Algebraic and Topological Persistence

by

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Abstract

This work will begin with a brief introduction, inspired by an applied context that has provided the foundation for this thesis. A substantial proportion of research in persistence theory has been conducted with the objective of applying persistent homology for the analysis of empirically-derived data. Nevertheless, we will adhere strictly to the theory of topological spaces and restrict ourselves to the provision of illustrative contexts for applications. This treatise addresses the theory of topological spaces (2) and the foundations of persistence theory (3). The subsequent discussion will address chain complexes (2.3.4) and the associated simplicial homology groups (2.2), as well as their relationship with singular homology theory (2.3). Moreover, we present the fundamental concepts of algebraic topology, including exact and short exact sequences (2.3.2) and relative homology groups derived from quotienting with subspaces of a topological space (2.4). These tools are used to prove the Excision Theorem (2.5) in algebraic topology. Subsequently, the theorem is applied to demonstrate the equivalence of simplicial and singular homology for triangulable topological spaces, i.e. those topological spaces which admit a simplicial structure (2.6). This enables a more general theory of homology to be adopted in the study of filtrations of point clouds.

The chapter on homological persistence (3) makes use of these tools throughout. We develop the theory of persistent homology (3.2.1), the homology of filtrations of topological spaces (3.1), and the corresponding dual concept of persistent cohomology (3.2.2, 3.3). In conclusion, we generalise both theories into the framework of zigzag persistence (3.4). Zigzag modules permit the treatment of maps in both directions along a filtration, making them highly suitable for local applications. This work aims to provide mathematicians with a robust foundation for productive engagement with the aforementioned theories. The majority of the proofs have been rewritten to clarify the relationships between the techniques discussed. The novel aspect of this contribution is the canonical presentation of persistence theory and the associated ideas through a rigorous mathematical treatment for triangulable topological spaces.

Dedication

I dedicate this thesis to those closest to me, who have provided invaluable support throughout this journey. I could not have written these pages or undertaken this path without the indispensable support I received.

My academic career took me through German and Italian studies, then to a major in Information Science with a focus on Media Informatics, culminating in a Master's degree from Regensburg. I then completed a three-year doctoral programme in Computer Science at Erlangen, after which I shifted my focus to theoretical mathematics. Throughout, I was driven by a desire to understand the underlying structures of language and computing. I am proud of these experiences and the insights they have given me.

I am grateful to my mother, Beata, who supported my decisions wholeheartedly once they were made, despite initial reservations.

I would like to thank my late father, Domenico, for teaching me to value the past more than the future.

I'd also like to thank my sister Dominique, who never let up on me about physics. She made sure I kept up with the subject whenever we had time to chat about it.

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And to all those unnamed, if these words strike a chord, I am aware that you have touched my life in significant ways.

I have learned a great deal from each of you.

Declaration

I hereby declare that I

- alone wrote the submitted Bachelor's thesis without illicit or improper assistance.
- did not use any materials other than those listed in the bibliography and that all passages taken from these sources in part or in full have been marked as citations and their sources cited individually in the thesis. Citations include the version (edition and year of publication) and paragraphs of the used materials.
- have not submitted this Bachelor's thesis to another institution and that it has never been used for other purposes or to fulfill other requirements, in part or in full.

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Contents

Chapter 1

Motivation

The development of persistence theory in topological data analysis (TDA) marks a significant advance in the quantitative analysis of complex, high-dimensional data sets. Conventional statistical methods frequently prove inadequate for capturing the intricate geometric and topological structures of such data, particularly when these are obscured by noise or nonlinear relationships. Persistence theory, and in particular persistent homology, provides a rigorous mathematical framework for the systematic identification and quantification of topologically relevant structures at varying levels of detail. Persistent homology is a mathematical concept that is employed for the analysis of homological features in data. These representations permit a precise description of the data structure and enable the distinction between significant features and noise. The persistent homology techniques are founded upon the principles of algebraic topology, wherein homology groups serve as algebraic invariants for the classification of topological spaces. In persistent homology, this concept is extended to a filtration where a real-valued function serves as the parameter of a nested sequence of topological spaces. The characteristics of this filtration are captured in persistence intervals, which indicate the degree of robustness associated with the features in question. The persistent homology is obtained by constructing simplicial complexes from the data through the efficient application of computational methods. In addition to their descriptive function, persistence diagrams and barcodes can be integrated into statistical and machine learning methods, enabling quantitative comparisons between data sets. This approach has been employed in a number of studies, including those referenced in Melodia et al. [22–25].

The theory of persistence is a valuable tool in TDA, as it remains stable in the analysis of data that has been subject to perturbations. This theory guarantees that minor alterations to the input data will only result in slight alterations to the persistence diagrams, thereby confirming the reliability of the topological features that have been extracted. This robustness is particularly beneficial when analysing data that is noisy or incomplete. Persistence theory serves to bridge the gap between abstract mathematical theory and the more practical field of data analysis. It has thus become a fundamental tool in this field.

1.1 History

The growth of persistence theory in TDA has been shaped by the seminal contributions of pioneering researchers, who have collectively established persistence as a core instrument for grasping the topological aspects of data.

The field of size theory: The origins of persistence theory can be traced back to the end of the 20th century, with the work of Patrizio Frosini and Massimo Ferri at the University of Bologna. Their research in set theory focused on the natural pseudodistance between functions defined on homeomorphic topological spaces [15, 17]. In particular, size theory, as applied to 0-dimensional homology, provided a framework for quantifying differences between topological spaces, and introduced a method for capturing persisting features across scales.

Fractal geometry: During her doctoral research at the University of Colorado Boulder, Vanessa Robins extended the application of persistence theory to fractal geometry. By means of alpha forms – a concept first proposed by Herbert Edelsbrunner et al. – Robins provided evidence of the efficacy of persistent homology in capturing the multiscale structure of fractal sets [14, 27].

Algebraic foundations: Herbert Edelsbrunner and his team at Duke University have made significant progress in formalising the algebra of persistence theory. They introduced fundamental concepts, including simplicial filtrations, which systematically construct topological spaces from data points by adding simplices in a hierarchical manner [13]. This filtration process tracks topological features, such as connected components, loops and voids, across different scales, leading to the birth and death of these features. The distinction between positive and negative simplices, introduced by Edelsbrunner's group, is crucial for understanding the emergence and decay of homological features within a filtration of point clouds.

1.2 Computational Aspects

The computational efficiency of persistence theory has been a significant factor in its extensive adoption across a range of scientific disciplines. This efficiency, underpinned by robust algorithmic principles, has established persistence theory as a key analytical tool for complex datasets.

Algorithmic developments: The algorithms for computing persistent homology, developed by Herbert Edelsbrunner and colleagues, are founded upon rigorous mathematical theory and optimised for practical application. These algorithms entail the construction and reduction of boundary matrices for the efficient computation of homology groups across a filtration of simplicial complexes.

Among these algorithms, the matrix reduction algorithm plays a pivotal role in the computation of persistence intervals. The practical implementation of these algorithms has led to the development of standard software packages, including `GUDHI`, `Ripser`, and `Dionysus` [26].

Applications in life sciences: In the field of life sciences, persistent homology has emerged as a powerful tool for the study of the structure and function of biological molecules, particularly proteins. Proteins are complex macromolecules, the function of which is intricately linked to their three-dimensional structure. Persistent homology is a method for identifying patterns within a protein's structure that persist across different scales. These patterns frequently correspond to critical functional regions, such as binding pockets or active centers, and provide insights into protein interactions and stability under diverse conditions [21]. In the field of neuroscience, persistence theory has been employed to examine brain networks, thereby providing a novel methodology for analysing the intricate connectivity patterns that underpin brain function. By constructing simplicial complexes from neural data, researchers utilise persistent homology to monitor alterations in brain region connectivity over time. This approach has yielded new insights into the manner in which brain networks reorganise during cognitive processes or in response to neurological diseases [18, 28].

Applications in machine learning: In the field of machine learning , persistent homology is a valuable tool for uncovering the underlying topological structure of data distributions. This allows for the effective completion of tasks such as clustering, classification, and anomaly detection. The topological features of data provide essential insights into the organisation of the data space. For example, persistent homology can identify clusters of data points that form distinct topological features, such as loops or voids, which correspond to different classes or subpopulations within the data set. This has been demonstrated in studies referenced in the literature [20, 22–25]. The incorporation of topological data into machine learning models improves their resilience and generalisation capabilities, particularly in the context of noisy or incomplete data.

Robustness to noise: A defining feature of persistence theory is its resilience to noise, which represents a substantial advantage in the context of real-world data analysis. persistence theory is concerned with the topological features that remain consistent across different scales, thereby filtering out noise-induced artefacts. This robustness is mathematically grounded in stability theorems, which guarantee that minor changes are induced in the persistence diagram by small perturbations in the input data [9].

1.3 Advanced Extensions

The adaptability and extensibility of persistence theory are exemplified by its sophisticated developments, which expand its applicability to more intricate mathematical and data analysis problems. Among these extensions, discrete morse theory, multiparameter persistence, and zigzag persistence represent notable ones, each addressing particular challenges and broadening the scope of TDA.

Discrete morse theory: The discrete morse theory, initially proposed by Robin Forman, represents an extension of the classical morse theory to discrete spaces, such as simplicial complexes. This extension is of particular value in TDA, as it facilitates the simplification of complex spaces while ensuring the preservation of essential topological characteristics. The construction of discrete Morse functions on simplicial complexes enables the reduction of the number of critical simplices, thereby facilitating more efficient persistent homology computations [16]. The critical simplices correspond to significant topological features, and focusing on these reduces the computational complexity of calculating persistence intervals. This approach is especially advantageous in large datasets, where the number of simplices can render traditional homology computations impractical.

Multiparameter persistence: Multiparameter persistence represents an extension of the traditional single-parameter filtration approach, whereby filtrations are considered that are indexed by multiple parameters simultaneously. This allows for a more comprehensive examination of topological characteristics, as distinct parameters facilitate the capture of diverse aspects of the data's structural elements. To illustrate, one might filter a dataset by both scale and density, thereby uncovering topological features that would otherwise remain invisible under a one-parameter filtration [5]. The use of multiple parameters results in a more complex algebraic structure, which in turn gives rise to computational and visualisation challenges associated with multiparameter persistence modules. In contrast to single-parameter persistence, where persistence diagrams or barcodes offer a comprehensive invariant, multiparameter persistence lacks a straightforward representation. In contrast, more complex invariants, such as generalized persistence diagrams or rank invariants, are employed to capture the intricate relationships between parameters.

Zigzag persistence: Zigzag persistence represents an extension of the traditional persistent homology framework to allow for the analysis of dynamic datasets, whereby the data may undergo change over time. In contrast to the standard persistence approach, which requires a monotonically increasing sequence of spaces, zigzag persistence permits both forward and backward inclusions throughout the filtration process [4]. This flexibility permits the analysis of topological features in settings where data is not static, such as time-varying networks or datasets undergoing changes due to external factors. Zigzag persistence is a methodology that captures the evolution of topological features, including their appearance, disappearance, and reappearance as the data changes. The algebraic structure underlying zigzag persistence is more intricate than that of standard persistence. It involves directed graphs and a more complex form of homological algebra.

1.4 Contribution

This work presents a comprehensive summary of persistent homology theory, unifying various proofs to provide a unified examination of persistence modules, persistent (co)homology, and zigzag persistence from an algebraic-topological perspective. The objective of this study is to provide a mathematically rigorous explanation for the remarkable success of persistent homology in data analytics. Our approach is based on the assumption that real-world data can be represented on a triangulable topological space and that simplicial structures allow us to derive invariants of this space. We provide a rigorous proof of the merits of this approach and demonstrate its clear and well-defined foundations. Moreover, we shed light on the interplay between cohomology and zigzag persistence on persistence intervals, filling in the gaps in the existing literature on this topic.

Chapter 2

Topological Spaces and Groups

Topological persistence is deeply rooted in algebraic topology. This is the study of topological spaces and functions based on algebraic objects and their properties. Examples include homotopy and homology theories, which are essential for understanding the construction and connectedness of surfaces, a central aspect of data analysis. Persistent homology, the central tool of topological persistence, extends classical homology to identify features across multiple scales. Introduced by Edelsbrunner et al. in their seminal paper [11], persistent homology examines multi-scale topological features through a filtration process - an indexed family of nested spaces that starts with the empty set and progressively covers the entire space under study. Each filtration stage represents a snapshot of some topological space at a certain resolutions, capturing the appearance and disappearance of multi-dimensional homology groups encoding topological properties such as connected components, holes and voids. Mathematically, the persistence of homological features is visualised using diagrams or barcode representations. These visual aids represent the emergence (birth) and disappearance (death) of topological features as the filter parameter changes. The duration of a feature's presence, represented by the length of its interval in the barcode, indicates its significance, with longer intervals suggesting features that represent the likely true characteristics of the underlying data rather than mere noise. The robustness of persistent homology, in particular its resistance to small perturbations in the data, is captured in the stability theorem. This theorem, proved by Cohen-Steiner, Edelsbrunner and Harer [1], states that small variations in the input data lead to small changes in the persistence barcodes. This property is crucial for practical applications, as it guarantees that the topological summaries are both reliable and meaningful for the actual underlying structures.

We start with basic concepts such as topological spaces and groups, which are crucial for understanding and encoding connectedness and other invariants. The discussion extends to simplicial complexes, which are essential for modelling data structures in topological data analysis. We explore simplicial and singular homology groups to accurately quantify topological features, and dwell on singular chain complexes and exact sequences to deepen the algebraic aspects of persistence theory. This will be useful in some of the later proofs when we discuss the algebraic nature of the persistence module.

2.1 Simplicial Complexes

We note that a set of points $X = \{x_0, x_1, \ldots, x_d\}$ in $\mathbb{R}^n$ is affinely independent if no affine subspace of dimension less than d contains all the points in X. Such a set of points is commonly called point cloud.

Definition 2.1.1 (d-Simplex) *[2, §2.1]* A d-dimensional simplex $\sigma^{(d)}$, or d-simplex, is the set of all convex combinations of $X = \{x_0, x_1, \ldots, x_d\} \subset \mathbb{R}^n$, where X consists of $d+1$ affinely independent points.

Formally, $\sigma^{(d)}$ is defined by:

$$\sigma^{(d)} := \left\{ \sum_{i=0}^{d} \lambda_i x_i \;\middle|\; \sum_{i=0}^{d} \lambda_i = 1,\ \lambda_i \geq 0 \right\}. \tag{2.1}$$

As a convention, the empty set is considered a face, corresponding to the simplex formed by the empty subset of vertices. Specifically, a 0-simplex corresponds to a single point, a 1-simplex to a line segment between two points, a 2-simplex to a triangle, and a 3-simplex to a tetrahedron. Notably, a d-simplex is homeomorphic to the d-dimensional disk D^d.

Theorem 2.1.1 (d-Disk to d-Simplex) *The d-simplex $\sigma^{(d)}$ is homeomorphic to the d-dimensional disk D^d.*

Proof Define the standard d-simplex $\sigma^{(d)}$ as

$$\sigma^{(d)} := \left\{ (x_0, \ldots, x_d) \in \mathbb{R}^{d+1} \;\middle|\; \sum_{i=0}^{d} x_i = 1,\ x_i \geq 0 \right\}, \tag{2.2}$$

and the d-dimensional disk D^d as

$$D^d := \left\{ (x_0, \ldots, x_{d-1}) \in \mathbb{R}^d \;\middle|\; \sum_{i=0}^{d-1} x_i^2 \leq 1 \right\}. \tag{2.3}$$

We construct a homeomorphism $f : \sigma^{(d)} \to D^d$ by

$$f(x_0, \ldots, x_d) = (\sqrt{x_0}, \ldots, \sqrt{x_{d-1}}), \tag{2.4}$$

where $x_d = 1 - \sum_{i=0}^{d-1} x_i$. This map is well-defined since

$$\sum_{i=0}^{d-1} (\sqrt{x_i})^2 = \sum_{i=0}^{d-1} x_i \leq 1. \tag{2.5}$$

The inverse $g : D^d \to \sigma^{(d)}$ is given by

$$g(y_0, \ldots, y_{d-1}) = (y_0^2, \ldots, y_{d-1}^2, 1 - \sum_{i=0}^{d-1} y_i^2), \tag{2.6}$$

ensuring that g is well-defined because $\sum_{i=0}^{d-1} y_i^2 \leq 1$ implies $1 - \sum_{i=0}^{d-1} y_i^2 \geq 0$. Both f and g are continuous and are inverses of each other, as shown by $f(g(y)) = y$ for all $y \in D^d$ and $g(f(x)) = x$ for all $x \in \sigma^{(d)}$. □

Furthermore, it is important to note that $\sigma^{(d)}$ represents the convex hull of the points $X = \{x_0, x_1, \ldots, x_d\}$, defined as the smallest convex subset of $\mathbb{R}^n$ that contains all of these points. The faces of the simplex $\sigma^{(d)}$, with vertex set X, are formed by the simplices corresponding to subsets of X. A d-face of a simplex consists of a subset of the vertices with cardinality $d+1$. The faces of a d-simplex with dimension less than d are known as its proper faces. Two simplices are considered properly situated if their intersection is either empty or a face of both simplices. By identifying simplices along entire faces, we can construct the corresponding simplicial complexes.

Definition 2.1.2 (Simplicial Complex) *[2, §2.2]* A simplicial complex K is a finite collection of simplices that satisfies the following properties:

1. For every simplex $\sigma^{(d)}$ in K, and every face $\tau^{(k)}$ of $\sigma^{(d)}$ with $k < d$, it follows that $\tau^{(k)}$ is also in K.
2. Any two simplices $\sigma^{(d)}$ and $\tau^{(k)}$ in K are properly situated; that is, their intersection is either empty or a face of both simplices.

The dimension of a simplicial complex K is defined as the highest dimension among its simplices. For a simplicial complex K in $\mathbb{R}^n$, the underlying space $|K|$ is the union of all the simplices in K. The topology of K is determined by the topology induced on $|K|$ by $\mathbb{R}^n$'s standard topology. Notably, when the vertex set is specified, a simplicial complex in $\mathbb{R}^n$ can be fully characterized by listing its simplices. Thus, it can be described purely in terms of combinatorics using abstract simplicial complexes.

Definition 2.1.3 (Abstract Simplicial Complex) *[2, §2.3]* Consider a finite set $V = \{v_0, \ldots, v_d\}$. An abstract simplicial complex $\tilde{K}$ with vertex set V is a collection of finite subsets of V that satisfies the following conditions:

1. Every singleton set $\{v_i\}$, where $v_i \in V$, is included in $\tilde{K}$.
2. If a set $\sigma^{(d)}$ is in $\tilde{K}$ and $\tau^{(k)}$ is a subset of $\sigma^{(d)}$, then $\tau^{(k)}$ must also be in $\tilde{K}$.

The abstract simplicial complex $\tilde{K}$ associated with a simplicial complex K is commonly referred to as its vertex scheme. Conversely, if an abstract complex $\tilde{K}$ serves as the vertex scheme for a complex K in $\mathbb{R}^n$, then K is known as a geometric realization of $\tilde{K}$.

Proposition 2.1.2 *Every finite abstract simplicial complex $\tilde{K}$ can be geometrically realized in Euclidean space.*

Proof Let $\{v_0, v_1, \ldots, v_d\}$ denote the vertex set of $\tilde{K}$, with $0 \leq d < n$ representing the number of vertices in $\tilde{K}$. Consider $\sigma^{(d-1)} \subset \mathbb{R}^n$, the simplex formed by the span of $\{e_1, e_2, \ldots, e_d\}$, where e_i represents the i-th unit vector. In this context, K refers to the subcomplex of $\sigma^{(d-1)}$ such that $[e_{i_0}, \ldots, e_{i_l}]$ is a l-simplex of K with $0 \leq l \leq d$ if and only if $[v_{i_0}, \ldots, v_{i_l}]$ is a simplex of $\tilde{K}$. $\square$

Pay attention, that this result is in particular interesting for data analysis, as computer aided methods deal with finite point sets. All realizations of an abstract simplicial complex are homeomorphic to each other. The specific realization mentioned above is referred to as the natural realization.

