex. However, $\overline{\mathrm{St}(\sigma)}$ is always a subcomplex of M.

The following example illustrates that the link of a simplex can be viewed as the representation of its neighbourhood.

Example 2.9. *Consider the following simplicial complex as well as the star and the link of some of its simplices.*



$\sigma \in M$	$\mathrm{St}(\sigma)$	$\mathrm{Lk}(\sigma)$
a	$\{a, ab, ac, ae, ag, abc\}$	$\{b, c, e, g, bc\}$
c	$\{c, ac, bc, abc\}$	$\{a, b, ab\}$
d	$\{d\}$	$\emptyset$
f	$\{f, ef\}$	$\{e\}$
g	$\{g, ag, bg\}$	$\{a, b\}$
ab	$\{ab, abc\}$	$\{c\}$
ag	$\{ag\}$	$\emptyset$
bc	$\{bc, abc\}$	$\{a\}$
abc	$\{abc\}$	$\emptyset$

Without loss of generality, let a *be the origin of* $\mathbb{R}^2$*. For* $\delta > 0$ *small enough, consider the neighbourhood of* a*:*

$$N(a) := \mathrm{B}_\delta(0) \cap \{x \in \sigma \mid \sigma \in M\} \subseteq \mathbb{R}^2.$$

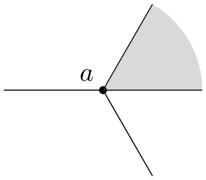


Figure 5: $N(a)$

Furthermore, consider the set of directions, for which there is a component of the link of a*:*

$$L(a) := \{x \in \sigma \mid \sigma \in \mathrm{Lk}(a)\} \subseteq \mathbb{R}^2.$$

We note, that $N(a)$ *and* $L(a)$ *are both fully represented by the same set of directions:*

$$\{\|w\|^{-1}w \mid w \in N(a) \setminus \{0\}\} = \{\|w\|^{-1}w \mid w \in L(a)\}$$

Therefore, the link of a simplicial complex does indeed represent its neighbourhood.

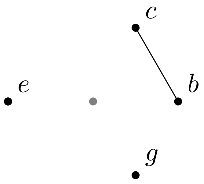


Figure 6: $L(a)$

2.2 Simplicial chain complexes

In this section, we introduce the notions of boundary matrices and chain complexes. For this, we observe maps from an $(n+1)$-dimensional simplex σ to its boundary, which is the set of n-dimensional faces of σ. We will see that it is possible to represent this maps by linear transformations between vector spaces. This will allow us to use linear algebra to compute homology. Hence, we start this section by introducing free vector spaces:

Definition 2.10 (free vector space). *A* ***free*** $\mathbb{K}$***-vector space*** *on a finite set* S *is the set of* $\mathbb{K}$*-linear combinations of the elements of* S *and is denoted by* $V_{\mathbb{K}}(S)$ *or by* $\langle S \rangle$*.*

Note that S is a basis of $V_{\mathbb{K}}(S)$, called the standard basis. Consider two finite sets S and T, as well as a map $f : T \to S$ between them. By extending linearly, we get a unique linear transformation $V_{\mathbb{K}}(f) : V_{\mathbb{K}}(T) \to V_{\mathbb{K}}(S)$, where for all linear combinations $t' \in \{\sum_{t \in T} a_t t \mid \forall t \in T : a_t \in \mathbb{K}\} = V_{\mathbb{K}}(T)$, we have that

$$V_{\mathbb{K}}(f)(t') = \sum_{t \in T} a_t V_{\mathbb{K}}(f)(t) = \sum_{t \in T} a_t f(t).$$

Let S and T be two finite sets. As mentioned above, they are bases of $V_{\mathbb{Z}/2\mathbb{Z}}(S)$ and $V_{\mathbb{Z}/2\mathbb{Z}}(T)$. Thus, we can define matrices mapping linear combinations of T to linear combinations of S.

Definition 2.11 ((S, T)-matrix).

1. *A matrix A where every row corresponds to exactly one $s \in S$ and every column corresponds to exactly one $t \in T$ is called (S, T)-matrix.*
2. *$\forall s \in S$, the row corresponding to s is denoted by $r(s)$.*
3. *$\forall t \in T$, the column corresponding to t is denoted by $c(t)$.*

Remark. Even though the definition of free vector spaces is given for a general field $\mathbb{K}$, we have defined (S, T)-matrices on the field $\mathbb{Z}/2\mathbb{Z}$. This choice is sufficient in most applications and we will not use any other field in this thesis.

Let M be a d-dimensional simplicial complex. We note that all simplices of M are of dimension less or equal to d. This observation motivates the following definition:

Definition 2.12. *Let $M \subseteq \mathbb{R}^d$ be a finite simplicial complex and let $n \in \mathbb{N}$ be arbitrary. Then,*

$$\Sigma_n(M) := \{\sigma \in M \mid \sigma \text{ is } n\text{-dimensional}\}$$

denotes the set of all n-dimensional simplices of M.

Remark. Since $\forall n \in \mathbb{N} : \Sigma_n(M)$ is finite, $V_{\mathbb{K}}(\Sigma_n(M))$ is a free vector space on $\Sigma_n(M)$, denoted by $C_n(M) := V_{\mathbb{Z}/2\mathbb{Z}}(\Sigma_n(M))$.

We proceed by defining the following $(\Sigma_n(M), \Sigma_{n+1}(M))$-matrix:

Definition 2.13 (boundary matrix). *The matrix $\partial_{n+1} = (a_{ij})$, where $\forall \sigma \in \Sigma_n(M)$ and $\forall \tau \in \Sigma_{n+1}(M)$, we have that*

$$a_{\sigma\tau} = \begin{cases} 1 & \text{if } \sigma \subseteq \tau \\ 0 & \text{otherwise} \end{cases}$$

is called $(n+1)$-dimensional ***boundary matrix*** *of M.*

Therefore, we have a sequence of $\mathbb{Z}/2\mathbb{Z}$-vector spaces $\{C_n(M)\}_{n \in \mathbb{N}}$, where for two consecutive vector spaces, there is a map between them given by a boundary matrix. Such a collection of spaces and maps is called simplicial chain complex.

Definition 2.14 (simplicial chain complex). *The **simplicial chain complex** $C_*(M)$ of M is the sequence of $\mathbb{Z}/2\mathbb{Z}$-vector spaces $\{C_n(M)\}_{n\in\mathbb{N}}$ together with linear transformations $(\partial_n : C_{n+1}(M) \to C_n(M))_{n\in\mathbb{N}}$ determined by the n-dimensional boundary matrices of M.*

Equivalently to the boundary homomorphisms in algebraic topology, the boundary matrices of simplicial complexes fulfil the following property:

Proposition 2.15. *For every finite simplicial complex M with an ordering of its simplices sets, and for every integer $n \in \mathbb{N}$, we have $\partial_n \cdot \partial_{n+1} = 0$.*

Proof. Let $(\sigma_1, \dots, \sigma_{m_1})$, $(\tau_1, \dots, \tau_{m_2})$ and $(\upsilon_1, \dots, \upsilon_{m_3})$ be orderings of the sets $\Sigma_n(M)$, $\Sigma_{n+1}(M)$ and $\Sigma_{n+2}(M)$. Let $i \in \{1, \dots, m_1\}$ and $j \in \{1, \dots, m_3\}$ be arbitrary. Then, the row of ∂_n corresponding to σ_i vanishes everywhere except at the columns $k \in \{1, \dots, m_2\}$ with $\sigma_i \subseteq \tau_k$. Similarly, the column of ∂_{n+1} corresponding to υ_j vanishes everywhere except at the columns $k \in \{1, \dots, m_2\}$ with $\tau_k \subseteq \upsilon_j$. Hence, the entry of the matrix $\partial_n \cdot \partial_{n+1}$ at row i and column j is equal the number of $\tau \in \Sigma_{n+1}(M)$ satisfying $\sigma_i \subseteq \tau \subseteq \upsilon_j$. This number is either 0 or 2 and hence 0 in the field $\mathbb{Z}/2\mathbb{Z}$. ☐

We can use this property to give a generalized definition of chain complexes.

Definition 2.16 (abstract chain complex). *An **abstract chain complex** C_* is a sequence of $\mathbb{K}$-vector spaces $(C_n)_{n\in\mathbb{N}}$ together with linear transformations $(\partial_n : C_{n+1} \to C_n)_{n\in\mathbb{N}}$ with the property that $\forall n \in \mathbb{N} : \partial_n \circ \partial_{n+1} = 0$. This condition is equivalent to the condition, that $\forall n \in \mathbb{N} : \mathrm{im}(\partial_{n+1}) \subseteq \ker(\partial_n)$.*

2.3 Simplicial homology

The goal of this section is to introduce the notion of homology on simplicial complexes. Homology is a topological invariant that counts the number of n-dimensional holes of a simplicial complex.

We start this section by defining cycles and boundaries:

Definition 2.17 (cycles and boundaries). *Let $n \in \mathbb{N}$ be an integer and let $C_*(M)$ be a simplicial chain complex.*

1. *$Z_n := \ker(\partial_n)$ denotes the kernel of ∂_n. The elements of Z_n are called **n-cycles**.*
2. *$B_n := \mathrm{im}(\partial_{n+1})$ denotes the image of ∂_{n+1}. The elements of B_n are called **n-boundaries**.*

To get a better intuition of cycles and boundaries, consider the following example:

Example 2.18. *Consider the abstract simplicial complex from Example 2.6:*

$$M = \{a, b, c, d, e, ab, ac, ad, ae, bc, bd, abd\}$$

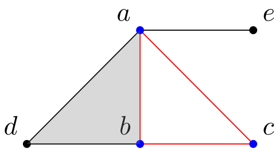
Furthermore, for all dimensions $n \in \mathbb{N}$, consider the free vector spaces $C_n(M)$. As every simplex is of dimension 2 or less, we see that $\forall n \geq 3 : C_n(M) = 0$. From the remark of Definition 2.10, it follows that:

1. *(a, b, c, d, e) is an ordered basis of $C_0(M) = \langle a, b, c, d, e\rangle$.*
2. *(ab, ac, ad, ae, bc, bd) is an ordened basis of $C_1(M)$.*
3. *(abd) is an ordered basis of $C_2(M)$.*

Now consider the boundary matrices of M.

$$\partial_1 = \begin{array}{c} \\ \text{a} \\ \text{b} \\ \text{c} \\ \text{d} \\ \text{e} \end{array} \begin{array}{c} \begin{array}{cccccc} \text{ab} & \text{ac} & \text{ad} & \text{ae} & \text{bc} & \text{bd} \end{array} \\ \begin{bmatrix} 1 & 1 & 1 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 & 1 & 1 \\ 0 & 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 & 0 \end{bmatrix} \end{array} \qquad \partial_2 = \begin{array}{c} \\ \text{ab} \\ \text{ac} \\ \text{ad} \\ \text{ae} \\ \text{bc} \\ \text{bd} \end{array} \begin{array}{c} \text{abd} \\ \begin{bmatrix} 1 \\ 0 \\ 1 \\ 0 \\ 0 \\ 1 \end{bmatrix} \end{array}$$

We observe that ∂_1 maps ab to $a + b$, bc to $b + c$ and ac to $a + c$. Since the boundary map is linear, $ab + bc + ac$ gets mapped to $2a + 2b + 2c$, which is equal to 0 in the field $\mathbb{Z}/2\mathbb{Z}$. Therefore, $ab + bc + ac$ is a 1-cycle of M. Also note that a, b, c are 0-boundaries of M.



We further observe that $ab + ad + bd$ is both a 1-cycle and a 1-boundary of M. Also, $ab + ac + bc$ is no 1-boundary. This is because the triangle abd is filled, while the triangle abc is not. Therefore, we can intuitively think of the simplex abd to fill the loop $ab + ad + bd$.

As we have seen in the example, if an element of $C_n(M)$ is a n-cycle but not a n-boundary, then it represents a n-dimensional hole. However, if an element of $C_n(M)$ is both a n-cycle and a n-boundary, then it does not correspond to a n-dimensional hole of M. Therefore, this motivates us to define the homology of a simplicial complex as the quotient of its cycles by its boundaries.

Definition 2.19 (homology). *Let $n \in \mathbb{N}$ be arbitrary and let $C_*(M)$ be a simplicial chain complex. The quotient space*

$$H_n(M) := Z_n/B_n$$

is called the n-dimensional ***homology group*** *of M.*

Note that the homology of a simplicial complex depends on the field on which the free vector spaces are defined. Intuitively, the n-dimensional homology of M represents its n-dimensional holes. Furthermore, the dimension of $H_n(M)$ can be thought of as the number of n-dimensional holes. Thus, we define the so-called Betti numbers:

Definition 2.20 (Betti number). *Let $n \in \mathbb{N}$ be an integer and let $C_*(M)$ be a simplicial chain complex. The integer*

$$\beta_n(M) \coloneqq \dim\left(H_n(M)\right)$$

*is called the n-th **Betti number** of M.*

2.4 Computing homology

Theoretically, we are able to compute the homology of every simplicial complex, just by using linear algebra to determine the kernels and images of its boundary matrices, as well as the quotients of them. However, with a few observations, we can develop an algorithm which makes computing homology a straitforward process. To ease notation, we first define simple matrices:

Definition 2.21 (Simple matrix). *Let S and T be two finite sets. Then, a (S,T)-matrix is called simple, if A has at most one entry equal to one in every row and every column, with all other entries being 0.*

We see that computing the kernels and images of simple (S,T)-matrices is easy.

Observation 2.22. *Let A be a simple (S,T)-matrix. Then:*

1. $\ker(L_A) = \langle\{s \in S \mid c(s) = 0\}\rangle \subseteq V_{\mathbb{Z}/2\mathbb{Z}}(S)$.
2. $\operatorname{im}(L_A) = \langle\{t \in T \mid r(t) \neq 0\}\rangle \subseteq V_{\mathbb{Z}/2\mathbb{Z}}(T)$.

Here, L_A denotes the linear transformation from $V_{\mathbb{Z}/2\mathbb{Z}}(T)$ to $V_{\mathbb{Z}/2\mathbb{Z}}(S)$ given by left multiplication of A.

Furthermore, we have the following result:

Observation 2.23. *Let R, S and T be finite sets. Furthermore, let A be a simple (R,S)-matrix and let B be a simple (S,T)-matrix such that $A \cdot B = 0$. Then, $\forall s \in S : c_A(s) \neq 0 \implies r_B(s) = 0$ and $r_B(s) \neq 0 \implies c_A(s) = 0$. Hence*

$$\{s \in S \mid r_B(s) \neq 0\} \subseteq \{s \in S \mid c_A(s) = 0\}.$$

From Observation 2.22, it follows that

$$\operatorname{im}(L_B) = \langle\{s \in S \mid r_B(s) \neq 0\}\rangle \subseteq \langle\{s \in S \mid c_A(s) = 0\}\rangle = \ker(L_A)$$

We see that the basis of $\operatorname{im}(L_B)$ is contained in the basis of $\ker(L_A)$. Therefore, computing their quotient is effortless:

$$\ker(L_A)/\operatorname{im}(L_B) = \langle\{s \in S \mid c_A(s) = r_B(s) = 0\}\rangle$$

Note that this is only possible when the columns of A and the rows of B both correspond to the same basis elements.

From linear algebra, we know that every matrix can be transformed into a simple matrix by performing finitely many row and column operations on it. Furthermore, these row operations correspond to basis changes on the corresponding vector fields.

