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Homology Computation on Cellular Structures in Image Context

S. Alayrangues, G. Damiand, L. Fuchs, P. Lienhardt, S. Peltier

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Abstract During the previous decade, many works have shown that topological properties are of interest in an image context. Among all topological invariants (Euler characteristic, Betti numbers, orientability...), homology groups are known to be powerful (in term of topological characterization) and computable in the same way in any dimension. In this paper, we recall briefly the cellular structures used in topology-based geometric modeling and image analysis, and propose different approaches for computing homology on such structures. These approaches are adaptations of classical methods from algebraic topology that had essentially been developed for simplicial or cubical complexes. We present two works in progress dealing with two different methods for computing homology information on structures derived from combinatorial maps: a method relying on the definition of a cellular border operator, the other following a constructive approach based on the works about effective homology.

1 Introduction

A wide range of combinatorial models exist to structure images [31]. They have been developed in several contexts from image analysis (e.g. Region Adjacency Graphs or RAG [40], dual graphs [28], orders [5, 17], topological maps [6, 12]) to topology-based geometric modeling (e.g. generalized maps [30], chains of maps [22]). They encode the topological structure of objects contained in images. To be fully efficient, they need to be associated with algorithms for computing topological properties of represented objects. Such topological invariants may help recognizing objects through partial topological characterization [37]. But they are also useful to supervise and control different processes applied on objects, e.g. to track the evolution of topological changes of an object throughout its construction and further modifications [13, 19, 32].

Many topological invariants have already been studied in an image context, but either they provide too few informations about the topology of an object (e.g. Euler characteristic [16]) or they cannot be efficiently computed or used (e.g. fundamental group [4, 34]). Homology information is an interesting compromise. But whereas homology theory has been developed on a wide class of structures [33, 35] (CW-complexes and subclasses), practical computation algorithms have only been designed for low dimensional [14, 15] and/or simplicial or cubical [25, 27, 37] complexes. Most of these algorithms are based onto two main approaches for computing homological features that have been developed in an algebraic topology context. The first historical method involves matrices reductions into their Smith Normal Form [26, 36] and requires the definition of a border operator (which is well-known on simplicial structures). Many variants and optimizations have been proposed to reduce the cost of matrices reductions (e.g. [20, 21, 24, 43]). The second method, called effective homology, relies on a constructive approach [25, 41]. It is based onto two main tools, namely reductions and homology equivalences and aims at making available algorithms able to compute homology information. Although there seems to exist no theoretical issue preventing from adapting both approaches and using similar methods onto cellular structures other than simplicial or cubical ones, no study has been achieved yet in an algebraic topology context. However promising breakthroughs have been accomplished, that deal with the

extension of the first approach onto cellular structures used in image context (simploidal sets [38], and a subclass of generalized maps [3]).

Our current works focus on cellular but triangulable structures which in practice correspond to most cellular structures used in computational geometry, topology-based geometric modeling and image analysis. We intend to address the problem of providing algorithms to compute homological information on such structures by adapting the two main algebraic approaches previously described. Triangulability is thus an essential property: it is actually required to validate our methods because the homology we compute on an object represented by a general cellular structure has to be equivalent to the simplicial one that can be obtained from the triangulation of the same object. The methods, we are interested in, have to be more general than the classic ones because they have to extend themselves regarding the kind of cells of the considered subdivisions (from simplices and cubical cells towards more general ones, quasi-manifolds[1] for instance). Moreover we intend to design specialized algorithms that use the properties of the studied cellular subdivisions and in particular benefit from the cellular optimization (i.e. the fact that a cellular subdivision is made of less cells than its simplicial analog).

In Section 2, a brief taxonomy of the cellular structures we are interested in is presented and the links between them highlighted. Section 3 describes the methodology we propose in order to provide new homology computation algorithms dedicated to such structures.

2 Cellular structures used in image context

Applications developed in computer imagery often require to be able to encode the topological structure of objects represented in images. Combinatorial models are used to fulfill this purpose. They provide indeed a decomposition of a topological structure into cells of different dimensions. Such a decomposition can be seen as a suitable discrete approximation of the topological structure of a continuous object or set of objects.