Proposition 2.1.3 (Equivalence of Geometric Realizations) *Let $\tilde{K}$ be an abstract simplicial complex. Then any two geometric realizations $|\tilde{K}|_1$ and $|\tilde{K}|_2$ of $\tilde{K}$ are homeomorphic.*

Proof Consider two geometrical realisations $|\tilde{K}|_1$ and $|\tilde{K}|_2$ of the abstract simplicial complex $\tilde{K}$. Each realisation $|\tilde{K}|_i$, $i \in \{1, 2\}$, is constructed by mapping the vertices of $\tilde{K}$ to points in $\mathbb{R}^d$, and identifying each simplex in $\tilde{K}$ with the convex hull of its image under that mapping. By construction, each simplex in $|\tilde{K}|_i$ corresponds homeomorphically to a standard l-simplex in $\mathbb{R}^d$ for the appropriate l for integers $0 \leq l \leq d$.

To create a homeomorphism between $|\tilde{K}|_1$ and $|\tilde{K}|_2$, define a map $f : |\tilde{K}|_1 \rightarrow |\tilde{K}|_2$ which acts on each vertex v of $\tilde{K}$ by mapping it from its image in $|\tilde{K}|_1$ to its image in $|\tilde{K}|_2$. Extend f linearly to each simplex in $|\tilde{K}|_1$, where a simplex is represented as a convex combination of the images of its vertices. Given the two geometric realisations $|\tilde{K}|_1$ and $|\tilde{K}|_2$ of $\tilde{K}$, where vertices v_i in $|\tilde{K}|_1$ are mapped to points p_i in $\mathbb{R}^d$ and in $|\tilde{K}|_2$ to points q_i, the map $f : |\tilde{K}|_1 \rightarrow |\tilde{K}|_2$ is defined so that for each vertex v_i corresponding to p_i in $|\tilde{K}|_1$ we set $f(p_i) = q_i$. This map is linearly extended over each simplex in $|\tilde{K}|_1$.

Specifically, for a point x and an integer $0 \leq k \leq d$ within a simplex of $|\tilde{K}|_1$, expressed as a convex combination $x = \sum_{j=1}^{k} \lambda_j p_{i_j}$, where $\{v_{i_1}, v_{i_2}, \ldots, v_{i_k}\}$

denote the vertices of the simplex and $\lambda_j \geq 0$ with $\sum_{j=1}^{k} \lambda_j = 1$, the function f is defined by $f(x) = \sum_{j=1}^{k} \lambda_j q_{i_j}$.

This ensures that f is a continuous and bijective map, preserving the simplicial structure and thus establishing f as a homeomorphism between $|\tilde{K}|_1$ and $|\tilde{K}|_2$.

f is continuous on each simplex because it is a linear transformation on compact convex subsets in $\mathbb{R}^d$. Since both $|\tilde{K}|_1$ and $|\tilde{K}|_2$ are topologised by the quotient of their respective disjoint unions of simplices under an equivalence relation that glues them along common faces, and since f preserves these gluing conditions, f is globally continuous. Every simplex and its face structure in $|\tilde{K}|_1$ maps uniquely onto a corresponding simplex and face structure in $|\tilde{K}|_2$, making f bijective.

Similarly, the inverse map $g : |\tilde{K}|_2 \to |\tilde{K}|_1$ can be constructed by reversing the roles of $|\tilde{K}|_1$ and $|\tilde{K}|_2$. It also maintains continuity for analogous reasons to f.

So $|\tilde{K}|_1$ and $|\tilde{K}|_2$ are homeomorphic. $\square$

Furthermore, it has been proven that any finite abstract simplicial complex of dimension d can be realized as a simplicial complex in $\mathbb{R}^{2d+1}$.

Theorem 2.1.4 (Realizations into $\mathbb{R}^{2d+1}$) *Any finite abstract simplicial complex of dimension d can be realized as a simplicial complex in $\mathbb{R}^{2d+1}$.*

Proof Let $\tilde{K}$ be a finite abstract simplicial complex of dimension d. We will construct an injective geometric realization $f : \tilde{K} \to \mathbb{R}^{2d+1}$.

First, define an injective map $\tilde{f} : V(\tilde{K}) \to \mathbb{R}^{2d+1}$ for the vertex set $V(\tilde{K})$ of $\tilde{K}$. Since $V(\tilde{K})$ is finite and $\mathbb{R}^{2d+1}$ has sufficient dimensionality, injectivity is guaranteed. Adjust $\tilde{f}$ if necessary to ensure the images of the vertices of each simplex $\sigma \in \tilde{K}$ are affinely independent. This can be achieved by slight perturbations within $\mathbb{R}^{2d+1}$, leveraging the ample dimensionality to avoid overlaps. We extend $\tilde{f}$ to a map $f : \tilde{K} \to \mathbb{R}^{2d+1}$ by defining it on each simplex $\sigma = [v_0, \ldots, v_k]$ through the unique affine map $v_i \mapsto \tilde{f}(v_i)$. The injective and affine properties of $\tilde{f}$ on vertices guarantee that f is injective over each simplex and preserves the simplicial structure. Specifically, for any simplices $\sigma, \tau \in \tilde{K}$, we have:

$$f(|\sigma| \cap |\tau|) = f(|\sigma|) \cap f(|\tau|). \tag{2.7}$$

Thus, f provides an injective geometric realization of $\tilde{K}$ as a simplicial complex in $\mathbb{R}^{2d+1}$. $\square$

2.2 Simplicial Homology

Given a set V representing the vertices of a d-simplex $\sigma^{(d)}$, we can establish an orientation for the simplex by selecting a specific ordering of the vertices. If the vertex ordering differs from our chosen order by an odd permutation, the orientation is considered reversed, while even permutations preserve the orientation. Thus, a simplex can have only two possible orientations. Moreover, the orientation of a d-simplex induces an orientation on its $(d-1)$-faces. Specifically, if $\sigma^{(d)} := (v_0, v_1, \dots, v_d)$ represents an oriented d-simplex, then the orientation of the $(d-1)$-face $\tau^{(d-1)}$ of $\sigma^{(d)}$, omitting the vertex v_i, is given by

$$\tau_i^{(d-1)} = (-1)^i (v_0, \dots, v_{i-1}, v_{i+1}, \dots, v_d). \tag{2.8}$$

Definition 2.2.1 (d-Chain) *[30, §2.3]* Given a set $\{\sigma_1^{(d)}, \dots, \sigma_k^{(d)}\}$ of arbitrarily oriented d-simplices in a complex K and an abelian group G, a d-chain c with coefficients $g_i \in G$ is defined as a formal sum:

$$c := g_0\sigma_0^{(d)} + g_1\sigma_1^{(d)} + \ldots + g_k\sigma_k^{(d)} = \sum_{i=0}^{k} g_i\sigma_i^{(d)}. \tag{2.9}$$

Henceforth, we will assume that $G = (\mathbb{Z}, +)$.

Lemma 2.2.1 *The set of simplicial d-chains C_d^Δ forms an abelian group $(C_d^\Delta, +)$.*

Proof The identity element of the group is the empty chain, given by:

$$e_{C_d^\Delta} = \sum_{i\in\emptyset} g_i\sigma_i^{(d)} = e_G = 0. \tag{2.10}$$

The sum of two chains is defined as:

$$c + c' = \sum_{i=0}^{k} g_i\sigma_i^{(d)} + \sum_{j=1}^{l} g_j'\sigma_j^{(d)}, \tag{2.11}$$

which simplifies to:

$$c + c' = \sum_{i=0}^{\min(k,l)} (g_i + g_i')\sigma_i^{(d)} + \begin{cases} \sum_{j=\min(k,l)+1}^{\max(k,l)} g_j\sigma_j^{(d)} & \text{if } k > l, \\ 0 & \text{if } k = l, \\ \sum_{j=\min(k,l)+1}^{\max(k,l)} g_j'\sigma_j^{(d)} & \text{if } k < l. \end{cases} \tag{2.12}$$

Hence, $c + c' \in C_d^\Delta$.

The associativity of the group operation in C_d^Δ follows directly from the associativity of the group operation in G.

The inverse element is given by:

$$c + (-c) = \sum_{i=0}^{k} g_i \sigma_i^{(d)} + \sum_{i=0}^{k} (-g_i) \sigma_i^{(d)} = \sum_{i=0}^{k} (g_i - g_i) \sigma_i^{(d)} = e_{C_d^\Delta}. \tag{2.13}$$

Thus, $(C_d^\Delta, +)$ is an abelian group. $\square$

Definition 2.2.2 (Boundary) *[19, p.106]* Let $\sigma^{(d)}$ be an oriented d-simplex in a complex K. The boundary of $\sigma^{(d)}$ is defined as the simplicial $(d-1)$-chain of K with coefficients in the abelian group G, given by

$$\partial(\sigma^{(d)}) = \sum_{i=0}^{d} (-1)^i \sigma_i^{(d-1)}, \tag{2.14}$$

where $\sigma_i^{(d-1)}$ is a $(d-1)$-face of $\sigma^{(d)}$. If $d = 0$, we define $\partial(\sigma^{(0)}) = 0$.

Since $\sigma^{(d)}$ is an oriented simplex, the $\sigma_i^{(d-1)}$ faces also have associated orientations. We extend the definition of the boundary linearly to elements of C_d^Δ.

Lemma 2.2.2 *The boundary operator is a group homomorphism*

$$\partial : C_d^\Delta \to C_{d-1}^\Delta. \tag{2.15}$$

Proof We define the boundary operator for a d-chain $c = \sum_{i=0}^{k} g_i \sigma_i^{(d)}$:

$$\begin{aligned} \partial(c) &= \sum_{i=0}^{k} g_i \partial(\sigma_i^{(d)}) && (2.16) \\ &= \sum_{i=0}^{k} g_i \sum_{j=0}^{d} (-1)^j \sigma_{i,j}^{(d-1)} && (2.17) \\ &= \sum_{i=0}^{k} \sum_{j=0}^{d} g_i (-1)^j \sigma_{i,j}^{(d-1)}, && (2.18) \end{aligned}$$

which is an element of C_{d-1}^Δ, where $\sigma_{i,j}^{(d-1)}$ are the $(d-1)$-faces of the d-simplices $\sigma_i^{(d)}$ in K.

To verify that ∂ is a group homomorphism, consider two d-chains $c =$

$\sum_{i=0}^{k} g_i\sigma_i^{(d)}$ and $c' = \sum_{j=0}^{l} g'_j\sigma_j^{(d)}$. We compute:

$$\partial(c + c') = \partial\left(\sum_{i=0}^{k} g_i\sigma_i^{(d)} + \sum_{j=0}^{l} g'_j\sigma_j^{(d)}\right) \tag{2.19}$$

$$= \sum_{i=0}^{k} g_i\partial(\sigma_i^{(d)}) + \sum_{j=0}^{l} g'_j\partial(\sigma_j^{(d)}) \tag{2.20}$$

$$= \partial(c) + \partial(c'). \tag{2.21}$$

Thus, ∂ is a group homomorphism. □

Example 2.2.3 *Let's consider the* 2*-simplex* $\sigma^{(2)}$ *with vertices* $v_0, v_1,$ *and* v_2*. The* 1*-faces of this simplex are:*

$$e_0 = (v_1, v_2), \quad \textit{connecting } v_1 \textit{ and } v_2, \tag{2.22}$$

$$e_1 = (v_2, v_0), \quad \textit{connecting } v_2 \textit{ and } v_0, \tag{2.23}$$

$$e_2 = (v_0, v_1), \quad \textit{connecting } v_0 \textit{ and } v_1. \tag{2.24}$$

Now, let's proceed with the computation:

$$\partial(\partial(\sigma^{(2)})) = \partial(e_0 + e_1 + e_2) \tag{2.25}$$

$$= \partial(e_0) + \partial(e_1) + \partial(e_2) \tag{2.26}$$

$$= \partial(v_1, v_2) + \partial(v_2, v_0) + \partial(v_0, v_1) \tag{2.27}$$

$$= [(v_2) - (v_1)] + [(v_0) - (v_2)] + [(v_1) - (v_0)] \tag{2.28}$$

$$= 0. \tag{2.29}$$

We observe that C_0^{Δ} *is an abelian group and that oppositely oriented simplices cancel each other out, resulting in:*

$$\partial(\partial(\sigma^{(2)})) = 0. \tag{2.30}$$

This property can be generalized to higher dimensions through induction. Therefore, since ∂ *is a linear operator and the chain c is a sum of d-simplices, we can conclude that:*

$$\partial^2(c) = 0 \quad \textit{for any d-chain c in } C_d^{\Delta}. \tag{2.31}$$

Consequently, the boundary of the boundary is zero. Moreover, if the boundary of a simplex is zero, it is referred to as a cycle. By this definition, we can deduce that the boundary of any simplex is a cycle.

Definition 2.2.4 (d-Cycle) *[19, p.106]* A d-chain is called a d-cycle if its boundary is equal to zero.

We denote the set of d-cycles of a complex K over the group $\mathbb{Z}$ as Z_d^{Δ}, the simplicial cycle group. It is important to note that Z_d^{Δ} is a subgroup of C_d^{Δ} and can also be expressed as:

$$Z_d^{\Delta} = \ker(\partial_d). \tag{2.32}$$

A d-cycle of a k-complex K is said to be homologous to zero if it can be expressed as the boundary of a $(d+1)$-chain in K, where $d = 0, 1, \ldots, k-1$. In other words, a cycle is considered a boundary if it can be 'filled in' by a higher-dimensional chain. This equivalence relation is denoted as $c \sim 0$.

Definition 2.2.5 (Boundary Group) *[30, §2.3]* The subgroup of Z_d^{Δ} consisting of boundaries is referred to as the simplicial boundary group B_d^{Δ}.

It is worth noting that B_d^{Δ} is equal to the image of the boundary operator ∂_{d+1}. Since B_d^{Δ} is a subgroup of Z_d^{Δ} and Z_d^{Δ} is an abelian group, every subgroup of Z_d^{Δ} is normal. Therefore, we can construct the group quotient:

$$H_d^{\Delta} = Z_d^{\Delta}/B_d^{\Delta}. \tag{2.33}$$

Definition 2.2.6 (Simplicial Homology Group) *[19, §2.1]* The group H_d^{Δ} represents the d-dimensional simplicial homology group of the complex K over $\mathbb{Z}$. It is expressed as the group quotient:

$$H_d^{\Delta} = \ker(\partial_d)/\mathrm{im}(\partial_{d+1}). \tag{2.34}$$

Next, we want to examine the structure of this homology group by shedding light on its connection to the connected components of a simplicial complex. We will find that the homology groups of the connected components of the complex, which in turn form a complex themselves, yield the direct sum of the homology group of the entire complex.

Definition 2.2.7 *A subcomplex is a subset S of the simplices belonging to a complex K, where S itself forms a complex.*

Definition 2.2.8 *The collection of all simplices in a complex K with dimension less than or equal to d is referred to as the d-skeleton of K.*

By definition, the d-skeleton forms a subcomplex.

Definition 2.2.9 *A complex K is considered connected if it cannot be expressed as the disjoint union of two or more non-empty subcomplexes. A geometric complex is path-connected if there exists a path consisting of 1-simplices connecting any vertex to any other vertex.*

Lemma 2.2.3 *A geometric complex is path-connected if and only if it is connected.*

Proof Suppose K is path-connected. Assume for contradiction that K can be expressed as the disjoint union of two non-empty subcomplexes L and M. Since K is path-connected, there exists a path of 1-simplices between any two vertices in K. Let $l \in L$ and $m \in M$ be any two vertices. By path-connectedness, there is a path from l to m, which contradicts the assumption that L and M are disjoint. Therefore, K is connected.

Suppose K is connected. Pick any vertex $v \in K$. Let L denote the subcomplex of K containing all vertices reachable from v via paths of 1-simplices. If $L \neq K$, then L and $K \setminus L$ form a disjoint union of two non-empty subcomplexes, contradicting the connectedness of K. Hence, $L = K$. □

Theorem 2.2.4 *[19, p.105ff]* Let $K_1, \ldots, K_p$ be the collection of all connected components of a complex K. Furthermore, let $H_{d_i}^{\Delta}$ represent the d-th simplicial homology group of K_i, and H_d^{Δ} denote the d-th simplicial homology group of K. Then, H_d^{Δ} is isomorphic to the direct sum $H_{d_1}^{\Delta} \oplus \cdots \oplus H_{d_p}^{\Delta}$.

Proof Let C_d^{Δ} represent the group of simplicial d-chains of K, and let K_i denote the i-th component of K. Define $C_{d_i}^{\Delta}$ as the group of simplicial d-chains of K_i. It is evident that $C_{d_i}^{\Delta}$ is a subgroup of C_d^{Δ}. Furthermore, we observe that C_d^{Δ} can be expressed as the direct sum of $C_{d_1}^{\Delta}, \ldots, C_{d_p}^{\Delta}$:

$$C_d^{\Delta} = C_{d_1}^{\Delta} \oplus \cdots \oplus C_{d_p}^{\Delta}. \tag{2.35}$$

Our goal is to demonstrate that a similar decomposition applies to the groups B_d^{Δ} and Z_d^{Δ}. By considering $B_{d_i}^{\Delta}$ as the image of ∂_{d+1} restricted to the subgroup $C_{d_i}^{\Delta}$, we can represent the group B_d^{Δ} as the direct sum of these restrictions:

$$B_d^{\Delta} = B_{d_1}^{\Delta} \oplus \cdots \oplus B_{d_p}^{\Delta}. \tag{2.36}$$

Thus, for any element $c \in C_{d+1}^{\Delta}$, we have:

$$c = c_1 + \cdots + c_p, \quad \partial_{d+1}(c) = \partial_{d+1}(c_1) + \cdots + \partial_{d+1}(c_p) \in B_d^{\Delta}, \tag{2.37}$$

where $c_i \in C_{(d+1)_i}^{\Delta}$.

Let us define $Z^{\Delta}_{d_i}$ as the intersection of the kernel of ∂_d and $C^{\Delta}_{d_i}$. It follows that Z^{Δ}_{d} can be expressed as the direct sum of $Z^{\Delta}_{d_1}, \ldots, Z^{\Delta}_{d_p}$:

$$Z^{\Delta}_{d} = Z^{\Delta}_{d_1} \oplus \cdots \oplus Z^{\Delta}_{d_p}. \tag{2.38}$$

To verify this, consider an element $c \in C^{\Delta}_{d}$ that belongs to Z^{Δ}_{d}. We require $\partial_d(c) = 0$. However, we can express $\partial_d(c)$ as $\partial_d(c_1) + \cdots + \partial_d(c_p)$. Therefore, for $\partial_d(c) = 0$, it must be that $\partial_d(c_i) = 0$, indicating that $c_i \in Z^{\Delta}_{d_i}$.

Since both Z^{Δ}_{d} and B^{Δ}_{d} can be decomposed componentwise, we conclude that:

$$Z^{\Delta}_{d}/B^{\Delta}_{d} = Z^{\Delta}_{d_1}/B^{\Delta}_{d_1} \oplus \cdots \oplus Z^{\Delta}_{d_p}/B^{\Delta}_{d_p}, \tag{2.39}$$

and consequently:

$$H^{\Delta}_{d} = H^{\Delta}_{d_1} \oplus \cdots \oplus H^{\Delta}_{d_p}. \tag{2.40}$$

□

Proposition 2.2.5 *[19, p.108f]* If K is a connected complex and c is a 0-chain with $I(c) = 0$, then $I(c) = 0$ is equivalent to $c \sim 0$, where $\sim$ denotes homology equivalence. Furthermore, in this case, the zeroth simplicial homology group $H^{\Delta}_0(K, \mathbb{Z})$ is isomorphic to the integers $\mathbb{Z}$.