Observation 2.24. *Consider a (S, T)-matrix A and a (T, U)-matrix B.*

1. *Let $s_1, s_2 \in S$ be distinct. Adding $r_A(s_1)$ to $r_A(s_2)$ yields a (S', T)-matrix A', where $S' = (S \setminus \{s_1\}) \cup \{s_1 - s_2\}$. Since the set S' is obtained by linearly combining elements of S, it generates the same free vector space as S. Furthermore, we know from linear algebra that A and A' represent the same linear transformation with respect to the bases S, T and S', T. As a consequence,* $\operatorname{im}(L_A) = \operatorname{im}(L_{A'})$.
2. *Let $u_1, u_2 \in U$ be distinct. Adding $c_B(u_1)$ to $c_B(u_2)$ yields a (T, U')-matrix B', where $U' = (U \setminus \{u_2\}) \cup \{u_2 + u_1\}$. With the same reasoning as above, we get that the matrices B and B' represent the same linear map and* $\ker(L_B) = \ker(L_{B'})$.
3. *Let $t_1, t_2 \in T$ be distinct. Adding $c_A(t_1)$ to $c_A(t_2)$ yields a (S, T')-matrix A', where $T' = (T \setminus \{t_2\}) \cup \{t_2 + t_1\}$ Now however, the matrices A and B have different bases of $V_{\mathbb{Z}/2\mathbb{Z}}(T)$. In order to match these bases again, we need to subtract $r_B(s_2)$ from $r_B(s_1)$ to get a (T', U)-matrix B'. Therefore* $\ker(L_A) = \ker(L_{A'})$ *and* $\operatorname{im}(L_B) = \operatorname{im}(L_{B'})$.

Therefore, the kernel and the image of a linear transformation are preserved under the operations described above. Furthermore, by only applying these operations to A and B, we can assure that the elements of $V_{\mathbb{K}}(S)$ representing the columns of A always match with elements representing the rows of B.

Let M be a finite simplicial complex and let $n \in \mathbb{N}$ be arbitrary. We now construct an algorithm to compute the n-dimensional homology of M. The algorithm is split into two steps. In the first step, we use Observation 2.24 to transform the n-dimensional boundary matrix ∂_n of M into a simple matrix. Then, we use Observation 2.24 again to transform the $(n+1)$-dimensional boundary matrix ∂_{n+1} of M into a simple matrix as well. We then can apply 2.23 to get the n-dimensional homology of M.

Algorithm 2.25. *Define $S := \Sigma_{n-1}(M)$, $T := \Sigma_n(M)$ and $U := \Sigma_{n+1}(M)$. Furthermore, let $A := \partial_n$ and let $B := \partial_{n+1}$. Note that A is a (S, T)-matrix, B is a (T, U)-matrix and $AB = 0$. Initialise $S' = S$, $T' = T$ and $U' = U$.*

Step 1:
Choose $s' \in S'$ and $t' \in T'$ such that $a_{s't'} \neq 0$.
Remove s' from S' and t' from T'.
$\forall s \in S'$ with $a_{st'} \neq 0$, perform the following operations:

1. *add $r_A(s')$ to $r_A(s)$.*
2. *remove s' from S.*

3. *add* $s' - s$ *to* S.

4. *redefine* s' *to be* $s' - s$.

These operations correspond to operations of the first type in Observation 2.24. $\forall t \in T'$ *with* $a_{s't} \neq 0$*, perform the following operations:*

1. *add* $c_A(t')$ *to* $c_A(t)$.

2. *subtract* $r_B(t)$ *from* $r_B(t')$.

3. *remove* t *from* T *and from* T'.

4. *add* $t + t'$ *to* T *and to* T'.

These operations correspond to operations of the second type in Observation 2.24. Note that now $a_{s't'}$ *is the only entry of* $r_A(s')$ *and* $c_A(t')$ *which is non-zero. Therefore, we can repeat* Step 1 *until* A *is transformed into a simple matrix.*

From $AB = 0$*, it follows that* $\forall t \in T$ *with* $c_A(t) \neq 0$*, we have that* $r_B(t) = 0$. *Furthermore, note that* $t \in T' \iff c_A(t) = 0$. *Thus,* $\forall t_1, t_2 \in T'$*, the change of basis caused by adding* $r_B(t_1)$ *to* $r_B(t_2)$ *does not affect* A.

Step 2:
Choose a $t' \in T'$ *and a* $u' \in U'$ *such that* $B_{t'u'} \neq 0$.
Remove t' *from* T' *and* u' *from* U'.
$\forall t \in T'$ *with* $b_{tu'} \neq 0$*, perform the following operations:*

1. *add* $r_B(t')$ *to* $r_B(t)$.

2. *remove* t' *from* T.

3. *add* $t' - t$ *to* T.

4. *redefine* t' *to be* $t' - t$.

These operations correspond to operations of the second type in Observation 2.24. $\forall u \in U'$ *with* $a_{t'u} \neq 0$*, perform the following operations:*

1. *add* $c_B(u')$ *to* $c_B(u)$.

2. *remove* u *from* U *and from* U'.

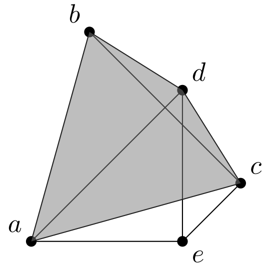
3. *add* $u + u'$ *to* U *and to* U'.

These operations correspond to operations of the third type in Observation 2.24. Note that now $b_{t'u'}$ *is the only entry of* $r_B(t')$ *and* $c_B(u')$ *which is non-zero. Therefore, we can repeat* Step 2 *until* B *is transformed into a simple matrix.*

Since all operations are of one of the types described in Observation 2.24, $\ker(A)$ *and* $\operatorname{im}(B)$ *are left invariant. Therefore, we can use Observation 2.23 to compute* $\ker(A)/\operatorname{im}(B)$

To close this chapter, we demonstrate this algorithm in an example.

Example 2.26. *Let M be the boundary of a tetrahedron together with three lines connecting three of its corners to a fifth point.*



Consider the sets of 0, 1 *and* 2 *dimensional simplices:*

$$\Sigma_0(M) = \{a, b, c, d, e\}$$

$$\Sigma_1(M) = \{ab, ac, ad, ae, bc, bd, cd, ce, de\}$$

$$\Sigma_2(M) = \{abc, abd, acd, bcd\}$$

Let ∂abc denote $ab + ac + bc$.

Consider the boundary matrices:

$$\partial_1 = \begin{array}{c} \\ \text{a} \\ \text{b} \\ \text{c} \\ \text{d} \\ \text{e} \end{array} \begin{array}{c} \begin{array}{ccccccccc} \text{ab} & \text{ac} & \text{ad} & \text{ae} & \text{bc} & \text{bd} & \text{cd} & \text{ce} & \text{de} \end{array} \\ \begin{bmatrix} 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 & 1 & 1 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 1 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 \end{bmatrix} \end{array} \qquad \partial_2 = \begin{array}{c|cccc} & \text{abc} & \text{abd} & \text{acd} & \text{bcd} \\ \hline \text{ab} & 1 & 1 & 0 & 0 \\ \text{ac} & 1 & 0 & 1 & 0 \\ \text{ad} & 0 & 1 & 1 & 0 \\ \text{ae} & 0 & 0 & 0 & 0 \\ \text{bc} & 1 & 0 & 0 & 1 \\ \text{bd} & 0 & 1 & 0 & 1 \\ \text{cd} & 0 & 0 & 1 & 1 \\ \text{ce} & 0 & 0 & 0 & 0 \\ \text{de} & 0 & 0 & 0 & 0 \end{array}$$

We start by performing all row operations of Step 1. *For this, we add the first row of ∂_1 to the second row. Furthermore, we replace a with $a - b$. Recall that $a - b = a + b$ in $\mathbb{Z}/2\mathbb{Z}$.*

$$\begin{array}{c|ccccccccc} & \text{ab} & \text{ac} & \text{ad} & \text{ae} & \text{bc} & \text{bd} & \text{cd} & \text{ce} & \text{de} \\ \hline \text{a+b} & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 & 0 \\ \text{b} & 0 & 1 & 1 & 1 & 1 & 1 & 0 & 0 & 0 \\ \text{c} & 0 & 1 & 0 & 0 & 1 & 0 & 1 & 1 & 0 \\ \text{d} & 0 & 0 & 1 & 0 & 0 & 1 & 1 & 0 & 1 \\ \text{e} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cccc} \text{abc} & \text{abd} & \text{acd} & \text{bcd} \\ \hline 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{array}$$

We proceed by performing the column operations of Step 1. *Thus, we add the first column of ∂_1 to columns* 2, 3 *and* 4. *Additionally, we subtract rows* 2, 3 *and* 4 *of ∂_2 from the first row. Finally, we adapt the bases.*

$$\begin{array}{c|ccccccccc} & \text{ab} & \text{ab+ac} & \text{ab+ad} & \text{ab+ae} & \text{bc} & \text{bd} & \text{cd} & \text{ce} & \text{de} \\ \hline \text{a+b} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{b} & 0 & 1 & 1 & 1 & 1 & 1 & 0 & 0 & 0 \\ \text{c} & 0 & 1 & 0 & 0 & 1 & 0 & 1 & 1 & 0 \\ \text{d} & 0 & 0 & 1 & 0 & 0 & 1 & 1 & 0 & 1 \\ \text{e} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cccc} \text{abc} & \text{abd} & \text{acd} & \text{bcd} \\ \hline 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{array}$$

Executing Step 1 *a second time yields:*

$$\begin{array}{c|ccccccccc} & \text{ab} & \text{ab+ac} & \text{ab+ad} & \text{ab+ae} & \text{bc} & \text{bd} & \text{cd} & \text{ce} & \text{de} \\ \hline \text{a+b} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{b+c} & 0 & 1 & 1 & 1 & 1 & 1 & 0 & 0 & 0 \\ \text{c} & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 1 & 0 \\ \text{d} & 0 & 0 & 1 & 0 & 0 & 1 & 1 & 0 & 1 \\ \text{e} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cccc} \text{abc} & \text{abd} & \text{acd} & \text{bcd} \\ \hline 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{array}$$

$$\begin{array}{c|ccccccccc} & \text{ab} & \text{ab+ac} & \text{ac+ad} & \text{ac+ae} & \partial\text{abc} & \text{ab+ac+bd} & \text{cd} & \text{ce} & \text{de} \\ \hline \text{a+b} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{b+c} & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \text{c} & 0 & 0 & 1 & 1 & 0 & 1 & 1 & 1 & 0 \\ \text{d} & 0 & 0 & 1 & 0 & 0 & 1 & 1 & 0 & 1 \\ \text{e} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cccc} \text{abc} & \text{abd} & \text{acd} & \text{bcd} \\ \hline 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{array}$$

Note that the third column of ∂_1 corresponds to the basis element $ac + ad$. This is because $ab + ac + ab + ad = 2ab + ac + ad$ and $2 = 0$ in $\mathbb{Z}/2\mathbb{Z}$.

We now repeat *Step 1* until ∂_1 is simple.

$$
\begin{array}{c|ccccccccc}
 & \text{ab} & \text{ab+ac} & \text{ac+ad} & \text{ad+ae} & \partial\text{abc} & \partial\text{abd} & \partial\text{acd} & \text{ac+ad+ce} & \text{de} \\
\hline
\text{a+b} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{b+c} & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{c+d} & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{d} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1 \\
\text{e} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 1
\end{array}
\qquad
\begin{array}{cccc}
\text{abc} & \text{abd} & \text{acd} & \text{bcd} \\
\hline
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
1 & 0 & 0 & 1 \\
0 & 1 & 0 & 1 \\
0 & 0 & 1 & 1 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0
\end{array}
$$

$$
\begin{array}{c|ccccccccc}
 & \text{ab} & \text{ab+ac} & \text{ac+ad} & \text{ad+ae} & \partial\text{abc} & \partial\text{abd} & \partial\text{acd} & \text{ac+ae+ce} & \text{ad+ae+de} \\
\hline
\text{a+b} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{b+c} & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{c+d} & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{d+e} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\
\text{e} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{array}
\qquad
\begin{array}{cccc}
\text{abc} & \text{abd} & \text{acd} & \text{bcd} \\
\hline
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
1 & 0 & 0 & 1 \\
0 & 1 & 0 & 1 \\
0 & 0 & 1 & 1 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0
\end{array}
$$

The goal now is to transform ∂_2 into a simple matrix as well. Therefore, we add columns 1, 2 and 3 of ∂_2 to the fourth column. To adjust the basis to these operations, we have to add abc, abd and acd to bcd, which corresponds to ∂abcd.

$$
\begin{array}{c|ccccccccc}
 & \text{ab} & \text{ab+ac} & \text{ac+ad} & \text{ad+ae} & \partial\text{abc} & \partial\text{abd} & \partial\text{acd} & \text{ac+ae+ce} & \text{ad+ae+de} \\
\hline
\text{a+b} & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{b+c} & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{c+d} & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{d+e} & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\
\text{e} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0
\end{array}
\qquad
\begin{array}{cccc}
\text{abc} & \text{abd} & \text{acd} & \partial\text{abcd} \\
\hline
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
1 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 \\
0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0
\end{array}
$$

Now we use Observation 2.22 to compute the cycles and boundaries of M:

$$Z_0 := \ker(\partial_0) \cong \langle a+b, b+c, c+d, d+e, e\rangle$$

$$B_0 := \operatorname{im}(\partial_1) \cong \langle a+b, b+c, c+d, d+e\rangle$$

Furthermore, we have that:

$$Z_1 := \ker(\partial_1) \cong \langle ac+ae+ce, ad+ae+de, \partial abc, \partial abd, \partial acd\rangle.$$

$$B_1 := \operatorname{im}(\partial_2) \cong \langle \partial abc, \partial abd, \partial acd\rangle.$$

Finally, we recall that ∂_3 has empty domain. Therefore:

$$Z_2 := \ker(\partial_2) \cong \langle \partial abcd\rangle$$

$$B_2 := \operatorname{im}(\partial_3) \cong 0$$

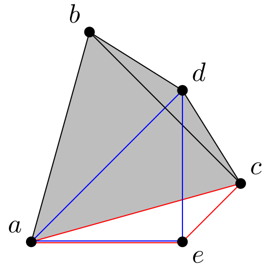
As desired, all generators of B_0, B_1 and B_2 are generators of Z_0, Z_1 and Z_2 too. Therefore, we just need to take the generators out of the cycles which are contained in the boundaries to get their quotient. With this, we can now compute the homology of M.

$$H_0(M) \cong \frac{\langle a+b,b+c,c+d,d+e,e\rangle}{\langle a+b,b+c,c+d,d+e\rangle} \cong \langle e\rangle$$

$$H_1(M) \cong \frac{\langle ac+ae+ce,ad+ae+de,\partial abc,\partial abd,\partial acd\rangle}{\langle \partial abc,\partial abd,\partial acd\rangle} \cong \langle ac+ae+ce, ad+ae+de\rangle$$

$$H_2(M) \cong \frac{\langle \partial abcd\rangle}{0} \cong \langle \partial abcd\rangle$$

To get a better understanding what this homology spaces are, we visualize its generators in a picture:



We see that $ac+ae+ce$ and $ad+ae+de$ are two loops which represent the two 1-dimensional holes of M. Furthermore, we observe that $\partial abcd$ represents the void which is enclosed by the boundary of the tetrahedron. Finally, e stands for the only connected component M has.

The Betti numbers of M are defined to be the dimension of the homologies. From linear algebra, we know that these dimensions are equal to the number of generators of the space. Therefore, $\beta_0(M) = 1$, $\beta_1(M) = 2$ and $\beta_2(M) = 1$. This means that M has one connected component, two 1-dimensional holes and one 2-dimensional hole, namely the void enclosed by the boundary of the tetrahedron.

3 Persistence

This chapter introduces persistent homology, an adaptation of homology to the setting of filtrations. It is mainly based on the article "Topological pattern recognition for point cloud data" [1].

3.1 Filtrations

We start this section by introducing filtrations, which are families of sets which are ordered by inclusion. Furthermore, we introduce tame functions, which are then used to define filtrations on simplicial complexes.

Definition 3.1 (filtered set).

