COMPLEXITY OF SIMPLICIAL HOMOLOGY AND INDEPENDENCE COMPLEXES OF CHORDAL GRAPHS

MICHAŁ ADAMASZEK AND JURAJ STACHO

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.

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 $\mathcal{T}$.

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

Input: A simplicial complex K represented as $\mathcal{T}$ and an integer $\ell \geq 0$ given in binary.

Output: TRUE if $\widetilde{H}_\ell(K) \ncong 0$ and FALSE if $\widetilde{H}_\ell(K) \cong 0$.

Here $\widetilde{H}_\ell(K)$ 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

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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* $\mathrm{Cl}(G)$, *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* $\widetilde{H}_{k-1}(\mathrm{Cl}(G)) \ncong 0$ *if and only if the complement* $\overline{G}$ *contains a strong induced matching of order* k*.*

The quasi-Rips graphs appearing in Theorem 1.2.(c) are generalizations of Rips graphs and were introduced in [5] as a way of modelling spatial uncertainty in the Rips graph construction. For all the necessary definitions see Section 2.

More about co-chordal graphs. We believe that our description of homology of clique complexes of co-chordal graphs can be of independent interest. This class of spaces has been studied quite successfully in the context of combinatorial topology and combinatorial commutative algebra [11, 9, 18, 24, 26]. The next theorem is an algorithmic counterpart to the hardness result of Theorem 1.2.(a). Here $\widetilde{H}_*(K) = \bigoplus_\ell \widetilde{H}_\ell(K)$ denotes the total homology of K (in all dimensions).

Theorem 1.3. *For the class of co-chordal graphs* G*:*

(a) *The homology problem for* $\mathrm{Cl}(G)$ *is in NP when the input is the graph* G*.*
(b) *There is an algorithm with running time* $O(|E(G)|^2)$ *which decides if* $\widetilde{H}_*(\mathrm{Cl}(G)) \cong 0$*.*

It is not clear if part (a) is true for arbitrary clique complexes, or for complexes represented by maximal faces. Naively, non-triviality of a homology group could be witnessed by a non-bounding cycle, but that may have size exponential in the size of the input.

For a co-chordal graph G the complex $\mathrm{Cl}(G)$ is homotopy equivalent to a wedge of spheres (Corollary 2.2), therefore $\widetilde{H}_*(\mathrm{Cl}(G)) \cong 0$ is equivalent to $\mathrm{Cl}(G)$ being contractible. The problem of deciding if $\mathrm{Cl}(G)$ is contractible for an arbitrary graph G is undecidable [23, Theorem 11].

This makes the clique complexes of co-chordal graphs an interesting boundary case for the complexity of the homology problem in the following sense: when G is co-chordal, testing for the non-triviality of $\widetilde{H}_\ell(\mathrm{Cl}(G))$ with ℓ as part of input is NP-hard, but detecting if $\mathrm{Cl}(G)$ has *any* non-trivial homology group is possible in polynomial time.

Organization of the paper. Section 2 contains preliminaries on topology and combinatorics. In that section we also deduce all the hardness results from Theorem 1.2.(a). In Section 3 we define strong induced matchings and prove Theorem 1.2.(a). Section 4 contains the algorithm of Theorem 1.3. Some final remarks and open problems are gathered in Section 5.

2. PRELIMINARIES

We assume a degree of familiarity with simplicial topology and basic graph theory and refer to the books by Kozlov [19] and West [25]. Below we briefly review the definitions and standardize notation.

Combinatorial topology. A *simplicial complex* K with vertex set V is a family $K \subseteq 2^V$ such that $A \in K$ and $B \subseteq A$ imply $B \in K$. We will identify a simplicial complex with its geometric realization. The elements of K are called *simplices* or *faces*. The dimension of a face $A \in K$ is $\dim A := |A| - 1$.

We write $\widetilde{H}_\ell(K;\mathbf{k})$ and $\widetilde{H}^\ell(K;\mathbf{k})$ for the reduced homology and cohomology groups of K with coefficients in $\mathbf{k}$. All of our results hold for arbitrary $\mathbf{k}$, and hence it will be omitted. Group isomorphism is denoted with $\cong$.

The symbol $\sqcup$ denotes disjoint union. The notation $\bigvee_{i\in I} X_i$ stands for the wedge sum of pointed spaces $\{X_i\}_{i\in I}$. By convention the wedge sum is just a point if $I = \emptyset$. We write ΣK for the suspension of a simplicial complex K. The symbol $\simeq$ denotes homotopy equivalence.

If K is a simplicial complex with vertex set V then we write $\mathfrak{B}(K)$ for the set of *maximal faces (facets)* of K, that is the set of inclusion-wise maximal elements of K. We also write $\mathfrak{C}(K)$ for the set of *minimal non-faces* of K, which are the inclusion-wise minimal elements of $2^V \setminus K$. [1] For a fixed vertex set V each of $\mathfrak{B}(K)$ and $\mathfrak{C}(K)$ uniquely determines K.

Suppose that $G = (V, E)$, with $E \subseteq \binom{V}{2}$ is an undirected graph without multiple edges or loops. The *complement* of G is the graph $\overline{G}$ with vertex set V and edge set $\binom{V}{2} \setminus E$. A *clique* of G is a subset of $V(G)$ whose elements are pairwise adjacent. An *independent set* of G is a subset of $V(G)$ whose elements are pairwise non-adjacent. Clearly a clique of G is an independent set of $\overline{G}$, and vice-versa.