Proof Let $\sigma^{(1)} = (v_0, v_1)$ be a 1-simplex. For the chain $c = \partial_1(g\sigma^{(1)}) = gv_1 - gv_0$, we have $c \sim 0$, and it is clear that $I(c) = g - g = 0$. Since $I(c + c') = I(c) + I(c')$, I is a group homomorphism. For any 1-chain $c \in C^{\Delta}_1$ of the form $\sum_{i=0}^{k} g_i\sigma_i^{(1)}$, where $\sigma_i^{(1)} = (v_i, v_{i+1})$, we have:

$$c = \partial_1(c) \sim 0 \implies I(c) = I(\partial_1(c)) = 0. \tag{2.41}$$

Consider two vertices v and w in K. Since K is connected, there exists a path between v and w consisting of 1-simplices $\sigma_i^{(1)} = (v_i, v_{i+1})$, $i = 0, \ldots, k-1$, where $v_0 = v$ and $v_k = w$. The boundary of the chain $c = \sum_{i=0}^{k} g\sigma_i^{(1)}$ is given by:

$$\partial_1(c) = \sum_{i=0}^{k} g\partial_1(\sigma_i^{(1)}) = \sum_{i=0}^{k} g[(v_{i+1}) - (v_i)] = gw - gv. \tag{2.42}$$

Since $\partial_1(c)$ is a boundary, we have $c = \partial_1(c) \sim 0$. Thus, $(gw - gv) \sim 0$, implying $gw \sim gv$. Therefore, any 0-chain c in K is homologous to the chain gv. We observe that homologous chains have equal indices, i.e., $I(c) = I(gv) = g$. Thus,

$c \sim gv \implies c \sim I(c)v$. This shows that if $I(c) = 0$, then $c \sim 0$. Hence, $I(c) = 0$ is equivalent to $c \sim 0$.

Since I is a homomorphism from $C_0^\Delta = Z_0^\Delta$ to $\mathbb{Z}$, for any 0-simplex c and $g \in \mathbb{Z}$, the chain $gc \in C_0^\Delta$ is a cycle with $I(gc) = g$. Therefore, $I(Z_0^\Delta) = \mathbb{Z}$. Since $I(c) = 0$ is equivalent to $c \sim 0$, we have $B_0^\Delta = \ker(I)$. This implies that:

$$H_0^\Delta = Z_0^\Delta / B_0^\Delta \cong \mathbb{Z}. \tag{2.43}$$

□

Corollary 2.2.6 *The* 0*-dimensional simplicial homology group of a complex K over $\mathbb{Z}$ can be represented as $\mathbb{Z}^p = \bigoplus_p \mathbb{Z}$, where p denotes the number of connected components present in K.*

Proof From Proposition 2.2.5, we know that if K is a connected complex, then the zeroth simplicial homology group $H_0^\Delta(K, \mathbb{Z})$ is isomorphic to $\mathbb{Z}$.

Consider a complex K that consists of p connected components $K_1, K_2, \ldots, K_p$. The 0-dimensional simplicial homology group $H_0^\Delta(K, \mathbb{Z})$ can be expressed as the direct sum of the 0-dimensional homology groups of its connected components:

$$H_0^\Delta(K, \mathbb{Z}) = H_0^\Delta(K_1, \mathbb{Z}) \oplus H_0^\Delta(K_2, \mathbb{Z}) \oplus \cdots \oplus H_0^\Delta(K_p, \mathbb{Z}). \tag{2.44}$$

Since each K_i is a connected component, by Proposition 2.2.5, each $H_0^\Delta(K_i, \mathbb{Z})$ is isomorphic to $\mathbb{Z}$. Therefore, we have:

$$H_0^\Delta(K, \mathbb{Z}) \cong \bigoplus_{i=1}^{p} \mathbb{Z} = \mathbb{Z}^p. \tag{2.45}$$

□

Example 2.2.10

- *The zeroth homology group of the circle is isomorphic to $\mathbb{Z}$. Consider a simplicial representation of the circle using four* 1*-simplices: $\sigma_0 = (v_0, v_1)$, $\sigma_1 = (v_1, v_2)$, $\sigma_2 = (v_2, v_3)$, and $\sigma_3 = (v_3, v_0)$. The group Z_0^Δ consists of sums over the four zero-simplices v_0, v_1, v_2, and v_3 with coefficients in $\mathbb{Z}$. Let c be a zero-chain with non-zero coefficients given by:*

$$c = g_0 v_0 + g_1 v_1 + g_2 v_2 + g_3 v_3. \tag{2.46}$$

To reduce it to an element of H_0^Δ, subtract the chain $c' = g_3 v_2 - g_3 v_3 \sim 0$:

$$c - c' = g_0 v_0 + g_1 v_1 + (g_2 - g_3) v_2. \tag{2.47}$$

By repeating this process, we obtain a new chain:

$$c'' = (g_0 - g_1 + g_2 - g_3)v_0. \tag{2.48}$$

Since $c'' \sim c$, it represents an element of H_0^Δ. Moreover, since $g_i \in \mathbb{Z}$, we can write $(g_0 - g_1 + g_2 - g_3) \in \mathbb{Z}$ as $c'' = gv_0$, where g is an element of $\mathbb{Z}$. Therefore, we can choose any g, implying that $H_0^\Delta \cong \mathbb{Z}$.

- We will demonstrate that $H_d^\Delta(S^d) \cong \mathbb{Z}$. The d-simplex $\sigma^{(d)}$ and the d-ball are homeomorphic, and their boundaries, which consist of $(d-1)$-simplices, are homeomorphic to the d-sphere. Thus, the appropriate simplicial structure to impose on S^d is that of the boundary of the $(d+1)$-simplex $\sigma^{(d+1)}$. Let $\{v_0, \ldots, v_d\}$ denote the set of vertices of $\sigma^{(d+1)}$. This set is not oriented, and the orientations of the $(d-1)$-simplices can be arbitrarily determined. We'll utilize their numbering to establish orientations.
  Consequently, all d-chains on this structure can be expressed as:

$$c = \sum_{i=0}^{d+1} g_i(v_0, \ldots, v_{i-1}, v_{i+1}, \ldots, v_d), \tag{2.49}$$

where $g_i \in \mathbb{Z}$.
Since $\sigma^{(d+1)}$ itself is not part of the structure, there are no boundaries in Z_d^Δ, the group of simplicial cycles. Thus, $H_d^\Delta = Z_d^\Delta / B_d^\Delta$ represents the group of simplicial cycles. If $c \in Z_d^\Delta$, then $\partial_{d+1}(c) = 0$. Using Eq. 2.49, we have:

$$\partial_{d+1}(c) = \partial_{d+1}\left(\sum_{i=0}^{d+1} g_i(v_0, \ldots, v_{i-1}, v_{i+1}, \ldots, v_d)\right) \tag{2.50}$$

$$= \sum_{i=0}^{d+1} g_i \left(\sum_{j=0}^{d+1} (-1)^j (v_0, \ldots, v_{i-1}, v_{i+1}, \ldots, v_{j-1}, v_{j+1}, \ldots, v_d)\right). \tag{2.51}$$

By rearranging this sum, we obtain terms of the form:

$$(g_k - g_l)(v_0, \ldots, v_{j-1}, v_{j+1}, \ldots, v_{i-1}, v_{i+1}, \ldots, v_d), \tag{2.52}$$

where $k, l = 0, \ldots, d+1$ for all $i, j = 0, \ldots, d$.
Each pair of d-simplices of $\sigma^{(d+1)}$ intersects along a $(d-1)$-face. Therefore, we obtain terms of the form given in Eq. 2.52 for each of these faces. From this, we deduce that if $\partial_d(c) = 0$, we must have $g_k = g_l$ for all $k, l = 0, \ldots, d+1$. In other words, $g_0 = g_1 = \cdots = g_{d+1}$. Consequently, our original d-chain is:

$$c = \sum_{i=0}^{d+1} g_0(v_0, \ldots, v_{i-1}, v_{i+1}, \ldots, v_d), \tag{2.53}$$

allowing us to choose g_0 from $\mathbb{Z}$. Thus, we conclude that $H_d^{\Delta}(S^d) \cong \mathbb{Z}$.

- *We demonstrate that $H_d^{\Delta}(D^d) = 0$. The simplest simplicial structure for D^d is that of the d-simplex $\sigma^{(d)}$. Consequently, all d-chains can be expressed as $c = g\sigma^{(d)}$, where $g \in \mathbb{Z}$. This form is never a boundary, implying that $H_d^{\Delta} = Z_d^{\Delta}$. However, $\partial_d(c) = 0$ is generally only true when $g = 0$. Thus, we conclude that $H_d^{\Delta}(D^d) \cong 0$.*

2.3 Singular Homology

In the context of lower dimensions, there is an intuitive understanding of when two topological spaces are fundamentally 'equivalent'. To formalise and strengthen this intuition, various methods have been developed, one of which is the concept of homeomorphism. It would be highly desirable to establish a relation between the homology groups of homeomorphic spaces. Interestingly, it has been found that the homology groups of two topological spaces are isomorphic if they are homeomorphic. This fact requires verification.

In order to achieve this objective, it is necessary to develop a methodology for comparing homology groups. However, it is not immediately evident how this can be accomplished with the tools that have been developed thus far. Indeed, this represents a significant challenge. To address this issue, we propose the introduction of the concept of singular homology. The fundamental principles underlying this concept are analogous to those that have been previously explored.

To compute $Z_d(X)$, we need to find the group of d-cycles in X. Since X is obtained by identifying opposite faces of $\partial_d\sigma^{(d)}$, a d-cycle in X corresponds to a d-cycle in $\partial_d\sigma^{(d)}$, which is not a boundary of a $(d+1)$-dimensional face of $\sigma^{(d)}$.

Definition 2.3.1 *A singular d-simplex in a topological space X is a continuous map $\tilde{\sigma}^{(d)} : \sigma^{(d)} \to X$.*

We define the boundary map ∂_d in a similar manner as before. The boundary map, denoted as ∂_d, is a function that operates on the chain group $C_d(X)$ and maps it to the chain group $C_{d-1}(X)$. It is defined as follows: For any singular d-simplex $\tilde{\sigma}^{(d)}$ in X, the boundary map $\partial_d(\tilde{\sigma}^{(d)})$ is obtained by summing over all the $(d-1)$-simplices that are obtained by removing one vertex from $\tilde{\sigma}^{(d)}$. Each term in the sum is multiplied by $(-1)^i$, where i represents the index of the removed vertex. In other words, if v_i represents the 0-simplex (vertex) of $\tilde{\sigma}^{(d)}$, then the boundary map can be expressed as:

$$\partial_d(\tilde{\sigma}^{(d)}) = \sum_i (-1)^i \tilde{\sigma}^{(d)}|_{[v_0,\dots,v_{i-1},v_{i+1},\dots,v_d]}. \tag{2.54}$$

Here, v_i is a map that takes the 0-simplex $\sigma^{(0)}$ to the corresponding vertex in X, such that $v_i : \sigma^{(0)} \to X$ is continuous.

As mentioned earlier, when we apply the boundary map twice to a d-chain c, denoted as $\partial^2(c)$ or $\partial_{d-1}(\partial_d(c))$, the result is always zero. This observation leads us to the idea of defining the singular homology groups in a similar way to the simplicial homology groups.

Definition 2.3.2 *The singular homology group $H_d(X)$ is the quotient:*

$$H_d(X) = \ker(\partial_d)/\mathrm{im}(\partial_{d+1}). \tag{2.55}$$

In the following section, we will explore how this definition of homology allows us to establish a simple relationship between homeomorphic spaces and their corresponding homology groups. This relationship becomes apparent when we consider the fact that the definitions of H_d and H_d^{Δ} are analogous. Intuitively, we would expect these two groups to be the same for triangulable topological spaces. However, this is not immediately obvious. One reason for this is that H_d^{Δ} is finitely generated, while the chain group $C_d(X)$, from which we derived H_d, is uncountable.

Interestingly, for spaces where both simplicial and singular homology groups can be calculated, these two groups are indeed equivalent. We will provide a proof for this later on. But before we do, let us present some facts about singular homology that support the intuition that H_d is isomorphic to H_d^{Δ}.

Proposition 2.3.1 *[19, p.108f]* In the context of a topological space X, $H_d(X)$ is isomorphic to the direct sum $H_d(X_1) \oplus \cdots \oplus H_d(X_p)$, where X_i represents the path-connected components of X.

This equivalence serves as the counterpart to Proposition 2.2.5.

Proof As the maps $\tilde{\sigma}^{(d)}$ are continuous, a singular simplex always has a path-connected image in X. Consequently, $C_d(X)$ can be expressed as the direct sum of subgroups $C_d(X_1) \oplus \cdots \oplus C_d(X_p)$. The boundary map ∂ functions as a homomorphism, thereby preserving this decomposition. Consequently, $\ker(\partial_d)$ and $\mathrm{im}(\partial_{d+1})$ also decompose:

$$H_d(X) \cong H_d(X_1) \oplus H_d(X_2) \oplus \cdots \oplus H_d(X_p). \tag{2.56}$$

□

Proposition 2.3.2 *The 0-dimensional homology group of a space X is the direct sum of $\mathbb{Z}$ copies, with each copy corresponding to a distinct path-component of X.*

Proof To establish the isomorphism $H_0(X) \cong \mathbb{Z}$, it is sufficient to consider the case where X is path-connected. For a 0-chain c, the boundary operator $\partial_0(c)$ is always zero since the boundary of any 0-simplex vanishes. Consequently, $\ker(\partial_0) = C_0(X)$, which implies that:

$$H_0(X) = C_0(X)/\mathrm{im}(\partial_1). \tag{2.57}$$

Define the map $I : C_0(X) \to \mathbb{Z}$ by:

$$I(c) = \sum_i g_i \quad \text{for } c = \sum_i g_i \tilde{\sigma}^{(0)} \in C_0(X). \tag{2.58}$$

Our goal is to demonstrate that $\ker(I) = \mathrm{im}(\partial_1)$. That is, for any 0-chain c, $I(c) = 0$ if and only if $c \sim 0$.

Suppose $I(c) = 0$ for $c = \sum_i g_i \tilde{\sigma}^{(0)}$. Since X is path-connected, we can express c as the boundary of a 1-chain:

$$c = \partial_1 \left(\sum_j g_j \tilde{\sigma}^{(1)} \right) \quad \text{implying } c \sim 0. \tag{2.59}$$

If $c \sim 0$, then $c = \partial_1 \left(\sum_j g_j \tilde{\sigma}^{(1)} \right)$ for some 1-chain $\sum_j g_j \tilde{\sigma}^{(1)}$. By linearity of I, we have:

$$I(c) = I\left(\partial_1 \left(\sum_j g_j \tilde{\sigma}^{(1)} \right) \right) = 0. \tag{2.60}$$

Thus, I induces an isomorphism between $H_0(X)$ and $\mathbb{Z}$ when X is path-connected.

For the general case where X has p path-components $X_1, \ldots, X_p$, we apply the above argument to each component. Therefore, $H_0(X)$ is isomorphic to the direct sum:

$$H_0(X) \cong \bigoplus_{i=1}^{p} \mathbb{Z}. \tag{2.61}$$

$\square$

This correspondence serves as the parallel to Corollary 2.2.6.

Example 2.3.3 *Alternative proof that $H_d(S^d) \cong \mathbb{Z}$. To prove that the d-th homology group of the d-sphere is isomorphic to $\mathbb{Z}$, we utilize the singular homology approach. The* *d-th singular chain group $C_d(S^d)$ consists of formal linear combinations of singular d-simplices in S^d with integer coefficients. First, we observe that S^d is a connected and compact topological space. According to the Hurewicz theorem, we have $H_d(S^d) \cong \pi_d(S^d)$, where $\pi_d(S^d)$ denotes the d-th homotopy group of S^d. Since S^d is simply connected for $d \geq 2$, it follows that $\pi_d(S^d) = 0$ for $d \geq 2$. However, for $d = 1$, $\pi_1(S^1) \cong \mathbb{Z}$.*

Now, to establish the isomorphism between $\pi_1(S^1)$ and $H_1(S^1)$, consider the singular 1-chain group $C_1(S^1)$, which consists of formal linear combinations of singular 1-simplices in S^1 with integer coefficients. Let c be a singular 1-chain in $C_1(S^1)$ expressed as:

$$c = \sum_i g_i \tilde{\sigma}_i^{(1)}, \tag{2.62}$$

where $g_i \in \mathbb{Z}$ and $\tilde{\sigma}_i^{(1)}$ are singular 1-simplices. The boundary of c is given by:

$$\partial_1(c) = \sum_i g_i \partial_1(\tilde{\sigma}_i^{(1)}). \tag{2.63}$$

Since S^1 is a 1-dimensional manifold, the boundary of any singular 1-simplex $\tilde{\sigma}_i^{(1)}$ is a formal linear combination of two points in S^1, each with opposite orientations:

$$\partial_1(\tilde{\sigma}_i^{(1)}) = p - q, \tag{2.64}$$

where p and q are points in S^1. Thus, we have:

$$\partial_1(c) = (p - q) \sum_i g_i, \tag{2.65}$$

where the sum $\sum_i g_i$ is an integer. Consequently, the boundary of any singular 1-chain c in $C_1(S^1)$ is of the form $(p - q)k$, where k is an integer.

This implies that:

$$H_1(S^1) = Z_1(S^1)/B_1(S^1) \cong \mathbb{Z}, \tag{2.66}$$

where $Z_1(S^1)$ is the group of 1-cycles and $B_1(S^1)$ is the group of 1-boundaries. In conclusion, $H_d(S^d) \cong \pi_d(S^d) = 0$ for $d \geq 2$, and $H_1(S^1) \cong \pi_1(S^1) \cong \mathbb{Z}$. Thus, the d-th homology group of the d-sphere is isomorphic to $\mathbb{Z}$.

2.3.1 Singular Chain Complexes

In order to demonstrate the equivalence of H_d^{Δ} and H_d, we will introduce a few concepts that will assist us in our proof.

Since $\tilde{\sigma}^{(d)}$ are continuous, a singular simplex has a path-connected image in X. Thus, we can express $C_d(X)$ as the direct sum of subgroups $C_d(X_1) \oplus \cdots \oplus C_d(X_p)$, where each subgroup corresponds to a distinct path-component of X. This decomposition is preserved by the boundary map ∂, which is a homomorphism. Thus, both $\ker(\partial_d)$ and $\mathrm{im}(\partial_{d+1})$ also split, leading to the conclusion that $H_d(X)$ is isomorphic to

$$H_d(X_1) \oplus H_d(X_2) \oplus \cdots \oplus H_d(X_p). \tag{2.67}$$

These ideas will serve as valuable tools in proving the equivalence of the groups H_d^{Δ} and H_d.

Definition 2.3.4 (Chain Complex) *A chain complex is a sequence of abelian groups $\{C_n\}_{n\in\mathbb{Z}}$ connected by homomorphisms $\partial_n : C_n \to C_{n-1}$ (called boundary operators), such that the composition of any two consecutive maps is zero, i.e., $\partial_{n-1} \circ \partial_n = 0$ for all n. Formally, a chain complex is:*

$$\cdots \xrightarrow{\partial_{n+2}} C_{n+1} \xrightarrow{\partial_{n+1}} C_n \xrightarrow{\partial_n} C_{n-1} \xrightarrow{\partial_{n-1}} \cdots \tag{2.68}$$

where $\partial_{n-1} \circ \partial_n = 0$.