Many combinatorial models have been developed so far to reach this goal. Most have been proposed in a given context, e.g. segmented images structuration [5, 6, 12, 17], topology-based geometric modeling [7, 11, 23, 29, 44]. Nevertheless, several works achieved in the past few years [1, 2, 8, 9, 29, 30, 31] have demonstrated that strong links and even partial equivalences exist between many of these structures independently from their area of application. Many of these combinatorial models actually aim at structuring manifold-like objects. The differences between such structures mainly come from the impossibility of combinatorially fully describing the continuous notion of manifold. Hence, this limitation constrains to make choices regarding the topological properties the structure has to grant (e.g. representation of orientable objects). More general structures have also been proposed to encode non-manifold objects.

These structures can be classified according to different criteria and the existing taxonomies show different levels of details. A detailed description and comparison of models used in topology-based geometric modeling can for instance be found in [31]. Such classifications may take into account the properties of the represented subdivisions (e.g. orientable or not), the kind of cells used (e.g. simplices, cubical cells, simploids), or the way cells are glued together (e.g. with or without multi-incidence, with or without self-bending, quasi-manifolds).

The rough classification criteria of cellular structures displayed on Fig. 1 is sufficient to illustrate the background of the problem we address. The computation of homology information has indeed essentially been achieved on simplicial structures, mostly on abstract simplicial complexes [36] but also on (semi-)simplicial sets [35]. More general structures regarding the nature of cells are the incidence graphs but they can only encode subdivisions without multi-incidence. One step further, the structures based on combinatorial maps (e.g. topological maps, generalized maps, complex maps formerly called chains of maps) can represent a wide range of subdivisions of (non-)manifold-like objects. Topological maps can only encode orientable subdivision. In addition, generalized maps can also represent non orientable subdivisions. Complex maps form an even

[1] Informally, an n-dimensional cellular quasi-manifold [30] is a collection of n-cells attached along $(n-1)$-cells such that at most two n-cells are incident to a given $(n-1)$-cell.

broader representation scheme because they impose even less constraints on the way cells are glued together.

	Without multi-incidence	*With multi-incidence*
Simplicial	Abstract Simplicial Complexes	(Semi-)Simplicial Sets
Cellular	Incidence Graphs	Map-based structures

Figure 1: Rough classification criteria.

Finally it has to be noted that any of these structures may be integrated in a hierarchical scheme [10, 18, 28, 42]. Some works have already been achieved in order to compute homology information on such multi-levels models. It has been shown that hierarchical structures can be of interest in order to control the geometry of homology generators [39]. But considering hierarchical structures implies first to correctly handle the computation of homology on the non hierarchical structures on which the different levels are constructed.

Our study of homology computation focuses hence on cellular structures derived from the notion of combinatorial maps (e.g. generalized maps and complex maps). Most of the other structures encoding manifold-like objects can be seen as subclasses of such structures. Moreover, their use in a hierarchical structure has already been examined [42]. More importantly, such structures contain in their definition their construction process which is a major advantage for homology computation following a constructive approach. Changes of topology can actually be tracked throughout the whole construction process.

3 Approaches for computing homology

Three main approaches may be considered to tackle the problem of homology computation on cellular triangulable structures. The first one consists in applying the simplicial methods on a triangulation of the studied object. Both other methods aim at adapting the two main algebraic approaches to the cellular case.

3.1 Application of simplicial methods

As we deal with triangulable structures, a simplicial complex or a (semi-)simplicial set encoding the studied object can always be associated with the cellular object. The triangulation is even implicitly included in the definition of the cellular structure. For instance, each simplex of the triangulation of a cellular structure encoded by an incidence graph is a path of incident cells in the graph. A similar interpretation can be achieved on maps. A classical result from topology states that the homology of an object is independent from the chosen subdivision but rather characterizes the object itself.

Though theoretically correct, this approach suffers from a major drawback. It loses indeed the optimizations that the cellular structure provides compared to its triangulated analog. The triangulation of an object represented by a cellular structure is actually made of many more cells than its initial representation (e.g. in $2D$, the barycenric subdivision of any single quadrangle is made of 8 triangles).