The *clique complex* $\mathrm{Cl}(G)$ of a graph G is the simplicial complex with vertex set $V(G)$ whose faces are all the cliques in G. The *independence complex* $I(G)$ is the simplicial complex whose faces are all the independent sets in G. We have $\mathrm{Cl}(G) = I(\overline{G})$.

For a finite metric space X with distance function $d_X : X \times X \to \mathbb{R}$ and a real number $r > 0$ the *Rips graph* $R(X;r)$ is the graph with vertex set X such that $x_1, x_2 \in X$ are adjacent in $R(X;r)$ if and only if $d_X(x_1, x_2) < r$. A *quasi-Rips graph with uncertainty interval* (r, r') on the space X is any graph Q for which $V(Q) = X$ and $E(R(X;r)) \subseteq E(Q) \subseteq E(R(X;r'))$. A *Rips complex* (resp. *quasi-Rips complex*) is the clique complex of a Rips (resp. quasi-Rips) graph. Rips complexes are used heavily in computational topology and quasi-Rips complexes are a relaxation which accommodates the possibility of non-precise distance measurements; see [5] for details.

If $G = (V, E)$ and $W \subseteq V$ then we write $G[W]$ for the induced subgraph of G with vertex set W. To simplify notation we write $G \setminus W$ for $G[V(G) \setminus W]$ and $G \setminus v$ for $G[V(G) \setminus \{v\}]$. For a vertex $v \in V(G)$ we define the open neighbourhood $N_G(v) = \{w : vw \in E(G)\}$ and the closed neighbourhood $N_G[v] = N_G(v) \cup \{v\}$. A subset $D \subseteq V(G)$ is called *dominating* if every vertex of $V(G) \setminus D$ is adjacent to some vertex of D.

If $\mathcal{P}$ is a class of graphs then co-$\mathcal{P}$ is the class of graphs G such that $\overline{G}$ is in $\mathcal{P}$. In particular, the class of clique complexes of graphs in co-$\mathcal{P}$ coincides with the class of independence complexes of graphs in $\mathcal{P}$.

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[1] If the simplicial complex K happens to be a matroid, then $\mathfrak{B}(K)$ is the set of *bases* and $\mathfrak{C}(K)$ is the set of *circuits* of K.

Chordal graphs. It will be convenient to prove our results in the language of independence complexes, rather than clique complexes. The core of our approach exploits topological properties of independence complexes of chordal graphs (which are the same as clique complexes of co-chordal graphs featured in Theorems 1.2.(a) and 1.3). Chordal graphs are a classical topic in structural and algorithmic graph theory and their independence complexes are well understood in the context of combinatorial topology and commutative algebra [11, 9, 18, 24, 26].

A graph is called *chordal* if it has no induced cycles of length four or higher. This class is closed under taking induced subgraphs. A vertex v of a graph G is called *simplicial*[2] if $N_G(v)$ is a clique of G. By a classical result of Dirac [6], every nonempty chordal graph G has a simplicial vertex. As a consequence, the vertices of G can be arranged in a *perfect elimination ordering*, that is a linear order $v_1, \dots, v_n$ such that v_i is simplicial in $G[\{v_i, \dots, v_n\}]$ for all $i = 1, \dots, n$. The existence of such an ordering characterizes chordal graphs.

For graphs with a simplicial vertex we have the following homotopy decomposition, originally due to Engström [11]. We include the proof for completeness.

Lemma 2.1. [11, Theorem 3.7] *If G is any graph and v is a simplicial vertex then there is a homotopy equivalence*

$$I(G) \simeq \bigvee_{w \in N_G(v)} \Sigma\, I(G \setminus N_G[w]).$$

Proof. If v is isolated then $I(G) \simeq *$, so the result holds. Otherwise let w be any vertex in $N_G(v)$. It suffices to show $I(G) \simeq I(G \setminus w) \vee \Sigma\, I(G \setminus N_G[w])$. Since v is still simplicial in $G \setminus w$ the lemma will then follow by induction.

In the complex $I(G)$ the link of w is $I(G \setminus N_G[w])$ and the deletion of w is $I(G \setminus w)$. It means that $I(G)$ is the mapping cone of the inclusion $\iota_w : I(G \setminus N_G[w]) \hookrightarrow I(G \setminus w)$.

Since $N_G[v] \subseteq N_G[w]$, every independent set in $G \setminus N_G[w]$ can be extended by v to an independent set in $G \setminus w$. It means that ι_w factors through the contractible cone $I(G \setminus N_G[w]) * \{v\}$. As a consequence ι_w is null-homotopic and its mapping cone is homotopy equivalent to $I(G \setminus w) \vee \Sigma\, I(G \setminus N_G[w])$. □

Applying Lemma 2.1 inductively yields the next corollary. It also follows from the fact that independence complexes of chordal graphs are vertex-decomposable [26, Corollary 7].

Corollary 2.2. *If G is chordal then $I(G)$ is homotopy equivalent to a wedge of spheres.*

Remark 2.3. If F is a forest then a vertex v of F is simplicial if and only if it is isolated or a leaf. In the latter case $N_F(v)$ is a singleton. Lemma 2.1 immediately yields a linear time algorithm that determines the homotopy type of $I(F)$, answering a question of Ehrenborg and Hetyei [9].