1. *A **filtered set** is a pair* (S, σ)*, consisting of a set* S *and a function* $\sigma : S \to \mathbb{R}$*.*
2. *A filtered set* (S, σ) *is called **finite**, if* S *is finite.*

Definition 3.2 (filtration). *A family of sets* $\{S_r\}_{r\in\mathbb{R}}$ *which is ordered by inclusion, meaning that*

$$\forall r_1, r_2 \in \mathbb{R} : r_1 \leq r_2 \implies S_{r_1} \subseteq S_{r_2},$$

*is called **filtration**.*

For a filtered set (S, σ), we see that $\{s \in S \mid \sigma(s) \leq r\}_{r\in\mathbb{R}}$ is a filtration. Furthermore, for a filtration $\{S_r\}_{r\in\mathbb{R}}$, we see that $\bigcup_{r\in R} S_r$ together with the function $\sigma : \bigcup_{r\in R} S_r \to \mathbb{R}$, where $\forall s \in \bigcup_{r\in R} S_r : \sigma(s) := \min\{r \in \mathbb{R} \mid s \in S_r\}$, is a filtered set. Therefore, there is a one-to-one correspondence between filtered sets and filtrations, which means that we can assign a filtration to any filtered set and vice versa.

We now continue to define tame functions, which are needed to build filtrations of simplicial complexes.

Definition 3.3 (homological critical value). *Let* T *be a topological space and let* $f : T \to \mathbb{R}$ *be a real-valued function. A **homological critical value** of* f *is a number* $a \in \mathbb{R}$ *for which there is an integer* $n \in \mathbb{N}$ *such that for all* $\varepsilon > 0$ *small enough, the map* $H_n(f^{-1}((-\infty, a - \varepsilon])) \to H_n(f^{-1}((-\infty, a + \varepsilon]))$ *induced by inclusion is not an isomorphism.*

The following example should give an intuition for homological critical values.

Example 3.4. *Consider the following simplicial complex:*

$$M = \{a, b, c, ab, ac, bc, abc\}$$

Note that M *is a triangle. Define* $f : M \to \mathbb{R}$ *such that*

1. $f(a) = f(b) = f(c) = 0$
2. $f(ab) = f(ac) = 1$
3. $f(bc) = 2$
4. $f(abc) = 3$

We observe that:

1. $\forall x \in (-\infty, 0) : f^{-1}((-\infty, x]) = \emptyset$ *and therefore* $\forall x \in (-\infty, 0) : \exists \varepsilon > 0$ *such that* $f^{-1}((-\infty, x]) = f^{-1}((-\infty, x])$.
2. $\forall x \in [0, 1) : f^{-1}((-\infty, x])) = \{a, b, c\}$ *and therefore* $\forall x \in (0, 1) : \exists \varepsilon > 0$ *such that* $f^{-1}((-\infty, x]) = f^{-1}((-\infty, x])$.
3. $\forall x \in [1, 2) : f^{-1}((-\infty, x])) = \{a, b, c, ab, ac\}$ *and therefore* $\forall x \in (1, 2) : \exists \varepsilon > 0$ *such that* $f^{-1}((-\infty, x]) = f^{-1}((-\infty, x])$.
4. $\forall x \in [2, 3) : f^{-1}((-\infty, x])) = \{a, b, c, ab, ac, bc\}$ *and therefore* $\forall x \in (2, 3) : \exists \varepsilon > 0$ *such that* $f^{-1}((-\infty, x]) = f^{-1}((-\infty, x])$.
5. $\forall x \in [3, \infty) : f^{-1}((-\infty, x])) = \{a, b, c, ab, ac, bc, abc\}$ *and therefore* $\forall x \in (3, \infty) : \exists \varepsilon > 0$ *such that* $f^{-1}((-\infty, x]) = f^{-1}((-\infty, x])$.

Note that, for every point $x \in \mathbb{R}$*, the preimage* $f^{-1}((-\infty, x))$ *is a simplicial complex.*
Let $x \in \mathbb{R} \setminus \{0, 1, 2, 3\}$*. Then, we have that* $\forall n \in N : \exists \varepsilon > 0$ *for which the map*

$$H_n(f^{-1}((-\infty, a - \varepsilon])) \to H_n(f^{-1}((-\infty, a + \varepsilon]))$$

induced by inclusion is the identity map and thus an isomorphism. Thus, x *is no homological critical value of* f*.*
Let $x \in \{0, 1\}$*. Then,* $\forall \varepsilon \in (0, 1)$ *we have that:*

1. $\beta_0(f^{-1}((-\infty, 0 - \varepsilon])) = 0$ *and* $\beta_0(f^{-1}((-\infty, 0 + \varepsilon])) = 3$
2. $\beta_0(f^{-1}((-\infty, 1 - \varepsilon])) = 3$ *and* $\beta_0(f^{-1}((-\infty, 1 + \varepsilon])) = 1$

As the dimensions of the 0*-dimensional homology do not match around the points* 1 *and* 2*, the inclusion maps again cannot be isomorphisms. Thus,* 0 *and* 1 *are homological critical values of* f*.*
Let $x \in \{2, 3\}$*. Similarly, we have that* $\forall \varepsilon \in (0, 1)$*:*

1. $\beta_1(f^{-1}((-\infty, 2 - \varepsilon])) = 0$ *and* $\beta_1(f^{-1}((-\infty, 2 + \varepsilon])) = 1$
2. $\beta_1(f^{-1}((-\infty, 3 - \varepsilon])) = 1$ *and* $\beta_1(f^{-1}((-\infty, 3 + \varepsilon])) = 0$

Therefore, the inclusions between $H_1(f^{-1}((-\infty, x-\varepsilon]))$ *and* $H_1(f^{-1}((-\infty, x+\varepsilon]))$ *cannot be isomorphisms. Hence,* 2 *and* 3 *are homological critical values of* f *as well.*

Definition 3.5 (tame function). *A real-valued function $f : T \to \mathbb{R}$ is called* ***tame****, if its number of homological critical values is finite.*

Remark. For a finite simplicial complex M, every real-valued function $f : M \to \mathbb{R}$ defined on M is tame.

In Example 3.4, we observed that the preimages of f are simplicial complexes. Furthermore, they are ordered by inclusion. As a consequence, we can now construct filtered sets of simplicial complexes using tame functions. Additionally, given a collection of simplicial complexes which is ordered by inclusion, we can see that only considering the simplices of a fixed dimension $n \in N$ conserves this ordering. Therefore, we will construct filtered sets generated by tame functions $f : M \to \mathbb{R}$ on the set of its n-dimensional simplices. Generally, the dimension of homology can be viewed as being fixed in this chapter.

Definition 3.6 (generated filtration). *Let $n \in \mathbb{N}$ be an arbitrary dimension, let M be a simplicial complex and let $f : M \to \mathbb{R}$ be a tame function with the property that $\forall \sigma \in M$ and for all faces τ of σ, we have that $f(\tau) \leq f(\sigma)$. Then, $(\Sigma_n(M), f|_{\Sigma_n(M)})$ is a filtered set.*

The condition on f is there to assure that at every time $r \in \mathbb{R}$, the subset of M consisting of all the simplices $\sigma \in M$ with $f(\sigma) \leq r$ is a subcomplex of M.

3.2 Persistent vector spaces

In this Section, we introduce persistent vector spaces, which are families of vector spaces together with families of linear transformations that fulfil a certain property Furthermore, we study how known concepts of linear algebra can be extended to a persistent setting. There, we get a notion of linear transformations between persistent vector spaces.

Definition 3.7 (persistent vector space). *A* ***persistent vector space*** *is a family of $\mathbb{K}$-vector spaces $\{V_r\}_{r\in\mathbb{R}}$ together with a family of linear transformations $\{L_V(r_1, r_2) : V_{r_1} \to V_{r_2}\}_{r_1 \leq r_2}$ such that*

$$\forall r_1, r_2, r_3 \in \mathbb{R} : r_1 \leq r_2 \leq r_3 \implies L_V(r_1, r_3) = L_V(r_2, r_3) \circ L_V(r_1, r_2).$$

The reason for the condition on the linear transformations will become apparent later. As for regular vector spaces, we want to define linear maps between two persistent vector spaces.

Definition 3.8 (linear transformations of persistent vector spaces). *Let $\{V_r\}_{r\in\mathbb{R}}$ and $\{W_r\}_{r\in\mathbb{R}}$ be two persistent vector spaces. A* ***linear transformation*** *from $\{V_r\}_{r\in\mathbb{R}}$ to $\{W_r\}_{r\in\mathbb{R}}$ is a family of linear transformations $\{f_r : V_r \to W_r\}_{r\in\mathbb{R}}$ such that*

$$\forall r_1, r_2 \in \mathbb{R} : r_1 \leq r_2 \implies f_{r_2} \circ L_V(r_1, r_2) = L_W(r_1, r_2) \circ f_{r_1}.$$

Also, we define subspaces and quotient spaces of persistent vector spaces.

Definition 3.9 (sub-persistent vector space). *Let* $\{V_r\}_{r\in\mathbb{R}}$ *be a persistent vector space. A* ***sub-persistent vector space*** *of* $\{V_r\}_{r\in\mathbb{R}}$ *is a family of sub-vector spaces* $\{U_r\}_{r\in\mathbb{R}}$ *such that*

$$\forall r_1, r_2 \in \mathbb{R} : r_1 \leq r_2 \implies \forall u \in U_{r_1} : L_V(r_1, r_2)(u) \in U_{r_2}.$$

Remark. For a linear transformation $\{f_r : V_r \to W_r\}_{r\in\mathbb{R}}$, its image $\mathrm{im}(f)$ is defined to be the sub-persistent vector space $\{\mathrm{im}(f_r)\}_{r\in\mathbb{R}}$.

Definition 3.10 (persistent quotient space). *Let* $\{V_r\}_{r\in\mathbb{R}}$ *be a persistent vector space and let* $\{W_r\}_{r\in\mathbb{R}}$ *be a sub-persistent vector space of* $\{V_r\}_{r\in\mathbb{R}}$*. Then*

$$\{V_r\}_{r\in\mathbb{R}}/\{W_r\}_{r\in\mathbb{R}} := \{V_r/W_r\}_{r\in\mathbb{R}}$$

is called ***persistent quotient space****, where* V_r/W_r *denotes the quotient space of the two* $\mathbb{K}$*-vector spaces* V_r *and* W_r*.*

Finally, we introduce a notation for free persistent vector spaces.

Definition 3.11 (persistent vector space on (S, σ)). *For all* $r \in \mathbb{R}$*, let*

$$W_r := V_{\mathbb{K}}(\{s \in S \mid \sigma(s) \leq r\})$$

be the free $\mathbb{K}$*-vector space on* $\{s \in S \mid \sigma(s) \leq r\}$*. For arbitrary* $r_1, r_2 \in \mathbb{R}$ *with* $r_1 \leq r_2$*, let*

$$L_S(r_1, r_2) : W_{r_1} \to W_{r_2}, w \mapsto w$$

be the inclusion map from W_{r_1} *to* W_{r_2}*. Then,* $\{W_r\}_{r\in\mathbb{R}}$ *together with the linear transformations* $\{L_S(r_1, r_2)\}_{r_1\leq r_2}$ *is called* ***free persistent vector space*** *on* (S, σ) *and is denoted by* $\{V_{\mathbb{K}}(S, \sigma)_r\}_{r\in\mathbb{R}}$*.*

Remark. $\{V_{\mathbb{K}}(S, \sigma)_r\}_{r\in\mathbb{R}}$ is a sub-persistent vector space of $(V_{\mathbb{K}}(S))_{r\in\mathbb{R}}$.

The following definition introduces finitely presented persistent vector spaces:

Definition 3.12 (finitely presented persistent vector space).

1. *A persistent vector space is called* ***free****, if it is isomorphic to* $\{V_{\mathbb{K}}(S, \sigma)_r\}_{r\in\mathbb{R}}$ *for a filtered set* (S, σ)*.*
2. *A free persistent vector space is called* ***finitely generated****, if it is isomorphic to* $\{V_{\mathbb{K}}(S, \sigma)_r\}_{r\in\mathbb{R}}$ *for a finite filtered set* (S, σ)*.*
3. *A persistent vector space is called* ***finitely presented****, if it is isomorphic to* $\{W_r\}_{r\in\mathbb{R}}/\mathrm{im}(f)$*, where* $\{V_r\}_{r\in\mathbb{R}}$ *and* $\{W_r\}_{r\in\mathbb{R}}$ *are two finitely generated persistent vector spaces and* $f : \{V_r\}_{r\in\mathbb{R}} \to \{W_r\}_{r\in\mathbb{R}}$ *is a linear transformation between them.*

For a better understanding of free persistent vector spaces, the following proposition classifies its elements:

Proposition 3.13. *For an arbitrary time $r \in \mathbb{R}$ and a linear combination $\sum_{\{s\in S\}} a_s s \in V_{\mathbb{K}}(S)$, we have:*

$$\sum_{\{s\in S\}} a_s s \in V_{\mathbb{K}}(S,\sigma)_r \iff \forall s \in S \text{ with } \sigma(s) > r : a_s = 0.$$

Proof. Let $y = \sum_{\{s\in S\}} a_s s \in V_{\mathbb{K}}(S)$ be a linear combination with the property that for all $s \in S$ with $\sigma(s) > r$, a_s vanishes. Hence $y = \sum_{\{s\in S|\sigma(s)\leq r\}} a_s s$. Since $\{s \in S \mid \sigma(s) \leq r\}$ is contained in $V_{\mathbb{K}}(S,\sigma)_r$, it follows that the sum lies in $V_{\mathbb{K}}(S,\sigma)_r$ too.
Now let $y = \sum_{\{s\in S\}} a_s s \in V_{\mathbb{K}}(S)$ such that there is at least a $s' \in S$ with $\sigma(s') > r$ and $a_{s'} \neq 0$. Since $s' \notin V_{\mathbb{K}}(S,\sigma)_r$, we have that also the linear combination is not contained in $V_{\mathbb{K}}(S,\sigma)_r$. □

This means that only the elements $s \in S$ which already appeared at time $r \in R$ are present in the vector space $V_{\mathbb{K}}(S,\sigma)_r$ and its basis.

3.3 Adapted matrices

In linear algebra, matrices are used to represent linear transformations between vector spaces. This section extends this notion of matrices to a persistent setting. This will simplify working with linear transformations between persistent vector spaces.

Definition 3.14 (adapted matrix). *Let $(S\sigma)$ and (T,τ) be two finite filtered sets. An (S,T)-matrix is called (σ,τ)-**adapted**, if the following condition holds:*

$$\forall s \in S, \forall t \in T : \sigma(s) > \tau(t) \implies a_{st} = 0.$$

By inserting $S = \Sigma_n(M)$ and $T = \Sigma_{n-1}(M)$, we see that the condition for a matrix being adapted is there to assure that the boundary of a simplex appears before the simplex itself.

Proposition 3.15. *Consider the following matrices:*

1. *Let A be a (σ,τ)-adapted (S,T)-matrix.*
2. *Let U be a (σ,σ)-adapted (S,S)-matrix.*
3. *Let V be a (τ,τ)-adapted (T,T)-matrix.*

Then, UAV is a (σ,τ)-adapted (S,T)-matrix too.

Proof. Let $s \in S$ and $t \in T$ be such that $\sigma(s) > \tau(t)$. Since U is (σ,σ)-adapted, it follows that $\forall s' \in S$ with $\sigma(s) > \sigma(s')$, we have that the entry of U corresponding to the row s and the column s' vanishes. Similarly, since A is (σ,τ)-adapted, it follows that $\forall s' \in S$ with $\sigma(s') > \sigma(t)$, we have that the entry of A corresponding to the row s' and the column t vanishes. Hence, the entry of UA corresponding to row s and column t vanishes. Therefore, UA is (σ,τ)-adapted. Analogously we get that AV is (σ,τ)-adapted and thus, we have that UAV is (σ,τ)-adapted too. □

In linear algebra, row operations on matrices corresponds to the multiplication of invertible matrices from the left. Similarly, column operations correspond to the multiplication with invertible matrices from the right. However, row and column operations do not preserve the adaptedness of a matrix in general. Therefore, we define (σ, τ)-adapted row and column operations.

Definition 3.16 ((σ, τ)-adapted row and column operation). *The (σ, τ)-adapted row operations and column operations consists of:*

1. *multiplying any row with a non-zero scalar.*
2. *multiplying any column with a non-zero scalar.*
3. *adding a multiple of $r(s_1)$ to $r(s_2)$ when $\sigma(s_1) \geq \sigma(s_2)$.*
4. *adding a multiple of $c(t_1)$ to $c(t_2)$ when $\tau(t_1) \leq \tau(t_2)$.*

The following corollary justifies the definition of adapted operations.