However this approach shall not be pushed aside to achieve our purpose. Whatever computation methods we want to develop on cellular structures, we have indeed to grant that their results are compliant with those of simplicial homology. Otherwise stated, the homology of an object computed by purely cellular methods has to be the same as the homology computed on a simplicial version of the same object.

Simplical methods have hence to be used not as a computational but as a validation tool to prove the accuracy of all other methods that can be developed to compute cellular homology.

3.2 Definition of a cellular border operator

The first algebraic method, we mentioned in the introduction, is based on the reduction of matrices in their Smith Normal Forms [26, 36]. Considered matrices encode the incidence relations linking cells of dimensions differing by exactly one. These incidence relations are usually formalized through the definition of a border operator, which is a linear morphism relating the cells of dimension k and the cells of dimension $(k-1)$. For instance, the border of an edge is a signed sum of its two end-vertices. The border of a triangle consists is a signed sum of the three edges composing its boundary.

The definition of a border operator on simplicial structures is well-known.

It is much more difficult to define such an operator on cellular structures. A suitable border operator $\partial^{\square}$ must indeed fulfill several requirements. It first has to be nilpotent of class 2 (i.e. $\partial^{\square}\partial^{\square} = 0$). Moreover, the cellular homology defined from the border operator must be equivalent to the simplicial homology. In other words, defining a border operator satisfying $\partial^{\square}\partial^{\square} = 0$ is not enough for computing the homology of a cellular object. For example, a border operator defined as the null morphism (i.e. the border of any cell of the subdivision is null) satisfies the property $\partial^{\square}\partial^{\square} = 0$, but this definition of a border operator is not consistent with the simplicial homology. Thus, the homology computed on the cellular object has to be isomorphic to the homology computed on the triangulation of the object. When we define a border operator for a cellular structure, the following points have to be proved in order to guarantee that the cellular homology defined from the cellular border operator is equivalent to the simplicial one:

- $\partial^{\square}\partial^{\square} = 0$,
- the border operators denoted by $\partial^{\square}$ on cellular structures and ∂ on simplicial ones commute with the triangulation operator τ i.e. for any chain of cells $c^{\square}$, we have $c^{\square}\tau\partial = c^{\square}\partial^{\square}\tau$,
- any simplicial cycle (resp. boundary) in the triangulation can be associated with a cellular cycle (resp. boundary). The converse is also true and is a consequence of the previous point.

This approach has already been developed onto two classes of cellular subdivisions. A border operator has indeed been defined on simploidal sets [38] where cells are cartesian products of simplices (e.g. in $3D$, cubes, prisms, and tetrahedra). Note that simploidal sets include simplicial and cubical structures as particular cases. More recently, such an operator has also been proposed on a subclass of generalized maps, whose cells are orientable and have complete boundaries [3].

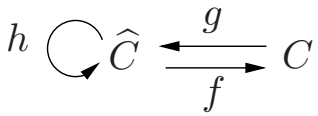
An optimization regarding the size of the incidence matrices is granted because any object subdivided into cells requires less cells than the same object subdivided into simplices. Researches currently in progress aim at proposing an efficient way to build the incidence matrices by optimizing the computation process of the incidence numbers in the cellular structure.

3.3 Constructive approach

The main idea of this approach is to compute the homology of an object while it is built. It is an extension of the approach developed by F. Sergeraert [41] and has already been applied in an image context through simplicial structures by P. Real *et al.* [25].

This method uses several tools developed for algebraic topology, among which the notion of reduction (Fig. 2(a)) and the notion of homology equivalence. A reduction process is illustrated on Fig. 3. Homology equivalences are used to relate three complexes (Fig. 2(b)): the object of interest (C) whose homology has to be computed, a very small homologically equivalent object (EC) and a big object ($\widehat{C}$) also homologically equivalent[2] and containing both the object and all operations used to build it. The whole homology information of the object C is contained in the very small object EC but the big object is required to link C and EC.