Remark 2.4. If G is any graph and e is the graph consisting of a single edge then $I(G \sqcup e) = \Sigma\, I(G)$. Moreover, if CG is the cone on G, that is the graph obtained by adding one new vertex adjacent to all of G, then $I(CG) = I(G) \vee S^0$. Both $G \sqcup e$ and CG are chordal if G is chordal. Successively applying these operations one shows that every finite wedge of spheres can appear as the homotopy type of an independence complex of a chordal graph.

Easy implications. We can now reduce all of the NP-hardness results to Theorem 1.2.(a).

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[2] This standard graph theory terminology unfortunately clashes with the other meaning of *simplicial* in this paper.

1.2 $\Longrightarrow$ 1.1.(b). Suppose G is a graph. We have $\mathfrak{C}(\mathrm{Cl}(G)) = E(\overline{G})$, i.e. the set of non-edges of G forms the description of $\mathrm{Cl}(G)$ via minimal non-faces, of size polynomial in the size of G. This reduces the homology problem for clique complexes of graphs to the homology problem for complexes given by vertices and minimal non-faces.

1.2.(a) $\Longrightarrow$ 1.1.(a). Given a co-chordal graph G with n vertices consider a simplicial complex K_G with vertex set $V(G)$ and with faces defined by the relation

$$A \in K_G \iff (V(G) \setminus A) \notin \mathrm{Cl}(G).$$

The complex K_G is the *Alexander dual* of $\mathrm{Cl}(G)$. We have

$$\mathfrak{B}(K_G) = \{V(G) \setminus \{x, y\} \ : \ xy \in E(\overline{G})\}$$

which means that the representation of K_G via vertices and maximal faces can be computed in polynomial time from G. We also have the relations

$$\widetilde{H}_{n-\ell-3}(K_G) \cong \widetilde{H}^{\ell}(\mathrm{Cl}(G)) \cong \widetilde{H}_{\ell}(\mathrm{Cl}(G))$$

where the first equality holds by Alexander duality [2], and the second one is a consequence of the fact that $\mathrm{Cl}(G)$ is homotopy equivalent to a wedge of spheres (Corollary 2.2). That reduces the homology problem for the pair $(\mathrm{Cl}(G), \ell)$ to the homology problem for $(K_G, n-\ell-3)$ in polynomial time.

1.1.(a) $\Longrightarrow$ 1.2.(b). Consider a simplicial complex K represented by n vertices $v_1, \ldots, v_n$ and m maximal faces $F_1, \ldots, F_m$. Let G_K be the bipartite graph with parts of size n and m, corresponding to the sets $V(K)$ and $\mathfrak{B}(K)$, such that there is an edge from v_i to F_j if and only if $v_i \notin F_j$. Clearly G_K can be constructed from the facet description of K in polynomial time. It is a folklore theorem (see for instance [1, Theorem 3.8]) that

$$I(G_K) \simeq \Sigma\, K.$$

In particular $\widetilde{H}_{\ell}(K) \cong \widetilde{H}_{\ell+1}(I(G_K)) \cong \widetilde{H}_{\ell+1}(\mathrm{Cl}(\overline{G_K}))$. That reduces the homology problem for complexes given by maximal faces to the homology problem for clique complexes of co-bipartite graphs.

1.2.(b) $\Longrightarrow$ 1.2.(c). Fix $0 < r < r'$. Every co-bipartite graph G can be realized as a quasi-Rips graph of a subset of $\mathbb{R}^1$ with uncertainty interval (r, r'), which can be seen by placing the vertices of the two parts of G on the real line in the intervals $(0, \frac{1}{2}(r'-r))$ and $(\frac{1}{2}(r'+r), r')$, respectively. Therefore every co-bipartite graph is a quasi-Rips graph in $\mathbb{R}^1$, and the reduction is immediate.

3. INDEPENDENCE COMPLEXES OF CHORDAL GRAPHS: HARDNESS

In this section we give a purely combinatorial characterization of homology classes in independence complexes of chordal graphs in terms of matchings. This leads to the proof of Theorem 1.2.(a) and Theorem 1.3.(a).

A *matching* of order k is the graph on $2k$ vertices that is a disjoint union of k edges. If M is a matching of order k then the independence complex $I(M)$ is the join of k copies of S^0, hence it is homeomorphic to S^{k-1}. More precisely, $I(M)$ is isomorphic to the boundary complex of the k-dimensional cross-polytope.

An *induced matching* M in G is an induced subgraph of G isomorphic to a matching. If M is a matching of order k in G then the subcomplex $I(M)$ of $I(G)$ is an embedded $(k-1)$-sphere. In particular, the inclusion $I(M) \hookrightarrow I(G)$ determines a homology class $\pm\alpha_M \in \widetilde{H}_{k-1}(I(G))$

(the sign depends on the choice of orientations which we will never have to concern ourselves with). Of course this class may be trivial. The next definition and lemma provide a simple witness of the non-triviality of α_M.

Definition 3.1. *A pair (M, D) is called a* strong induced matching *(s.i.m.) of order k in a graph G if*

(a) *M is an induced matching of order k in G,*
(b) *$|D| = k$ and D contains exactly one vertex from each edge of M,*
(c) *D is a maximal independent set of G.*

Conditions (a) and (b) imply that D is an independent set of G and then (c) is equivalent to asking that D is dominating. See Figure 2 for an example.