Corollary 3.17. *Let A be a (σ, τ)-adapted (S, T)-matrix. If a (S, T)-matrix B is obtained by applying finitely many (σ, τ)-adapted row and column operations on A, then there is an invertible (σ, σ)-adapted (S, S)-matrix U and an invertible (τ, τ)-adapted (T, T)-matrix V such that $B = UAV$.*

Proof. We prove this corollary via induction on the number of adapted operations used.
Base case: Let B be the matrix A, where the row corresponding to $s \in S$ is multiplied by $\lambda \in \mathbb{K} \setminus \{0\}$. Let $U = (u_{ij})$ be the (S, S)-matrix with

$$u_{i,j} = \begin{cases} 0 & \text{if } i \neq j \\ \lambda^{-1} & \text{if } r(s) = i = j \\ 1 & \text{otherwise} \end{cases}$$

Then $UB = A$. Since U only has non-zero entries where the row and the column correspond to the same $s \in S$, it follows that U is indeed (σ, σ)-adapted.
Let $\lambda \in \mathbb{K}$ be arbitrary and let $s_1, s_2 \in S$ be such that $\sigma(s_1) \geq \sigma(s_2)$. Let B be the matrix A, where $r(s_1)$ is added λ times to $r(s_2)$. Let $U = (u_{ij})$ be the (S, S)-matrix with

$$u_{i,j} = \begin{cases} 1 & \text{if } i = j \\ -\lambda & \text{if } r(s_2) = i \text{ and } r(s_1) = j \\ 0 & \text{otherwise} \end{cases}$$

Then $UB = A$. Since $\sigma(s_2) \leq \sigma(s_1)$, it follows that U is indeed (σ, σ)-adapted. For the analog column operations, the same reasoning can be applied.
Induction hypothesis: Let $n \in \mathbb{N}$ be arbitrary and let A_n denote the matrix A after performing n adapted operations on it. Then there is an invertible (σ, σ)-adapted (S, S)-matrix U and an invertible (τ, τ)-adapted (T, T)-matrix V such that $A_n = UAV$.

Induction step: Let $n \in \mathbb{N}$ be arbitrary. Consider A_{n+1} to be any matrix that can be obtained by performing $n+1$ adapted operation on A. Furthermore, let A_n denote the matrix where only the first n of these adapted operation are performed. Due to the induction hypothesis, there is an invertible (σ, σ)-adapted matrix U and an invertible (τ, τ)-adapted matrix V such that $A_n = UAV$. Note that A_{n+1} can be obtained by performing one adapted operation on A_n. Assume that, without loss of generality, this is an adapted row operation. Thus, according to the base case, we can find an invertible (σ, σ)-adapted matrix such that $A_{n+1} = U'A_n$. Therefore, we have $A_{n+1} = U'UAV$. Since U and U' are both (σ, σ)-adapted, it follows from Proposition 3.15 that $U'U$ is (σ, σ)-adapted too, proving the claim. □

As a consequence, we can work with adapted matrices and adapted row operations as we are used to from linear algebra. However, when applying a row or column operation, we should never forget to check if the operation is an adapted one. In practice, by ordering the rows and columns of an adapted matrix before performing operations on it, working with it gets much easier, since we know that we can add a row to another one, if and only if it is higher up in the matrix. Another property of matrices in linear algebra is that they can be used to represent linear transformations between vector spaces. In the following propositions, it will become clear that we can find a similar one-to-one correspondence between adapted matrices and linear transformations between two persistent vector spaces.

Proposition 3.18. *Every linear transformation between two finitely generated persistent vector spaces* $f : \{V_{\mathbb{K}}(T, \tau)_r\}_{r \in \mathbb{R}} \to \{V_{\mathbb{K}}(S, \sigma)_r\}_{r \in \mathbb{R}}$ *determines a unique* (σ, τ)*-adapted* (S, T)*-matrix* $A(f)$*.*

Proof. Let $\{f_r : V_{\mathbb{K}}(T, \tau)_r \to V_{\mathbb{K}}(S, \sigma)_r\}_{r \in \mathbb{R}}$ be an arbitrary linear transformation between two finitely generated persistent vector spaces. Since S and T are finite, $R_S := \max\{\sigma(x) \mid s \in S\}$ and $R_T := \max\{\tau(x) \mid x \in T\}$ are finite too. Let R be the bigger of these values. Then $\forall r \geq R$, we have that $V_{\mathbb{K}}(S, \sigma)_r = V_{\mathbb{K}}(S)$ and $V_{\mathbb{K}}(T, \tau)_r = V_{\mathbb{K}}(T)$. Consider the basis $B_{\mathbb{K}}(S) := \{s \in S\}$ of $V_{\mathbb{K}}(S)$ and the basis $B_{\mathbb{K}}(T) := \{t \in T\}$ of $V_{\mathbb{K}}(T)$. Then, following from linear algebra, there is a unique transformation matrix $A(f)$ of f_R with respect to these bases. Hence, for all $t \in T$, we have that $f(t) = \sum_{\{s \in S\}} a_{st} s$.
Let $t \in B_{\mathbb{K}}$ be arbitrary. Clearly, $t \in V_{\mathbb{K}}(T, \tau)_{\tau(t)}$ and $f(t) \in V_{\mathbb{K}}(S, \sigma)_{\tau(t)}$. According to Proposition 3.13, for all $s \in S$ with $\sigma(s) > \tau(t)$, we have that $a_{st} = 0$. Thus, $A(f)$ is (σ, τ)-adapted. □

Proposition 3.19. *Every* (σ, τ)*-adapted* (S, T)*-matrix* A *determines a unique linear transformation between two finitely generated persistent vector spaces* $f_A : \{V_{\mathbb{K}}(T, \tau)_r\}_{r \in \mathbb{R}} \to \{V_{\mathbb{K}}(S, \sigma)_r\}_{r \in \mathbb{R}}$*.*

Proof. Let A be an arbitrary (σ, τ)-adapted (S, T)-matrix. For an arbitrary time $r \in \mathbb{R}$, by expanding linearly, we get a unique linear transformation

$f_r : V_{\mathbb{K}}(T,\tau)_r \to V_{\mathbb{K}}(S,\sigma)_r$, where for $t \in T$ with $\tau(t) \leq r$, we have

$$f_r(t) = \sum_{s \in S} a_{st} s.$$

This sum lies is $V_{\mathbb{K}}(S,\sigma)_r$, since for all non-zero a_{st}, we have $\sigma(s) \leq \tau(t) \leq r$. Let now $r_1 \leq r_2$ be arbitrary. Recall that L_S and L_T are both inclusion maps. Hence

$$f_{r_2} \circ L_T(r_1, r_2) = L_S(r_1, r_2) \circ f_{r_1}$$

and thus, $f_A = \{f_r\}_{r \in \mathbb{R}}$ is a linear transformation between two finitely generated persistent vector spaces. ☐

Proposition 3.20. *There is a one-to-one correspondence between (σ,τ)-adapted (S,T)-matrices A and linear transformation between finitely generated persistent vector spaces $f : \{V_{\mathbb{K}}(T,\tau)_r\}_{r\in\mathbb{R}} \to \{V_{\mathbb{K}}(S,\sigma)_r\}_{r\in\mathbb{R}}$.*

Proof. Let (S,σ) and (T,τ) be two filtered sets. For every linear transformation $g : \{V_{\mathbb{K}}(T,\tau)_r\}_{r\in\mathbb{R}} \to \{V_{\mathbb{K}}(S,\sigma)_r\}_{r\in\mathbb{R}}$, we have that $f_{A(g)} = g$. Similarly, for every (σ,τ)-adapted (S,T)-matrix B, we have that $A(f_B) = B$. Therefore, there is indeed a one-to-one correspondence. ☐

Thanks to this correspondence, we are now able to work with adapted matrices instead of linear transformations. This will ease the computation of kernels and images of linear transformation immensely.

Definition 3.21 (persistent boundary matrix). *The (σ,τ)-adapted matrix determined by a linear transformation between two finitely generated persistent vector spaces is called **persistent boundary matrix**.*

Until now, we have not really discussed finitely presented persistent vector spaces yet. Therefore, we now proceed by investigating the nature of finitely presented persistent vector spaces.

Proposition 3.22. *Let A be a (σ,τ)-adapted (S,T)-matrix. Then*

$$\theta(A) := \{V_{\mathbb{K}}(S,\sigma)_r\}_{r\in\mathbb{R}}/\mathrm{im}(f_A)$$

is a finitely presented persistent vector space. Furthermore, for every finitely presented persistent vector space $\{V_r\}_{r\in\mathbb{R}}$, there is a (σ,τ)-adapted (S,T)-matrix such that $\{V_r\}_{r\in\mathbb{R}} \cong \theta(A)$.

Proof. Since f_A is a linear map between $\{V_{\mathbb{K}}(T,\tau)_r\}_{r\in\mathbb{R}}$ and $\{V_{\mathbb{K}}(T,\tau)_r\}_{r\in\mathbb{R}}$, it follows by definition that θ is finitely presented. Furthermore, as $\{V_r\}_{r\in\mathbb{R}}$ and $\{W_r\}_{r\in\mathbb{R}}$ in the definition of finitely presented vector spaces are finitely generated, we can find two finite filtered sets (S,σ) and (T,τ) such that $\{V_r\}_{r\in\mathbb{R}}$ and $\{W_r\}_{r\in\mathbb{R}}$ are isomorphic to $\{V_{\mathbb{K}}(S,\sigma)_r\}_{r\in\mathbb{R}}$ and $\{V_{\mathbb{K}}(S,\sigma)_r\}_{r\in\mathbb{R}}$. Also, for every g in the definition of finitely presented vector spaces, we can find a (σ,τ)-adapted (S,T)-matrix A with $g = f(A)$. This finishes the proof. ☐

Example 3.23. *Consider the simplicial complex* $M = \{a, b, c, ab, ac, bc\}$*. Let* $S := \Sigma_0(M) = \{a, b, c\}$ *and* $T := \Sigma_1(M) = \{ab, ac, bc\}$ *denote the set of* 0*-dimensional and* 1*-dimensional simplices of* M*. Define* $\sigma : S \to \mathbb{R}$ *such that* $\sigma(a) = \sigma(b) = 0$ *and* $\sigma(c) = 1$*. Furthermore, define* $\tau : T \to \mathbb{R}$ *such that* $\tau(ab) = \tau(ac) = 1$ *and* $\tau(bc) = 2$*. We have that*

$$V_{\mathbb{K}}(S, \sigma)_r = \begin{cases} 0 & \textit{if } r \in (-\infty, 0) \\ \langle a, b\rangle & \textit{if } r \in [0, 1) \\ \langle a, b, c\rangle & \textit{if } r \in [1, \infty) \end{cases}$$

Consider the following (σ, τ)*-adapted matrix:*

$$A = \begin{array}{c} \\ \text{(a,0)} \\ \text{(b,0)} \\ \text{(c,1)} \end{array} \begin{array}{c} \begin{array}{ccc} \text{(ab,1)} & \text{(ac,1)} & \text{(bc,2)} \end{array} \\ \begin{bmatrix} 1 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & 1 \end{bmatrix} \end{array}$$

Using Proposition 3.19, we can get $f_A = \{f_r\}_{r \in \mathbb{R}}$*, where*

1. $f_r(ab) = \begin{cases} a + b & \textit{if } r \geq 1 \\ 0 & \textit{otherwise} \end{cases}$

2. $f_r(ac) = \begin{cases} a + c & \textit{if } r \geq 1 \\ 0 & \textit{otherwise} \end{cases}$

3. $f_r(bc) = \begin{cases} b + c & \textit{if } r \geq 2 \\ 0 & \textit{otherwise} \end{cases}$

Therefore, we have that $\operatorname{im}(f_A) = \{\operatorname{im}(f_r)\}_{r \in \mathbb{R}}$ *with*

$$\operatorname{im}(f_r) = \begin{cases} 0 & \textit{if } r \in (-\infty, 1) \\ \langle a + b, a + c\rangle & \textit{if } r \in [1, 2) \\ \langle a + b, a + c, b + c\rangle & \textit{if } r \in [2, \infty) \end{cases}$$

With this, we can get $\theta(A) = \{V_{\mathbb{K}}(S, \sigma)_r / \operatorname{im}(f_r)\}_{r \in \mathbb{R}}$*, where*

$$V_{\mathbb{K}}(S, \sigma)_r / \operatorname{im}(f_r) \begin{cases} 0 & \textit{if } r \in (-\infty, 0) \\ \frac{\langle a,b\rangle}{0} \cong \langle a, b\rangle & \textit{if } r \in [0, 1) \\ \frac{\langle a,b,c\rangle}{\langle a+b,a+c\rangle} \cong \langle c\rangle & \textit{if } r \in [1, 2) \\ \frac{\langle a,b,c\rangle}{\langle a+b,a+c,b+c\rangle} \cong \langle c\rangle & \textit{if } r \in [2, \infty) \end{cases}$$

Let $\forall r \in \mathbb{R} : M_r$ *be the sub-complex of* M *which consists of all simplices* $s \in \Sigma_0(M)$ *with* $\sigma(s) \leq r$ *and* $t \in \Sigma_0(M)$ *with* $\tau(t) \leq r$*. Then, for all* $r \in \mathbb{R}$*, the dimension of* $V_{\mathbb{K}}(S, \sigma)_r / \operatorname{im}(f_r)$ *is equal to the number of connected components of* M_r*.*

Therefore, θ can represent every finitely presented persistent vector space using an adapted matrix. Similarly to what we already know from linear algebra, the following proposition now gives us an invariance condition for θ.

Proposition 3.24. *Consider the following matrices:*

1. *Let A be a (σ, τ)-adapted (S, T)-matrix.*
2. *Let U be an invertible (σ, σ)-adapted (S, S)-matrix.*
3. *Let V be an invertible (τ, τ)-adapted (T, T)-matrix.*

Then, we have that

$$\theta(A) \cong \theta(UAV).$$

Proof. Following from Proposition 3.15, we get that UAV is (σ, τ)-adapted. Therefore f_{UAV} is a linear transformation between persistent vector spaces. Note that $\mathrm{im}(f_A)$ is the only thing of $\theta(A)$, that depends on A. From linear algebra, we know that the image of A is isomorphic to the image of UAV, since U and V are invertible. Thus, we get that $\theta(A) \cong \theta(UAV)$. $\square$

This result motivates the idea of representing more complicated persistent vector spaces as a direct sum of simpler persistent vector spaces.

3.4 Decomposition theorem

With the results of the previous sections, we are now able to state the decomposition theorem and define persistence diagrams. First, however, we need to define elementary persistent vector spaces.

Definition 3.25 (elementary persistent vector space). *Let $a \in [0, \infty)$ be an arbitrary birth time and let $b \in (0, \infty]$ be an arbitrary death time with $a < b$. For all $r \in \mathbb{R}$, define*

$$P_r := \begin{cases} \mathbb{K} & \text{if } r \in [a, b) \\ 0 & \text{otherwise} \end{cases}$$

For arbitrary $r_1, r_2 \in \mathbb{R}$, define

$$L(r_1, r_2) := \begin{cases} \mathrm{id}_{\mathbb{K}} & \text{if } r_1, r_2 \in [a, b) \\ 0 & \text{otherwise} \end{cases}$$

*Then, $\{P_r\}_{r \in \mathbb{R}}$ together with $\{L(r_1, r_2)\}_{r_1 \leq r_2}$ is a finitely presented persistent vector space called **elementary persistent vector space** on $[a, b)$ and denoted by $P(a, b)$.*

Intuitively, the persistent vector space $P(a, b)$ describes that a homology class is born at time a and dies at time b. We will now see that every finitely presented vector space can be decomposed into elementary persistent vector spaces.