Example 2.3.5 *The groups $C_d(X)$ represent the collection of singular d-chains that form a part of a chain complex, where the boundary operator ∂_d is the map between these groups in the respective dimension:*

$$\cdots \to C_{d+1}(X) \xrightarrow{\partial_{d+1}} C_d(X) \xrightarrow{\partial_d} C_{d-1}(X) \to \cdots \tag{2.69}$$

$$\cdots \to C_1(X) \xrightarrow{\partial_1} C_0(X) \xrightarrow{\partial_0} 0. \tag{2.70}$$

Definition 2.3.6 *A chain map f between two chain complexes $(A, \partial^{(A)})$ and $(B, \partial^{(B)})$ is a collection of maps $f_d : A_d \to B_d$ such that for each d, the following condition holds:*

$$\partial_d^{(B)} \circ f_d = f_{d-1} \circ \partial_d^{(A)}. \tag{2.71}$$

Thus, it holds that

$$\begin{array}{ccccccccc}
\cdots & \xrightarrow{\partial_{d+2}^{(A)}} & A_{d+1} & \xrightarrow{\partial_{d+1}^{(A)}} & A_d & \xrightarrow{\partial_d^{(A)}} & A_{d-1} & \xrightarrow{\partial_{d-1}^{(A)}} & \cdots \\
 & & \downarrow{\scriptstyle f_{d+1}} & & \downarrow{\scriptstyle f_d} & & \downarrow{\scriptstyle f_{d-1}} & & \\
\cdots & \xrightarrow{\partial_{d+2}^{(B)}} & B_{d+1} & \xrightarrow{\partial_{d+1}^{(B)}} & B_d & \xrightarrow{\partial_d^{(B)}} & B_{d-1} & \xrightarrow{\partial_{d-1}^{(B)}} & \cdots .
\end{array} \tag{2.72}$$

Theorem 2.3.3 (Chain Maps) *[29, §1.3.1]* A chain map f between two chain complexes $(A, \partial^{(A)})$ and $(B, \partial^{(B)})$ induces a homomorphism between their respective homology groups.

Proof Given a chain map f between two chain complexes $(A, \partial^{(A)})$ and $(B, \partial^{(B)})$, we want to show that f induces a homomorphism $f_\star : H_d(A) \to H_d(B)$.

By definition of a chain map, we have $f_{d-1} \circ \partial_d^{(A)} = \partial_d^{(B)} \circ f_d$. Let $[c] \in Z_d(A)$ be a cycle in A, i.e., $\partial_d^{(A)}(c) = 0$. Applying f to this equation, we obtain:

$$f_{d-1}(\partial_d^{(A)}(c)) = \partial_d^{(B)}(f_d(c)). \tag{2.73}$$

Since $\partial_d^{(A)}(c) = 0$, we have:

$$f_{d-1}(0) = \partial_d^{(B)}(f_d(c)), \tag{2.74}$$

which implies that $\partial_d^{(B)}(f_d(c)) = 0$. Thus, $f_d(c)$ is a cycle in B.

Now, let $[b] \in B_d(A)$ be a boundary in A, i.e., there exists $a \in A_{d+1}$ such that $\partial_{d+1}^{(A)}(a) = b$. Applying f to both sides, we obtain:

$$f_d(\partial_{d+1}^{(A)}(a)) = \partial_{d+1}^{(B)}(f_{d+1}(a)). \tag{2.75}$$

Since $\partial_{d+1}^{(A)}(a) = b$, we have:

$$f_d(b) = \partial_{d+1}^{(B)}(f_{d+1}(a)). \tag{2.76}$$

Therefore, $f_d(b)$ is a boundary in B.

From the above, we see that f maps cycles in A to cycles in B and boundaries in A to boundaries in B. Hence, f induces a well-defined map $f_\star : H_d(A) \to H_d(B)$.

To show that $f_\star$ is a homomorphism, let $[c_1], [c_2] \in H_d(A)$ be two homology classes. We want to show that $f_\star([c_1] + [c_2]) = f_\star([c_1]) + f_\star([c_2])$. Let c_1 and c_2 be representatives of $[c_1]$ and $[c_2]$, respectively. Then, $[c_1] + [c_2]$ is represented by $c_1 + c_2$. Applying f to both sides, we have:

$$f_d(c_1 + c_2) = f_d(c_1) + f_d(c_2). \tag{2.77}$$

Since $f_d(c_1)$ and $f_d(c_2)$ are cycles in B, we have:

$$[f_d(c_1 + c_2)] = [f_d(c_1)] + [f_d(c_2)]. \tag{2.78}$$

Therefore, $f_\star([c_1] + [c_2]) = f_\star([c_1]) + f_\star([c_2])$. $\square$

2.3.2 Exact and Short Exact Sequences

We can apply Theorem 2.3.3 to the case of singular homology. Consider two topological spaces X and Y. For any map $f : X \to Y$, we can define an induced homomorphism $f_\star : C_d(X) \to C_d(Y)$ by composing singular d-simplices $\tilde{\sigma}^{(d)} : \sigma^{(d)} \to X$ with f. Specifically, we have

$$f_\star := f \circ \tilde{\sigma}^{(d)} : \sigma^{(d)} \to Y. \tag{2.79}$$

We can extend this definition by applying $f_\star$ to d-chains in $C_d(X)$. This gives us the following commutative diagram:

$$\begin{array}{ccccccccc} \cdots & \xrightarrow{\partial_{d+2}} & C_{d+1}(X) & \xrightarrow{\partial_{d+1}} & C_d(X) & \xrightarrow{\partial_d} & C_{d-1}(X) & \xrightarrow{\partial_{d-1}} & \cdots \\ & & \big\downarrow{\scriptstyle f_{d+1}} & & \big\downarrow{\scriptstyle f_d} & & \big\downarrow{\scriptstyle f_{d-1}} & & \\ \cdots & \xrightarrow{\partial_{d+2}} & C_{d+1}(Y) & \xrightarrow{\partial_{d+1}} & C_d(Y) & \xrightarrow{\partial_d} & C_{d-1}(Y) & \xrightarrow{\partial_{d-1}} & \cdots. \end{array} \tag{2.80}$$

The chain map f_d gives rise to a homomorphism $f_\star : H_d(X) \to H_d(Y)$. It becomes evident that if X and Y are homeomorphic, meaning there exists a homeomorphism $f : X \to Y$, then the induced map $f_\star$ is an isomorphism.

To formalize the relationships between the homology groups of a topological space X, a subset $A \subset X$, and the quotient space X/A, we introduce the concept of exact sequences.

Definition 2.3.7 (Exact Sequences) *An arrangement of elements in the form*

$$\cdots \to A_{d+1} \xrightarrow{\alpha_{d+1}} A_d \xrightarrow{\alpha_d} A_{d-1} \to \cdots \tag{2.81}$$

is referred to as an exact sequence when the A_i are abelian groups and the α_i are homomorphisms, and it satisfies the condition that $\ker(\alpha_d) = \operatorname{im}(\alpha_{d+1})$ *for all d.*

Remark 2.3.8

- *The condition* $\ker(\alpha_d) = \operatorname{im}(\alpha_{d+1})$ *implies that* $\operatorname{im}(\alpha_{d+1})$ *is a subset of* $\ker(\alpha_d)$*, which is equivalent to $\alpha_d \circ \alpha_{d+1} = 0$. Therefore, an exact sequence can be seen as a chain complex.*
- *Since* $\ker(\alpha_d)$ *is a subset of* $\operatorname{im}(\alpha_{d+1})$*, the homology groups of an exact sequence are trivial.*

Proposition 2.3.4 *[29, §1.3.1]* We can establish the following equivalences:

1. $0 \to A \xrightarrow{a} B$ is exact $\iff \ker(a) = 0$, or a is injective.
2. $A \xrightarrow{a} B \to 0$ is exact $\iff \operatorname{im}(a) = B$, or a is surjective.
3. $0 \to A \xrightarrow{a} B \to 0$ is exact if and only if a is an isomorphism.
4. A sequence of the form
$$0 \to A \xrightarrow{a} B \xrightarrow{b} 0 \tag{2.82}$$
is said to be exact if and only if the following conditions hold:
   - The map $a : A \to B$ is injective, meaning that $\ker(a) = 0$.

- The map $b : B \to 0$ is surjective, meaning that $\mathrm{im}(b) = 0$.
- The kernel of b is equal to the image of a, i.e., $\ker(b) = \mathrm{im}(a)$.
- If $a : A \hookrightarrow B$ is an inclusion, then $B/\mathrm{im}(a) \cong B/A$.

These exact sequences are called short exact sequences.

Proof

1. Assume $0 \to A \xrightarrow{a} B$ is exact. This means $\mathrm{im}(0) = \ker(a)$, which implies $\ker(a) = 0$ since the image of the zero map is always the trivial group. Therefore, a is injective.
   Conversely, suppose $\ker(a) = 0$. We need to show $\mathrm{im}(0) = \ker(a)$. Since $\ker(a) = 0$, the only element mapped to the identity in B is the zero element of A. Thus, the sequence $0 \to A \xrightarrow{a} B$ is exact.
2. Assume $A \xrightarrow{a} B \to 0$ is exact. This means $\mathrm{im}(a) = \ker(0)$, which implies $\mathrm{im}(a) = B$ since the kernel of the zero map is always the entire group. Therefore, a is surjective.
   Conversely, suppose $\mathrm{im}(a) = B$. We need to show $\mathrm{im}(a) = \ker(0)$. Since $\mathrm{im}(a) = B$, every element in B has a preimage in A under the map a. Thus, the sequence $A \xrightarrow{a} B \to 0$ is exact.
3. Assume $0 \to A \xrightarrow{a} B \to 0$ is exact. From the exactness, we have $\ker(a) = \mathrm{im}(0) = 0$ and $\mathrm{im}(a) = \ker(0) = B$. Therefore, a is both injective and surjective, hence an isomorphism.
   Conversely, suppose a is an isomorphism, meaning a is both injective (no kernel) and surjective (maps onto B). Thus, $0 \to A \xrightarrow{a} B \to 0$ is exact, satisfying $\mathrm{im}(0) = \ker(a)$ and $\mathrm{im}(a) = \ker(0)$.
4. Assume the sequence $0 \to A \xrightarrow{a} B \xrightarrow{b} 0$ is exact. a is injective, and $\mathrm{im}(a) = \ker(b)$. As b is the zero map and surjective, $B/\mathrm{im}(a) = 0$, implying $B = \mathrm{im}(a)$. Therefore, a is an isomorphism, thus $B \cong A$.
   Conversely, if a is an isomorphism, $\ker(a) = 0$ and $\mathrm{im}(a) = B$.

$\square$

2.4 Relative Homology

The concept we will now discuss is that of relative homology groups. Let X be a topological space and A a subspace of X. We define $C_d(X, A)$ as the quotient group $C_d(X)/C_d(A)$. This means that chains in A are considered equivalent to the trivial chains in $C_d(X)$.

Since the boundary operator $\partial_d : C_d(X) \to C_{d-1}(X)$ also maps $C_d(A)$ to $C_{d-1}(A)$, a natural boundary map on the quotient group $\partial_d : C_d(X, A) \to$

$C_{d-1}(X, A)$ is obtained. This gives rise to the following sequence:

$$\cdots \to C_{d+1}(X, A) \xrightarrow{\partial_{d+1}} C_d(X, A) \xrightarrow{\partial_d} C_{d-1}(X, A) \to \cdots. \tag{2.83}$$

This sequence forms a chain complex because $\partial_{d+1} \circ \partial_d = 0$. We can then define the relative homology groups $H_d(X, A)$ as the homology groups of this chain complex.

We propose two important facts about $H_d(X, A)$:

Proposition 2.4.1 *[19, §2.1]*

1. Elements in $H_d(X, A)$ are represented by relative cycles, which are d-chains c in $C_d(X)$ such that $\partial_d(c) \in C_{d-1}(A)$.
2. A relative cycle c is trivial in $H_d(X, A)$ if and only if it is a relative boundary, i.e., c is the sum of a chain in $C_d(A)$ and the boundary of a chain in $C_{d+1}(X)$.

Proof

1. Assume $[c] \in H_d(X, A)$ represents a homology class of a chain $c \in C_d(X)$. Since $[c]$ is a class in the relative homology group, $\partial_d(c) \in C_{d-1}(A)$, implying that c is a relative cycle because its boundary maps into A.
   Conversely, if $\partial_d(c) \in C_{d-1}(A)$, then c qualifies as a relative cycle by definition, and any chain homologous to c in $C_d(X)$ that differs from c by a boundary in $C_d(A)$ will also have its boundary in $C_{d-1}(A)$, confirming $[c]$ as an element of $H_d(X, A)$.
2. For a chain c in $C_d(X)$ to be a relative boundary, it must be expressible as $c = a + \partial_{d+1}(b)$ where $a \in C_d(A)$ and $b \in C_{d+1}(X)$. Applying the boundary operator, we have:

$$\partial_d(c) = \partial_d(a) + \partial_d(\partial_{d+1}(b)) = \partial_d(a) + 0 = \partial_d(a). \tag{2.84}$$

   Since $\partial_d(a) \in C_{d-1}(A)$ and $\partial_{d+1}\partial_d = 0$ (as boundaries of boundaries are zero), c is a cycle relative to A, making it trivial in $H_d(X, A)$.
   Conversely, if a relative cycle c is trivial in $H_d(X, A)$, then it must be homologous to a boundary in $C_d(A)$, meaning there exists $a \in C_d(A)$ and $b \in C_{d+1}(X)$ such that $c = a + \partial_{d+1}(b)$.

□

Before we further investigate the decomposition of the relative homology groups into exact sequences, we need an intermediate result for commutative diagrams, which facilitates further argumentation. This intermediate result is also known as the Snake Lemma.

Definition 2.4.1 (Cokernel and Coset) *Let A and B be abelian groups (or modules), and let $a : A \to B$ be a homomorphism. The cokernel of a, denoted by coker(a), is* *defined as the quotient group*

$$\textit{coker}(a) = B/\textit{im}(a). \tag{2.85}$$

For any element $y \in B$, cl(y) represents the coset of y in coker(a), defined by

$$\textit{cl}(y) = y + \textit{im}(a). \tag{2.86}$$

This is the set of all elements in B that differ from y by an element of $\mathrm{im}(a)$. Or, two elements $y_1, y_2 \in B$ satisfy $\mathrm{cl}(y_1) = \mathrm{cl}(y_2)$ if and only if $y_1 - y_2 \in \mathrm{im}(a)$.

Lemma 2.4.2 (Snake Lemma) *[29, §1.2.6]* Consider the following commutative diagram with exact rows:

$$\begin{array}{ccccccccc} 0 & \longrightarrow & A' & \xrightarrow{f'} & A & \xrightarrow{f} & A'' & \longrightarrow & 0 \\ & & \Big\downarrow{\scriptstyle a'} & & \Big\downarrow{\scriptstyle a} & & \Big\downarrow{\scriptstyle a''} & & \\ 0 & \longrightarrow & B' & \xrightarrow{g'} & B & \xrightarrow{g} & B'' & \longrightarrow & 0. \end{array} \tag{2.87}$$

There exists an exact sequence:

$$\ker(a') \xrightarrow{\delta} \ker(a) \xrightarrow{\delta} \ker(a'') \xrightarrow{\delta} \cdots \tag{2.88}$$

$$\cdots \xrightarrow{\delta} \mathrm{coker}(a') \xrightarrow{\delta} \mathrm{coker}(a) \xrightarrow{\delta} \mathrm{coker}(a'') \tag{2.89}$$

with the connecting homomorphism δ.

Proof Consider $x'' \in \ker(a'') \subseteq A''$. Since f is surjective, there exists $x \in A$ such that $f(x) = x''$. We have $a''(x'') = 0$, hence $a''(f(x)) = 0$. By commutativity, $g(a(x)) = 0$, so $a(x) \in \ker(g) = \mathrm{im}(g')$. Thus, there exists $y' \in B'$ such that $g'(y') = a(x)$.

Set $\delta(x'') = \mathrm{cl}(y') \in \mathrm{coker}(a')$. If $x'' = f(x_1'')$, choose x such that $f(x) = x''$, then $a(x) = g'(y_1')$ and $\delta(x'') = \mathrm{cl}(y_1')$. If $x = x_2 + f(x_1)$, then $a(x) = a(x_2) + a(f(x_1))$, with $g(a(x_1)) = 0$ and $a(f(x_1)) \in \mathrm{im}(g')$, so δ is independent of the choice of x. Linear maps remain linear under δ.

Suppose $y'' \in \ker(\delta)$. This means $y'' \in \ker(a'')$ and $\delta(y'') = 0$. There exists $x \in A$ such that $f(x) = y''$ and $a(x) = g'(z')$ for some $z' \in B'$. Since $\delta(y'') = \mathrm{cl}(z') = 0$, we have $z' \in \mathrm{im}(a')$, so $z' = a'(w')$ for some $w' \in A'$. Hence, $a(x) = g'(a'(w')) = a(g(w'))$, so $x - g(w') \in \ker(a)$. Therefore, $y'' = f(x) = f(x - g(w')) \in \mathrm{im}(f)$, showing that $\ker(\delta) = \mathrm{im}(\ker(a) \to \ker(a''))$.

Suppose $y \in \mathrm{coker}(a)$ such that $y \in \ker(\mathrm{coker}(a) \to \mathrm{coker}(a''))$. This means $y = \mathrm{cl}(z)$ for some $z \in B$ with $a(z) = g'(w')$ for some $w' \in B'$. Since $z \in \ker(g)$, we have $z = g(x)$ for some $x \in A$. Thus, $y = \mathrm{cl}(z) = \mathrm{cl}(g(x)) = 0$, showing exactness. $\square$

Theorem 2.4.3 *[19, p.115ff]* The relative homology groups $H_d(X, A)$ are part of the exact sequence:

$$\cdots \to H_d(A) \to H_d(X) \to H_d(X, A) \to H_{d-1}(A) \to \cdots \tag{2.90}$$
$$\cdots \to H_0(X, A) \to 0. \tag{2.91}$$

Proof Consider the following diagram:

$$\begin{tikzcd}
0 \arrow[r] & C_d(A) \arrow[r, hook, "i"] \arrow[d, "\partial_d"] & C_d(X) \arrow[r, two heads, "j"] \arrow[d, "\partial_d"] & C_d(X, A) \arrow[r] \arrow[d, "\partial_d"] & 0 \\
0 \arrow[r] & C_{d-1}(A) \arrow[r, hook, "i"] & C_{d-1}(X) \arrow[r, two heads, "j"] & C_{d-1}(X, A) \arrow[r] & 0.
\end{tikzcd} \tag{2.92}$$

Here, i is the inclusion map $C_d(A) \hookrightarrow C_d(X)$, and j is the quotient map $C_d(X) \twoheadrightarrow C_d(X, A)$. Both rows are exact, and the diagram commutes. This gives rise to a long exact sequence of homology groups by the Snake Lemma 2.4.2.

To clarify, consider the chain complexes

$$A_\bullet = \{C_d(A), \partial_d\}_{d\in\mathbb{N}}, \tag{2.93}$$
$$B_\bullet = \{C_d(X), \partial_d\}_{d\in\mathbb{N}}, \tag{2.94}$$
$$C_\bullet = \{C_d(X, A), \partial_d\}_{d\in\mathbb{N}}. \tag{2.95}$$

The vertical maps i and j are chain maps and thus induce homomorphisms on homology groups $i_\star : H_d(A) \to H_d(X)$ and $j_\star : H_d(X) \to H_d(X, A)$. The exactness of the rows implies that $\ker(j_\star) = \mathrm{im}(i_\star)$.

The connecting homomorphism $\partial : H_d(X, A) \to H_{d-1}(A)$ can be defined as follows: for any class $[c] \in H_d(X, A)$ represented by a cycle $c \in C_d(X)$ with $\partial_d(c) \in C_{d-1}(A)$, choose a chain $b \in C_d(X)$ such that $j(b) = c$. Since c is a cycle, $\partial_d(b) \in \ker(j) = \mathrm{im}(i)$, so there exists a chain $a \in C_{d-1}(A)$ such that $\partial_d(b) = i(a)$. Define $\partial([c]) = [a] \in H_{d-1}(A)$.

We need to verify that the map ∂ is well-defined:

- Uniqueness: If b and b' both map to c via j, then $b - b' \in \ker(j) = \mathrm{im}(i)$. Thus, there exists $a' \in C_{d-1}(A)$ such that $b - b' = i(a')$. Hence,

  $$\partial_d(b) = \partial_d(b') + \partial_d(i(a')) = \partial_d(b') + i(\partial_{d-1}(a')). \tag{2.96}$$

  So, $[a] = [a']$ in $H_{d-1}(A)$, ensuring the uniqueness of $\partial([c])$.
- Homologous chains: If c and c' are homologous in $H_d(X, A)$, then $c - c' = \partial_d(c'')$ for some $c'' \in C_{d+1}(X, A)$. Thus, $b - b' = \partial_{d+1}(c'')$ in $C_d(X)$, and the same argument as above applies.