Lemma 3.2. *If (M, D) is a strong induced matching in G then the homology class $\pm\alpha_M \in \widetilde{H}_{k-1}(I(G))$ is non-trivial.*

Proof. The cycle representing the class α_M contains in its support the oriented simplex $[D]$. Since D is a maximal face of $I(G)$, it does not appear in the image of the boundary map, and therefore the cycle representing α_M is not a boundary. □

Remark 3.3. Homology classes in $I(G)$ defined by strong induced matchings in G were introduced by Jonsson [15] under the name *cross-cycles*. In general, homology classes defined by matchings appear in a number of contexts. They are the typical generators of homology for independence complexes of random graphs [16]. Moreover, they are the minimal generators, in the sense that every homology class in $\widetilde{H}_{k-1}$ of a clique or independence complex must be supported on at least $2k$ vertices [16, Lemma 5.3]. This motivates our interest in their algorithmic properties.

Remark 3.4. To our best knowledge strong induced matchings have not been studied in (algorithmic) graph theory. In this remark we discuss two related problems.

A *maximum induced matching (m.i.m.)* is an induced matching of largest cardinality in the graph. A *dominating induced matching (d.i.m.)* is an induced matching M such that every edge of G is either in M or incident to some edge of M. Every d.i.m. is a m.i.m. [4], but no other implication holds between the properties of s.i.m., m.i.m. and d.i.m. A graph need not have a strong or dominating induced matching. In this respect the notion of s.i.m. is closer to that of a d.i.m.

Finding either a maximum, dominating or strong induced matching is NP-hard in general graphs and polynomial-time in chordal graphs. This is shown in [3] for m.i.m., in [20] for d.i.m. and in this paper for s.i.m. The hardness proofs are rather straightforward in all cases. The algorithms for chordal graphs are based on the structure of clique-neighbourhoods in chordal graphs in the case of [3], on a reduction to series-parallel graphs in [20] and on the tree model of a chordal graph in this paper. It is the interplay between induced matchings and vertex-dominating subsets in the definition of a s.i.m. that makes the s.i.m. problem quite distinct from the other two.

To clarify the boundary cases we remark that if G is the empty graph (that means $V(G) = \emptyset$) then $(M, D) = (\emptyset, \emptyset)$ is a s.i.m. in G of order 0.

The next main result builds the bridge between topology and graph theory for chordal graphs.

Theorem 3.5. *Suppose G is a chordal graph and $k \geq 0$. Then G has a strong induced matching of order k if and only if $\widetilde{H}_{k-1}(I(G)) \ncong 0$.*

Proof. If G has a strong induced matching of order k then $\widetilde{H}_{k-1}(I(G)) \ncong 0$ follows from Lemma 3.2. The other implication will be proved by induction on $|V(G)|$.

If $V(G) = \emptyset$, then $I(G) = \emptyset$ is the simplicial complex with empty vertex set. We have $\widetilde{H}_{k-1}(\emptyset) \ncong 0$ if and only if $k = 0$. In this case the pair $(\emptyset, \emptyset)$ is a s.i.m. of order 0 in G and we established the base of induction.

Now let G be a chordal graph with at least one vertex and suppose that $\widetilde{H}_{k-1}(I(G)) \ncong 0$. Let v be any simplicial vertex of G. By Lemma 2.1 we have

$$0 \ncong \widetilde{H}_{k-1}(I(G)) \cong \bigoplus_{w \in N_G(v)} \widetilde{H}_{k-2}(I(G \setminus N_G[w])).$$

It follows that there exists a vertex $w \in N_G(v)$ such that $\widetilde{H}_{k-2}(I(G \setminus N_G[w])) \ncong 0$. The graph $G \setminus N_G[w]$ is chordal, so by induction it has a strong induced matching (M', D') of order $k-1$. Now define a new pair (M, D) of order k in G by setting

$$M = M' \cup \{wv\}, \qquad D = D' \cup \{w\}.$$

The vertices in M induce a matching since neither v nor w are adjacent to any vertex of $V(M') \subseteq V(G \setminus N_G[w])$. Every vertex of $V(G) \setminus D$ is either in $N_G[w]$, and then it is adjacent to w, or in $G \setminus N_G[w]$, and then it is adjacent to an element of D'. It follows that (M, D) is a s.i.m. of order k in G. □

Remark 3.6. One can show that even more is true. If G is chordal then the homology group $\widetilde{H}_{k-1}(I(G); \mathbf{k})$ is generated, as a $\mathbf{k}$-module, by the classes α_M where M varies over all strong induced matchings (M, D) of order k in G. The proof is a simple extension of the proof of Theorem 3.5. We are not going to use this result, so we omit the details.

We have thus reduced the homology problem for independence complexes of chordal graphs to the problem of detecting a strong induced matching of a specified order in a chordal graph. We will now prove that the latter problem is NP-complete. Combined with Theorem 3.5 that immediately yields Theorem 1.2.(a) and Theorem 1.3.(a).

Theorem 3.7. *The problem of deciding, given a chordal graph G and an integer k, whether G has a strong induced matching of order k, is NP-complete.*

To prove this theorem we first need to establish an auxiliary hardness reduction.

Lemma 3.8. *The problem of deciding, given a chordal graph G and an integer k, whether G has a maximal independent set of size exactly k, is NP-complete.*

Proof. The proof is by reduction from the following problem: given an arbitrary graph H and an integer k, does H have a dominating set of size exactly k? This problem is NP-complete, since finding a minimum size dominating set in H is NP-complete [13, Problem GT2].

