

On the Incremental Computation of Simplicial Homology

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Abstract

Homology groups are a fundamental algebraic invariant in algebraic topology that allows the discrimination of topological spaces. Methods to compute the homology groups of a simplicial complex are known in general, but they require expensive matrix computations. For specific classes of simplicial complexes, both geometric and incremental methods are known. However, these classes generally preclude the presence of torsion in the homology groups. This paper investigates the possibility of an incremental homology type computation that can account for torsion and thus apply to a larger class of simplicial complexes than previous results.

Keywords: algebraic topology, homology, algorithmic complexity

1 Introduction

Topology is the study of geometric structure on sets. One of the big questions of topology is to determine when are two spaces essentially the same. Algebraic topology is a branch of topology which computes algebraic objects which remain invariant when the underlying structure remains the same. These algebraic invariants include homology groups which encapsulate certain characteristics about the underlying structure of the space. In this paper I consider the homology groups of a certain class of spaces known as simplicial complexes. Algorithms to compute these homology groups are known, but they are generally inefficient. This project will investigate the efficiency of various algorithms to compute these homology groups. Improving the efficiency of such algorithms is applicable in experimental mathematics, where computers can perform computations beyond the reach of human work.

2 Background

2.1 Previous Results

The computation of simplicial homology via reduction of the boundary matrices to Smith normal form is rather classic. For sparse matrices, [1] gives an efficient algorithm to compute the homology groups. This algorithm works in full generality; it will compute the homology of any simplicial complex regardless of factors such as orientability. However, the algorithm presented in [1] is probabilistic and the worst case analysis of the algorithm is unsatisfactory. [4] describes a method by which simplicial complexes embedded in \mathbb{R}^3 may be transformed into a homotopically equivalent three-dimensional manifold, for which the homology groups may be computed efficiently via classical results of the structure of such spaces. This method allows deterministic computation of the homology type of a simplicial complex embedded in \mathbb{R}^3 in linear time, even faster than the probabilistic methods proposed by [1] for general simplicial complexes. For the remainder of this paper, we investigate extensions of this method to dimensions higher than 3.

2.2 Definitions

In this paper, we deal solely with triangulated spaces, so a general notion of a topological space is unnecessary. We define a k -simplex as the convex hull of $k + 1$ affinely independent points in Euclidean space. A simplicial complex is the union of a set of simplices such that the faces of any simplex in the complex are also in the complex, and the intersection of two simplices of the same dimension is either empty or a face of both. We will refer to n -dimensional Euclidean space as \mathbb{R}^n and the n -dimensional halfspace as \mathbb{R}_{\geq}^n , the set of points in \mathbb{R}^n with nonnegative first coordinate. We will assume that manifolds in this paper are closed and with boundary, so an n -dimensional manifold is a space such that there is a neighborhood around each point homeomorphic to either \mathbb{R}^n or \mathbb{R}_{\geq}^n . A continuous map between topological spaces is a map $f : X \rightarrow Y$ is a map such that for every open set $U \subseteq Y$, the preimage $f^{-1}(U)$ is an open set in X . A homeomorphism is a bijective map that is continuous and has a continuous inverse. An embedding of a space X into \mathbb{R}^n is a map $f : X \rightarrow \mathbb{R}^n$ that maps X homeomorphically onto its image.

3 Preliminary Results

3.1 The Abstract Incremental Algorithm

In this section, we will establish an abstract algorithm for incrementally computing the homology type of a simplicial complex. We will work with a given simplicial complex $K = \bigcup_{i=1}^N \sigma_i$, where σ_i ranges over all the simplexes of K such that $K_i = \bigcup_{j=1}^i \sigma_j$ is a valid simplicial complex for all i . In this incremental algorithm, we will compute the homology type of K_i for all i , starting from $i = 1$. The homology type of K_1 is trivial to compute: $H_n(K_1) = 0$ for all n .