[2]Similar sequences of equivalences are used in many other areas of Mathematics, e.g. fraction equivalences: for instance, the three fractions 21/15, 42/30 and 14/10 are equivalent (according to fraction equivalences) but 42/30 is defined with much bigger integers. To go a little further, according to this analogy, the objects C, $\widehat{C}$ and EC would respectively correspond to the fractions 21/15, 42/30 and 14/10. Note also that 42/30 can be simplified into 21/15 and 14/10 but 21/15 cannot be simplified into 14/10.



(a) Reduction process of the complex $\widehat{C}$ onto the complex C. This process is described by three morphisms [41]. To simplify the notations, the reduction of $\widehat{C}$ onto C is often denoted by $\widehat{C} \Rightarrow C$

(b) Homology equivalences relating an object C, a big object $\widehat{C}$ and a small one EC.

Figure 2: Reduction process and homology equivalences.

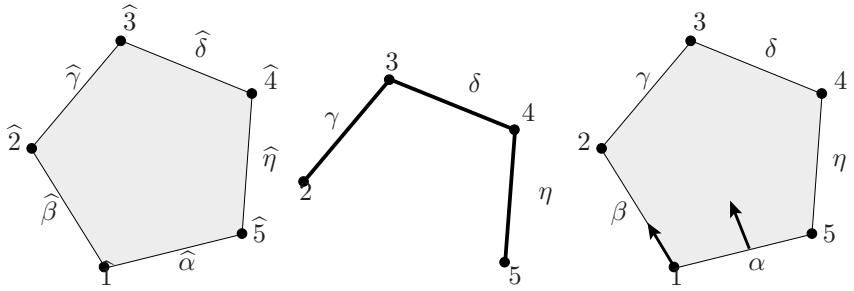


Figure 3: An example of a "big" complex, $\widehat{C}_*$ (a). A "small" complex, C_*, (b). And a reduction from $\widehat{C}_*$ to C_* : with the formalism of Fig. 2(a), g is the inclusion map of C_* in $\widehat{C}_*$, f the projection of $\widehat{C}_*$ onto C_* and h is depicted by black arrows on each cell of C_* whose image under h is not trivial (c).

Effective homology uses one more tool, the notion of cone of morphisms[3] (Fig. 4). For computational topology purpose, a cone of a morphism can simply be seen as a way to represent a morphism as a chain complex. Informally the cone of a morphism $f : M \to N$ is a direct sum of M and N such that the morphism f is involved in the border operation of $M \oplus N$. Such a representation makes it possible to build an homologically equivalent object from the morphisms used to build it.

Effective homology approach is based on the following theorem which is here expressed rather informally. A more formal presentation can be found in [41].

Theorem 3.1 *(Effective homology theorem (illustrated on Fig. 5))*

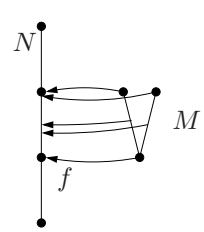
Given two objects A and B and two associated homology equivalences, $A \Leftarrow \widehat{A} \Rightarrow EA$ and $B \Leftarrow \widehat{B} \Rightarrow EB$. Let C be a third object. If the morphisms i, r, j, s relating A, B and C as displayed on Fig. 5 can be constructed, then the applications $\widehat{i}$ and $\widehat{Ei}$ respectively mapping $\widehat{A}$ to $\widehat{B}$, and EA to EB can be deduced from them. Moreover an homology equivalence for the object C can be straightforwardly deduced by building the cones of both morphisms $\widehat{i}$ and Ei.

Morphisms[4] i, r, j, s have to fulfill the following requirements:

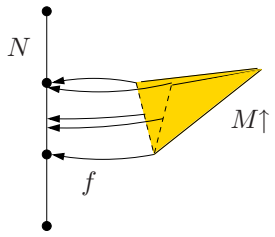
- $ri = id_A$
- $ir + sj = id_B$
- $js = id_C$

[3]This notion of *cone of morphism* is different from the notion of *cone operation* which will be defined later on generalized maps

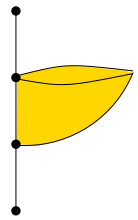
[4]Formally r, s and i, j are respectively *graded-module* and *chain-complex* morphisms [41].