Now suppose we are given an arbitrary graph H with n vertices. Construct a graph G with $7n$ vertices as follows (see Figure 1):

$$\begin{aligned} V(G) &= \{v_0, v_1, v_2, v_3, v_4, v_5, v_6 \;:\; v \in V(H)\} \\ E(G) &= \{v_0w_0 \;:\; v, w \in V(H)\} \cup \{v_0w_1 \;:\; vw \in E(H)\} \\ &\quad \cup \{v_0v_1, v_1v_2, v_1v_4, v_1v_5, v_1v_6, v_2v_3 \;:\; v \in V(H)\} \end{aligned}$$

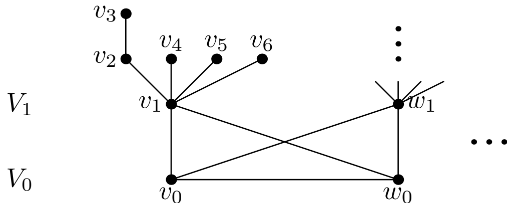

FIGURE 1. The gadget used in Lemma 3.8.

For simplicity define $V_i = \{v_i \ : \ v \in V(H)\} \subseteq V(G)$ for $i = 0, \dots, 6$. Note that V_0 is a clique of G. The graph G is chordal; a perfect elimination ordering is to remove vertices of V_3 followed by V_2, V_4, V_5, V_6, V_1 and finally the vertices of V_0 in any order.

Now we prove the following claim: H has a dominating set of size k if and only if G has a maximal independent set of size $4n - 2k$. This reduction will clearly prove the lemma.

First suppose that H has a dominating set D of size k. Define a subset D' of $V(G)$ by

$$D' = \{v_1, v_3 \ : \ v \in D\} \cup \{v_2, v_4, v_5, v_6 \ : \ v \notin D\}.$$

It is obvious that $|D'| = 2|D| + 4(n - |D|) = 4n - 2k$, that D' is independent and that every vertex of $V_1 \cup \cdots \cup V_6$ is either in D' or adjacent to a vertex of D'. Consider any vertex $v_0 \in V_0$. If $v \in D$ then v_0 is adjacent to $v_1 \in D'$. If $v \notin D$ then $vw \in E(H)$ for some $w \in D$ and therefore $v_0 w_1 \in E(G)$ with $w_1 \in D'$. That proves D' is a dominating (hence maximal) independent set.

Conversely, suppose that G contains an independent dominating set D' of size $4n - 2k$. For every $v \in V(H)$ either $v_2 \in D'$ or $v_3 \in D'$. Further, we have the implications

$$\begin{aligned} v_2 \in D' \quad &\Longrightarrow \quad v_2, v_4, v_5, v_6 \in D', \ v_1, v_3 \notin D', \\ v_3 \in D' \quad &\Longrightarrow \quad \begin{cases} v_3, v_4, v_5, v_6 \in D', \ v_1, v_2 \notin D', \text{ or} \\ v_1, v_3 \in D', \ v_2, v_4, v_5, v_6 \notin D'. \end{cases} \end{aligned}$$

In particular $|D' \cap (V_1 \cup \cdots \cup V_6)|$ is even. Since V_0 is a clique, we have $|D' \cap V_0| \le 1$. Because $|D'|$ is even, these conditions imply $D' \cap V_0 = \emptyset$.

Define a subset of $V(H)$ by $D = \{v \in V(H) \ : \ v_1 \in D'\}$. By the above observations

$$4n - 2k = |D'| = 2|D| + 4(n - |D|)$$

and so $|D| = k$. Since D' was dominating in G, every vertex $v \in V(H)$ is either in D, or it is adjacent to some $w \in D$ for which $v_0 w_1 \in E(G)$. This shows that D is dominating in H, as required. ☐

We can now prove the main result of this section.

Proof of Theorem 3.7. The problem is clearly in NP. To prove NP-hardness we describe a polynomial-time reduction from the problem of Lemma 3.8.

Consider a chordal graph G and an integer k. We construct a graph G' from G by substituting a clique of size two for every vertex of G. More precisely, G' is defined as follows:

$$\begin{aligned} V(G') &= \{v_0, v_1 \ : \ v \in V(G)\} \\ E(G') &= \{v_0 v_1 \ : \ v \in V(G)\} \cup \{v_0 w_0, v_0 w_1, v_1 w_0, v_1 w_1 \ : \ vw \in E(G)\} \end{aligned}$$

Note that G' is chordal, since chordal graphs are closed under clique substitution.

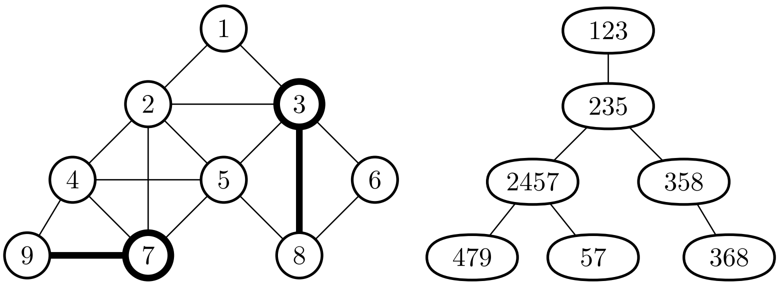

Figure 2. *(Left)* A chordal graph with a strong induced matching of order 2; the set $D = \{3, 7\}$ is a dominating independent set. *(Right)* A tree model of this graph (see Section 4).

