

SPECIAL SESSIONS

Applications of Computer Algebra - ACA2018



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S4

Applied Computational Algebraic Topology

Tuesday

Tue 19th, 10:30 - 11:00, Aula 9 – Eduardo Sáenz-de-Cabezón:

Reductions of monomial resolutions for the computation of high dimensional simplicial homology

Tue 19th, 11:30 - 12:00, Aula 9 – Julián Cuevas-Rozo:

New algorithms for computing homology of finite topological spaces

Tue 19th, 12:00 - 12:30, Aula 9 – Pedro Real:

Computing Homotopy Information of 4D Digital Objects in Parallel

Tue 19th, 12:30 - 13:00, Aula 9 – Pedro Real:

Maximal Stable Homological Regions and AT-models

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Aim and cope

Algebraic Topology was in its origin an area of pure mathematics with deep algebraic and geometrical roots, which has had an intense development in the last 120 years. However, in this period this discipline has become the core of several areas of application-oriented research using algebraic topology methods in biology, statistics, engineering, computer science. . . The growing number of these interactions has given rise to the field of applied and computational algebraic topology.

This session is therefore mainly devoted to the computational aspects of this emerging field in all possible directions which include, but are not restricted to:

- Computational algebraic topology
- Computational homological algebra
- Computational topological dynamics
- Coding theory and cohomology of groups
- Topological analysis and processing of digital images
- Topological analysis of data
- Stochastic algebraic topology

- Topological pattern recognition
- Topological robotics
- Topology, computer science and parallelism

New algorithms for computing homology of finite topological spaces

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We present some algorithms to compute the homology of finite topological spaces, which have been implemented in the Kenzo system by combining techniques of point reduction of finite topologies and discrete vector fields.

Keywords: Finite topological space, simplicial complex, discrete vector field, homology.

1 Introduction

A useful correspondence between finite topological spaces and finite simplicial complexes is due to McCord [6], who assigns to each finite T_0 space X a simplicial complex $\mathcal{K}(X)$, called the *order complex of X* , in such a way that X and $\mathcal{K}(X)$ are weak homotopy equivalent. In addition, McCord proves that weak homotopy types of compact polyhedra are in one-to-one correspondence with those of finite topological spaces.

In the last years the theory of finite topological spaces has experimented a new impulse from works by Barmak and Minian [2] about the study of homotopy and weak homotopy types, among many other results; for example, they show that elementary collapses of compact polyhedra correspond to elimination of *weak points* of finite T_0 -spaces. On the other hand, Minian [7] introduced a version of discrete Morse theory for posets that satisfy the *h -regularity* property; the incidence graphs of simplicial complexes are *h -regular* so that Minian's results apply to any finite topological space coming from the simplicial context.

More recently, Cianci and Ottina [3] have generalized Minian's results by defining an appropriate spectral sequence that converges to the homology of a finite T_0 -space and showing that, in the particular case of *quasicellular posets*, the computation is more tractable. In this work we present the implementation of some algorithms in the Kenzo system [5] to compute topological invariants of finite spaces. The Kenzo system was developed by Francis Sergeraert and some coworkers and it allows the user to compute homotopy and homology invariants of spaces by using their simplicial versions. Our algorithms combine theoretical results by Barmak and Minian and some previous ideas implemented in Kenzo, as the technique of discrete vector fields.

2 Computation of homology in finite spaces

Given a finite T_0 -space (X, \mathcal{T}) where $X = \{x_1, \dots, x_n\}$, the *topogenous matrix* associated to X is the n -square matrix $T_X = [t_{ij}]$ defined by

$$t_{ij} = \begin{cases} 1 & , x_i \in U_j \\ 0 & , x_i \notin U_j \end{cases}$$

where U_j is the minimal open set that contains x_j . There exists a well-known result due to Alexandroff [1] providing a one-to-one correspondence between finite topological spaces and posets (the order relation is given by: $x_i \leq x_j \iff x_i \in U_j$). In this way, the topogenous matrix can be regarded as the incidence matrix corresponding to the order relation and U_x is the set of elements that are less than or equal to x . Moreover, in the previous work [4] it is shown how to modify T_X in order to obtain an upper triangular permutation-similar matrix, such that it is associated to a T_0 -space which is homotopically equivalent to X . For this reason, we assume that a finite T_0 -space X has an enumeration of its elements in such a way that its topogenous matrix is upper triangular. Usually a poset is represented by its Hasse diagram $\mathcal{H}(X)$, given by edges (x, y) such that $x < y$ and there does not exist z such that $x < z < y$.