This establishes the long exact sequence:

$$\cdots \to H_d(A) \to H_d(X) \to H_d(X,A) \to H_{d-1}(A) \to \cdots \tag{2.97}$$
$$\cdots \to H_0(X,A) \to 0. \tag{2.98}$$

□

Proposition 2.4.4 *The map $\partial_d : H_d(C) \to H_{d-1}(A)$ is a homomorphism.*

Proof Let $[c_1], [c_2] \in H_d(C)$ be two homology classes, where $c_1, c_2 \in C_d(X,A)$ are cycles. By definition, let $[a_1] = \partial_d([c_1])$ and $[a_2] = \partial_d([c_2])$. This means that c_1 and c_2 are represented by chains $b_1, b_2 \in C_d(X)$ such that $j(b_1) = c_1$ and $j(b_2) = c_2$.

Since b_1 and b_2 are cycles modulo A, we have:

$$\partial_d(b_1) = i(a_1) \quad \text{and} \quad \partial_d(b_2) = i(a_2). \tag{2.99}$$

We need to show that:

$$\partial_d([c_1] + [c_2]) = [a_1] + [a_2]. \tag{2.100}$$

Consider the sum $c_1 + c_2 \in C_d(X,A)$. By the properties of the quotient map j we yield:

$$j(b_1 + b_2) = j(b_1) + j(b_2) = c_1 + c_2. \tag{2.101}$$

Thus, $b_1 + b_2 \in C_d(X)$ is a preimage of $c_1 + c_2$ under the quotient map j. Furthermore, the boundary of $b_1 + b_2$ is:

$$\partial_d(b_1 + b_2) = \partial_d(b_1) + \partial_d(b_2) = i(a_1) + i(a_2) = i(a_1 + a_2). \tag{2.102}$$

Therefore, the cycle $c_1 + c_2$ maps to the cycle $a_1 + a_2$ under ∂_d, which implies on the respective equivalence classes:

$$\partial_d([c_1] + [c_2]) = [a_1 + a_2] = [a_1] + [a_2]. \tag{2.103}$$

□

Lemma 2.4.5 *[19, p.115ff]* The given sequence,

$$\cdots \to H_d(A) \xrightarrow{i_\star} H_d(B) \xrightarrow{j_\star} H_d(C) \xrightarrow{\partial_d} \cdots \tag{2.104}$$
$$\cdots \xrightarrow{\partial_d} H_{d-1}(A) \xrightarrow{i_\star} H_{d-1}(B) \to \cdots \tag{2.105}$$

is exact.

Proof We need to show that the sequence is exact at each point.

1. Exactness at $H_d(B)$: We need to show that $\ker(j_\star) = \mathrm{im}(i_\star)$. Since $j \circ i = 0$, it follows that $j_\star \circ i_\star = 0$, so $\mathrm{im}(i_\star) \subseteq \ker(j_\star)$.
2. Exactness at $H_d(C)$: We need to show that $\ker(\partial_d) = \mathrm{im}(j_\star)$. By definition, if $[b] \in \mathrm{im}(j_\star)$, then $j_\star([b]) = [c] \in H_d(C)$ where c is a cycle. Therefore, $\partial_d([c]) = 0$, and thus $\mathrm{im}(j_\star) \subseteq \ker(\partial_d)$.
3. Exactness at $H_{d-1}(A)$: We need to show that $\ker(i_\star) = \mathrm{im}(\partial_d)$. If $[c] \in \mathrm{im}(\partial_d)$, then c is a relative boundary. This implies that there exists $b \in B_d$ such that $c = j(b)$. Since $\partial_d(b) = 0$, it follows that $i_\star([c]) = 0$, thus $\mathrm{im}(\partial_d) \subseteq \ker(i_\star)$.
4. Exactness at $H_d(A)$: Let $[b] \in \ker(j_\star)$, meaning $j_\star([b]) = [c] = 0$ in $H_d(C)$. This implies that c is a boundary, i.e., there exists a chain $c' \in C_{d+1}$ such that $c = \partial_{d+1}(c')$. Since j is surjective, $c' = j(b')$ for some $b' \in B_{d+1}$. Thus, $j(b) = \partial_{d+1}(c') = \partial_{d+1} \circ j(b')$, which leads to:
$$j(b - \partial_{d+1}(b')) = 0. \tag{2.106}$$
Hence, $b - \partial_{d+1}(b') = i(a)$ for some $a \in A_d$. Since i is injective, a is a cycle because:
$$i \circ \partial_d(a) = \partial_d \circ i(a) = \partial_d(b - \partial_{d+1}(b')) = \partial_d(b) = 0, \tag{2.107}$$
given that b is a cycle. Thus, $i_\star([a]) = [b]$, and $\mathrm{im}(i_\star) = \ker(j_\star)$.
5. Exactness at $H_d(C)$: Let $[c] \in \ker(\partial_d)$. This means that c is a relative cycle such that $\partial_d([c]) = 0$. Hence, there exists $b \in B_d$ such that $j(b) = c$. Therefore, $\ker(\partial_d) \subseteq \mathrm{im}(j_\star)$.
6. Exactness at $H_{d-1}(A)$: Let $[a] \in \ker(i_\star)$, meaning $i_\star([a]) = 0$ in $H_{d-1}(B)$. Thus, $i(a) = \partial_d(b)$ for some $b \in B_d$. Since $\partial_d(j(b)) = j(\partial_d(b)) = j \circ i(a) = 0$, $j(b)$ is a cycle. Therefore, $\partial_d([j(b)]) = [a]$, which demonstrates that $\ker(i_\star) \subseteq \mathrm{im}(\partial_d)$.

□

Proposition 2.4.6 *[19, p.117f]* The sequence
$$\cdots \to H_d(A) \xrightarrow{i_\star} H_d(X) \xrightarrow{j_\star} H_d(X,A) \xrightarrow{\partial_d} \cdots \tag{2.108}$$
$$\cdots \xrightarrow{\partial_d} H_{d-1}(A) \to \cdots \to H_0(X,A) \to 0 \tag{2.109}$$
is exact.

Proof The exactness of this sequence is a standard result of algebraic topology, which follows from the long exact sequence of the pair (X, A). The maps in this sequence are defined as follows

- $i_\star$ is induced by the inclusion map $i : A \hookrightarrow X$.
- $j_\star$ is induced by the quotient map $j : X \hookrightarrow X/A$, where each chain in X is mapped to its homology class in X/A modulo the image of chains in A.
- ∂_d is the boundary homomorphism connecting homology groups, defined by the boundary of a relative cycle in $H_d(X, A)$, which by definition of a chain complex is a cycle in A in one dimension lower.

The exactness at each point, for example in $H_d(X, A)$, implies that the image of $j_\star$ of $H_d(X)$ is equal to the kernel of ∂_d. This shows that any cycle in $H_d(X, A)$ that becomes trivial in $H_{d-1}(A)$ must come from a cycle in X that is not affected by cycles in A. The exactness in $H_{d-1}(A)$ further implies that the image of ∂_d is exactly the kernel of $i_\star$ that corresponds to cycles in A that are bounderies in X but not in A itself.

The exactness of the entire sequence thus results from the properties of the chain maps and the boundary operators defined in the chain complexes of A, X and X/A. The additional observation that $\partial_d([c])) = [\partial_d(c)]$ for each relative cycle $c \in H_d(X, A)$ extends the continuity of the exact sequence by the boundary mapping, since it connects the homology in one dimension in A with the relative homology in X and A. $\square$

2.5 Excision Theorem

In addition, we refer to the Excision Theorem, a fundamental result in algebraic topology. Simply put, the Excision Theorem allows one to analyse the homology of a space by effectively 'excising' or removing a smaller subspace under certain topological conditions. These conditions usually involve the smaller subspace being 'negligible' in some sense, such as being contained within another subspace. Essentially, this theorem guarantees that, given these conditions, the homology of the original space is preserved compared to the homology of the space with the smaller subspace removed.

To prove the Excision Theorem, we will need the famous Five Lemma.

Lemma 2.5.1 (The Five Lemma) *[19, p.120]* Consider a commutative diagram with exact rows:

$$\begin{array}{ccccccccc}
A & \xrightarrow{i} & B & \xrightarrow{j} & C & \xrightarrow{k} & D & \xrightarrow{l} & E \\
\downarrow{\scriptstyle\alpha} & & \downarrow{\scriptstyle\beta} & & \downarrow{\scriptstyle\gamma} & & \downarrow{\scriptstyle\delta} & & \downarrow{\scriptstyle\epsilon} \\
A' & \xrightarrow{i'} & B' & \xrightarrow{j'} & C' & \xrightarrow{k'} & D' & \xrightarrow{l'} & E'.
\end{array} \tag{2.110}$$

If $\alpha, \beta, \delta, \epsilon$ are isomorphisms, then γ is also an isomorphism.

Proof Commutativity of the diagram ensures that γ is a homomorphism. To show that γ is bijective, we consider:

- Surjectivity: Let $c' \in C'$. Since δ is surjective, there exists $d \in D$ such that $k'(c') = \delta(d)$. Because ϵ is injective, $\epsilon(l(d)) = l'(\delta(d)) = l'(k'(c')) = 0$, thus $l(d) = 0$. By exactness, $d = k(c)$ for some $c \in C$. Therefore, $k'(c' - \gamma(c)) = 0$, and exactness implies $c' - \gamma(c) = j'(b')$ for some $b' \in B'$. With β surjective, $b' = \beta(b)$ for some $b \in B$, hence $\gamma(c + j(b)) = c'$, proving surjectivity of γ.
- Injectivity: Assume $\gamma(c) = 0$. Injectivity of δ and exactness yield $\delta(k(c)) = 0$ and $k(c) = 0$, thus $c = j(b)$ for some $b \in B$. Since $\gamma(j(b)) = j'(\beta(b)) = 0$ and β is injective, $b = i(a)$ for some $a \in A$, giving $c = j(i(a)) = 0$. Therefore, γ has a trivial kernel and is injective.

$\square$

Theorem 2.5.2 (Excision Theorem) *[19, §2.20] Given subspaces $Z \subset A \subset X$ such that $\overline{Z} \subseteq \mathrm{int}(A)$, the inclusion $(X \setminus Z, A \setminus Z) \hookrightarrow (X, A)$ induces isomorphisms in homology*:

$$H_n(X \setminus Z, A \setminus Z) \to H_n(X, A) \quad \text{for all } n. \tag{2.111}$$

Equivalently, for subspaces $A, B \subset X$ whose interiors cover X, the inclusion $(B, A \cap B) \hookrightarrow (X, A)$ induces isomorphisms:

$$H_n(B, A \cap B) \to H_n(X, A) \quad \text{for all } n. \tag{2.112}$$

The equivalence is demonstrated by setting $B = X \setminus Z$ and $Z = X \setminus B$, thereby $A \cap B = A \setminus Z$. The condition $\overline{Z} \subseteq \mathrm{int}(A)$ translates to $X = \mathrm{int}(A) \cup \mathrm{int}(B)$. The proof involves barycentric subdivision, which aids in the computation of homology groups using small singular simplices. In metric spaces, 'smallness' is determined by the diameters of simplices, while in general topological spaces, it is defined by their containment within elements of a cover $\mathcal{U}$. Define $\mathcal{U} = \{U_j\}_{j \in J}$, an open cover of X and J an arbitrary index set, and let $C_n^{\mathcal{U}}(X)$ be the subgroup of $C_n(X)$ consisting of chains $\sum_i n_i \sigma_i$ with each σ_i contained within one of the U_j. The boundary operator $\partial : C_n(X) \to C_{n-1}(X)$ preserves this containment, forming a chain complex $C_n^{\mathcal{U}}(X) \to C_{n-1}^{\mathcal{U}}(X)$. The homology groups of this complex are denoted by $H_n^{\mathcal{U}}(X)$.

Proposition 2.5.3 *According to [19, §2.21], the inclusion $\iota : C_n^{\mathcal{U}}(X) \hookrightarrow C_n(X)$ is a chain homotopy equivalence. There exists a chain map $\rho : C_n(X) \to C_n^{\mathcal{U}}(X)$ such that the compositions $\iota \circ \rho$ and $\rho \circ \iota$ are chain homotopic to the identity, implying that ι induces isomorphisms $H_n^{\mathcal{U}}(X) \cong H_n(X)$ for all n.*

Proof We follow Hatcher's proof [19, §2.21]. The proof is divided into four steps, which initially are geometric and become more algebraic over time.

1. Barycentric Subdivision of Simplices [19, §2.21 (1)]: We recall that the points of a d-simplex $[v_0, \ldots, v_d]$ are given by linear combinations of the form $\sum_i t_i v_i$ with $\sum_i t_i = 1$ and $t_i \geq 0$ for all i.

Definition 2.5.1 (Barycenter) *The barycenter of a d-simplex $[v_0, \ldots, v_d]$ is the point $b = \sum_i t_i v_i$, where the barycentric coordinates are given by $t_i = \frac{1}{d+1}$ for all i.*

Definition 2.5.2 (Barycentric Subdivision) *The barycentric subdivision of a d-simplex $[v_0, \ldots, v_d]$ is the decomposition into d simplices $[b, w_0, \ldots, w_{d-1}]$. The $(d-1)$-simplex $[w_0, \ldots, w_{d-1}]$ is a face in the barycentric subdivision of $[v_0, \ldots, \hat{v}_i, \ldots, v_d]$.*

The base case for $d = 0$ is the barycentric subdivision of $[v_0]$, which is simply $[v_0]$ itself. Inductively, it follows that the barycentric subdivision of $[v_0, \ldots, v_d]$ includes the barycenters of all k-dimensional faces $[v_{i_0}, \ldots, v_{i_k}]$ of $[v_0, \ldots, v_d]$ for $0 \leq k \leq d$. If $k = 0$, we obtain the original vertices v_i, as the barycenter of a 0-simplex is the 0-simplex itself. The barycenter of $[v_{i_0}, \ldots, v_{i_k}]$ has coordinates

$$t_i = \begin{cases} \frac{1}{k+1}, & \text{if } i = i_0, \ldots, i_k, \\ 0, & \text{otherwise.} \end{cases} \tag{2.113}$$

The n-simplices thus form the structure of a simplicial complex.

The diameter of a simplex is defined as the maximum distance between its vertices. Consider a point v and a point of the form $\sum_i t_i v_i$ within the simplex $[v_0, \ldots, v_n]$.

The distance between these two points satisfies the inequality

$$\begin{aligned} \left| v - \sum_i t_i v_i \right| &= \left| \sum_i t_i (v - v_i) \right| && (2.114) \\ &\leq \sum_i t_i \left| v - v_i \right| && (2.115) \\ &\leq \sum_i t_i \max_i \left| v - v_i \right| && (2.116) \\ &= \max_i \left| v - v_i \right|. && (2.117) \end{aligned}$$

This inequality holds due to the convex combination of the vertices and the properties of the norm. Therefore, the distance between any point within the simplex and any of its vertices is bounded above by the maximum distance between the vertices of the simplex.

Let b_i denote the barycenter of the face $[v_0, \ldots, \hat{v}_i, \ldots, v_n]$, where the barycentric coordinates are equal to $\frac{1}{n}$ for each vertex except for v_i, which has $t_i = 0$. It follows that $b = \frac{1}{n+1} v_i + \frac{n}{n+1} b_i$. The sum of the coefficients is 1, so b lies on the line segment $[v_i, b_i]$, and the distance from b to v_i is $\frac{n}{n+1}$ times the length of $[v_i, b_i]$. Therefore, the distance from b to v_i is bounded by $\frac{n}{n+1}$ times the diameter of $[v_0, \ldots, v_n]$. This bound is independent of the shape of the simplex. If two points w_j and w_k in a simplex are not the barycenter, then these points lie on a proper face of $[v_0, \ldots, v_n]$. Thus, the same bound applies inductively to all 0-simplices. For the repeated r-fold barycentric subdivision, we obtain

$$\left(\frac{n}{n+1}\right)^r \xrightarrow{r \to \infty} 0, \tag{2.118}$$

which implies that the barycentric subdivision can be made with an arbitrarily small diameter.

2. Barycentric Subdivision of Linear Chains [19, §2.21 (2)]: We construct now the subdivision operator $S : C_n(X) \to C_n(X)$ and show, that it is chain homotopic to the identity map.

For a convex set Y in Euclidean space, the linear maps $\lambda : \sigma^{(n)} \to Y$ generate a subgroup of $C_n(Y)$, which we denote by $LC_n(Y)$, the so-called linear chains. The boundary operator $\partial : C_n(Y) \to C_{n-1}(Y)$ maps $LC_n(Y)$ to $LC_{n-1}(Y)$, hence the linear chains form a subcomplex of the singular chain complex of Y. We define the unique map $\lambda : \sigma^{(n)} \to Y$ by $[w_0, \ldots, w_n]$, where w_i is the image of the i-th vertex of $\sigma^{(n)}$ under λ. To avoid the constant case distinction regarding the 0-simplices, we complete the complex $LC(Y)$ by defining $LC_{-1}(Y) = \mathbb{Z}$, generated by the equivalence class of the empty simplex $[\emptyset]$, with $\partial[w_0] = [\emptyset]$ for all 0-simplices $[w_0]$. Let us now go into more detail.

Consider the n-simplex $\sigma^{(n)}$, defined as convex hull of its vertices $\{v_0, \ldots, v_n\}$ in Euclidean space. A linear map $\lambda : \sigma^{(n)} \to Y$ is determined by the images of the vertices v_i, and thus λ is entirely defined by the points $w_i = \lambda(v_i)$ in Y. The image $\lambda(\sigma^{(n)})$ is a linear simplex in Y, and the subgroup $LC_n(Y)$ consists of formal sums of such linear simplices. The boundary of a linear simplex $[w_0, \ldots, w_n]$ is given by the alternating sum

$$\partial[w_0, \ldots, w_n] = \sum_{i=0}^{n} (-1)^i [w_0, \ldots, \hat{w}_i, \ldots, w_n], \tag{2.119}$$

where $\hat{w}_i$ denotes the omission of the vertex w_i. Since each face of a linear simplex is itself a linear simplex, ∂ maps $LC_n(Y)$ into $LC_{n-1}(Y)$, ensuring that $LC_\bullet(Y)$ is a subcomplex of the singular chain complex $C_\bullet(Y)$.

Finally, to extend the chain complex to include negative degrees, we define the group $LC_{-1}(Y)$ to be the integers $\mathbb{Z}$, generated by the empty simplex $[\emptyset]$. The boundary of any 0-simplex $[w_0]$ is defined to be the empty simplex, i.e., $\partial[w_0] = [\emptyset]$, for all 0-simplices $[w_0]$. This extension allows us to treat the boundary operator uniformly across all dimensions, including the trivial case where the simplex has no vertices.

Each point $b \in Y$ defines a homomorphism $b : LC_n(Y) \to LC_{n+1}(Y)$ on the basis elements, given by $b([w_0, \ldots, w_n]) \mapsto [b, w_0, \ldots, w_n]$. Now, applying the boundary operator ∂ to $b(\alpha)$, we obtain

$$\partial b([w_0, \ldots, w_n]) = [w_0, \ldots, w_n] - b(\partial[w_0, \ldots, w_n]). \tag{2.120}$$

Due to linearity, it follows that

$$\partial b(\alpha) = \alpha - b(\partial\alpha) \quad \text{for any } \alpha \in LC_n(Y). \tag{2.121}$$

This shows the equivalence of the equations $\partial b(\alpha) = \alpha - b(\partial\alpha)$ and $\partial b + b\partial = \mathrm{id}$, meaning that b is a chain homotopy between the identity map and the zero map of the completed complex $LC(Y)$.

As a consequence, the subdivision homomorphism $S : LC_n(Y) \to LC_n(Y)$ can be defined inductively over n. Now let $\sigma^{(n)}$ be a generator of $LC_n(Y)$, and let b_λ be the image of the barycentre of $\sigma^{(n)}$ under λ. We define the value of $S(\lambda)$ as $b_\lambda(S\partial\lambda)$, such that $b_\lambda : LC_{n-1}(Y) \to LC_n(Y)$.