The proof will be completed if we verify the following claim: G has a maximal independent set of size k if and only if G' has a strong induced matching of order k.

Suppose D is a maximal independent set of size k in G. Let $M' = \{v_0v_1 \ : \ v \in D\}$ and $D' = \{v_0 \ : \ v \in D\}$. Since D is an independent set of G, the matching M' of G' is an induced matching of order k. The condition that D is dominating in G easily implies that D' is dominating in G'. Thus G' contains a strong induced matching (M', D') of order k.

Conversely, suppose that G' contains a strong induced matching (M', D') of order k. Define $D = \{v \in V(G) \ : \ v_0 \in D' \text{ or } v_1 \in D'\}$. Clearly, $|D| = |D'| = k$ and D is an independent dominating set of G. □

Theorems 3.7 and 3.5 together imply Theorem 1.2.(a) and Theorem 1.3.(a).

4. More about strong induced matchings

In this section we continue the study of homology classes defined by strong induced matchings. First we observe that deciding the existence of such classes in independence complexes of arbitrary graphs is computationally hard.

Proposition 4.1. *The problem of deciding, given an arbitrary graph G, whether G has any strong induced matching, is NP-complete.*

Proof. The problem is clearly in NP. To prove that it is also NP-hard we construct a reduction from 3SAT. An instance $\mathcal{I}$ of 3SAT has clauses $C_1, \ldots, C_m$ and variables $v_1, \ldots, v_n$. We may assume that no variable appears in the same clause both positively and negatively. We write $\overline{v_i}$ for the negation of v_i.

Given an instance $\mathcal{I}$ of 3SAT, we construct a graph G as follows. The vertex set of G is $\{c_1, \ldots, c_m,\ v_1, \ldots, v_n, \overline{v_1}, \ldots, \overline{v_n}\}$. There are edges $v_1\overline{v_1}, \ldots, v_n\overline{v_n}$ and there is an edge between v_i and c_j if the literal v_i appears in the clause C_j, while there is an edge between $\overline{v_i}$ and c_j if $\overline{v_i}$ appears in C_j. Finally, the set $\{c_1, \ldots, c_m\}$ forms a clique. We will prove that $\mathcal{I}$ has a satisfying truth assignment if and only if G has a strong induced matching.

Suppose that $\mathcal{I}$ has a satisfying truth assignment $\varphi : \{v_1, \ldots, v_n\} \to \{\mathsf{true}, \mathsf{false}\}$. Define $M = \{v_1\overline{v_1}, \ldots, v_n\overline{v_n}\}$ and $D = \{v_i \ : \ \varphi(v_i) = \mathsf{true}\} \cup \{\overline{v_i} \ : \ \varphi(v_i) = \mathsf{false}\}$. By construction, M is an induced matching containing D, and D is an independent set. Since ϕ is a satisfying truth assignment, every vertex c_j is adjacent to at least one vertex of D. It shows that D is dominating in G, and therefore (M, D) is a s.i.m. in G.

Conversely, suppose that G has a strong induced matching (M, D). Suppose that D contains some vertex c_j (since $\{c_1, \dots, c_m\}$ is a clique, there can be at most one such c_j). Let v_i be any variable that appears in C_j (rename $\overline{v_i}$ to v_i if necessary). Then c_j is not adjacent to $\overline{v_i}$ and the maximality of D implies that $\overline{v_i} \in D$. In that case either $\overline{v_i}v_i \in M$ or $\overline{v_i}c_{j'} \in M$ for some $j' \neq j$, both contradicting the fact that M is an induced matching. This proves that $D \cap \{c_1, \dots, c_m\} = \emptyset$ which also shows that for each $i \in \{1 \dots n\}$, either v_i or $\overline{v_i}$ belongs to D but not both. Define a truth assignment φ by setting $\varphi(v_i)$ to true if $v_i \in D$, and to false if $\overline{v_i} \in D$. Since D is dominating, every vertex c_j is adjacent to a vertex from D, and so every clause C_j contains a literal which evaluates to true. This shows that $\mathcal{I}$ has a satisfying assignment and completes the proof. □

In the remainder of this section we are going to show that the situation is quite different for chordal graphs.

Theorem 4.2. *There is an algorithm which finds a strong induced matching in a chordal graph G, or decides there is no such matching, in time $O(|E(G)|^2)$.*

Note that because of Theorem 3.5 this implies Theorem 1.3.(b). Observe the contrast with Theorem 3.7, where we showed that the problem becomes NP-hard if one asks for a s.i.m. of a prescribed order.

To construct the algorithm we are going to use the representation of chordal graphs as intersection graphs of subtrees of a fixed tree. This approach, common in algorithmic graph theory, has not been used before to study topological properties of chordal graphs, where all known results exploit the structure of chordal graphs via perfect elimination orderings.

We will now introduce the intersection model. More details can be found in [25] and [14, Chapter 4]. For every chordal graph G there exists a tree T such that (see Figure 2)

- every node of T is labelled with a subset of $V(G)$,
- for every vertex $v \in V(G)$, the nodes of T which contain v induce a subtree of T,
- $vw \in E(G)$ if and only if there is a node of T which contains both v and w.

We call any such tree T a *tree model* of G. In fact a graph is chordal if and only if it has a tree model. For a chordal graph G a tree model with $O(|V(G)|)$ nodes can be found in linear time, and henceforth we will always assume that a chordal graph G is given together with one, fixed tree model T. The nodes of T will be denoted with capital letters $X, Y, \dots$.