Next, we need to analyze the incremental step. We wish to compute the homology type of $K_i = K_{i-1} \cup \sigma_i$ from the homology type of K_{i-1} . To do this, we will appeal to the Mayer-Vietoris Sequence. Given two spaces A and B which cover a space X , the Mayer-Vietoris Sequence relates the homology groups of A , B , $A \cap B$, and X . We'll apply this to our simplicial complex with $A = K_{i-1}$, $B = \sigma_i$, and $X = K_i$. The Mayer-Vietoris Sequence then tells us that the sequence

$$H_n(K_{i-1} \cap \sigma_i) \rightarrow H_n(K_{i-1}) \oplus H_n(\sigma_i) \rightarrow H_n(K_i) \rightarrow H_{n-1}(K_{i-1} \cap \sigma_i) \rightarrow H_{n-1}(K_{i-1})$$

is exact for all n .

However, this relation can be simplified significantly. $K_{i-1} \cap \sigma_i = \partial\sigma_i$, the boundary of σ_i , as K_i must be a valid simplicial complex, so the simplices forming $\partial\sigma_i$ must be in K_i , but they are also not σ_i , so they were in K_{i-1} as well while the interior of σ_i was not. Furthermore, σ_i is homotopy equivalent to a single point, so $H_n(\sigma_i) = 0$ for all n . Using these simplifications, we find that the sequence

$$H_n(\partial\sigma_i) \rightarrow H_n(K_{i-1}) \rightarrow H_n(K_i) \rightarrow H_{n-1}(\partial\sigma_i) \rightarrow H_{n-1}(K_{i-1}) \quad (1)$$

is exact for all n .

Let us now consider three cases. If σ_i is a k -simplex, we consider $n = k - 1$, $n = k$, and $n \neq k - 1, k$ separately.

First, consider $n \neq k - 1, k$. Then we have $H_n(\partial\sigma_i) = H_{n-1}(\partial\sigma_i) = 0$. Therefore, (1) tells us that $0 \rightarrow H_n(K_{i-1}) \rightarrow H_n(K_i) \rightarrow 0$ is exact, and it follows that $H_n(K_{i-1}) \simeq H_n(K_i)$. Since this map from $H_n(K_{i-1}) \rightarrow H_n(K_i)$ is induced by the inclusion map $\iota : K_{i-1} \rightarrow K_i$, the generating set for $H_n(K_i)$ is the same as the generating set for $H_n(K_{i-1})$.

Second, consider $n = k - 1$. Then we have $H_n(\partial\sigma_i) \simeq \mathbb{Z}$ and $H_{n-1}(\partial\sigma_i) = 0$. Then (1) yields that $H_{k-1}(\partial\sigma_i) \xrightarrow{\iota_*} H_{k-1}(K_{i-1}) \rightarrow H_{k-1}(K_i) \rightarrow 0$ is exact, so $H_{k-1}(K_i) = H_{k-1}(K_{i-1})/\iota_*(H_{k-1}(\partial\sigma_i))$, where ι_* is the map induced by the inclusion $\iota : \partial\sigma_i \hookrightarrow K_{i-1}$.

Finally, consider $n = k$. Then we have $H_n(\partial\sigma_i) = 0$ and $H_{n-1}(\partial\sigma_i) \simeq \mathbb{Z}$. Then (1) yields that the sequence $0 \rightarrow H_k(K_{i-1}) \rightarrow H_k(K_i) \xrightarrow{\partial_*} \mathbb{Z} \xrightarrow{\iota_*} H_{k-1}(K_{i-1})$ is exact. $\partial_*(H_k(K_i))$ is a subgroup of \mathbb{Z} , all of which are isomorphic to \mathbb{Z} . Let x be an n -cycle that contains σ_i such that the coefficient of σ_i is minimal but positive. Suppose that the coefficient of σ_i in x is a . Then for any k -cycle y , the coefficient of σ_i will be a multiple of a , or else we can subtract an appropriate multiple of x to find a k -cycle with a smaller coefficient of σ_i . Therefore, we can write any k -cycle as $cx + y$, where x is our specific cycle containing σ_i and y is a k -cycle class in K_{i-1} . Then the homology class of this k -cycle is simply $c[x] + [y]$ where $[x]$ is a new generator and $[y]$ is a homology class in $H_k(K_{i-1})$. All the requisite properties of the addition operations can be verified to see that $H_k(K_i) \simeq \mathbb{Z} \times H_k(K_{i-1})$ where the new generator is our specific k -cycle x containing σ_i the minimum positive number of times.