Theorem 3.26 (decomposition theorem). *For every finitely presented persistent vector space* $\{V_r\}_{r\in\mathbb{R}}$*, there are birth times* $a_1, \ldots, a_n \in \mathbb{R}$ *and death times* $b_1, \ldots, b_n \in \mathbb{R}$ *with* $\forall i \in \{1, \ldots, n\} : a_i < b_i$*, such that*

$$\{V_r\}_{r\in\mathbb{R}} \cong \bigoplus_{i=1}^{n} P(a_i, b_i).$$

Furthermore, n *is bounded from above by the number of elements in* S*.*

Proof. Let A be the (σ, τ)-adapted (S, T)-matrix such that $\{V_r\}_{r\in\mathbb{R}} \cong \theta(A)$.
Case 1: Assume that A has at most one entry in every row and every column equal to 1 and every other entry is equal to 0. Let $\{(s_i, t_i) \in S \times T \mid i \in \{1, \ldots, m\}\}$ be the pairs such that $a_{s_i,t_i} = 1$ and let $\{s'_1, \ldots, s'_{n-m}\} = S \setminus \{s_1, \ldots, s_m\}$ be the remaining elements of S. Then, for an arbitrary $r \in \mathbb{R}$ and for all $i \in \{1, \ldots, m\}$ with $\tau(t_i) \leq r$, we have that $f_r(t_i) = s_i$. Thus

$$\theta(A) = \{V_{\mathbb{K}}(S, \sigma)_r\}_{r\in\mathbb{R}}/\mathrm{im}(f_A) \cong \bigoplus_{i=1}^{m} P(\sigma(s_i), \tau(t_i)) \oplus \bigoplus_{i=1}^{n-m} P(\sigma(s'_i), \infty).$$

Case 2: Now let A be arbitrary. According to Proposition 3.24, it suffices to find a (σ, σ)-adapted (S, S)-matrix U and a (τ, τ)-adapted (T, T)-matrix V such that UAV has at most one entry in every row and every column equal to 1 and every other entry is equal to 0. Let $S' := \{s \in S \mid r(s) \neq 0\}$ and let $s' \in S'$ be such that $\forall s \in S' : \sigma(s') \geq \sigma(s)$. Similarly, let $T' := \{t \in T \mid a_{s't} \neq 0\}$ and let $t' \in T'$ be such that $\forall t \in T' : \tau(t') \leq \tau(t)$. Then, for all $s \in S' \setminus \{s'\}$, we can add $r(s')$ to $r(s)$, getting $a_{st'} = 0$. Hence $a_{s't'}$ is the only non-zero entry in $c(t')$. Similarly, for all $t \in T' \setminus \{t'\}$ we can add $c(t')$ to $c(t)$, getting $a_{s't} = 0$. Hence $a_{s't'}$ is the only non-zero entry in $r(s')$. By removing $r(s')$ and $c(t')$ and by iteratively applying this process, we get the statement. $\square$

As usual, when we know about the existence of a decomposition, we are also interested in the uniqueness of it.

Proposition 3.27 (uniqueness of the decomposition). *Let* $\{V_r\}_{r\in\mathbb{R}}$ *be a finitely presented persistent vector space and let* $\bigoplus_{i=1}^{m} P(a_i, b_i)$ *and* $\bigoplus_{i=1}^{n} P(a'_i, b'_i)$ *be two decompositions of* $\{V_r\}_{r\in\mathbb{R}}$*. Then* $m = n$ *and there is a permutation* π *of the set* $\{1, \ldots, n\}$ *such that* $\forall i \in \{1, \ldots, n\} : (a_i, b_i) = (a'_{\pi(i)}, b'_{\pi(i)})$*.*

Proof. We first define

$$a_{\min} := \min\{a_i \mid\in \{1, \ldots, m\}\} \text{ and analogously } a'_{\min} := \min\{a'_i \mid\in \{1, \ldots, n\}\}.$$

Then, we have that $a_{\min} = \min\{r \in \mathbb{R} \mid V_r \neq 0\} = a'_{\min}$. Similarly, define

$$b_{\min} := \min\{b_i \mid a_i = a_{\min}\} \text{ and analogously } b'_{\min} := \min\{b'_i \mid a'_i = a'_{\min}\}.$$

We then have $b_{\min} = \min\{r' \in \mathbb{R} \mid \ker(L(r, r')) \neq 0\} = b'_{\min}$.
This proves that $P(a_{\min}, b_{\min})$ appears in both decompositions. However, note that we did not yet account for multiplicities. To take care of that, we define

$$I := \{i \in \mathbb{N} \mid (a_i, b_i) = (a_{\min}, b_{\min})\} \text{ and } I' := \{i \in \mathbb{N} \mid (a'_i, b'_i) = (a_{\min}, b_{\min})\}.$$

With that, we can now define the sub-persistent vector spaces

$$\{W_r\}_{r\in\mathbb{R}} := \bigoplus_{i\in I} P(a_{\min}, b_{\min}) \text{ and analogously } \{W_r\}_{r\in\mathbb{R}} := \bigoplus_{i\in I'} P(a_{\min}, b_{\min}).$$

We then have that both $\{W_r\}_{r\in\mathbb{R}}$ and $\{W'_r\}_{r\in\mathbb{R}}$ are equal to the nullspace of the following linear transformation:

$$\operatorname{im}(L(a_{\min}, r)) \xrightarrow{L(r,b_{\min})|_{\operatorname{im}(L(a_{\min},r))}} V_{b_{\min}}$$

Thus, $I = I'$ and the multiplicity of $P(a_{\min}, b_{\min})$ is the same in both decompositions. Finally, we have

$$\{V_r\}_{r\in\mathbb{R}}/\{W_r\}_{r\in\mathbb{R}} = \bigoplus_{i=1}^{m} P(a_i, b_i)/\bigoplus_{i\in I} P(a_{\min}, b_{\min}) = \bigoplus_{i\in\{1,\ldots,m\}\setminus I} P(a_i, b_i)$$

$$\{V_r\}_{r\in\mathbb{R}}/\{W'_r\}_{r\in\mathbb{R}} = \bigoplus_{i=1}^{n} P(a'_i, b'_i)/\bigoplus_{i\in I} P(a_{\min}, b_{\min}) = \bigoplus_{i\in\{1,\ldots,n\}\setminus I} P(a_i, b_i)$$

By iteratively applying this procedure, we get the result. □

Therefore, for every persistent vector space, we can get a unique set of birth times and a unique set of death times. These values turn out to be quite useful and are usually represented as a so called barcode or in a so called persistence diagram. For the following, we are particularly interested in the latter one.

Definition 3.28 (persistence diagram). *Let* $\bigoplus_{i=1}^{n} P(a_i, b_i)$ *be the decomposition of a finitely presented persistent vector space* $\{V_r\}_{r\in\mathbb{R}}$*. Then*

$$\{(a_i, b_i) \in \mathbb{R} \times (\mathbb{R} \cup \{\infty\}) \mid i \in \{1, \ldots, n\}\}$$

together with all point on the diagonal with infinite multiplicity is called the ***persistence diagram*** *of* $\{V_r\}_{r\in\mathbb{R}}$*. Furthermore,*

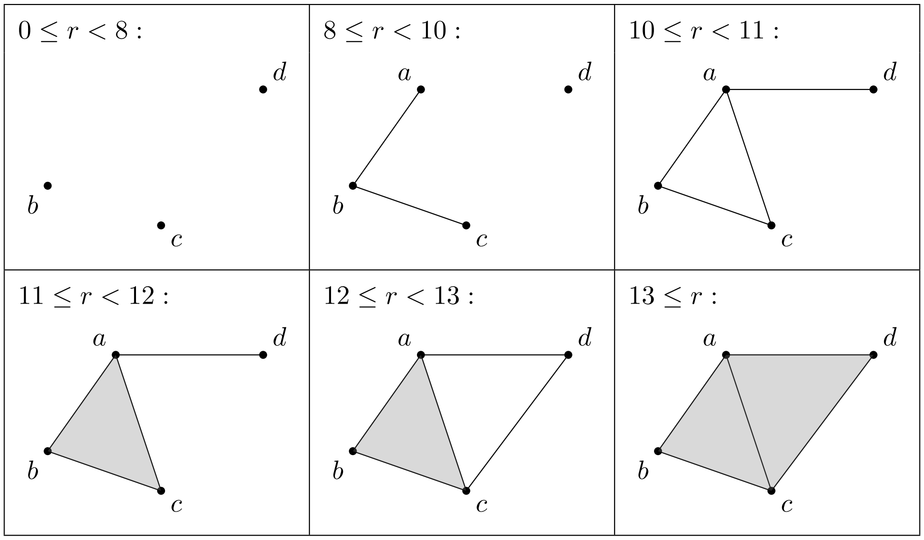
1. $X(S, \sigma)$ *denotes the persistence diagram corresponding to the filtered set* (S, σ)*.*
2. $\mathcal{D}$ *denotes the set of all persistence diagrams.*

Remark. Note that every persistence diagram has only finitely many off diagonal points, since the sum in the decomposition theorem is finite. The number of off diagonal points is bounded from above by the cardinality of the generating set as a direct consequence of the n being bounded in the decomposition theorem.

To compute the persistent homology of a filtration, we can almost use the same algorithm we used to compute the homology of a simplex. However, we can no longer choose the rows and columns in the beginning of the first and the second step arbitrarily. Instead, we choose them according to the time they appear as we did in the proof of the decomposition theorem. In particular, we choose the

rows such that they maximise their appearance time. Similarly, we choose the columns to minimize their appearance time. This ensures that every operation performed in the algorithm is adapted.
The following examples now show this algorithm in action:

Example 3.29. *Consider the following filtration:*



We can get this filtration by taking M to be the last simplicial complex and defining $f : M \to \mathbb{R}$ to take the time value at which the face appears in the subcomplex. We now compute the persistence diagrams $X_0(M, f)$ and $X_1(M, f)$. For that, we first define the boundary matrices.

$$\partial_1 = \begin{array}{c|ccccc|} & \text{(ab,8)} & \text{(bc,8)} & \text{(ac,10)} & \text{(ad,10)} & \text{(cd,12)} \\ \text{(a,8)} & 1 & 0 & 1 & 1 & 0 \\ \text{(b,0)} & 1 & 1 & 0 & 0 & 0 \\ \text{(c,0)} & 0 & 1 & 1 & 0 & 1 \\ \text{(d,0)} & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \partial_2 = \begin{array}{c|cc|} & \text{(abc,11)} & \text{(acd,13)} \\ \text{(ab,8)} & 1 & 0 \\ \text{(bc,8)} & 1 & 0 \\ \text{(ac,10)} & 1 & 1 \\ \text{(ad,10)} & 0 & 1 \\ \text{(cd,12)} & 0 & 1 \end{array}$$

Define $v = ab + ad + bc$ and $w = ab + ad + bc + cd$. We now apply the procedure described above. Observe that a maximises the appearance time of 0-dimensional simplices and ab minimizes the appearance time of 1-dimensional simplices. Therefore, we use the row of ∂_1 corresponding to a to cancel out every further entry in the column corresponding to ab.

$$\begin{array}{cccccc} & (ab,8) & (bc,8) & (ac,10) & (ad,10) & (cd,12) \\ (a+b,8) & 1 & 0 & 1 & 1 & 0 \\ (b,0) & 0 & 1 & 1 & 1 & 0 \\ (c,0) & 0 & 1 & 1 & 0 & 1 \\ (d,0) & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cc} (abc,11) & (acd,13) \\ 1 & 0 \\ 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 1 \end{array}$$

Now, we use the column of ∂_2 *corresponding to a to cancel out every further entry in the row corresponding to a.*

$$\begin{array}{cccccc} & (ab,8) & (bc,8) & (ab+ac,10) & (ab+ad,10) & (cd,12) \\ (a+b,8) & 1 & 0 & 0 & 0 & 0 \\ (a,0) & 0 & 1 & 1 & 1 & 0 \\ (c,0) & 0 & 1 & 1 & 0 & 1 \\ (d,0) & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cc} (abc,11) & (acd,13) \\ 0 & 0 \\ 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 1 \end{array}$$

By repeating this procedure, we transform ∂_1 *into a simple matrix:*

$$\begin{array}{cccccc} & (ab,8) & (bc,8) & (ab+ac,10) & (ab+ad,10) & (cd,12) \\ (a+b,8) & 1 & 0 & 0 & 0 & 0 \\ (b+c,0) & 0 & 1 & 1 & 1 & 0 \\ (c,0) & 0 & 0 & 0 & 1 & 1 \\ (d,0) & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cc} (abc,11) & (acd,13) \\ 0 & 0 \\ 1 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 1 \end{array}$$

$$\begin{array}{cccccc} & (ab,8) & (bc,8) & (\partial abc,10) & (v,10) & (cd,12) \\ (a+b,8) & 1 & 0 & 0 & 0 & 0 \\ (b+c,0) & 0 & 1 & 0 & 0 & 0 \\ (c,0) & 0 & 0 & 0 & 1 & 1 \\ (d,0) & 0 & 0 & 0 & 1 & 1 \end{array} \qquad \begin{array}{cc} (abc,11) & (acd,13) \\ 0 & 0 \\ 0 & 0 \\ 1 & 1 \\ 0 & 1 \\ 0 & 1 \end{array}$$

$$
\begin{array}{c|ccccc|}
 & \text{(ab,8)} & \text{(bc,8)} & (\partial\text{abc,10}) & \text{(v,10)} & \text{(cd,12)} \\
\text{(a+b,8)} & 1 & 0 & 0 & 0 & 0 \\
\text{(b+c,0)} & 0 & 1 & 0 & 0 & 0 \\
\text{(c+d,0)} & 0 & 0 & 0 & 1 & 1 \\
\text{(d,0)} & 0 & 0 & 0 & 0 & 0
\end{array}
\qquad
\begin{array}{|cc|}
\text{(abc,11)} & \text{(acd,13)} \\
0 & 0 \\
0 & 0 \\
1 & 1 \\
0 & 1 \\
0 & 1
\end{array}
$$

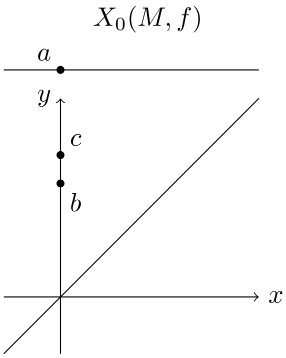
$$
\begin{array}{c|ccccc|}
 & \text{(ab,8)} & \text{(bc,8)} & (\partial\text{abc,10}) & \text{(v,10)} & \text{(w,12)} \\
\text{(a+b,8)} & 1 & 0 & 0 & 0 & 0 \\
\text{(b+c,0)} & 0 & 1 & 0 & 0 & 0 \\
\text{(c+d,0)} & 0 & 0 & 0 & 1 & 0 \\
\text{(d,0)} & 0 & 0 & 0 & 0 & 0
\end{array}
\qquad
\begin{array}{|cc|}
\text{(abc,11)} & \text{(acd,13)} \\
0 & 0 \\
0 & 0 \\
1 & 1 \\
0 & 0 \\
0 & 1
\end{array}
$$

We see that adding the first column of ∂_2 to its second column is adapted:

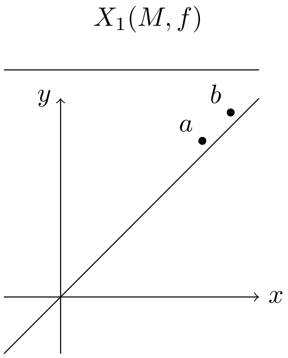
$$
\begin{array}{c|ccccc|}
 & \text{(ab,8)} & \text{(bc,8)} & (\partial\text{abc,10}) & \text{(v,10)} & \text{(w,12)} \\
\text{(a+b,8)} & 1 & 0 & 0 & 0 & 0 \\
\text{(b+c,0)} & 0 & 1 & 0 & 0 & 0 \\
\text{(c+d,0)} & 0 & 0 & 0 & 1 & 0 \\
\text{(d,0)} & 0 & 0 & 0 & 0 & 0
\end{array}
\qquad
\begin{array}{|cc|}
\text{(abc,11)} & \text{(abc+acd,13)} \\
0 & 0 \\
0 & 0 \\
1 & 0 \\
0 & 0 \\
0 & 1
\end{array}
$$

According to the proof of the decomposition theorem, the 1*-dimensional persistent vector space is isomorphic to* $P(10, 11) \oplus P(12, 13)$*. At time* 10*, a loop* ∂abc *is born which gets filled in by* abc *at time* 11*. Similarly, at time* 12*, a second loop* $\partial abcd$ *is born which gets filled in by* $abc + acd$ *at time* 13*.*

Therefore, we have the following persistence diagrams:



$a = (0,\infty), b = (0,8), c = (0,10)$



$a = (10,11), b = (12,13)$

The longer a homology class survives, the more it contributes to the general shape of the point cloud. Therefore, a point of a persistence diagram which is far away from the diagonal represents a more significant topological feature than a point closer to the diagonal.

