Efficient Computation of Homology Groups of Simplicial Complexes Embedded in Euclidean Space
TJHSST Senior Research Project Proposal
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1   Introduction and Background

Topology is the study of geometric structure on sets of points. One of the big questions of topology is to determine when are two spaces essentially the same. Algebraic topology is a branch of topology that computes algebraic objects that remain invariant when the underlying structure remains the same. These algebraic invariants include homology groups. In this project I consider the homology groups specifically of simplicial complexes embedded in Euclidean space. 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   Procedure and Methodology

The focus of this project is the development of more efficient algorithms for computing homology groups of simplicial complexes subject to various constraints. As such, the bulk of the project will be mathematical research with

implementation of the various algorithms in C++ using the GNU Multiprecision Library (GMP). The main purpose of implementation will be to verify the complexity analysis done. Additionally, the implementations will allow for cross-checking and to further verify that the algorithms constructed are, at least experimentally, correct. OpenGL will be used in preliminary stages in order to display the intermediate steps of computation to allow for easier human verification. Various algorithms are already known for computing homology groups, both in general and under various constraints. To find more efficient algorithms for computing homology groups, the proofs of these algorithms will be extended to include inputs with weaker constraints or higher dimensionality.

3   Expected Results

This project is expected to generate various algorithms to efficiently compute the homology groups of simplicial complexes and cellular complexes using known properties of the input such as sparsity of the boundary homomorphisms or an embedding of the underlying space into low dimensional Euclidean space. These algorithms would be applicable in fields such as experimental mathematics where the size of triangulations exceeds the capacity of human effort.