The beginning of the induction shows that $S([\emptyset]) = [\emptyset]$ applies, so that S is the identity on $LC_{-1}(Y)$. Consequently, this mapping is also the identity on $LC_0(Y)$, as the following applies for $n = 0$:

$$S([w_0]) = w_0(S(\partial[w_0])) = w_0(S([\emptyset])) = w_0([\emptyset]) = w_0. \tag{2.122}$$

Provided that λ is an embedding with $\mathrm{ran}(\lambda) = [w_0, \ldots, w_n]$, $S(\lambda)$ can be defined as the sum of the n-simplices in the barycentric subdivision of $[w_0, \ldots, w_n]$. Since $S = \mathbb{I}$ applies to $LC_0(Y)$ and $LC_{-1}(Y)$, it follows for all further $n \in \mathbb{N}$ that

$$\begin{aligned}
\partial S\lambda &= \partial b_\lambda(S\partial\lambda), && (2.123)\\
&= S\partial\lambda - b_\lambda\partial(S\partial\lambda) \quad \text{since } \partial b_\lambda = \mathbb{I} - b_\lambda\partial, && (2.124)\\
&= S\partial\lambda - b_\lambda S(\partial\partial\lambda) \quad \text{since } \partial S(\partial\lambda) = S\partial(\partial\lambda) \text{ for all } n, && (2.125)\\
&= S\partial\lambda \quad \text{since } \partial\partial = 0. && (2.126)
\end{aligned}$$

Thus, the chain map $S : LC(Y) \to LC(Y)$ satisfies $\partial S = S\partial$.

Next, we define a chain homotopy $T : LC_n(Y) \to LC_{n+1}(Y)$ between S and the identity, such that the following diagram commutes:

$$\begin{tikzcd}
\cdots \arrow[r] & LC_2(Y) \arrow[r] \arrow[d, "S"] & LC_1(Y) \arrow[r] \arrow[d, "S"] \arrow[dl, "T"] & LC_0(Y) \arrow[r] \arrow[d, "{S,\mathbb{I}}"] \arrow[dl, "T"] & LC_{-1}(Y) \arrow[r] \arrow[d, "{S,\mathbb{I}}"] \arrow[dl, "{T,0}"] & 0 \\
\cdots \arrow[r] & LC_2(Y) \arrow[r] & LC_1(Y) \arrow[r] & LC_0(Y) \arrow[r] & LC_{-1}(Y) \arrow[r] & 0.
\end{tikzcd} \tag{2.127}$$

We define T on $LC_n(Y)$ inductively by setting $T = 0$ for $n = -1$ and $T\lambda = b_\lambda(\lambda - T\partial\lambda)$ for $n \geq 0$. This formula is an inductive definition of the barycentric subdivision of $\sigma^{(n)} \times \mathbb{I}$ obtained by the union of all simplices in $\sigma^{(n)} \times \{0\} \cup \partial\sigma^{(n)} \times \mathbb{I}$ to the barycentre of $\sigma^{(n)} \times \{1\}$. The chain homotopy formula is $\partial T + T\partial = \mathbb{I} - S$. This is trivial for $LC_{-1}(Y)$, where $T = 0$ and $S = \mathbb{I}$. The formula for $LC_n(Y)$ for all $n \geq 0$ is given by:

$$
\begin{aligned}
\partial T\lambda &= \partial b_\lambda(\lambda - T\partial\lambda), && (2.128)\\
&= \lambda - T\partial\lambda - b_\lambda\partial(\lambda - T\partial\lambda) && (2.129)\\
&= \lambda - T\partial\lambda - b_\lambda[\partial\lambda - \partial T(\partial\lambda)] && (2.130)\\
&= \lambda - T\partial\lambda - b_\lambda[S(\partial\lambda) + T\partial(\partial\lambda)] && (2.131)\\
&= \lambda - T\partial\lambda - S\lambda. && (2.132)
\end{aligned}
$$

Now we can drop the group $LC_{-1}(Y)$ again, and the relation $\partial T + T\partial = \mathbb{I} - S$ still holds since T is zero for $LC_{-1}(Y)$.

3. Barycentric Subdivision of General Chains [19, §2.21 (3)]: Consider the chain complex $C_n(X)$. Define the operator $S : C_n(X) \to C_n(X)$ by $S\sigma = \sigma_\star S\sigma^{(n)}$, where $\sigma : \sigma^{(n)} \to X$ is a singular n-simplex, and $S\sigma^{(n)}$ denotes the barycentric subdivision of the standard n-simplex $\sigma^{(n)}$. The barycentric subdivision $S\sigma^{(n)}$ is a signed sum of the n-simplices that make up the subdivision of $\sigma^{(n)}$.

We will now prove that S is a chain map, i.e., that S commutes with the boundary operator, $S\partial = \partial S$. For a singular n-simplex σ, we compute:

$$
\begin{aligned}
\partial S\sigma &= \partial(\sigma_\star S\sigma^{(n)}) = \sigma_\star\partial(S\sigma^{(n)}) = \sigma_\star S(\partial\sigma^{(n)}) && (2.133)\\
&= \sigma_\star S\left(\sum_i (-1)^i \sigma_i^{(n)}\right) = \sum_i (-1)^i \sigma_\star S(\sigma_i^{(n)}) && (2.134)\\
&= \sum_i (-1)^i S(\sigma|\sigma_i^{(n)}) = S\left(\sum_i (-1)^i \sigma|\sigma_i^{(n)}\right) = S(\partial\sigma). && (2.135)
\end{aligned}
$$

Next, define the operator T on $C_n(X)$ by $T\sigma = \sigma_\star T\sigma^{(n)}$, where $\sigma_\star$ denotes the pullback by $T\sigma^{(n)}$. We will show that T provides a chain homotopy between the subdivision operator S and the identity map, satisfying $T\partial + \partial T = \mathbb{I} - S$. The verification is as follows:

$$
\begin{aligned}
\partial T\sigma &= \partial(\sigma_\star T\sigma^{(n)}) = \sigma_\star(\partial T\sigma^{(n)}) && (2.136)\\
&= \sigma_\star(\sigma^{(n)} - S\sigma^{(n)} - T\partial\sigma^{(n)}) && (2.137)\\
&= \sigma - S\sigma - \sigma_\star T\partial\sigma^{(n)} && (2.138)\\
&= \sigma - S\sigma - T(\partial\sigma). && (2.139)
\end{aligned}
$$

4. Iterated Barycentric Subdivision [19, §2.21 (4)]: A chain homotopy between the identity map $\mathbb{I}$ and the iterate S^m is given by the operator $D_m = \sum_{0\leq i<m} TS^i$. The following calculation verifies this:

$$\partial D_m + D_m\partial = \sum_{0\leq i<m} (\partial TS^i + TS^i\partial) = \sum_{0\leq i<m} (\partial TS^i + T\partial S^i) \tag{2.140}$$

$$= \sum_{0\leq i<m} (\partial T + T\partial)S^i = \sum_{0\leq i<m} (\mathbb{I} - S)S^i \tag{2.141}$$

$$= \sum_{0\leq i<m} (S^i - S^{i+1}) = \mathbb{I} - S^m. \tag{2.142}$$

In the calculation, we use the fact that $\partial T + T\partial = \mathbb{I} - S$, which shows that D_m serves as a homotopy between the identity map $\mathbb{I}$ and S^m. For each singular n-simplex $\tilde{\sigma}^{(n)} : \sigma^{(n)} \to X$, there exists an integer m such that $S^m(\sigma)$ lies in $C_n^{\mathcal{U}}(X)$, where $\mathcal{U}(X)$ is an open cover of X. In this context, $C_n^{\mathcal{U}}(X)$ denotes the chain complex where simplices are refined to align with the cover $\mathcal{U}$. This holds because, for sufficiently large m, the simplices of $S^m(\sigma^{(n)})$ have diameters smaller than a Lebesgue number for the cover of $\sigma^{(n)}$ by the open sets $(\tilde{\sigma}^{(n)})^{-1}(\mathrm{int}(U_j))$.[1]

We define the operator $D : C_n(X) \to C_{n+1}(X)$ by $D\tilde{\sigma}^{(n)} := D_{m(\tilde{\sigma}^{(n)})}(\tilde{\sigma}^{(n)})$ for each singular n-simplex $\tilde{\sigma}^{(n)} : \sigma^{(n)} \to X$. Our objective is to find a chain map $\rho : C_n(X) \to C_n(X)$ whose image lies in $C_n^{\mathcal{U}}(X)$, and which satisfies the chain homotopy equation

$$\partial D + D\partial = \mathbb{I} - \rho. \tag{2.143}$$

A straightforward approach is to define ρ directly from this equation. Specifically, we set

$$\rho = \mathbb{I} - \partial D - D\partial. \tag{2.144}$$

We can easily verify that ρ is a chain map by calculating:

$$\partial\rho(\tilde{\sigma}^{(n)}) = \partial\tilde{\sigma}^{(n)} - \partial^2 D\tilde{\sigma}^{(n)} - \partial D\partial\tilde{\sigma}^{(n)} = \partial\tilde{\sigma}^{(n)} - \partial D\partial\tilde{\sigma}^{(n)}, \tag{2.145}$$

$$\rho(\partial\tilde{\sigma}^{(n)}) = \partial\tilde{\sigma}^{(n)} - \partial D\partial\tilde{\sigma}^{(n)} - D\partial^2\tilde{\sigma}^{(n)} = \partial\tilde{\sigma}^{(n)} - \partial D\partial\tilde{\sigma}^{(n)}. \tag{2.146}$$

[1] The Lebesgue number is a positive real number ϵ such that any set with diameter less than ϵ is contained within some element of the cover. The existence of such a number is guaranteed by the compactness of $\sigma^{(n)}$. Since m may vary depending on $\tilde{\sigma}^{(n)}$, we define $m(\tilde{\sigma}^{(n)})$ as the smallest integer such that $S^m(\tilde{\sigma}^{(n)})$ lies in $C_n^{\mathcal{U}}(X)$.

To ensure that ρ maps $C_n(X)$ to $C_n^{\mathcal{U}}(X)$, we compute $\rho(\tilde{\sigma}^{(n)})$:

$$\begin{aligned}
\rho(\tilde{\sigma}^{(n)}) &= \tilde{\sigma}^{(n)} - \partial D\tilde{\sigma}^{(n)} - D(\partial\tilde{\sigma}^{(n)}) \\
&= \tilde{\sigma}^{(n)} - \partial D_{m(\tilde{\sigma}^{(n)})}(\tilde{\sigma}^{(n)}) - D(\partial\tilde{\sigma}^{(n)}) \\
&= S_{m(\tilde{\sigma}^{(n)})}(\tilde{\sigma}^{(n)}) + D_{m(\tilde{\sigma}^{(n)})}(\partial\tilde{\sigma}^{(n)}) - D(\partial\tilde{\sigma}^{(n)}),
\end{aligned} \tag{2.147}$$

where the last equality follows from $\partial D_{m(\tilde{\sigma}^{(n)})} + D_{m(\tilde{\sigma}^{(n)})}\partial = \mathbb{I} - S_{m(\tilde{\sigma}^{(n)})}$.

The term $S_{m(\tilde{\sigma}^{(n)})}(\tilde{\sigma}^{(n)})$ lies in $C_n^{\mathcal{U}}(X)$ by the definition of $m(\tilde{\sigma}^{(n)})$. The remaining terms, $D_{m(\tilde{\sigma}^{(n)})}(\partial\tilde{\sigma}^{(n)}) - D(\partial\tilde{\sigma}^{(n)})$, are linear combinations of terms of the form $D_{m(\tilde{\sigma}^{(n)})}(\tilde{\sigma}_j^{(n)}) - D_{m(\tilde{\sigma}_j^{(n)})}(\tilde{\sigma}_j^{(n)})$, where $\tilde{\sigma}_j^{(n)}$ denotes the restriction of $\tilde{\sigma}^{(n)}$ to a face of $\sigma^{(n)}$. Since $m(\tilde{\sigma}_j^{(n)}) \le m(\tilde{\sigma}^{(n)})$, the difference $D_{m(\tilde{\sigma}^{(n)})}(\tilde{\sigma}_j^{(n)}) - D_{m(\tilde{\sigma}_j^{(n)})}(\tilde{\sigma}_j^{(n)})$ consists of terms $TS^i(\tilde{\sigma}_j^{(n)})$ with $i \ge m(\tilde{\sigma}_j^{(n)})$. These terms lie in $C_n^{\mathcal{U}}(X)$ because the operator T maps $C_{n-1}^{\mathcal{U}}(X)$ into $C_n^{\mathcal{U}}(X)$. Viewing ρ as a chain map from $C_n(X)$ to $C_n^{\mathcal{U}}(X)$, the equation $\partial D + D\partial = \mathbb{I} - \iota\rho$ holds, where $\iota : C_n^{\mathcal{U}}(X) \hookrightarrow C_n(X)$ is the inclusion map. Moreover, $\rho\iota = \mathbb{I}$ since D is identically zero on $C_n^{\mathcal{U}}(X)$. This follows because $m(\tilde{\sigma}^{(n)}) = 0$ for any $\tilde{\sigma}^{(n)} \in C_n^{\mathcal{U}}(X)$, implying that the sum defining $D\tilde{\sigma}^{(n)}$ is empty. Consequently, ρ is a chain homotopy inverse to ι. $\square$

We may now prove the Excision Theorem, which states that for a space $X = A \cup B$, the inclusion map induces an isomorphism $H_n(B, A\cap B) \cong H_n(X, A)$.

Proof Consider the open cover $\mathcal{U} = \{A, B\}$ of X, and define the chain complex $C_n(A + B)$ as the subgroup of $C_n(X)$ generated by chains in A and chains in B, i.e., $C_n(A + B) = C_n(A) + C_n(B)$. The inclusion $C_n(A + B) \subset C_n(X)$ induces a map on the quotient complexes:

$$C_n(A + B)/C_n(A) \to C_n(X)/C_n(A). \tag{2.148}$$

Recall that we previously established the identities

$$\partial D + D\partial = \mathbb{I} - \iota\rho, \tag{2.149}$$

$$\rho\iota = \mathbb{I}, \tag{2.150}$$

where D is a chain homotopy, ι denotes the inclusion, and ρ is the associated chain map. These identities persist after passing to the quotient complexes, thus the inclusion induces an isomorphism on homology:

$$H_n(C_\bullet(A + B)/C_\bullet(A)) \cong H_n(C_\bullet(X)/C_\bullet(A)). \tag{2.151}$$

Now, consider the quotient chain complex $C_n(B)/C_n(A \cap B)$. This complex is naturally isomorphic to $C_n(A+B)/C_n(A)$ since both are spanned by singular n-simplices in B that are not entirely contained in A. Therefore, the inclusion map induces an isomorphism:

$$C_n(B)/C_n(A \cap B) \cong C_n(A+B)/C_n(A). \tag{2.152}$$

Given that these quotient complexes are free with bases consisting of singular n-simplices in B not contained in A, the induced map is indeed an isomorphism. Consequently, the inclusion $(B, A \cap B) \hookrightarrow (X, A)$ induces an isomorphism on homology:

$$H_n(B, A \cap B) \cong H_n(X, A). \tag{2.153}$$

□

2.6 Equivalence of $H_d^{\Delta}(X)$ and $H_d(X)$

We want to establish the equivalence of the homology groups $H_d^{\Delta}(X)$ and $H_d(X)$. Note that simplicial homology groups $H_d^{\Delta}(X)$ are defined only for simplicial complexes, whereas singular homology groups $H_d(X)$ can be computed for any topological space. This generality is advantageous, since homeomorphic spaces have isomorphic singular homology groups, allowing the introduction of a simplicial structure into any triangulible topological space.

To prove the equivalence between $H_d^{\Delta}(X)$ and $H_d(X)$, we establish an isomorphism between these groups for all dimensions d. A homomorphism naturally follows from the map $C_d^{\Delta}(X) \to C_d(X)$, which sends every d-simplex in X to a singular simplex via the mapping $\tilde{\sigma}^{(d)} : \sigma^{(d)} \to X$. This induces a homomorphism from $H_d^{\Delta}(X)$ to $H_d(X)$.

Theorem 2.6.1 **($H_d^{\Delta}(X) \cong H_d(X)$)** *[19, p.102f]* For each integer d, the homomorphisms from the simplicial homology group $H_d^{\Delta}(X)$ to the singular homology group $H_d(X)$ are isomorphisms. Hence, the simplicial and singular homology groups are equivalent for all dimensions.

Proof Consider a simplicial complex X. For each k-skeleton X^k, the inclusion $X^{k-1} \subset X^k$ leads to the following commutative diagram of exact sequences:

X^k/X^{k-1} contains only simplices of dimension k, thus, $C_d(X^k, X^{k-1})$ is trivial for $d \neq k$ and a free abelian group for $d = k$, with a basis formed by the k-simplices of X.

$$\begin{array}{ccccccccc}
H_{d+1}^{\Delta}(X^k, X^{k-1}) & \longrightarrow & H_d^{\Delta}(X^{k-1}) & \longrightarrow & H_d^{\Delta}(X^k) & \longrightarrow & H_d^{\Delta}(X^k, X^{k-1}) & \longrightarrow & H_{d-1}^{\Delta}(X^{k-1}) \\
\downarrow & & \downarrow & & \downarrow & & \downarrow & & \downarrow \\
H_{d+1}(X^k, X^{k-1}) & \longrightarrow & H_d(X^{k-1}) & \longrightarrow & H_d(X^k) & \longrightarrow & H_d(X^k, X^{k-1}) & \longrightarrow & H_{d-1}(X^{k-1})
\end{array}$$

Figure 2.1: Commutative diagram of exact sequences for homology and relative homology of a triangulable topological space X.

We define a characteristic map $\Phi : \coprod_i (\sigma_i^{(k)}, \sigma_i^{(k-1)}) \to (X^k, X^{k-1})$, inducing a homeomorphism

$$\Phi_* : \coprod_i \sigma_i^{(k)} / \coprod_i \sigma_i^{(k-1)} \to X^k / X^{k-1}.$$

By the Excision Theorem,

$$H_d^{\Delta}\left(\coprod_i (\sigma_i^{(k)}, \sigma_i^{(k-1)})\right) \cong H_d(X^k, X^{k-1}) \cong H_d(X^k / X^{k-1}),$$

establishing isomorphisms for $H_d(X^k, X^{k-1})$.

Using induction and assuming that the necessary homology isomorphisms hold for dimensions less than k, we extend the isomorphism to all dimensions:

$$H_k^{\Delta}(X^k, X^{k-1}) \cong H_k(X^k, X^{k-1}). \tag{2.154}$$

The Five Lemma supports the isomorphism between $H_k^{\Delta}(X^k, X^{k-1})$ and $H_k(X^k, X^{k-1})$. Thus, we conclude that

$$H_d^{\Delta}(X^k, X^{k-1}) \to H_d(X^k, X^{k-1})$$

is an isomorphism for all d, verifying the equivalence of simplicial and singular homology for all k. $\square$

Chapter 3

Homological Persistence

The focus of this chapter is on persistent homology and shows how it identifies multiscale topological features using filtrations of complexes on point clouds. We discuss barcode isomorphisms and persistence modules that visualise and explain the stability of the detected features within a filtration against perturbations of the data. The chapter concludes with persistent chain complexes and the cohomology of these structures, which improve our understanding of the evolution of the topology of filtrations on point clouds. We also explore distances between persistence modules and the stability theorem to provide metrics for comparing topological features and ensure the statistical robustness of persistent homology.

3.1 Filtrations of Complexes

In the following individual (co)homology groups are defined with coefficients in a fixed field $\mathbb{F}$ and form a graded module over $\mathbb{F}[x]$. Replacing the field $\mathbb{F}$ by the ring $\mathbb{Z}$ leads to substantial problems, but most results still hold for principal ideal domains, as discussed in [30, §3.1].