3.5 Stability

In this section, we state the bottleneck stability theorem. It implies that a small change of a simplicial complex does not cause a massive change in its corresponding persistence diagrams. To even be able to talk about differences of persistence diagrams, we first have to define metrics on the space of persistence diagrams. Let us thus start by defining the Wasserstein distance and the bottleneck distance.

Definition 3.30 (Wasserstein and bottleneck distance). *Let $X, Y \in \mathcal{D}$ be two persistence diagrams. Consider the set of all bijections between X and Y, denoted by Φ. Then, for $p \in \mathbb{N}$, we have that*

$$\mathrm{dist}_p : \mathcal{D}^2 \to \mathbb{K}, (X,Y) \mapsto \inf_{\varphi \in \Phi} \Big(\sum_{x \in X} \|x - \varphi(x)\|_\infty^p \Big)^{\frac{1}{p}}$$

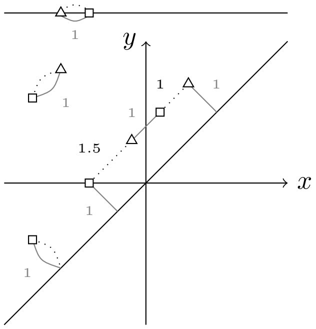
defines a metric on $\mathcal{D}$, called the ***p-Wasserstein distance****. Similarly*

$$\mathrm{dist}_\infty : \mathcal{D}^2 \to \mathbb{K}, (X,Y) \mapsto \inf_{\varphi \in \Phi} (\sup_{x \in X} \|x - \varphi(x)\|_\infty)$$

defines a metric on $\mathcal{D}$, called the ***bottleneck distance****.*

Example 3.31. *Let X and Y be two persistence diagrams.*

Consider the following diagram, where the off-diagonal points of X are represented as triangles and the off-diagonal points of Y are represented as squares. The dotted lines represents a bijection $\varphi \in \Phi$, for which the infimum in the definitions of the Wasserstein distance is reached. Similary, the gray lines represent a bijection $\varphi \in \Phi$ for which the infimum in the definition of the bottleneck distance *is reached. The number next to a line connecting two points is equal to the supremum norm of the difference of them.*



Therefore, we see that:

1. $\mathrm{dist}_p(X,Y) = (4\cdot 1^p + 1.5^p)^{\frac{1}{p}}$
2. $\mathrm{dist}_\infty(X,Y) = 1$

Note that if X and Y have different amounts of points on the additional line representing the persisting homology classes, then both the Wasserstein distance and the bottleneck distance between X and Y are infinite.

In the following proposition, we compare the Wasserstein distance and the bottleneck distance.

Proposition 3.32. *Let $p \in \mathbb{N}$ be an arbitrary integer and let $X, Y \in \mathcal{D}$ be two finite persistence diagrams. Let X^* and Y^* denote the sets of off-diagonal points of X and Y Then:*

$$\mathrm{dist}_p(X,Y) \leq (|X^*| + |Y^*|)\mathrm{dist}_\infty(X,Y).$$

Proof. Let $\varphi \in \Phi_{XY}$ be arbitrary. Then:

$$\begin{aligned}\mathrm{dist}_p(X,Y) &\leq \Big(\sum_{x\in X^*} \|x-\varphi(x)\|_\infty^p + \sum_{y\in Y^*} \|y-\varphi^{-1}(y)\|_\infty^p\Big)^{\frac{1}{p}} \\ &\leq \sum_{x\in X^*} \|x-\varphi(x)\|_\infty + \sum_{y\in Y^*} \|y-\varphi^{-1}(y)\|_\infty \\ &\leq |X^*| \sup_{x\in X^*} \|x-\varphi(x)\|_\infty + |Y^*| \sup_{y\in Y^*} \|y-\varphi^{-1}(y)\|_\infty\end{aligned}$$

As φ was arbitrary, we get that $\mathrm{dist}_p(X,Y) \leq \mathrm{dist}_\infty(X,Y)$. ☐

When we want to use persistence diagrams to represent spaces, it is of at most importance to know that the persistence diagrams of a filtered sets (S,σ_1) and (S,σ_2) are close whenever σ_1 and σ_2 are close. This is the content of the following theorem:

Theorem 3.33 (bottleneck stability theorem). *Let M be a simplicial complex and let $f, g : M \to \mathbb{K}$ be two continuous tame functions. Then, $\forall n \in \mathbb{N}$:*

$$\mathrm{dist}_\infty(X_n(M,f), X_n(M,g)) \leq \|f-g\|_\infty.$$

A proof of the bottleneck stability theorem can be found in [2].

4 Persistent homology transform

The goal of this chapter is to introduce the persistent homology transform, which represents a simplicial complex M as a collection of persistence diagrams. Furthermore, we show that we can use the persistent homology transform to represent shapes. This chapter is based on the article "Persistent homology transform for modeling shapes and surfaces" [5].

4.1 Sublevel sets

In this section, we introduce sublevel sets, which are filtrations depending on the height $r \in \mathbb{R}$ in a given direction $v \in S^{d-1}$. Therefore, we start by defining height functions.

Definition 4.1 (height function). *For a finite simplicial complex $M \subseteq \mathbb{R}^d$ and a direction $v \in S^{d-1}$, the map*

$$h_v : M \to \mathbb{R}, \sigma \mapsto \sup_{x \in \sigma}(x \cdot v)$$

is called the ***height function*** *of M in the direction of v. Here, $\cdot$ denotes the standard inner product on $\mathbb{R}^d$.*

Remark. Due to the convexity of simplices, we have that $\forall \sigma \in M : \exists \sigma' \in \Sigma_0(M)$ such that $h_v(\sigma) = h_v(\sigma')$. Therefore, for every simplex $\sigma \in M$, there is a vertex x of M with $h_v(\sigma) = x \cdot v$.

We see that a height function h_v maps a simplex σ to the smallest height r, where σ is fully contained beneath the height r. Lying beneath r means, that if we rotate our space such that v is pointing in direction e_1, then the first coordinate of every point in σ is smaller or equal to r. Due to the convexity of σ, $h_v(\sigma)$ can be viewed as the height of the highest corner-point of σ or the smallest height for which all vertices contained in σ lie beneath the height r. We already know, that for a dimension $n \in \mathbb{N}$, we can get a filtered set $(\Sigma_n(M), h_v|_{\Sigma_n(M)})$. Therefore, the height function can indeed give us a filtration of a simplicial complex.

Definition 4.2 (sublevel set). *Let M be a simplicial complex, let $v \in S^{d-1}$ be a direction and let $r \in \mathbb{R}$ be arbitrary. Then*

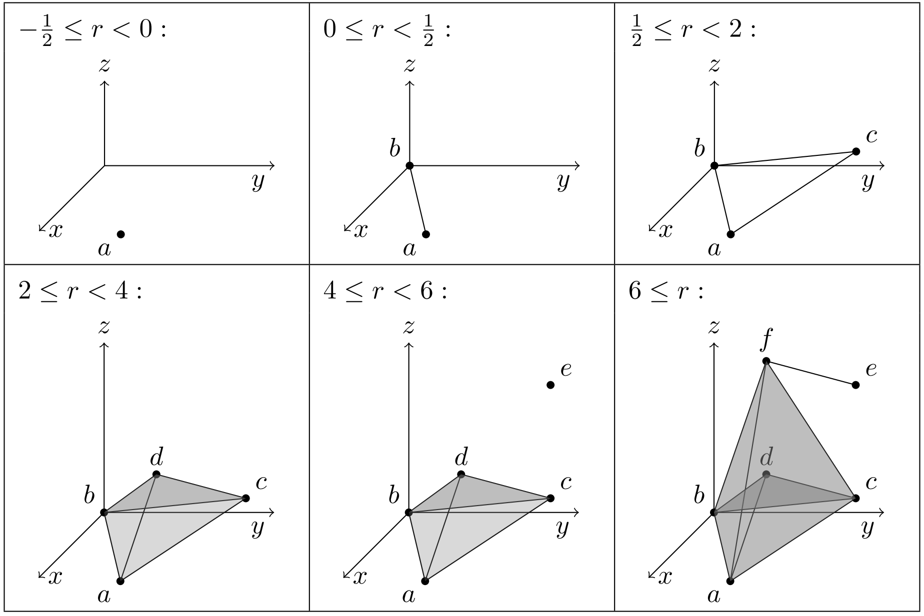
$$M_{h_v}(r) := \{\sigma \in M \mid h_v(\sigma) \leq r\}$$

is called ***sublevel set*** *of M.*

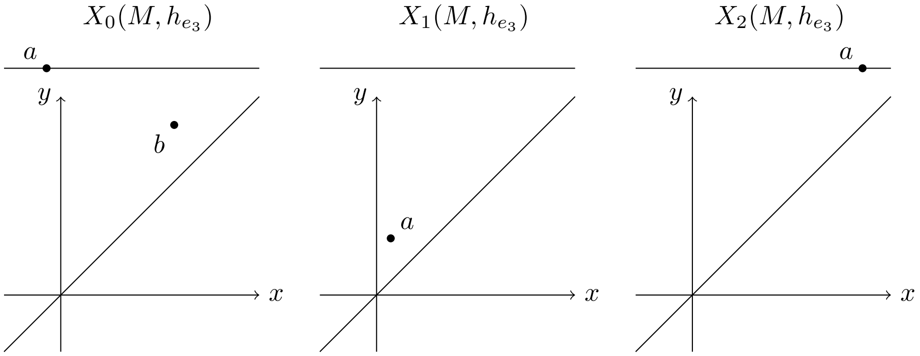
We immediately see that $\{M_{h_v}(r)\}_{r \in \mathbb{R}}$ is a filtration of M, corresponding to the filtered set $(\Sigma_n(M), h_v|_{\Sigma_n(M)})$. Hence, we can compute the persistence diagrams $X_n(M, h_v)$ of this filtrations. Clearly, $X_n(M, h_v)$ depends on the choice of $v \in S^{d-1}$, since for different directions, other parts of the simplicial complex lie beneath a given height.

The following example shows a filtration which corresponds to a simplicial complex and a height function. It illustrates how the homology changes with growing height.

Example 4.3. *Consider the filtration:*



This filtration corresponds to the height function in the direction e_3. By following the same steps as in Example 3.29, we can compute the persistence diagrams of this filtration:



$a = (-\frac{1}{2}, \infty), b = (4, 6)$. $a = (\frac{1}{2}, 2)$. $a = (6, \infty)$.

If we, on the other hand pick the direction to be e_1, the 1-dimensional persistence diagram $X_1(M, h_{e_1})$ is empty and for the direction $-e_3$, we have that $X_0(M, h_{-e_3})$ consists only of the point $(-6, \infty)$.

Using the bottleneck stability theorem, we can now show that the map which links a direction $v \in S^{d-1}$ to the n-dimensional persistence diagram we get from the height function h_v is Lipschitz and hence continuous.

Lemma 4.4. *For all integers $n \in \mathbb{N}$ and for every finite simplicial complex M, the map $S^{n-1} \to \mathcal{D}, v \mapsto X_n(M, h_v)$ is Lipschitz with respect to* $\operatorname{dist}_\infty$ *and* dist_p.

Proof. Let $n \in \mathbb{N}$ be arbitrary. Since M is finite, we have that $\forall i \in \mathbb{N} : \Sigma_i(M)$ is finite too. Hence, for $c_1 := \max\{\|x\|_2 \mid x \in \Sigma_0(M)\}$, we have that $M \subseteq \overline{\mathrm{B}_{c_1}(0)}$. Furthermore, the number of off-diagonal points in any persistence diagram is bounded from above by $c_2 := |\Sigma_n(M)|$. Let $v_1, v_2 \in S^{k-1}$ and $x \in M$ be arbitrary. Then

$$|h_{v_1}(x) - h_{v_2}(x)| = |x \cdot v_1 - x \cdot v_2| \leq \|x\|_2 \|v_1 - v_2\|_2 \leq c_1 \|v_1 - v_2\|_2.$$

Since this inequality holds for all $x \in M$, it also holds for the $x \in M$ which maximizes $|h_{v_1}(x) - h_{v_2}(x)|$. Thus

$$\|h_{v_1} - h_{v_2}\|_\infty \leq c_1 \|v_1 - v_2\|_2.$$

From the bottleneck stability theorem, it follows that

$$\operatorname{dist}_\infty(X_n(M, h_{v_1}), X_n(M, h_{v_2})) \leq c_1 \cdot \|v_1 - v_2\|_2.$$

Thus, the map $v \mapsto X_n(M, h_v)$ is indeed Lipschitz with respect to $\operatorname{dist}_\infty$ and hence continuous. From 3.32, we know $\operatorname{dist}_p(X, Y) \leq 2c_2 \cdot \operatorname{dist}_\infty(X, Y)$. Hence:

$$\operatorname{dist}_p(X, Y) \leq 2c_2 \cdot c_1 \cdot \|v_1 - v_2\|_2.$$

Therefore, the map $v \mapsto X_n(M, h_v)$ is also Lipschitz with respect to dist_p. □

Since for every dimension $n \in \mathbb{N}$ this map is Lipschitz, mapping a direction $v \in S^{d-1}$ to the tuple of all persistence diagrams of dimension less then d is continuous too. This map is called persistent homology transform.

Definition 4.5 (persistent homology transform). *The* ***persistent homology transform*** *of a finite simplicial complex $M \subseteq \mathbb{R}^d$ is the following map:*

$$\operatorname{PHT}(M) : S^{d-1} \to \mathcal{D}^d, v \mapsto (X_0(M, h_v), X_1(M, h_v), \ldots, X_{d-1}(M, h_v)).$$

4.2 Injectivity of the persistent homology transform

In this section we prove that the persistent homology transform of a triangulated object contains every information about the shape of the object.

First, however, we observe that changes in homology only occur at the height of vertices. What we precisely mean with that is stated in this following lemma:

Lemma 4.6. *Let $v \in S^d$ be a direction and let $r \in \mathbb{R}$ be a height. If the sublevel sets $\{\sigma \in M \mid h_v(\sigma) < r\}$ and $\{\sigma \in M \mid h_v(\sigma) \leq r\}$ have different homology, then there is a vertex x of M with $r = x \cdot v$.*

Proof. Let $v \in S^d$ be arbitrary. From the proof of the decomposition theorem, we know that for every dimension $n \in \mathbb{N}$ and every point (a, b) in a persistence diagram $X_n(M, h_v)$, there are simplices $\sigma, \tau \in \Sigma_n(M)$ such that $a = h_v(\sigma)$ and $b = h_v(\tau)$ or $b = \infty$. Hence, if $\forall n \in \mathbb{N}$ and $\forall (a, b) \in X_n(M, h_v)$, we have that $r \neq a$ and $r \neq b$, then we know that $\forall \sigma \in M : h_v(\sigma) \neq r$ and hence:

$$\{\sigma \in M \mid h_v(\sigma) < r\} \text{ and } \{\sigma \in M \mid h_v(\sigma) \leq r\} \text{ have the same homology.}$$

Therefore, if they have different homology, there is a dimension $n \in \mathbb{N}$ and a point $(a, b) \in X_n(M, h_v)$ such that $r = a$ or $r = b$. Furthermore, there is a simplex $\sigma \in \Sigma_n(M)$ such that $r = h_v(\sigma)$. Finally, from the Remark 4.1, we know that there is a vertex x of M, for which we have $r = h_v(\sigma) = x \cdot v$. ☐

Recall that $\mathcal{M}_3^d$ is the set of 3-dimensional simplicial complexes, which are reduced to its simplest form. Now, we prove that the map which links finite simplicial complexes of $\mathcal{M}_3^*$ to its persistent homology transform is injective:

Theorem 4.7. *The map* $\mathcal{M}_3^* \to (S^2 \to \mathcal{D}^3), M \mapsto \mathrm{PHT}(M)$ *is injective.*

Proof. The proof is given as an algorithm which reconstructs a finite simplicial complex M form its persistent homology transform. Since this reconstruction is unique, there cannot be two simplicial complexes in $\mathcal{M}_3^*$ which map to the same persistent homology transform. Therefore, the existence and uniqueness of this reconstruction implies that the map is injective.