Putting these together, we have the following tasks that need to be completed to create a bona fide algorithm for incrementally computing the homology type and generating set of a complex:

- Write the homology class of $\partial\sigma_i$ as a linear combination of the generating set for $H_{k-1}(K_{i-1})$.

- Compute the quotient of $H_{k-1}(K_{i-1})$ by the subgroup generated by the homology class of $\partial\sigma_i$.
- Detect whether a new k -simplex is part of a k -cycle.
- If it exists, compute a k -cycle with the minimal positive coefficient of σ_i .

3.2 The One Dimensional Algorithm

Let us first consider the simple case of a one dimensional finite simplicial complex. The result that we will expect from this algorithm is a number telling us the number of connected components and the number of independent cycles in the complex, as well as a list of those components and independent cycles.

Because our simplex is one dimensional, $H_n(K_i) = 0$ for all $n \geq 2$ and all i . Furthermore, we only need to consider two operations: adding a 0-simplex and adding a 1-simplex.

Assume we are working on the step to compute the homology type and generators for K_i from that of K_{i-1} . Let us first consider the case where σ_i is a 0-simplex. This 0-simplex was not already in our complex, so it is not part of the boundary of any 1-simplex. Therefore, this 0-simplex is independent of everything in $H_0(K_{i-1})$, so we have $H_0(K_i) \simeq H_0(K_{i-1}) \times \mathbb{Z}$, where the new generator is simply the 0-cycle composed of this simplex.

Second, suppose σ_i is a 1-simplex. We know that $\partial\sigma_i$ is of the form $y - x$ for two points x and y . Let us treat σ_i as a path from x to y . There are now two cases:

In the first case, the two bounding points of σ_i are in different connected components (they have distinct homology classes in K_{i-1}). Then we have that $H_0(K_i) \simeq H_0(K_{i-1}) / \iota_*(H_0(\partial\sigma_i))$. Therefore, when we mod by the subgroup generated by $[\partial\sigma_i]$, we are simply modding by the relation $[x] \sim [y]$, so the result is that two elements of the generating set, corresponding to $[x]$ and $[y]$, are associated. This simply corresponds to a reduction of the homology group and its generating set. No other elements of the generating set are affected.

In the second case, the two bounding points of σ_i are in the same connected component. Then if we add σ_i to an existing path from y to x , we have a 1-cycle that contains σ_i exactly once, so it is a cycle containing σ_i the minimal positive number of times. We then know that $H_1(K_i) \simeq H_1(K_{i-1}) \times \mathbb{Z}$ where the new generator is our found 1-cycle.

3.3 Implementation Details

Because of the low-dimensionality of this case, the task of writing $\partial\sigma_i$ as a linear combination of the generating set for $H_{k-1}(K_{i-1})$ is rendered moot by the fact that the generators simply correspond to the connected components that the two endpoints lie in. Updating the generator corresponding to each point is a relatively simple task. When we need to merge two generators, we choose either one of them and mark all of the 0-simplices in its connected component as belonging to the other connected component. In this way, each connected component retains a canonical name, so that we may easily find all the 0-simplices in any given component.

Therefore, the only remaining task is that of finding the path from y to x in the last step of the above section. To do this, we will use a floodfill algorithm. Breadth-first search is used so that the shortest path is found and used. Because of the low-dimensionality, these cycles are never modified in the generating set for the first homology group, so we use the shortest path to simplify the output.

Each of these two operations is at most linear in the number of simplices, so this algorithm takes at most quadratic time in the number of simplices.

References

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