Upon selecting an arbitrary node R as the root, we can view T as a rooted tree. We write $Y \prec X$ if Y is a descendant of X and $Y \preceq X$ if $Y \prec X$ or $Y = X$. The relation $\preceq$ is a partial order on the nodes of T with the unique largest element R. For a vertex $v \in V(G)$ we denote by $\mathsf{top}(v)$ the unique largest node of T containing v. Note that $vw \in E(G)$ if and only if $\mathsf{top}(v)$ contains w or $\mathsf{top}(w)$ contains v.

If $W \subseteq V(G)$ then by removing from T all vertex labels not in W we obtain a tree model of $G[W]$. Optionally, one can also remove all empty nodes and get a collection of trees, each a tree model of one connected component of $G[W]$.

For a node X of T we write G_X for the subgraph of G induced by vertices v with $\mathsf{top}(v) \preceq X$. Note that $G = G_R$. Moreover, let T_X be obtained from T by restricting to nodes Y with $Y \preceq X$ and to vertex labels v with $\mathsf{top}(v) \preceq X$. Then T_X is a tree model of G_X.

A strong induced matching (M, D) with $M = \{u_i v_i \ : \ i = 1, \dots, k\}$ and $D = \{u_i \ : \ i = 1, \dots, k\}$ will be called *canonical* (with respect to a fixed rooted tree model T) if $\mathsf{top}(u_i) \succeq \mathsf{top}(v_i)$ for $i = 1, \dots, k$.

Lemma 4.3. *Let G be a chordal graph with a fixed rooted tree model T. If G has a strong induced matching, then it has a canonical one of the same order.*

Proof. If $V(G)=\emptyset$ then $(\emptyset,\emptyset)$ is the only s.i.m. in G, and it is canonical.

Suppose G has at least one vertex and let (M,D) be a s.i.m. in G. Pick any vertex v which minimizes $\mathsf{top}(v)$ with respect to $\preceq$. Then every vertex u adjacent to v must appear in $\mathsf{top}(v)$, which implies that v is simplicial. Since D is dominating and independent, it must contain exactly one element x of $N_G[v]$. Now we perform a local modification which only affects the edge of M containing x as follows. If $xy\in M$ then we set

$$(M',D')=\begin{cases}(M,\ D\setminus\{v\}\cup\{y\}) & \text{if } x=v,\\ (M\setminus\{xy\}\cup\{xv\},\ D) & \text{if } x\neq v.\end{cases}$$

In either case we get a new s.i.m. (M',D') such that

$$M'=\{uv\}\cup M'',\ D'=\{u\}\cup D''$$

for some $u\in N_G(v)$. By minimality of $\mathsf{top}(v)$ we have $\mathsf{top}(u)\succeq\mathsf{top}(v)$. Now (M'',D'') is a s.i.m. in $G\setminus N_G[u]$. By induction, it can be replaced with one that is canonical with respect to the tree model of $G\setminus N_G[u]$ obtained from T, and therefore enjoying the same relation $\preceq$ on its nodes. This ends the proof. ☐

Let $\mathcal{M}(G)$ denote the set of all canonical strong induced matchings in G (of all orders). If $(M,D),(M',D')\in\mathcal{M}(G)$ then we write $(M,D)\preceq(M',D')$ if for every $u\in D$ there exists $u'\in D'$ such that $\mathsf{top}(u)\preceq\mathsf{top}(u')$. That makes $(\mathcal{M}(G),\preceq)$ a pre-order. As we will see in the proof of Theorem 4.4, whenever this pre-order is non-empty, it has a largest element (not necessarily unique).

If D contains a vertex u such that $\mathsf{top}(u)=R$ then (M,D) is automatically a largest element of $(\mathcal{M}(G),\preceq)$. We will call such (M,D) *rooted*.

We can now describe the algorithm. It proceeds bottom–up along the rooted tree model of G and for each node X it finds some largest, with respect to $\preceq$, canonical s.i.m. in G_X. We assume that the answer has already been computed for all G_Y with $Y\prec X$. The final answer is obtained for $X=R$, the root of the tree.

Theorem 4.4. *Algorithm 1 returns a largest element of $(\mathcal{M}(G_X),\preceq)$ or returns NONE if G_X has no strong induced matching.*

Proof. First we will show that if G_X has a rooted s.i.m. then Algorithm 1 will exit with an answer in line 8. Any s.i.m. returned in line 8 is canonical and rooted, and therefore a largest element of $(\mathcal{M}(G_X),\preceq)$.

Let $M'=\{uv\}\cup M''$ and $D'=\{u\}\cup D''$ be a canonical s.i.m. in G_X such that $\mathsf{top}(u)=X$. Then (M'',D'') is a canonical s.i.m. in $G_X\setminus(N[u]\cup N[v])=G_{Y_1}\sqcup\cdots\sqcup G_{Y_s}$. Note that there are no edges between different subgraphs G_{Y_i}. It follows that each G_{Y_i} has a s.i.m. ($\mathcal{M}(G_{Y_i})\neq\emptyset$) and $M''=\bigcup M_i''$, $D''=\bigcup D_i''$, where (M_i'',D_i'') is a canonical s.i.m. in G_{Y_i}. Let us show that the pair (M,D) defined in line 7 is a s.i.m. in G_X. The only non-trivial fact is that D is dominating in G_X. Pick any vertex $x\in V(G_X)$. If $xu\in E(G_X)$ then we are done. If $\mathsf{top}(x)\preceq Y_i$ for some i then $x\in V(G_{Y_i})$ and x is adjacent to some element of D_i by the definition of (M_i,D_i). In all other cases, since (M',D') is a s.i.m. in G_X, x must be adjacent to some $y\in D_i''$. Since (M_i,D_i) is a largest element of $(\mathcal{M}(G_{Y_i}),\preceq)$, there is a vertex $z\in D_i$ such that $\mathsf{top}(z)\succeq\mathsf{top}(y)$. Since x appears in the node $\mathsf{top}(y)$ and it appears