Since the proof is quite lengthy, we split it into three steps. In a first step, we introduce some tools and notions to talk about relative homology around vertices. We then proceed by studying the relations between this relative homologies and different links of a simplex in a second step. Finally, we construct two algorithms in a third step, which are able to find the vertices and links of a simplicial complex using its persistent homology transform.

Step 1: Let $x \in M$ be an arbitrary vertex and let $v \in S^2$ be an arbitrary direction. Since h_v has at most finitely many homological critical values, there is a $\delta > 0$ such that h_v has no homological critical value in the open interval $(h_v(x) - \delta, h_v(x))$. Consider the following two sublevel sets:

1. $M(x, v) := M_{h_v}(h_v(x)) = \{\sigma \in M \mid \forall x' \in \sigma : h_v(x') \leq h_v(x)\}$
2. $M(x, v)^- := M_{h_v}(h_v(x) - \delta) = \{\sigma \in M \mid \forall x' \in \sigma : h_v(x') \leq h_v(x) - \delta\}$

From the definition of relative homology, we get the following long exact sequence:

$$\cdots \xrightarrow{\partial_{n+1}} H_n(M(x, v)^-) \xrightarrow{i_n} H_n(M(x, v)) \longrightarrow H_n(M(x, v), M(x, v)^-) \xrightarrow{\partial_n}$$
$$\xrightarrow{\partial_n} H_{n-1}(M(x, v)^-) \xrightarrow{i_{n-1}} H_{n-1}(M(x, v)) \longrightarrow \cdots$$

Here, i_n denotes the inclusion map between $H_n(M(x,v)^-)$ and $H_n(M(x,v))$. It follows that $\forall n \geq 3 : H_n(M(x,v), M(x,v)^-) = 0$ and:

$$\begin{aligned} H_0(M(x,v), M(x,v)^-) &\cong \operatorname{coker}(i_0) \\ H_1(M(x,v), M(x,v)^-) &\cong \ker(i_0) \oplus \operatorname{coker}(i_1) \\ H_2(M(x,v), M(x,v)^-) &\cong \ker(i_1) \oplus \operatorname{coker}(i_2) \end{aligned}$$

Now let us consider the Betti numbers $\tilde{\beta}_n(x,v) := \dim H_n(M(x,v), M(x,v)^-)$. Then, we have that $\forall n \geq 3 : \tilde{\beta}_n(x,v) = 0$ and:

$\tilde{\beta}_0(x,v)$ is equal to the number of points in $X_0(M,h_v)$ born at time $h_v(x)$.

$\tilde{\beta}_1(x,v)$ is equal to the number of points in $X_0(M,h_v)$ dying at time $h_v(x)$ plus the number of points in $X_1(M,h_v)$ born at time $h_v(x)$.

$\tilde{\beta}_2(x,v)$ is equal to the number of points in $X_1(M,h_v)$ dying at time $h_v(x)$ plus the number of points in $X_2(M,h_v)$ born at time $h_v(x)$.

Note that the points in the persistence diagrams are counted with multiplicity. Consider the change in the Euler characteristic from $M(x,v)^-$ to $M(x,v)$, namely

$$\tilde{\chi}(x,v) := \tilde{\beta}_0(x,v) - \tilde{\beta}_1(x,v) + \tilde{\beta}_2(x,v).$$

Step 2: Suppose we know the set of vertices $\Sigma_0(M)$. Let $x \in \Sigma_0(M)$ be an arbitrary vertex. From now on, we only consider essential edges. Essential edges are edges, which appear in every representation of M in its reduced form. For example, the boundary edges of a square are essential, but the diagonal is not.

Without loss of generality, translate M such that x is the origin.

Assume that x is isolated. This means that $\mathrm{Lk}(x) = \emptyset$ or equivalently that there is no edge in M containing x. We then have that for all directions $v \in S^2$, an H_0-class is born at height $h_v(x)$. Furthermore, x does not contribute to any other change in homology.

Assume that x is not isolated. Let e be an oriented edge out of x. Then, for a direction $v \in S^2$ with $e \cdot v < 0$, where x is the only vertex at height $h_v(x)$, there is no H_0-class being born at height $h_v(x)$. This is because e is contained in $M(x,v)$ and thus connects x to $M(x,v)^-$.

Hence x being isolated is equivalent to the condition that $\forall v \in S^2$, an H_0 class is born at height $h_v(x)$. With this, we can find all isolated vertices knowing the PHT. Thus, let from now on $x \in \{x_1, \ldots, x_m\}$ be a non-isolated vertex and let e be an edge out of x.

Without loss of generality, rotate M such that e is pointing to the north pole and let $u \in S^2$ denote this direction.

Let $S(e) := \{w \in S^2 \mid w \cdot u = 0\}$ denote the set of all directions perpendicular to e. Note that the directions in $S(e)$ are the directions pointing to the equator of the sphere. Let $v \in S(e)$ be arbitrary. Define $S(e, v) \coloneqq \{w \in S(e) \mid w \cdot v < 0\}$. This is the semicircle pointing away from v. Furthermore, define $L(e)$ to be the projection of the link of e onto the plane perpendicular to e. Let $N(e) \subseteq S(e)$ denote the set of directions in which there is at least a point in $L(e)$. Now consider the function $f_e : S(e) \to \mathbb{N}$, where a direction v gets mapped to the number of connected components in $N(e) \cap S(e, v)$. We observe the following:

0. Assume $f_e(v) = 0$. This means that $\mathrm{Lk}(e) \cap M(x, v) = \emptyset$ or equivalently that there is no face in $M(x, v)$ containing e. For $w \in S^2$ lying in the southern hemisphere, the edge e does not contribute a path to M_x^-.

   (a) If x is connected to $M(x, w)^-$, then there is no change in homology at height $h_w(x)$.

   (b) If x is not connected in $M(x, w)$, then there is a H_0-class being born and no other changes in homology at height $h_w(x)$.

   For $w \in S^2$ lying in the northern hemisphere, we have that e contributes a path from x to $M(x, w)^-$.

   (a) If x is connected to $M(x, w)^-$, then the addition of e causes either the birth of a H_1-class or the death of a H_0-class at height $h_v(x)$.

   (b) If x is not connected in $M(x, w)$, then the addition of e causes no change in homology at height $h_v(x)$.

   Hence, either $\tilde{\beta}_0(x, w)$ decreases by one or $\tilde{\beta}_1(x, w)$ increases by one when we pass a direction w with the same longitude as v through the equator. Therefore, passing though v from north to south decreases the relative Euler characteristic by one.

1. Assume $f_e(v) = 1$. Then, passing a direction w though v from north to south does not change $\tilde{\chi}(x, w)$. This is because a part of the link is already contained in the sublevel set $M(x, w)^-$, when w is of the same longitude as v.

2. Assume $f_e(v) = 2$. Then, passing though the equator with a direction w of the same longitude as v either increases $\tilde{\beta}_2(x, w)$ by one or decreases $\tilde{\beta}_1(x, w)$ by one. The first case corresponds to when two already connected components join in x and the second when the two components were not jet connected. Finally, we see that by passing though v from north to south increases the relative Euler characteristic by one.

k. Assume $\exists k \in \mathbb{N}$ with $k \geq 2$ such that $f_e(v) = k$. Then passing a direction w though v from north to south increases $\tilde{\chi}(x, w)$ by $k - 1$. This is as we can generalize the case of 2 for arbitrary k. We define a graph G. For each of the k connected component of $S(e, v) \cap N(e)$, we add a vertex to G. Two vertices are connected, if there is a face containing x in M between the connected components corresponding to the vertices. Then, the connected components of G represent the second case and we see that $\tilde{\beta}_1$ decreases by the number of connected components minus one. Furthermore, for every connected component,$\tilde{\beta}_2$ is increased by the number of vertices inside it minus one. For every combination of connected components the graph G can have, the change of $\tilde{\beta}_2 - \tilde{\beta}1$ stays the same, namely as an increase of $k-1$. Therefore, by passing though v from north to south increases the relative Euler characteristic by $k-1$.

Thus, by knowing the changes in homology, we can reconstruct f_e. Furthermore, since we only considered essential edges, there is at least one direction for which the number of components different from 1. Hence it follows that the inclusion of every vertex x causes a change in homology.

Step 3: With this observations, we are now able to give an algorithm to find all the vertices of M and an algorithm to find their links by knowing the persistent homology transform of M:

Finding vertices: Knowing the persistent homology transform of M, by repeatedly applying the following four steps, we can find all the vertices of M.

1. Choose a dimension $n \in \{0,1,2\}$ and a direction $v \in S^2$ such that $X_n(M, h_v)$ is non-empty. Furthermore, choose a point $(a_v, b_v) \in X_n(M, h_v)$.
2. Since $S^2 \to \mathcal{D}, v \mapsto X_n(M, h_v)$ is continuous, we can find a $r > 0$ such that $\forall u \in \mathrm{B}_r(v) \cap S^2 : \exists (a_u, b_u) \in X_n(M, u)$ with the property that the map $\mathrm{B}_r(v) \cap S^2 \to \mathbb{R}^2, u \mapsto (a_u, b_u)$ is continuous.
3. If there is a $r' \in \mathbb{R}$ with $0 < r' \leq r$ and a point $x' \in \mathbb{R}^3$ such that $\forall u \in \mathrm{B}_{r'}(v) : a_u = h_u(x')$, then x' is a vertex of M.
4. If there is a $r' \in \mathbb{R}$ with $0 < r' \leq r$ and a point $x' \in \mathbb{R}^3$ such that $\forall u \in \mathrm{B}_{r'}(v) : b_u = h_u(x')$, then x' is a vertex of M.

From 4.6, step (3) and step (4) follow immediately. Step (3) accounts for homology classes being born at time $h_u(x)$ and Step (4) accounts for homology classes dying at time $h_u(x)$. Since the inclusion of every vertex causes at least a change in a persistence diagram, we can truly find all the vertices with this algorithm.

Finding links: First, we choose a direction $v_0 \in S^2$ such that $\forall x_1, x_2 \in V(M) : h_{v_0}(x_1) \neq h_{v_0}(x_2)$. This condition means that v_0 is a direction for which all vertices lie on a different height. Let now $\{x_1, \ldots, x_m\} = \Sigma_0(M)$ with $\forall i \in \{1, \ldots, m-1\} : h_{v_0}(x_i) \leq h_{v_0}(x_{i+1})$ be an ordering of the set of vertices. By repeatedly applying the following steps and increasing i after every iteration, we can fully determine the link of every simplex in M.

1. Notice that, at the i-th step, we know the sublevel set $M(x_i, v_0)$. Consider $S^2 \to \mathbb{Z}, v \mapsto \tilde{\chi}(x, v)$. This is the partition of the sphere of directions into regions with the same relative homology at height of x. Consider a great circle and the direction $v \in S^2$ perpendicular to the great circle with $v \cdot v_0 > 0$. Then, there is an edge in direction v or $-v$. Such a v exist, since

there is always a $w \in S^2$ perpendicular to a great circle and if $w \cdot v_0 < 0$, then we can just take $-w$. Also $w \cdot v_0 = 0$ will not happen since then we would have an edge in direction w or $-w$, which would imply that there are two vertices at height $h_{v_0}(x_i)$.

2. If there is no edge in $M(x_i, v_0)$ out of x in direction $-v$, then there must be an edge out of x in direction v. Furthermore, with f_e we get the link of e.

3. If there is an edge e' in $M(x_i, v_0)$ out of x in direction $-v$, then we have to investigate $f_{e'}$ and f_e. If $f_{e'} = f_e$ then every change in homology can be attributed to e' and hence there is no edge in direction v. Otherwise, there is such an edge. Furthermore, with $f_e - f_e'$, we get the link of e.

□

Now consider the case where domain is the set of finite simplicial complexes in $\mathbb{R}^2$. It is possible to state a similar proof as in the 3-dimensional case, however, we can also think about the two dimensional Euclidean space as lying inside the three dimensional Euclidean space.

Theorem 4.8. *The map* $\mathcal{M}_2 \to (S^1 \to \mathcal{D}^2), M \mapsto \mathrm{PHT}(M)$ *is injective.*

Proof. Consider $R^2 = \{(a, b, 0) \in \mathbb{R}^3\}$ and $S^2 = \{(v_1, v_2, 0) \in S^3\}$. Hence we can think of $\mathcal{M}_2$ as lying inside $\mathcal{M}_3$. Let thus $M \in \mathcal{M}_2$ be a simplicial complex in $\mathbb{R}^3$. Note that, for all vertices x of M, we have that $x \cdot e_3 = 0$. Let $v = (v_1, v_2, v_3) \in S^2 \setminus \{-e_3, e_3\}$ be a direction in $\mathbb{R}^3$ which is not perpendicular to the plane on which M is lying. Now consider:

$$w = (w_1, w_2, 0) = \frac{1}{\sqrt{v_1^2 + v_2^2}}(v_1, v_2, 0) \in S^2.$$

Then, w is the unit vector in direction $(v_1, v_2, 0)$. Let $\sigma \in M$ be arbitrary. Observe:

$$h_v(\sigma) \leq r \iff \forall (x_1, x_2, x_3) \in \sigma : (x_1, x_2, x_3) \cdot (v_1, v_2, v_3) \leq r.$$

Since for all $(x_1, x_2, x_3) \in \sigma$, we have that $x_3 = 0$, we get:

$$h_v(\sigma) \leq r \iff \forall (x_1, x_2, 0) \in \sigma : (x_1, x_2, 0) \cdot (v_1, v_2, 0) \leq r.$$

Furthermore, we see:

$$h_v(\sigma) \leq r \iff \forall (x_1, x_2, 0) \in \sigma : (x_1, x_2, 0) \cdot (w_1, w_2, 0) \leq \frac{r}{\sqrt{v_1^2 + v_2^2}}.$$

Finally, we have that $h_v(\sigma) \leq r \iff h_w(\sigma) \leq \frac{r}{\sqrt{v_1^2+v_2^2}}$ and:

$$M_{h_v}(r) = M_{h_w}(\frac{r}{\sqrt{v_1^2 + v_2^2}}).$$

Therefore, from knowing $X_0(M, w)$ and $X_1(M, w)$, we can get $X_0(M, v)$ and $X_1(M, v)$. Finally, we know that $X_n(M, e_3)$ and $X_n(M, -e_3)$ only consist of the point $(0, \infty)$ with multiplicity equal to $\dim(H_n(M))$.

Let $M, M' \in \mathcal{M}_2$ be two simplicial complexes. Notice that $\forall v \in S^2$, we clearly have that $X_2(M, h_v) = X_2(M', h_v) = \emptyset$.

Assume that $\forall w \in S^1 : X_0(M, h_w) = X_0(M', h_w)$ and $X_1(M, h_w) = X_1(M', h_w)$. The observation from above then yields, that for all directions $v \in S^2$, we have:

1. $X_0(M, h_v) = X_0(M', h_v)$
2. $X_1(M, h_v) = X_1(M', h_v)$
3. $X_2(M, h_v) = X_2(M', h_v)$

From the injectivity of the4.7, we then get that $M = M'$. Therefore, the map $\mathcal{M}_2 \to (S^1 \to \mathcal{D}^2), M \mapsto \mathrm{PHT}(M)$ is indeed injective. ☐

Finally, we want to give a proof for the 1-dimensional case. Notice, since S^0 consists of two separate points, this proof does not use any continuity arguments. Nevertheless, the injectivity is quite a simple observation.