We investigate the persistent topology of filtered topological spaces, with a primary focus on the prototypical example of a filtered cell complex. This structure is defined by a sequence $\mathcal{X}$ of cell complexes:

$$\mathcal{X} : \emptyset \subset X_1 \subset X_2 \subset \cdots \subset X_n = X_\infty, \tag{3.1}$$

where X_1 starts with a single vertex σ_1, and each subsequent complex X_i is constructed by adding a single cell to the previous complex:

$$X_i := X_{i-1} \cup \sigma_i. \tag{3.2}$$

Here, the indexing set is $\{1, 2, \ldots, n\}$. Additionally, associated real values a_i are assigned to these indices, satisfying $a_1 \leq a_2 \leq \cdots \leq a_n$. This formulation clearly delineates the stepwise enlargement of the complex, illustrating the dynamic evolution of its topology as new cells are incrementally incorporated.

We will use the same running example as in [10, §2.2].

Example 3.1.1 *The chosen illustrative example involves a cellular filtration of the 2-sphere, denoted by $\mathcal{S}^2$. This process constructs a cell complex and introduces an ordering among the cells to facilitate differentiation between them. The development of the filtration can be articulated as follows [10, §2.2]:*

$$\begin{aligned}
\mathcal{S}^2 : \ & \emptyset \\
& \subset \ S_1 = \{\sigma_1\} \\
& \subset \ S_2 = \{\sigma_1, \sigma_2\} \\
& \subset \ S_3 = \{\sigma_1, \sigma_2, \sigma_3 := (\sigma_1, \sigma_2)\} \\
& \subset \ S_4 = \{\sigma_1, \sigma_2, \sigma_3, \sigma_4 := (\sigma_2, \sigma_1)\} \\
& \subset \ S_5 = \{\sigma_1, \sigma_2, \sigma_3, \sigma_4, \sigma_5 := (\sigma_3, \sigma_4)\} \\
& \subset \ S_6 = \{\sigma_1, \sigma_2, \sigma_3, \sigma_4, \sigma_5, \sigma_6 := (\sigma_4, \sigma_3)\}.
\end{aligned}$$

In this sequence, the cell σ_1 symbolizes the initial point. The set S_2 incorporates two distinct points. In S_3, a path connecting σ_1 and σ_2 is introduced. S_4 augments this path with its reverse from σ_2 to σ_1 clearly distinguishing it from σ_3. Finally, S_5 and S_6 progressively differentiate between cells that represent the upper and lower halves of the sphere, respectively.

3.2 Persistence Modules

The persistent homology is obtained by applying the homology functor to a filtration of a topological space. This section will examine the concept of persistent modules, which serve to describe persistent homology from a mathematical perspective. Similarly, as filtrations describe the evolution of a simplicial complex under a one-parameter or multi-parameter family, the persistence module describes the evolution of associated vector spaces. In the case of homology vector spaces or modules, the dimension or rank of the associated homomorphisms is the Betti number, which indicates the number of k-dimensional holes of a topological space in the intuitive sense.

Definition 3.2.1 (Persistence Module) *[7, §1.1]* A persistence module is a collection of vector spaces $\{V_i\}_{i\in I}$ over a partially ordered index set $(I, \leq)$ together with linear maps

$$\phi_r^s : V_r \to V_s, \quad \forall r \leq s, \tag{3.3}$$

such that $\phi_r^t = \phi_s^t \circ \phi_r^s$ and $\phi_r^r = \mathbb{I}_{V_r}$ for all $r \leq s \leq t$.

We rephrase this definition in categorical language, which makes it easier for us to define the normal form of persistence modules. Persistence modules have a decomposition into interval modules, which cannot be further decomposed. Therefore, an interval modulus is a persistence module that cannot be decomposed.

Let $\mathbb{F}$ be a field and $\mathrm{Vect}_{\mathbb{F}}$ the category of finite dimensional vector spaces over $\mathbb{F}$. The real numbers are a partially ordered category $(\mathbb{R}, \leq)$. In the following we consider the real persistence module.

Definition 3.2.2 (Persistence module) *[7, §1.3]* A persistence module is a functor $V : (\mathbb{R}, \leq) \to \mathrm{Vect}_F$. It is uniquely defined by a family $\{V_r\}_{r\in\mathbb{R}}$ of finite dimensional vector spaces over $\mathbb{F}$ together with morphisms $\phi_r^s : V_r \to V_s, r \leq s$, so that the diagram commutes:

$$\begin{tikzcd} V_r \arrow[r, "\phi_r^s"] \arrow[d, "\phi_r^t"'] & V_s \\ V_t. \arrow[ur, "\phi_t^s"'] & \end{tikzcd} \tag{3.4}$$

A morphism of persistence modules is a natural transformation. This can be written as $f_r : V_r \to V_r'$, which is compatible with the mappings ϕ_r^s. This defines the category Pers of persistence modules.

The category of persistence modules is abelian. A notable consequence of the aforementioned results is that a part of the constructions for persistence modules remain valid when the category of finite-dimensional vector spaces over a field is replaced by another abelian category. This includes, for instance, vector spaces over other fields. It is also possible to consider persistence modules over cochain complexes in place of vector spaces. In the following section, we will make a number of simplifying assumptions:

a) For all $r \in \mathbb{R}\backslash S$, where S is a finite subset, there exists a neighbourhood U_r of r such that the map $\phi_u^{u'}$ is an isomorphism for all $u \leq u'$ in U_r.
b) $V_u = 0$ for u sufficiently small.
c) For all $t \in \mathbb{R}$ and for all $s \leq t$ with $t - s$ sufficiently small, the mapping ϕ_s^t is an isomorphism.

The conditions a) and b) are referred to as finite type conditions. Condition a) implies that there is a finite number of 'jumps', while we have that $V_u = V_\infty$ for u large enough. Condition c) is called semi-continuity and can be visualised by the following indecomposable interval modules:

Normal Form

3.2.1 Persistent Homology on Complexes

In the context of algebraic topology, applying the homology functor H to a filtration of a complex $\mathcal{X}$ yields a sequence of algebraic structures:

$$\mathsf{H}(\mathcal{X}): \quad \mathsf{H}(X_1) \to \mathsf{H}(X_2) \to \cdots \to \mathsf{H}(X_n), \tag{3.5}$$

where $\mathsf{H}(-)$ generally represents either the k-th dimensional homology, denoted by $H_k(-;\mathbb{F})$, or the total homology, expressed as $H_\bullet(-;\mathbb{F})$. Here, this diagram characterizes a sequence of abelian groups or finite-dimensional vector spaces, interconnected through vector space homomorphisms, forming what is known as a persistence module.

Persistence modules are central to understanding how the features of a space evolve over time. They can typically be decomposed into a direct sum of interval modules [12, §8]. Each interval module is associated with an ordered pair of integers (p, q) where $1 \leq p \leq q \leq n$, within a finite filtration. These pairs (p, q) signify topological features that persist over an index set $I := \{p, \ldots, q\}$, where $\inf\{I\} = p$ and $\sup\{I\} = q$. Conventionally, these tuples are interpreted as half-open intervals $[a_p, a_{q+1})$, with $a_{n+1} = \infty$ being a customary notation when the sequence extends beyond the largest indexed space.

The decomposition of a persistence module into its constituent interval modules is represented in a persistence diagram or a barcode. This barcode is a multiset of ordered tuples (p, q) or, alternatively, a multiset of half-open intervals $[a_p, a_{q+1})$. This collection is formally expressed through the forgetful functor **Pers**$(-)$:

$$\begin{aligned} \mathbf{Pers}(\mathsf{H}(\mathcal{X})) &= \{(p_1, q_1), \ldots, (p_m, q_m)\} && (3.6) \\ &\cong \{[a_{p_1}, a_{q_1+1}), \ldots, [a_{p_m}, a_{q_m+1})\}. && (3.7) \end{aligned}$$

In practical applications, intervals where $a_p = a_{q+1}$ are usually omitted, as they represent ephemeral topological features.

Example 3.2.3 *In the further elaboration of the example [10, §2.2], we consider the topological subspaces S_1, S_3, S_5, all of which are contractible. Meanwhile, S_2, S_4, S_6 are homeomorphic to the 0-sphere, 1-sphere, and 2-sphere, respectively. This structural distinction leads to four distinct intervals in the persistence diagram of the total homology of a sphere, specifically $\mathcal{S}^2$:*

$$\begin{aligned} \boldsymbol{Pers}(H_\bullet(\mathcal{S}^2)) &= \{(1,6)_0, (2,2)_0, (4,4)_1, (6,6)_2\} && (3.8) \\ &= \{(1,\infty)_0, (2,3)_0, (4,5)_1, (6,\infty)_2\}. && (3.9) \end{aligned}$$

Here, the subscript k in $(p, q)_k$ or $[a_p, a_{q+1})_k$ denotes a topological feature in the k-

$$
\begin{aligned}
H_\bullet(\mathcal{X}): &\quad H_\bullet(X_1) \to \cdots \to H_\bullet(X_{n-1}) \to H_\bullet(X_n),\\
H^\bullet(\mathcal{X}): &\quad H^\bullet(X_1) \leftarrow \cdots \leftarrow H^\bullet(X_{n-1}) \leftarrow H^\bullet(X_n),\\
H_\bullet(X_\infty, \mathcal{X}): &\quad H_\bullet(X_n) \to H_\bullet(X_n, X_1) \to \cdots \to H_\bullet(X_n, X_{n-1}),\\
H^\bullet(X_\infty, \mathcal{X}): &\quad H^\bullet(X_n) \leftarrow H^\bullet(X_n, X_1) \leftarrow \cdots \leftarrow H^\bullet(X_n, X_{n-1}).
\end{aligned}
$$

Figure 3.1: The four standard persistence modules.

dimensional homology.

3.2.2 The Four Standard Persistence Modules

The standard module of persistent homology, $H_\bullet(\mathcal{X})$, illustrates how the absolute homology groups $H_\bullet(X_i)$ relate to each other as the index i changes. Similar observations can be made by considering the absolute cohomology groups $H^\bullet(X_i)$, the relative homology groups $H_\bullet(X_n, X_i)$, and the relative cohomology groups $H^\bullet(X_n, X_i)$ [10, §2.4].

The persistence diagram for absolute cohomology is represented as a multiset of integer pairs (p, q), where $1 \leq p \leq q \leq n$ for a finite filtration. For relative homology and cohomology, the persistence diagram consists of a multiset of tuples (p, q) where $0 \leq p \leq q \leq n-1$ for a finite filtration. In each case, we interpret (p, q) as a half-open interval $[a_p, a_{q+1})$ with the convention that $a_0 = -\infty$ and $a_{n+1} = \infty$ [10, §2.4].

Example 3.2.4 *For $\mathcal{S}^2$ we yield*

$$
\begin{aligned}
\textbf{\textit{Pers}}(H_\bullet(S_6, \mathcal{S}^2)) &= \{(0,0)_0, (2,2)_1, (4,4)_2, (0,5)_2\} && (3.10)\\
&= \{[-\infty, 1)_0, [2,3)_1, [4,5)_2, [-\infty, 6)_3\}. && (3.11)
\end{aligned}
$$

At index 2 there is a nontrivial element of $H_1(S_6, S_2)$ represented by any arc connecting the two points of S_2 [10, §2.4] – the homology class is $[\sigma_3] = [\sigma_4]$. This class vanishes in $H_1(S_6, S_3)$, thus we yield the interval $[2, 3)$.

3.3 Persistent (Co)homology

Inverse problems primarily involve inferring geometric shapes from measurements like path integrals. Classical methods such as Fourier transforms provide extensive information but struggle with nonlinearity and ill-posed conditions, requiring substantial regularization. Topology, particularly through persistent homology, offers alternative methods for deducing topological rather than geometric information. This approach is especially useful in high-dimensional, discrete sets of points, exemplified in the finite case by geological sonar to detect subterranean features based on density variations [10, §1]. Persistent homology identifies topological features represented as intervals in a barcode or persistence diagram, crucial for understanding the presence and persistence of features such as holes or voids in topological spaces. This method is statistically robust and can provide both qualitative and quantitative insights into point sets, which we suspect to lie on some compact topological object [6, 8].

In this section, we continue to examine the consequences of absolute and relative homology and cohomology groups for filtrations of cell complexes, such as the introduced simplicial complexes. In particular, we derive the theory in the context of filtered simplicial complexes upon sets of points, embedded into some metric space. While we can apply the entire theory to simplicial complexes and their (co)homology, cell complexes provide a much broader context and significantly simplify notation in many instances.

In particular, there are at least four naturally arising persistent objects that can be extracted from a filtration of any topological space. We follow the results of de Silva, Morozov, and Vejdemo-Johansson for our explanations [10, §1]. They are

$$\text{persistent} \begin{Bmatrix} \text{absolute} \\ \text{relative} \end{Bmatrix} \begin{Bmatrix} \text{homology} \\ \text{cohomology} \end{Bmatrix}.$$

We address the computation of barcodes for all four types of persistent objects. We demonstrate that both absolute and relative (co)homologies yield identical barcodes and that transitions between these states are facilitated by established duality principles. The duality between homology and cohomology is akin to the duality in vector spaces, whereas a global duality specific to persistent topology allows for a unique interchange:

$$\begin{aligned} \text{Absolute homology} &\rightleftarrows \text{relative cohomology.} \\ \text{Absolute cohomology} &\rightleftarrows \text{relative homology.} \end{aligned}$$

The main results from the literature suggest that a single calculation is sufficient to compute all four persistent objects due to the commutative nature of the global duality.

3.3.1 Barcode Isomorphisms

We characterise the multisets for persistence modules that are decomposable into interval modules. The persistence diagram partitions into $\mathbf{Pers}_0$, comprising finite intervals $[a, b)$ as per [10, §2.3], and $\mathbf{Pers}_\infty$, consisting of intervals $[a, \infty)$. This leads to the decomposition $\mathbf{Pers} = \mathbf{Pers}_0 \cup \mathbf{Pers}_\infty$.

In this chapter, we establish that persistent homology and cohomology yield the same intervals, or barcodes, for both absolute and relative (co-)homology frameworks. This equivalence necessitates invoking the universal coefficient theorem from algebraic topology, which we will prove beforehand. The universal coefficient theorem for cohomology elegantly ties together the cohomology of a space with coefficients in any abelian group G to the homology of the space with integer coefficients.

Specifically, as notation for this proof, $H_n(X;\mathbb{Z})$ and $H^n(X;\mathbb{Z})$ denote the n-th singular homology and cohomology groups with coefficients in $\mathbb{Z}$, respectively. We further involve $\mathrm{Hom}(A,G)$, denoting group homomorphisms from an abelian group A to another abelian group G, and $\mathrm{Ext}^1(A,G)$ [19, §4.3], which measures obstructions in the splitting of a short exact sequence of abelian groups. Further, we use the properties of derived functors [29, §2.7].

Theorem 3.3.1 (Universal Coefficients for Cohomology) *[19]* Let X be a topological space and G an abelian group. For any integer $n \geq 0$, there is a short exact sequence:

$$0 \to \mathrm{Ext}^1(H_{n-1}(X;\mathbb{Z}),G) \to H^n(X;G) \to \cdots \tag{3.12}$$

$$\cdots \to \mathrm{Hom}(H_n(X;\mathbb{Z}),G) \to 0, \tag{3.13}$$

which splits, though not canonically.

Proof Let $C_\bullet(X)$ be the singular chain complex of a topological space X with integer coefficients. The homology groups $H_n(X;\mathbb{Z})$ are defined as:

$$H_n(X;\mathbb{Z}) := \ker(\partial_n)/\mathrm{im}(\partial_{n+1}), \tag{3.14}$$

where ∂_n are the boundary maps in $C_\bullet(X)$. The chain group $C_n(X)$ consists of formal sums of singular n-simplices in X with integer coefficients. The boundary maps $\partial_n : C_n(X) \to C_{n-1}(X)$ are defined by

$$\partial_n(\sigma) = \sum_{i=0}^{n}(-1)^i \sigma|_{[v_0,\ldots,\hat{v}_i,\ldots,v_n]}, \tag{3.15}$$

where $\sigma : \Delta^n \to X$ is a singular simplex, and $\sigma|_{[v_0,\ldots,\hat{v}_i,\ldots,v_n]}$ denotes the restriction of σ to the i-th face of the simplex, omitting the i-th vertex.

The functor $\mathrm{Hom}(-,G)$ applied to $C_n(X)$ yields a group $\mathrm{Hom}(C_n(X),G)$, and the coboundary δ^n for the cochain complex $\mathrm{Hom}(C_\bullet(X),G)$ is

$$\delta^n(f) = f \circ \partial_{n+1} \tag{3.16}$$

for $f \in \mathrm{Hom}(C_{n+1}(X), G)$. This leads to the cohomology groups

$$H^n(X; G) := \ker(\delta^n)/\mathrm{im}(\delta^{n-1}). \tag{3.17}$$

We consider the projective resolution of $C_\bullet(X)$ to effectively apply the Ext functor. Recall that for any abelian group A,

$$\mathrm{Ext}^1(A, G) = R^1 \mathrm{Hom}(A, G), \tag{3.18}$$

where R^1 denotes the first right derived functor of Hom [29, §2.7]. To show this equality, we begin by taking a projective resolution of A [29, p.39f]:

$$\cdots \to P_2 \to P_1 \to P_0 \to A \to 0, \tag{3.19}$$

where each P_i is a projective abelian group. Then we can apply the functor $\mathrm{Hom}(-, G)$ to the projective resolution:

$$0 \to \mathrm{Hom}(P_0, G) \to \mathrm{Hom}(P_1, G) \to \mathrm{Hom}(P_2, G) \to \cdots. \tag{3.20}$$

This sequence is exact on the left because $\mathrm{Hom}(-, G)$ is left exact and each P_i is projective. The first right derived functor $R^1 \mathrm{Hom}(A, G)$ is defined as the cohomology of this sequence at the location corresponding to P_1:

$$R^1 \mathrm{Hom}(A, G) = \frac{\ker(\mathrm{Hom}(P_1, G) \to \mathrm{Hom}(P_2, G))}{\mathrm{im}(\mathrm{Hom}(P_0, G) \to \mathrm{Hom}(P_1, G))}. \tag{3.21}$$

The group $\mathrm{Ext}^1(A, G)$ classifies extensions of A by G, equivalent to the kernel / image calculation in the cohomology of the Hom-sequence:

$$\mathrm{Ext}^1(A, G) = R^1 \mathrm{Hom}(A, G). \tag{3.22}$$

Given $H_n(X; \mathbb{Z})$, consider the short exact sequence obtained from the projective resolution of $\mathbb{Z}$:

$$0 \to \mathbb{Z} \to F \to H_n(X; \mathbb{Z}) \to 0, \tag{3.23}$$

where F is free. Applying $\mathrm{Hom}(-, G)$ gives

$$0 \to \mathrm{Hom}(H_n(X; \mathbb{Z}), G) \to \mathrm{Hom}(F, G) \to \cdots \tag{3.24}$$

$$\cdots \to \mathrm{Hom}(\mathbb{Z}, G) \to \mathrm{Ext}^1(H_n(X; \mathbb{Z}), G) \to 0. \tag{3.25}$$

We apply $\mathrm{Ext}^\bullet$, which gives rise to the long exact sequence of Ext groups:

$$0 \to \mathrm{Hom}(H_n(X;\mathbb{Z}), G) \to H^n(X;G) \to \cdots \tag{3.26}$$

$$\cdots \to \mathrm{Ext}^1(H_{n-1}(X;\mathbb{Z}), G) \to 0. \tag{3.27}$$

Finally, we verify exactness and splitting. The term $\mathrm{Ext}^1(H_{n-1}(X;\mathbb{Z}), G)$ measures the non-trivial extensions of G by $H_{n-1}(X;\mathbb{Z})$, which corresponds to the obstructions to lifting $H_{n-1}(X;\mathbb{Z})$ linearly over G. The term $\mathrm{Hom}(H_n(X;\mathbb{Z}), G)$ represents the group homomorphisms from $H_n(X;\mathbb{Z})$ to G, which naturally includes in $H^n(X;G)$. The sequence is exact at each stage by the properties of derived functors and their application to the singular chain complex. The sequence ends with 0 because Ext^1 of a projective (or free) module vanishes, and $\mathbb{Z}$ is free. The sequence splits because the functor $\mathrm{Hom}(-, G)$ preserves products and coproducts. However, the way it splits is not canonical and depends on the choice of a splitting homomorphism, which is not unique.

