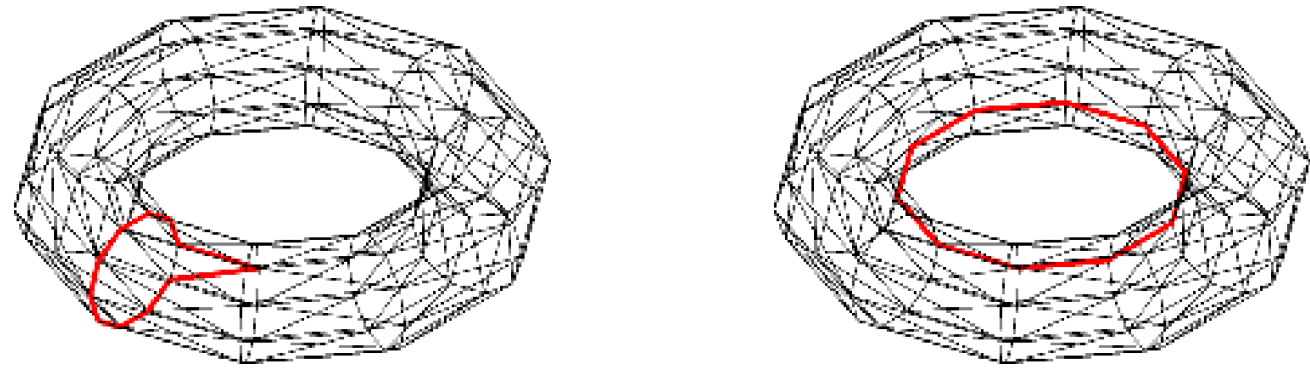# On the Incremental Computation of Simplicial Homology of Triangulated Surfaces

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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 project is focused on the incremental computation of both homology groups and generating sets. This has applications to such fields as object recognition when doing image processing.

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 that 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 three dimensions, these characteristics can be thought of as the holes through the object and the voids within the object. In this project I consider the homology groups of a certain class of spaces known as simplicial complexes. The incremental approach taken in this project is designed to allow for efficient updates of the homology groups and their generating sets when a single new simplex is added, allowing, updates to the homology groups if a new surface is found without rerunning the entire computation. One possible choice of generators for the first homology group of the torus are shown above and those for the Klein bottle to the right.

Definitions

• A k-dimensional simplex is the convex hull of k+1 points in general position.
• A k-chain is a sum of k-dimensional simplices
• A simplicial complex is a collection of simplices such that the boundary of each simplex is in the complex and any two simplices are either the same, disjoint, or the intersection is a face of both.
• A k-cycle is a k-chain with trivial boundary.
• The kth homology group of a simplicial complex is the quotient of the group of k-cycles by the group of boundaries of (k+1)-chains.
• The torsion coefficient of a k-cycle is the number of times it must be added to itself in order to be trivial in the k-th homology group and 0 if it never is.

Basis For Algorithm

The Mayer-Vietoris Sequence. Gives an exact sequence relating homology groups of a complex composed of smaller complexes:

$$\cdots \rightarrow H_{n+1}(X) \xrightarrow{\partial_*} H_n(A \cap B) \xrightarrow{(i_*,j_*)} H_n(A) \oplus H_n(B) \xrightarrow{k_*-l_*} H_n(X) \xrightarrow{\partial_*}$$
$$\xrightarrow{\partial_*} H_{n-1}(A \cap B) \rightarrow \cdots \rightarrow H_0(A) \oplus H_0(B) \xrightarrow{k_*-l_*} H_0(X) \rightarrow 0$$

The Algorithm

In this project, an algorithm was created that allows for the incremental computation of homology groups of simplicial complexes. The incremental step of the algorithm consists of the following four main components:
1. Determine whether the k-dimensional complex is part of a k-cycle.
2. Augment the generating sets with new cycles, starting with a torsion coefficient of 0.
3. Write the boundary of a new simplex in terms of the generating set for the current homology group.
4. Compute the quotient of the homology group by the new relation, updating the generating set simultaneously.

Implementation Details

In order to facilitate the writing of a cycle in terms of generators, a set of cycles called fundamental cycles and representations of these cycles in terms of the current generators are maintained throughout the algorithm. A representation of any given cycle in terms of the fundamental cycles is easy to construct, and then the maintained representations can be used to translate that representation into a representation in terms of the generators.

Discussion

This incremental method for computing serves as a useful intermediate between highly algebraic methods and highly geometric methods for computing homology type and homology generators in generality. While this method is not as generally applicable as purely algebraic methods, it also surpasses geometric algorithms by removing the constraint that the triangulation should be embedded in R^3, and particular should be orientable. Additionally, due to the incremental nature of the algorithm, on-line computation of homology is now possible. For applications where the simplicial complex takes a significant time to build, this method can be run concurrently and so effectively the only time required is the time for the final update. Therefore, for such applications this method could surpass even the extremely refined algebraic methods, as the matrix reduced in each step is much simpler than that of the complete boundary homomorphism.