Efficient Computation of Homology Groups of Simplicial Complexes Embedded in Euclidean Space TJHSST Senior Research Project Computer Systems Lab 2009-2010

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Abstract

Homology groups are an important concept in algebraic topology. The homology groups of a simplicial complex represent certain characteristics of the structure that can distinguish it from other simplicial complexes. Methods to compute homology groups from a triangulation are well studied, but most such methods focus on the matrix operations required to reduce a matrix to Smith normal form. This paper investigates the use of geometric structure of Euclidean space in order to create space and time efficient algorithms to compute homology groups of complexes embedded in Euclidean space.

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 algorithms 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. [3] 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}^n_{\geq} , 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}^n_{\geq} . A continuous map between topological spaces is a map $f: X \to Y$ 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 $f: X \to \mathbb{R}^n$ that maps X homeomorphically onto its image.

3 Preliminary Results

To be completed.

4 The Main Result

To be completed.

5 Discussion

To be completed.

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