Theorem 4.9. *The map* $\mathcal{M}_1 \to (S^0 \to \mathcal{D}^1), M \mapsto \mathrm{PHT}(M)$ *is injective.*

Proof. First note that 1 and -1 are the only two directions. Also note that every point in the persistence diagram has second coordinate equal to ∞. First, let $x_1, \ldots, x_m \in \mathbb{R}$ with $x_1 < \ldots < x_m$ be such that

$$H_0(M, h_1) = \{(x_i, \infty) \mid i \in \{1, \ldots, m\}\}.$$

Now let $y_1, \ldots, y_m \in \mathbb{R}$ with $y_1 < \ldots < y_m$ be such that

$$H_0(M, h_{-1}) = \{(-y_i, \infty) \mid i \in \{1, \ldots, m\}\}.$$

Then $M = [x_1, y_1] \cup \ldots \cup [x_m, y_m]$. This is because walking in direction 1, we find the beginning of all the connected components and walking in direction -1, we find the end of all the connected components. Note that m is equal to the number of connected components of M. Furthermore, if $x_i = y_i$, then x_i is an isolated vertex. ☐

It is conjectured, that the map $\mathcal{M}_d \to (S^{d-1} \to \mathcal{D}^d), M \mapsto \mathrm{PHT}(M)$ is injective for all dimension $d \in \mathbb{N}$.

4.3 Euler characteristic curve transform

The goal of this section is to construct a third transform, the so-called Euler characteristic curve transform. For that we start by generalizing the Euler characteristic [4] to the d-dimensional case.

Definition 4.10 (Euler characteristic). *Let M be a finite simplicial complex in $\mathbb{R}^d$. Then*

$$\chi(M) := \sum_{i=1}^{d} (-1)^i \cdot |\Sigma_i(M)|$$

is called the ***Euler characteristic*** *of M.*

We see that for $d = 3$, we get the usual Euler characteristic, which is known to describe the topology of a shape quite well in a single number. Furthermore, the Euler characteristic is linked to the theory of homology in the following way:

Theorem 4.11. *Let M be a finite simplicial complex in $\mathbb{R}^d$. Then*

$$\chi(M) = \sum_{i=1}^{n} (-1)^i \cdot \dim(H_i(M)).$$

A proof of this theorem can be found in [4].

This now motivates us to define the Euler characteristic curve transform.

Definition 4.12 (Euler characteristic curve transform). *Let $M \subseteq \mathbb{R}^d$ be a finite simplicial complex. For a direction $v \in S^{d-1}$, define*

$$\chi(M, h_v) : \mathbb{R} \to \mathbb{Z}, r \mapsto M_{h_v}(r).$$

Then, the Euler characteristic curve transform of M is the following map:

$$\mathrm{ECT}(M) : S^{d-1} \to (\mathbb{R} \to \mathbb{Z}), v \mapsto \chi(M, h_v).$$

Since we can get the Euler characteristic curve transform from knowing the persistent homology transform, it appears, that the Euler characteristic curve transform is weaker than the persistent homology transform. However, from the proof of Theorem 4.7, it follows that for $d \leq 3$, the Euler characteristic curve transform suffices to reconstruct a triangulation.

Thus, the following proposition is a direct consequence from the proof of 4.7.

Proposition 4.13. *For $d \in \{1, 2, 3\}$, the map $\mathcal{M}_d \to (\mathbb{R} \to \mathbb{Z}), M \mapsto \mathrm{ECT}(M)$ is injective.*

4.4 0-dimensional persistent homology transform

In this section, we observe that for simplicial complexes M which are homeomorphic to a circle or a sphere, the 0-dimensional persistence diagrams already contain the whole information needed for the persistent homology transform of M:

Proposition 4.14. *Let $v \in S^1$ be an arbitrary direction and let $M \subseteq \mathbb{R}^2$ be a simplicial complex which is homeomorphic to S^1. Then, we can construct $X_1(M, h_v)$ from knowing $X_0(M, h_{-v})$.*

Proof. Since M is homeomorphic to a circle, we know that there is exactly one H_0-class in $H_0(M)$ and that there is exactly one H_1-class in $H_1(M)$. This means that for every direction $w \in S^1$, there is exactly one point in $X_0(M, h_w)$ that never dies and there is exactly one point in $X_1(M, h_w)$ that never dies. Furthermore, $X_1(M, h_v)$ only consists of this one point that never dies. Let thus (a, ∞) be this point. Let $(b, c) \in X_0(M, h_{-v})$ be the left most point in the 0-dimensional persistence diagram. This means that the first coordinate of every other point in $X_0(M, h_{-v})$ is greater or equal to b. Then, we have $a = -b$, since the height where the H_1-class is born is the height where M ends. This height however is exactly minus the height in opposite direction where M starts. ☐

Proposition 4.15. *Let $v \in S^2$ be an arbitrary direction and let $M \subseteq \mathbb{R}^3$ be a simplicial complex which is homeomorphic to S^2. Then, we can construct $X_2(M, h_v)$ and $X_1(M, h_v)$ from knowing $X_0(M, h_{-v})$.*

Proof. Since M is homeomorphic to a sphere, we know that there is exactly one H_0-class in $H_0(M)$, there in no H_1-class in $H_1(M)$ and that is exactly one H_2-class in $H_2(M)$ too. Hence, for every direction $w \in S^1$, there is exactly one point in $X_0(M, h_w)$, no point in $X_1(M, h_w)$ and exactly one point again in $X_2(M, h_w)$ that never dies. Furthermore, $X_2(M, h_v)$ only consists of this one point that never dies. Let thus (a, ∞) be this point. Let $(b, c) \in X_0(M, h_{-v})$ be the left most point in the 0-dimensional persistence diagram. This means that the first coordinate of every other point in $X_0(M, h_{-v})$ is greater or equal to b. Then, we have $a = -b$, since the height where the H_2-class is born is the height where M ends. This height however is exactly minus the height in opposite direction where M starts. Let $(a, b) \in H_0(M, h_{-v})$ be a point with $a < b < \infty$. Then, $(-b, -a) \in H_1(M, h_{-v})$. This is because the connected component we find in on direction is exactly the part missing to fill in the hole. ☐

This motivates us to define the so-called 0-dimensional persistent transform.

Definition 4.16. *The 0-th dimensional persistence homology transform of a finite simplicial complex M is the following map:*

$$\mathrm{PHT}_0\mathrm{T}(M) : S^d \to \mathcal{D}, v \mapsto X_0(M, h_v).$$

If M is isomorphic to S^1 or S^2, then it follows immediately from Proposition 4.14, Proposition 4.15 and Theorem 4.7, that the map linking M to its 0-dimensional persistent homology transform is injective as well.

4.5 Using the PHT to distinguish bones

This section shows how we can use the persistent homology transform to differentiate shapes.
The following proposition shows how we can use a metric on persistence diagrams to measure distances between simplicial complexes. This will then allow us to find differences of triangulations by comparing their persistent homology transform.

Proposition 4.17. *For an integer* $d \in \{1, 2, 3\}$*,*

$$\mathrm{dist}_{\mathcal{M}_d} : \mathcal{M}_d^2 \to \mathbb{K}, (M_1, M_2) \mapsto \sum_{i=0}^{d} \int_{S^{d-1}} \mathrm{dist}_1(X_i(M_1, h_v), X_i(M_2, h_v))dv$$

defines a metric on $\mathcal{M}_d$*.*

Proof. Identity property: Let $M_1, M_2 \in \mathcal{M}_d$ be arbitrary. It follows directly from the injectivity of $\mathcal{M}_3 \to (S^2 \to \mathcal{D}^3), M \mapsto \mathrm{PHT}(M)$, that:

$$M_1 = M_2 \iff \mathrm{PHT}(M_1) = \mathrm{PHT}(M_2).$$

From the definition of PHT, we get

$$\mathrm{PHT}(M_1) = \mathrm{PHT}(M_2) \iff \forall v \in S^d, \forall i \in \{0, \dots, d\} : X_i(M_1, h_v) = X_i(M_2, h_v).$$

As dist_1 is a metric on $\mathcal{D}$, we have $\forall v \in S^d, \forall i \in \{0, \dots, d\}$:

$$X_i(M_1, h_v) = X_i(M_2, h_v) \iff \mathrm{dist}_1(X_i(M_1, h_v), X_i(M_2, h_v)) = 0.$$

Furthermore, dist_1 is continuous and non-negative. Therefore, $\forall i \in \{0, \dots, d\}$, the following are equivalent:

1. $\forall v \in S^{d-1} : \mathrm{dist}_1(X_i(M_1, h_v), X_i(M_1, h_v)) = 0$
2. $\int_{S^{d-1}} \mathrm{dist}_1(X_i(M_1, h_v), X_i(M_1, h_v))dv = 0$

Since integrals of non-negative continuous functions vanish if and only if the function itself vanishes, the following are equivalent as well:

1. $\forall i \in \{1, \dots, d\} : \int_{S^{d-1}} \mathrm{dist}_1(X_i(M_1, h_v), X_i(M_1, h_v))dv = 0$
2. $\mathrm{dist}_{\mathcal{M}_d}(M_1, M_2) = 0$

Thus, $\mathrm{dist}_{\mathcal{M}_d}$ indeed satisfies the identity property. *Symmetry:* Let $M_1, M_2 \in \mathcal{M}_d$ be arbitrary. Since $\forall i \in \{1, \dots, d\}, \forall v \in S^d : \mathrm{dist}_1(X_i(M_1, h_v), X_i(M_2, h_v))$ is symmetric, $\mathrm{dist}_{\mathcal{M}_d} M_1, M_2$ is symmetric too.

Triangle inequality: Let $M_1, M_2, M_3 \in \mathcal{M}_d$ be arbitrary. Since dist_1 fulfills the triangle inequality and due to monotonicity and additivity of integrals, we get

$$\begin{aligned}
\operatorname{dist}_{\mathcal{M}_d}(M_1, M_3) &= \sum_{i=0}^{d} \int_{S^{d-1}} \operatorname{dist}_1(X_i(M_1, h_v), X_i(M_3, h_v))dv \\
&\leq \sum_{i=0}^{d} \int_{S^{d-1}} \sum_{j=1}^{2} \operatorname{dist}_1(X_i(M_j, h_v), X_i(M_{j+1}, h_v))dv \\
&= \sum_{j=1}^{2} \sum_{i=0}^{d} \int_{S^{d-1}} \operatorname{dist}_1(X_i(M_j, h_v), X_i(M_{j+1}, h_v))dv \\
&= \operatorname{dist}_{\mathcal{M}_d}(M_1, M_2) + \operatorname{dist}_{\mathcal{M}_d}(M_2, M_3).
\end{aligned}$$

Therefore, $\operatorname{dist}_{\mathcal{M}_d}$ indeed defines a metric on $\mathcal{M}_d$. $\square$

Since there are uncountable many directions, the image of the persistent homology transform consists of uncountable many persistence diagrams. Thus, it is not possible to compute the persistent homology transform of a simplicial complex in finite time. However, by sampling a finite number of directions $v_1, \ldots, v_k \in S^{d-1}$, we can approximate the actual value close enough. Therefore, consider

$$\operatorname{dist}^*_{\mathcal{M}_d} : \mathcal{M}_d^2 \to \mathbb{K}, (M_1, M_2) \mapsto \frac{1}{k} \sum_{i=1}^{d} \sum_{j=1}^{k} \operatorname{dist}_1(X_i(M_1, h_{v_j}), X_i(M_2, h_{v_j})).$$

Since $v \mapsto X_n(M, h_v)$ and dist_1 are both continuous, we see that for sampling more and more direction, $\operatorname{dist}^*_{\mathcal{M}_d}$ approximates $\operatorname{dist}_{\mathcal{M}_d}$ better and better.

Katharine Turner, Sayan Mukherjee and Doug M. Boyer use $\operatorname{dist}^*_{\mathcal{M}_d}$ to compare the shapes of heel bones from extant and extinct primates in the paper "Persistent homology transform for modeling shapes and surfaces" [5].

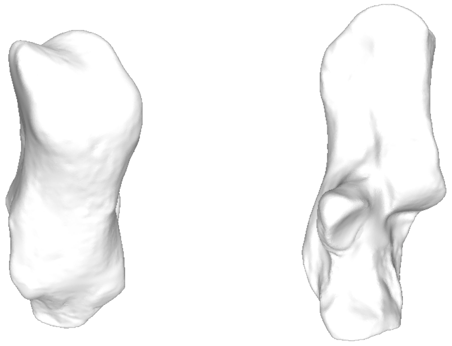


Figure 7: Scan of a heel bone, viewed from the front and the back. (Source [5])

The data they worked with consist of microCT scans from 106 heel bones called calcanei. Some of these heel bones originate from the extinct primate species Adapiforms, Omomyiforms and Parapithecids. The other bones originate from Cercopithecoids, Hominoids, Platyrrhines and Strepsirrhines, which are extant species of primates. These scans were then approximated with finite simplicial complexes $M_1, \ldots, M_{106}$ and aligned automatically.

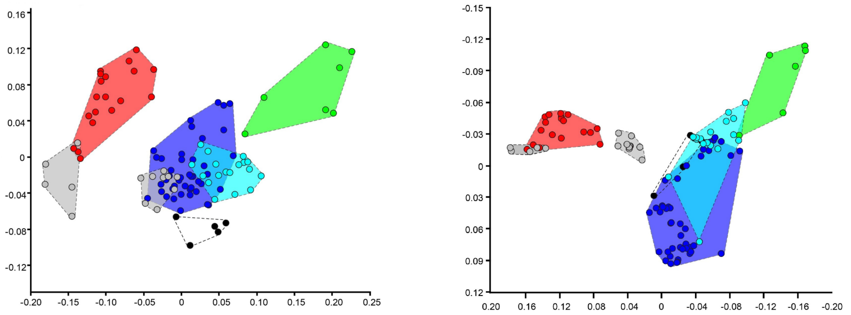
Then, they subdivided a regular icosahedron to get 162 evenly spaced directions $v_1, \ldots, v_{162} \in S^2$. In particular, they split all 20 of its faces into 16 smaller equilateral triangles by subdividing each of its 30 edges into 4 segments of equal length. This procedure adds 3 new vertices to every edge and 3 additional vertices to each face, excluding those that lie on one its three boundary edges. Therefore, the subdivision has 162 evenly spaced vertices, which are used as the sampled directions.

With them, they computed $\forall i, j \in \{1, \ldots, 106\}$ the distance $\operatorname{dist}^*_{\mathcal{M}_3}(M_i, M_j)$ between the two bones belonging to M_i and M_j. Finally, they generated three multidimensional scaling plot to visualise the clusters of similar bones.

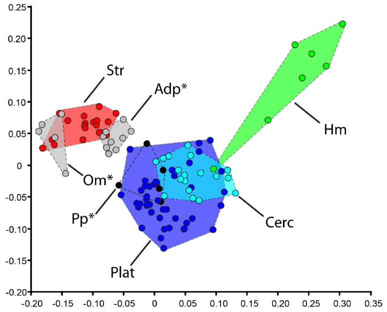
1. For the first plot, they measures the distances between bones by comparing 27 landmark points, which were manually placed on every bone.
2. For the second plot, they compared 1000 automatically positioned pseudo-landmarks to measure the distances between bones.
3. For the third plot, they used the distances $\operatorname{dist}^*_{\mathcal{M}_3}(M_i, M_j)$ from above ass distances between the bones.

1. Manually placed landmarks:

2. Automatically placed landmarks:



3. Persistent homology



Adp:	Adapiforms
Cerc:	Cercopithecoids
Hm:	Hominoids
Om:	Omomyiforms
Pp:	Parapithecids
Plat:	Platyrrhines
Str:	Strepsirrhines

Figure 8: Phenetic clusterings of phylogenetic groups of primate heel bones. (Source [5])

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