If X is a finite T_0 -space, the *order complex* $\mathcal{K}(X)$ associated to X is the simplicial complex whose simplices are the nonempty chains of X . The simplicial complex $\mathcal{K}(X)$ can be used to compute the topological invariants of X ; the problem is the size of $\mathcal{K}(X)$, which limits the possible computations on it. In fact, the McCord morphism [6] provides a weak homotopy equivalence between X and $\mathcal{K}(X)$. Nevertheless, there exist methods that can be directly apply to finite spaces. For instance, Stong [9] proved that by sequentially removing some particular points in a finite T_0 -space X , a minimal space, which is homotopy equivalent to X , is obtained; this space is called a *core* of X . Moreover, to decide if two spaces have the same homotopy type is equivalent to verify that their cores are homeomorphic.

With regard to homology, some results given in [2], [7] can help us to develop algorithms for computing homology groups of some particular classes of finite topological spaces. A space X is called *h-regular* if for every $x \in X$, the order complex $\mathcal{K}(\hat{U}_x)$ is homotopy equivalent to the sphere S^{n-1} , where n is the *degree* of x , that is, the maximum of the cardinality of the chains of \hat{U}_x (\hat{U}_x denotes the subspace $U_x - \{x\}$ in the poset associated to X). In the same way, a *cellular* poset X is a graded poset such that for every $x \in X$, \hat{U}_x has the homology of S^{n-1} , where n is the degree of x .

We say that an edge (x, y) in the Hasse diagram $\mathcal{H}(X)$ is *admissible* if the subposet $\hat{U}_y - \{x\}$ is homotopically trivial. A poset is *admissible* if all its edges are admissible. It can be proved that any admissible poset is h-regular and the face poset $\mathcal{X}(K)$ (the poset given by the simplices of K ordered by subset inclusion) of any regular CW-complex K (in particular, of any finite simplicial complex) is admissible.

Given a cellular poset X , its *cellular chain complex* (C_*, d) is defined in [7] by

$$C_p(X) = \bigoplus_{\deg(x)=p} H_{p-1}(\hat{U}_x) \quad (1)$$

where $H_k(Y)$ denotes the k -homology group of Y .

Then, the following result [7, Theorem 3.7] provides a framework to compute homology.

Theorem 1. Let X be a cellular poset and let (C_*, d) be its cellular chain complex. Then $H_*(C_*) = H_*(X)$.

In order to improve the efficiency, one can consider discrete vector fields, a basic tool in homology computations. Let X be an h -regular poset and let $\mathcal{H}(X)$ be its Hasse diagram. A matching M is a *Morse matching* provided that the directed graph $\mathcal{H}(X)$ is acyclic and M is called *admissible* if all its edges are admissible. Corollary 3.15 in [7] asserts that the homology of a cellular poset X coincides with the homology of a complex (\bar{C}_*, \bar{d}) , obtained by restricting only to those direct summands of (1) corresponding to the set C_M of critical points of M (those points that are not incident to any edge in M).

Theorem 2. Let X be a cellular poset with an admissible Morse matching M defined on it. Then $H_*(\bar{C}_*) = H_*(X)$, where (\bar{C}_*, \bar{d}) is defined by

$$\bar{C}_p(X) = \bigoplus_{\substack{\deg(x)=p \\ x \in C_M}} H_{p-1}(\hat{U}_x). \quad (2)$$

3 New algorithms and its implementation

In this section we are going to present some algorithms developed in Kenzo allowing the user to make topological computations over finite spaces. In particular, we provide algorithms to determine the core and the order complex of a space X . Moreover, we present an ongoing work for the computation of homology groups by using discrete vector fields.

An element x is a *beat point* of the space X if either \hat{U}_x has a maximum or the set $\{y \in X : x < y\}$ has a minimum. A *core* of a finite T_0 -space X is a strong deformation retract of X which has no beat points; in [9] it is proved that the core can be obtained by removing one by one all the beat points of X .

Given an element $x_k \in X$, we have implemented an algorithm to decide if x_k is a beat point by using the topogenous matrix $T_X = [t_{ij}]$ as follows: consider the sets $I_k = \{i : t_{ik} = 1, i \neq k\}$ and $J_k = \{j : t_{kj} = 1, j \neq k\}$ and the numbers $M_k = \max I_k$, $m_k = \min J_k$; if either $I_k = \{i : t_{i, M_k} = 1\}$ or $J_k = \{i : t_{m_k, j} = 1\}$ then x_k is a beat point. Once we know that x_k is a beat point, we can delete the k -th row and column in order to obtain a smaller topogenous matrix that represents the space $X - \{x_k\}$; continuing this process, after a finite number of steps, we will have the topogenous matrix of a core of X .

In [2] another kind of points that preserves the weak homotopy type is defined; these points are called *weak points* and satisfy the following property: x is a weak point if the link of x (the subspace consisting of all the elements comparable with x , different to x) is contractible. Since the algorithm to find the core of a space is already implemented, we have a procedure to decide if x_k is a weak point: consider the set $L_k = \{l \neq k : t_{lk} = 1 \text{ or } t_{kl} = 1\}$ and delete the r -th row and column from T_X for all $r \notin L_k$ in order to obtain the topogenous matrix $T_{\hat{C}_{x_k}}$ of the link; then, the matrix of the core of this link has size 1 if and only if x_k is a weak point.