In the generalization of the universal coefficient theorem to the case of modules over a principal ideal domain, the Ext^1 terms vanish since $\mathbb{F}$ is a field, thus we obtain $H^n(X;\mathbb{F}) \cong \mathrm{Hom}(H_n(X;\mathbb{F}), \mathbb{F})$ [19, p.198 §3.3.1]. □

Theorem 3.3.2 *For all integers $d \geq 0$, it holds that [10, §2.3]:*

$$\textbf{\textit{Pers}}(H_d(\mathcal{X})) = \textbf{\textit{Pers}}(H^d(\mathcal{X})), \tag{3.28}$$

$$\textbf{\textit{Pers}}(H_d(X_\infty, \mathcal{X})) = \textbf{\textit{Pers}}(H^d(X_\infty, \mathcal{X})). \tag{3.29}$$

Proof When considering coefficients in a field $\mathbb{F}$ rather than in a ring, the universal coefficient theorem assures us of a natural isomorphism between the d-th cohomology group and the homomorphisms from the d-th homology group to the base field:

$$H^d(X;\mathbb{F}) \cong \mathrm{Hom}(H_d(X;\mathbb{F}), \mathbb{F}). \tag{3.30}$$

Therefore, the associated maps

$$H_d(X_i;\mathbb{F}) \to H_d(X_j;\mathbb{F}) \quad \text{and} \quad H^d(X_i;\mathbb{F}) \leftarrow H^d(X_j;\mathbb{F}) \tag{3.31}$$

are adjoint and hence possess the same rank. Since the persistence intervals over a field are uniquely determined by the dimension and rank of the homology vector spaces, it follows that this holds for both homology and cohomology. Consequently, they share the same barcode. □

Consider a filtration $X_1 \subseteq X_2 \subseteq \cdots \subseteq X_n$ of a topological space X, extending to X_∞ where X_∞ is the direct limit of the filtration. The homology groups $H_d(X_n)$ for some fixed dimension d serve as the initial terms for the relative homology groups $H_d(X_\infty, X)$. Since $H_d(X)$ is consistent with $H_d(X_n)$ as n approaches infinity, these sequences can be unified into a single sequence:

$$H_d(X) \to H_d(X_\infty, X). \tag{3.32}$$

For this concatenated sequence, the indices are denoted as

$$\{1, 2, \ldots, n = 0^\flat, 1^\flat, 2^\flat, \ldots, (n-1)^\flat\}, \tag{3.33}$$

using the $\flat$ symbol to indicate relative homology part of the sequence.

This structure allows us to discuss the persistence diagram associated with this homological configuration. The persistence intervals in this diagram can generally be categorized into three types:

- (p, q) where $1 \leq p \leq q < n$, denoted as $[p, q+1)$ or $[a_p, a_{q+1})$.
- $(p^\flat, q^\flat)$ where $0 < p \leq q \leq n-1$, denoted as $[p^\flat, q^\flat + 1)$ or $[a_{p^\flat}, a_{q^\flat+1})$.
- $(p, q^\flat)$ where $1 \leq p \leq n$ and $0 \leq q \leq n-1$, represented as $[p, q^\flat + 1)$ or $[a_p, a_{q^\flat+1})$.

Corollary 3.3.3 *The barcode* $\textbf{Pers}(H_d(\mathcal{X}) \to H_d(X_\infty, \mathcal{X}))$ *comprises the following collections of intervals [10, §2.5]:*

- *An interval* $[a, b)$ *for every interval* $[a, b)$ *in* $\textbf{Pers}_0(H_d(\mathcal{X}))$.
- *An interval* $[a^\flat, b^\flat)$ *for every interval* $[a, b)$ *in* $\textbf{Pers}_0(H_{d-1}(\mathcal{X}))$.
- *An interval* $[a, a^\flat)$ *for every interval* $[a, \infty)$ *in* $\textbf{Pers}_\infty(H_d(\mathcal{X}))$.

Proof We begin by analyzing the first two types of intervals in the persistence diagram $\textbf{Pers}(H_d(X) \to H_d(X_\infty, X))$.

These intervals either do not intersect the intermediate term $H_d(X_n)$ or terminate before it. Consequently, they correspond precisely to the finite intervals in $\textbf{Pers}(H_d(X))$ and $\textbf{Pers}(H_d(X_\infty, X))$, clarifying the first two cases. The correspondence $\textbf{Pers}_0(H_d(X_\infty, X)) = \textbf{Pers}_0(H_{d-1}(X))$ helps in mapping these relationships.

The third case requires examining intervals of the form $[a, b^\flat)$ and proving that they are invariably of the form $[a, a^\flat)$, which means that the paired intervals $[a, \infty)$ and $[-\infty, a)$ in $\textbf{Pers}_\infty(H_d(\mathcal{X}))$ and $\textbf{Pers}_\infty(H_d(X_\infty, \mathcal{X}))$ are restrictions of a single interval $[a, a^\flat)$ in the concatenated sequence [10, p.6]. To establish this, we compare the ascending filtration defined by the images of $H_d(X_i)$ in $H_d(X_n)$ for $i = 1, 2, \ldots, n-1$ (denoted as $\mathrm{Im}(H_d(X_i) \to H_d(X_n))$) with the descending filtration defined by the kernels of $H_d(X_n)$ in $H_d(X_\infty, X)$ for $i = 1, 2, \ldots, n-1$ (denoted as $\mathrm{Ker}(H_d(X_n) \to H_d(X_n, X_i))$). This examination revolves around the fundamental properties of the homology groups in a filtration setting.

For each index i, the image and kernel correspond to the same subspace of $H_d(X_n)$. This equivalence is guaranteed by the homology long exact sequence associated with the pair (X_n, X_i), which links the relative and absolute homology groups. Specifically, the exact sequence implies that any cycle in $\mathrm{Im}(H_d(X_i) \to H_d(X_n))$ that becomes a boundary in $H_d(X_n, X_i)$ must vanish, thus equating the image and kernel. As a result, both filtrations align perfectly, establishing that the third type of interval indeed maps to self-closing intervals of the form $[a, a^\flat)$. $\square$

3.3.2 Persistent Chain Complexes

Alternatively, following [10, §2.6], the standard persistence module can be described via a filtered cell complex $\mathcal{X} := \sigma_1 \cup \cdots \cup \sigma_d$, so that the persistence module can be expressed as the sequence

$$\mathcal{C}: \quad C_1 \to C_2 \to \cdots \to C_d,$$

for a finite filtration, where each $C_i := \langle \sigma_1, \ldots, \sigma_i \rangle$ is a vector space (or an abelian group) over a field $\mathbb{F}$, generated by the elements $\sigma_1, \ldots, \sigma_i$. The boundary operator is defined by $\partial \sigma_j = \sum_{i<j} \lambda_{ij} \sigma_i$ for $\lambda_{ij} \in \mathbb{F}$ for all $i, j \in \{1, \ldots, d\}$.

Then $C_\bullet(X_i) = (C_i, \partial_i)$ is the chain complex for the absolute homology of X_i, and $C_\bullet(\mathcal{X}) = (\mathcal{C}, \partial)$ represents the persistent version for $\mathcal{X}$. This leads to the definition of the persistent absolute homology of $\mathcal{X}$ as

$$H_\bullet(\mathcal{X}) = H(\mathcal{C}, \partial): \quad \frac{\ker(\partial_1)}{\mathrm{im}(\partial_1)} \to \frac{\ker(\partial_2)}{\mathrm{im}(\partial_2)} \to \cdots \to \frac{\ker(\partial_d)}{\mathrm{im}(\partial_d)}.$$

For the persistent absolute cohomology $H^\bullet(\mathcal{X})$, we define

$$\mathcal{C}^\flat: \quad C_1^\flat \leftarrow C_2^\flat \leftarrow \cdots \leftarrow C_d^\flat,$$

where $C_i^\flat = \mathrm{Hom}(C_i, \mathbb{F}) = \langle \sigma_1^\flat, \sigma_2^\flat, \ldots, \sigma_i^\flat \rangle$, with $\{\sigma_i^\flat\}$ as the dual basis of $\{\sigma_i\}$. The coboundary $\delta = \partial^\flat$ is defined as the adjoint of ∂. Then $C^\flat(\mathcal{X}) = (\mathcal{C}^\flat, \delta)$ and $H^\bullet(\mathcal{X}) = H(\mathcal{C}^\flat, \delta) = \ker(\delta)/\mathrm{im}(\delta)$. This too constitutes a persistence module, with morphisms in the reverse direction.

Example 3.3.1 *For $\mathcal{S}^2$, the boundary operator is given by*

$$\partial \sigma_1 = \partial \sigma_2 = 0, \tag{3.34}$$

$$\partial \sigma_3 = \partial \sigma_4 = \sigma_1 - \sigma_2, \tag{3.35}$$

$$\partial \sigma_5 = \partial \sigma_6 = \sigma_3 - \sigma_4. \tag{3.36}$$

This information can also be summarized in a matrix. Similarly, the coboundary operator

$$
\begin{tikzcd}
 & \vdots \arrow[d, "\partial_{n+2}"] & \vdots \arrow[d, "\partial_{n+2}"] & \vdots \arrow[d, "\partial_{n+2}"] & \vdots \arrow[d, "\partial_{n+2}"] & \\
\cdots \arrow[r, "f^{i-2}_{n+1}"] & C^{i-1}_{n+1} \arrow[r, "f^{i-1}_{n+1}"] \arrow[d, "\partial_{n+1}"] & C^{i}_{n+1} \arrow[r, "f^{i}_{n+1}"] \arrow[d, "\partial_{n+1}"] & C^{i+1}_{n+1} \arrow[r, "f^{i+1}_{n+1}"] \arrow[d, "\partial_{n+1}"] & C^{i+2}_{n+1} \arrow[r, "f^{i+2}_{n+1}"] \arrow[d, "\partial_{n+1}"] & \cdots \\
\cdots \arrow[r, "f^{i-2}_{n}"] & C^{i-1}_{n} \arrow[r, "f^{i-1}_{n}"] \arrow[d, "\partial_{n}"] & C^{i}_{n} \arrow[r, "f^{i}_{n}"] \arrow[d, "\partial_{n}"] & C^{i+1}_{n} \arrow[r, "f^{i+1}_{n}"] \arrow[d, "\partial_{n}"] & C^{i+2}_{n} \arrow[r, "f^{i+2}_{n}"] \arrow[d, "\partial_{n}"] & \cdots \\
\cdots \arrow[r, "f^{i-2}_{n-1}"] & C^{i-1}_{n-1} \arrow[r, "f^{i-1}_{n-1}"] \arrow[d, "\partial_{n-1}"] & C^{i}_{n-1} \arrow[r, "f^{i}_{n-1}"] \arrow[d, "\partial_{n-1}"] & C^{i+1}_{n-1} \arrow[r, "f^{i+1}_{n-1}"] \arrow[d, "\partial_{n-1}"] & C^{i+2}_{n-1} \arrow[r, "f^{i+2}_{n-1}"] \arrow[d, "\partial_{n-1}"] & \cdots \\
 & \vdots & \vdots & \vdots & \vdots &
\end{tikzcd}
$$

Figure 3.2: A persistence complex, where moving to the right increases the filtration index, while moving downwards decreases the dimension.

is given by

$$\delta\sigma_1^\flat = -\delta\sigma_2^\flat = \sigma_3^\flat + \sigma_4^\flat, \tag{3.37}$$

$$\delta\sigma_3^\flat = -\delta\sigma_4^\flat = \sigma_5^\flat + \sigma_6^\flat, \tag{3.38}$$

$$\delta\sigma_5^\flat = \delta\sigma_6^\flat = 0. \tag{3.39}$$

This data can analogously be summarized in a transposed matrix [10, p.7].

The relative homology and cohomology persistence modules are then defined as the homology of the persistence modules [10, p.7]:

$$(C_d/\mathcal{C}): \quad C_d \to (C_d/C_1) \to (C_d/C_2) \to \cdots \to (C_d/C_{d-1}), \tag{3.40}$$

$$(C_d/\mathcal{C})^\flat: \quad C_d^\flat \leftarrow (C_d/C_1)^\flat \leftarrow (C_d/C_2)^\flat \leftarrow \cdots \leftarrow (C_d/C_{d-1})^\flat. \tag{3.41}$$

We note that the mappings $\to$ from $\mathcal{C}$ and the mappings $\leftarrow$ from $(C_d/\mathcal{C})^\flat$ are injective, while the mappings $\leftarrow$ from $\mathcal{C}^\flat$ and the mappings $\to$ from $(C_d/\mathcal{C})$ are surjective. Thus, absolute and relative cohomology are structurally similar but qualitatively different from absolute homology and relative homology.

Theorem 3.3.4 *(Persistence Partition) [10, §2.6]* Let $\mathcal{C}$ be given and ∂ as above, then there exists a partition

$$\{1, 2, \ldots, d\} = P^{\bowtie} \sqcup P \sqcup N$$

with a bijective pairing $P \leftrightarrow N$, such that

$$p \text{ is paired with } n \iff [p, n) \in \mathbf{Pairs}(\mathcal{C}, \partial). \tag{3.42}$$

Furthermore, there is a basis $\hat{\sigma}_1, \hat{\sigma}_2, \dots, \hat{\sigma}_d$ of C_d such that

1. $C_i = \langle \hat{\sigma}_1, \dots, \hat{\sigma}_i \rangle$ for each i.
2. $\partial \hat{\sigma}_p = 0$ for all $p \in P^{\bowtie}$.
3. $\partial \hat{\sigma}_n = \hat{\sigma}_p$, and thus $\partial \hat{\sigma}_p = 0$, for all $[p, n) \in \mathbf{Pairs}$.

It follows that the persistence diagram $\mathbf{Pers}(H(\mathcal{C}, \partial))$ consists of $[a_p, \infty)$ for $p \in P^{\bowtie}$ together with intervals $[a_p, a_n)$ for $[p, n) \in \mathbf{Pairs}$.

Proof Let $\mathcal{C} = \{C_i\}_{i \in I}$ be a filtered chain complex associated with a topological space, structured over a field $\mathbb{F}$ for any finite index set I. The filtration indices $1, 2, \dots, d$, where $d = |I|$, classify the stages at which elements are born or die in homology. The partition of $\{1, 2, \dots, d\}$ into $P^{\bowtie} \sqcup P \sqcup N$ is then constructed such that:

- $P^{\bowtie}$ contains indices corresponding to elements that persist indefinitely, i.e., those for which $\partial \sigma_i = 0$ and σ_i does not become a boundary at any higher index.
- P and N are paired bijectively, where each $p \in P$ (births) corresponds uniquely to an $n \in N$ (deaths), signifying the termination of the homological feature introduced at p. This pairing is determined through the matrix reduction of ∂, ensuring that every cycle born at stage p becomes a boundary at stage n.

We then construct a basis $\hat{\sigma}_i$ such that for each i, $\hat{\sigma}_i$ is a generator of C_i. Specifically, if $i \in P^{\bowtie}$, then $\partial \hat{\sigma}_i = 0$, indicating these elements are cycles that persist indefinitely. For pairs $[p, n) \in \mathbf{Pairs}(\mathcal{C}, \partial)$ with $p \in P$ and $n \in N$, set $\partial \hat{\sigma}_n = \hat{\sigma}_p$ and $\partial \hat{\sigma}_p = 0$, reflecting the fact that the cycle $\hat{\sigma}_p$ born at p becomes a boundary at n and thus ceases to contribute to homology past n.

Hence, the persistence diagram $\mathbf{Pers}(H(\mathcal{C}, \partial))$ contains intervals $[a_p, \infty)$ for each $p \in P^{\bowtie}$, indicating persistent homological features and intervals $[a_p, a_n)$ for each $[p, n) \in \mathbf{Pairs}$, describing features with finite lifespans, starting as a cycle at p and terminating as a boundary at n. □

In 3.3.4 the index sets are defined as follows [10, p.8]:

- P identifies the positive simplices that remain unpaired,
- $P^{\bowtie}$ identifies the positive simplices that do become paired,
- N identifies the negative simplices.

The vectors $\hat{\sigma}_p$ and $\hat{\sigma}_n$ are cycles characterized by their leading terms σ_p and σ_n respectively, while the vector $\hat{\sigma}_n$ is a chain with leading term σ_n. This chain 'kills' the homology class of its paired cycle $\hat{\sigma}_p$ through the boundary relation $\partial \hat{\sigma}_n = \hat{\sigma}_p$.

Theorem 3.3.5 *For all integers $d \geq 0$ it holds that [10, §2.4]:*

$$\boldsymbol{Pers}(H_d(\mathcal{X}) \cong \boldsymbol{Pers}(H_{d+1}(\mathcal{X}),$$
$$\boldsymbol{Pers}(H_d(X_\infty, \mathcal{X}) \cong \boldsymbol{Pers}(H_d(X_\infty, \mathcal{X}).$$

Proof TBD □

Remark 3.3.2 *In this case, we get an isomorphism of multisets. This is due to the identification of the intervals $[a, \infty) \leftrightarrow [-\infty, a)$ for* $\boldsymbol{Pers}_\infty$*. Thus, persistent homology and relative homology barcodes carry the same information, with a dimension shift for the finite intervals [10, §2.4].*

3.3.3 Cohomology of Chain Complexes

3.4 Zigzag Persistence

The zigzag persistence framework is initiated by constructing a zigzag diagram of topological or vector spaces. This diagram consists of a sequence of spaces $S_1, S_2, \ldots, S_n$, where each adjacent pair (S_i, S_{i+1}) is connected by a map $S_i \to S_{i+1}$ or $S_i \leftarrow S_{i+1}$ [3, §1]. In contrast to the classical approach to persistent homology, the linking maps can now point in arbitrary directions. The major limitation of traditional persistence is its reliance on a nested family $\{S_t\}_{t\in[0,\infty]}$, where $S_t \subseteq S_{t'}$ whenever $t \leq t'$. This constraint applies to both the theoretical framework and the algorithms. Zigzag persistence overcomes this limitation. When the variable t is discretized to a finite set, the family of simplicial complexes can be represented as a diagram of spaces: $S_1 \to S_2 \to \cdots \to S_n$, where the arrows denote inclusion maps. Applying the k-dimensional homology functor $H_k(-;\mathbb{F})$ with coefficients in a field $\mathbb{F}$, we obtain a diagram of vector spaces: $V_1 \to V_2 \to \cdots \to V_n$, where $V_i = H_k(S_i;\mathbb{F})$, the persistence module. Persistence is effective because persistence modules can be classified up to isomorphism, with each barcode corresponding to an isomorphism type.

Zigzag persistence aims to achieve a similar classification for diagrams where the arrows may point in either direction, thereby generalizing the framework of traditional persistence. In this section, we follow the work of Carlsson and de Silva [3, §2.1].

3.4.1 Zigzag Modules

We consider a sequence of vector spaces and linear maps of length n, which point in both directions:

$$\mathsf{V}: \quad V_1 \xleftrightarrow{p_1} V_2 \xleftrightarrow{p_2} \cdots \xleftrightarrow{p_{n-1}} V_n. \tag{3.43}$$

Each $\xleftrightarrow{p_i}$ represents either a forward map $\xrightarrow{f_i}$ or a backward map $\xleftarrow{g_i}$. We call the sequence V a zigzag diagram of vector spaces or a zigzag module over $\mathbb{F}$. The sequence of symbols f and g is called the type of V. For example, a diagram of type $\tau = fgg$ would be $V_1 \xrightarrow{f_1} V_2 \xleftarrow{g_2} V_3 \xleftarrow{g_3} V_4$. The length of a type τ is the length of the diagram of type τ. Thus, fgg has length 4. If the length and type of a zigzag module are known, it is called a τ-module of length n and is included in the class τMod of τ-modules.

3.4.2 Decompositions of Zigzag Modules

3.4.3 Zigzag Modules and Filtrations

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Index