Algorithm 1 Strong induced matching in a chordal graph

```
Input: A chordal graph $G$ with a rooted tree model $T$ and a node $X$ of $T$.
Output: A largest element of $(\mathcal{M}(G_X), \preceq)$ or NONE if $\mathcal{M}(G_X) = \emptyset$.
1: if $V(G_X) = \emptyset$ then return $(\emptyset, \emptyset)$
2: for all $uv \in E(G_X)$ with $\mathsf{top}(u) = X$ do
3:     delete the nodes containing $u$ or $v$ from $T_X$
4:     let $Y_1, \dots, Y_s$ be the roots of the resulting forest
5:     if $\mathcal{M}(G_{Y_i}) \neq \emptyset$ for all $i$ then
6:         let $(M_i, D_i)$ be a largest element of $(\mathcal{M}(G_{Y_i}), \preceq)$
7:         let $M = \{(u,v)\} \cup M_1 \cup \cdots \cup M_s$, $D = \{u\} \cup D_1 \cup \cdots \cup D_s$
8:         if $(M, D)$ is a s.i.m. in $G_X$ then return $(M, D)$
9:     end if
10: end for
11: let $Z_1, \dots, Z_t$ be the children of $X$ in $T$
12: if $\mathcal{M}(G_{Z_i}) \neq \emptyset$ for all $i$ then
13:     let $(M_i, D_i)$ be some largest element of $(\mathcal{M}(G_{Z_i}), \preceq)$
14:     let $M = M_1 \cup \cdots \cup M_t$, $D = D_1 \cup \cdots \cup D_t$
15:     if $(M, D)$ is a s.i.m. in $G_X$ then return $(M, D)$
16: end if
17: return NONE
```

in some node outside T_{Y_i} because $\mathsf{top}(x) \not\preceq Y_i$, it must also appear in $\mathsf{top}(z)$. It means that $xz \in E(G_X)$, and we are done also in this case.

We showed that if the algorithm reaches line 11 then G_X does not have a rooted s.i.m. It means that every canonical s.i.m. in G_X contains only vertices v with $\mathsf{top}(v) \prec X$.

Suppose now that G_X has some non-rooted canonical s.i.m. (M', D'). Since there are no edges between different subgraphs G_{Z_i} and G_{Z_j} of G_X, we have $(M', D') = \bigcup (M'_i, D'_i)$, where (M'_i, D'_i) is a canonical s.i.m. of G_{Z_i}. Let (M_i, D_i) and (M, D) be the pairs found in line 14 of the algorithm. To show that (M, D) is a s.i.m. in G_X we need to verify only that D is dominating in G_X. Pick any vertex $x \in V(G_X)$. If $\mathsf{top}(x) \preceq Z_i$ for some i then x is adjacent to an element of D_i by definition of (M_i, D_i). If, on the other hand, $\mathsf{top}(x) = X$ then x is adjacent to some element $y \in D'_i$ because (M', D') is a s.i.m. in G_X. We find $z \in D_i$ so that $\mathsf{top}(z) \succeq \mathsf{top}(y)$ and conclude that $xz \in E(G_X)$ as before. It shows that (M, D) is a canonical s.i.m. in G_X. Since $(M_i, D_i) \succeq (M'_i, D'_i)$ in $\mathcal{M}(G_{Z_i})$, we have $(M, D) \succeq (M', D')$ in $\mathcal{M}(G_X)$. As (M', D') was arbitrary that proves that the pair (M, D) returned in line 15 is a largest element of $(\mathcal{M}(G_X), \preceq)$.

It follows that the algorithm returns NONE if and only if $\mathcal{M}(G_X) = \emptyset$, which ends the proof. □

To complete the proof of Theorem 4.2 it remains to bound the total running time of Algorithm 1 invoked bottom–up for all nodes X of T. Suppose G has n vertices and m edges. Then testing if a particular pair (M, D) is a s.i.m. can be done in time $O(m)$. Every edge of G is processed exactly once in line 2 and the number of nodes of T is $O(n)$. That means the running time is $O(m^2 + nm) = O(m^2)$ as required.

5. Open problems

It would be interesting to prove that other variants of the homology problem are also NP-hard when K is given by maximal faces or when $K = \mathrm{Cl}(G)$ is given as the graph G. In particular, the *homological dimension* problem asks if $\widetilde{H}_i(K) \cong 0$ for all $i \geq \ell$ and the *homological connectivity* problem asks if $\widetilde{H}_i(K) \cong 0$ for all $i \leq \ell$. The complexity status of these questions is open.

In the case of independence complexes of chordal graphs Theorem 3.5 reduces the above questions to the problem of finding a strong induced matching of maximal, resp. minimal order. Even the complexity of those special cases is open.

In the geometric context we conjecture that the homology problem remains NP-hard for clique complexes of Rips graphs of finite subsets of $\mathbb{R}^2$.

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