We can also compute the order complex of any finite topology making use of its topogenous matrix. More exactly, if we consider the matrix N_T obtained from T_X by subtracting the identity matrix i.e. $N_T = T_X - \mathbb{I}_n$, we have the following proposition.

Proposition. [4] For each $0 \leq k \leq n - 1$, the entry $[N_T^k]_{ij}$ represents the number of chains of $k + 1$ elements with x_i as minimum and x_j as maximum.

The above result allows us to find all the chains of elements in X from the successive powers of N_T , and therefore Kenzo is able to compute the order complex of a finite space.

With regard to homology, in order to define an admissible Morse matching on $\mathcal{H}(X)$, we have modified the algorithm proposed in [8, Section 5.2] (for computing admissible discrete vector fields for digital images), with the purpose it can be applied to any cellular space. In addition, the involved calculations to verify the cellularity condition improve the efficiency by means of the sequential construction of the discrete vector field. At first instance, we consider those edges (x, y) where the core of $\hat{U}_x - \{y\}$ is a single point (in this case, $\hat{U}_x - \{y\}$ is contractible), which is a stronger condition than being homotopically trivial, and combine this with the modified algorithm in [8] in order to obtain admissible vectors up to degree $p - 1$. Then, we can compute all the homology groups $H_{p-1}(\hat{U}_x)$ appearing in (2) by applying Theorem 2 to $X := \hat{U}_x$ together with those vectors contained in it. In this manner, the Kenzo system uses in a recursive way Theorem 2 and the modified algorithm in [8] to construct an admissible discrete vector field and also to check the cellularity condition in each step.

It should be mentioned that the class of finite topological spaces to which these results can be applied has been extended in [3] to *quasicellular* spaces. The idea is to replace the degree function by the definition of a morphism $\rho : X \rightarrow \mathbb{N}_0$ satisfying some particular conditions, in such a way that Theorems 1 and 2 are still valid and our algorithms can also be applied.

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Maximal Stable Homological Regions and AT-models*

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Keywords: Maximal Stable Homological Regions, Homological Segmentation, AT-model

Let X be a finite cell complex. Working with $Z/2Z$ as the ground ring, we construct from an AT-model [1] a partition of X as a set of cells, called a *homological segmentation* of X . Its regions are strongly related to the specification of the homological holes of X as set of cells in which paths cutting or delineating them live. This method can be curiously seen as a purely homological version of the computer vision procedure named *maximally stable extremal regions (MSER)* proposed by Matas et al [2], which is used as a method of blob detection in digital images. In this sense, we show some experiments with three-dimensional digital objects in order to analyze the mathematical notion of homological segmentation within the context of topological object recognition.

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Computing Homotopy Information of 4D Digital Objects in Parallel*

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Keywords: four-dimensional digital object, primal-dual abstract cell complex, homology, homotopy,

Let $X \subset I$ be a digital object embedded in a 4-dimensional digital image I . Working with a primal-dual abstract cell complex (pACC, for short) version $pACC(X)$ of X , we design an algorithm in which elementary homotopy operations can be exhaustively applied to $pACC(X)$ in order to obtain a smaller pACC (in terms of cells and connexions between them) whose cells are strongly related to the integer algebraic homological generators of $pACC(X)$. An ambiance-based parallel version of this previous algorithm can be designed from which homology and homotopy Information of X can be derived in a straightforward manner.

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Reductions of monomial resolutions for the computation of high dimensional simplicial homology

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Abstract

In this paper we propose an algorithm for the computation of monomial resolutions that can be useful for obtaining the reduced homology of simplicial complexes. The algorithm is based on the reduction of known resolutions using the support of smaller ones. We start with a combinatorial resolution that is highly non minimal but easy to obtain, such as Taylor resolution. On the other hand, we compute in a combinatorial way the support of a smaller resolution (without computing the differentials in this resolution). In this step we use Mayer-Vietoris tree algorithm to obtain the support of a mapping cone resolution. Finally the last step consists on reducing the differential of the Taylor resolution using the information in the support of the mapping cone resolution to have smaller matrices, from which we compute the homology of the given simplicial complex.

Usually, a simplicial complex is given by a list of its facets. It is important to note that we use the ideal generated by the complements of the facets of the simplicial complex, which is equivalent to use the ideal generated by the minimal nonfaces, however, passing from one representation to the other is computationally demanding. Due to the size of the matrices involved in this process, our algorithm is particularly useful for simplicial complexes of high dimensions, since the matrices in the usual algorithm grow exponentially in terms of dimension of the complex, and those in our approach grow exponentially in terms of the number of facets of the complex.

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