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Complexity of simplicial homology and independence complexes of chordal graphs $\stackrel{\star}{\approx}$



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ABSTRACT

We prove the NP-hardness of computing homology groups of simplicial complexes when the size of the input complex is measured by the number of maximal faces or the number of minimal non-faces. The latter case implies NP-hardness of the homology problem for clique and independence complexes of graphs.

Our approach is based on the observation that the homology of an independence complex of a chordal graph can be described using what we call strong induced matchings in the graph (also known as cross-cycles). We show that finding such a matching of a specified size in a chordal graph is NP-hard.

We further study the computational complexity of finding any cross-cycle in arbitrary and chordal graphs.

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1. Introduction

The main purpose of this paper is to study the difficulty of computing homology groups for certain representations of simplicial complexes. Homology groups, together with their persistent versions, are topological invariants of fundamental importance in applications of computational topology [7], and various kinds of simplicial complexes are commonly used to represent data sets. We will be concerned with the following family of decision problems parametrized by an input type T.

Problem HOMOLOGY $_{\mathcal{T}}(K, \ell)$

Input: A simplicial complex *K* represented as \mathcal{T} and an integer $\ell \ge 0$ given in binary. **Output:** TRUE if $\widetilde{H}_{\ell}(K) \cong 0$ and FALSE if $\widetilde{H}_{\ell}(K) \cong 0$.

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Here $\tilde{H}_{\ell}(K)$ denotes the ℓ -th reduced homology group of K and all the results of this paper are true with arbitrary coefficients. The computational complexity of the problem depends on the input type \mathcal{T} which determines how the simplicial complex K is represented. We will now discuss various choices of \mathcal{T} and introduce our results.

The list of all simplices. In the applications in computational topology the size of *K* is usually measured in terms of the number *n* of all simplices. In other words, it is assumed that *K* is represented by the list of all its simplices. In this case the homology problem can be formulated directly as a linear algebra problem for matrices of size at most $n \times n$. Over the integers it can be solved by reduction to the Smith normal form in time $O(n^{3.37\cdots})$ [22]. For coefficients in a field Gaussian elimination is likely to be the most efficient method [8]. Either way, the problem can be solved in polynomial time (although a lot of non-trivial optimization is required to handle data sets with, say, $n = 10^9$ simplices, occurring in practice).

The representation of K via the list of all simplices is not very efficient. Below we will discuss two succinct kinds of representations which occur in practice, and which lead to complexes with n exponential in the size of the input. One would expect that the homology problem for such inputs is NP-hard. Surprisingly though, the complexity of these natural problems has not been investigated before.

Before we proceed, note that for most reasonable representations of K (in particular the ones studied next), the homology problem is solvable in polynomial time for any fixed ℓ as well as for complexes of dimension bounded by any fixed d. This is because the relevant part of the chain complex has polynomial size, and can be generated in polynomial time, where the degree of the polynomial is a function of ℓ or d. The subsequent matrix operations thus take time polynomial in the size of the input.

Maximal faces, minimal non-faces. Kaibel and Pfetsch [17, Problem 33] asked if the homology problem is NP-hard when *K* is represented by the list of facets (maximal faces). We answer this question, and its dual, affirmatively.

Theorem 1.1. The homology problem is NP-hard when the input complex K is represented by either (a) the list of vertices and the list of maximal faces or (b) the list of vertices and the list of minimal non-faces.

The representation via maximal faces is quite natural, and in fact most existing simplicial homology software accepts this kind of input. The most prominent class of complexes naturally described by minimal non-faces are clique complexes, and among them Rips complexes; see below.

It has recently been shown that computing the Euler characteristic of a simplicial complex given by maximal faces is #*P*-hard [21]. We note in passing one other famous problem involving such representations. Suppose we have two simplicial complexes K_1 and K_2 , with the same vertex set, where K_1 is given by its maximal faces and K_2 is given by its minimal non-faces. Then the decision problem "Does $K_1 = K_2$?", better known as *monotone dualization* or *hypergraph transversal* has received a lot of attention in the theoretical computer science community [10]. Its complexity status is open; a quasi-polynomial time algorithm is known [12]. An equivalent version of this problem asks to decide if a simplicial complex *K* given by maximal faces is Alexander dual to itself.

Clique complexes. Another class of spaces we are interested in are clique (or flag) complexes. A clique complex of a graph G is the simplicial complex whose simplices are all the cliques (complete subgraphs) of G. These complexes appear in applications as Rips complexes, that is clique complexes of Rips graphs, used to capture the notion of proximity in metric spaces. In this scenario the entire simplicial complex is determined by the graph, which becomes the most natural and efficient input representation. We will prove that the homology problem for this representation of clique complexes is also NP-hard.

Theorem 1.2. The homology problem is NP-hard for the class of clique complexes Cl(G), when the input is the graph *G*. Moreover, it remains NP-hard if *G* is restricted to any of the following classes:

(a) co-chordal graphs,

(b) co-bipartite graphs,

(c) quasi-Rips graphs of finite subsets of \mathbb{R}^1 with any fixed uncertainty interval.

All the hardness results in this paper will be deduced from Theorem 1.2.(a). Co-chordal graphs are complements of chordal graphs (in general, co- \mathcal{P} are the complements of graphs in \mathcal{P}), and the latter can be defined for instance as intersection graphs of subtrees of a tree. To prove Theorem 1.2.(a) we will construct a more direct combinatorial model of homology generators in clique complexes of co-chordal graphs, which we call *strong induced matchings* in the graph's complement (Definition 3.1). They correspond to embedded spheres isomorphic to the boundary complexes of cross-polytopes, called *cross-cycles* by Jonsson [15]. The following theorem, which we prove in Section 3, is our main link between topological and combinatorial properties of co-chordal graphs.

Theorem 3.5. If G is co-chordal then $\widetilde{H}_{k-1}(Cl(G)) \not\cong 0$ if and only if the complement \overline{G} contains a strong induced matching of order k.

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