(a) f morphism $M \to N$.



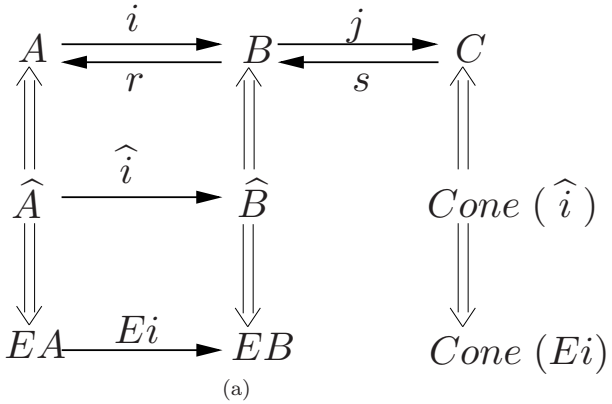
(b) $M\uparrow$ is deduced from M by replacing each k-cell of M by a $(k+1)$-cell. The border operator of $M\uparrow$ is straightforwardly deduced from the border operator of M. $f : M \to N$ completes the border operator of $N \oplus M\uparrow$.



(c) cone(f): each cell is either an element of N or an element of $M\uparrow$. The border operator is constructed from the border operators of N and M and from f.

Figure 4: Cone of a morphism.

This theorem is well suited to a constructive approach. Indeed, let C be an object built from two other objects A and B through a construction process, which is fully described by the morphisms i, r, s and j. If, for each object involved in the construction (i.e. A and B), homology equivalences as described above are memorized then two morphisms relating both corresponding small objects (EA and EB) and very big objects ($\widehat{A}$ and $\widehat{B}$) can be deduced from morphisms relating A and B. The cones of both morphisms are finally used to construct an accurate homology equivalence for the object C. Fig. 6 shows an illustration of the effective homology diagram for a step of an identification operation.



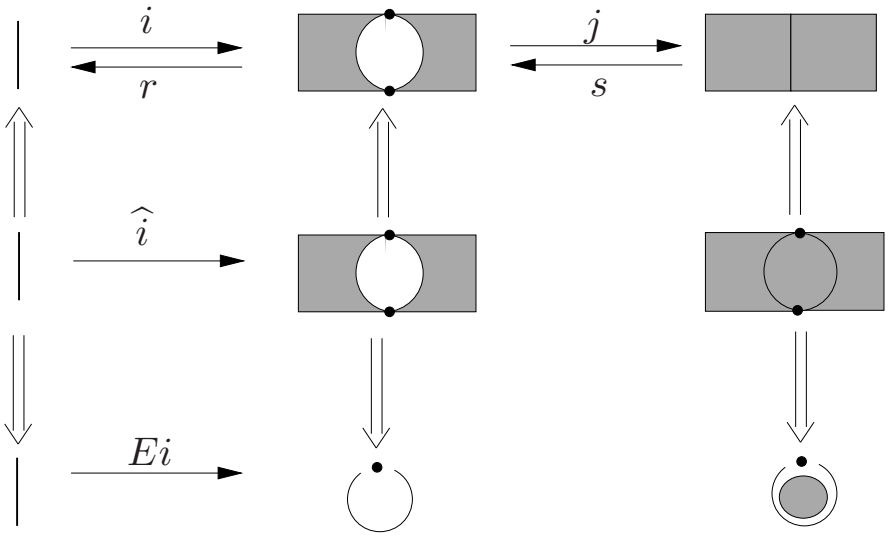
(a)

Figure 5: Effective homology diagram.

This approach seems promising for generalized maps and more generally for structures derived from combinatorial maps because the construction processes of an object represented by such a structure is implicitly included in the structure itself, and the big object $\widehat{C}$ shall not be bigger than the studied object C.

We focus thus on the generalized map structure. Every generalized map can be incrementally constructed from dimension 0 to dimension n by applying two building operations, namely the cone operation and the identification (see Fig. 7).

The main issue for computing homology on generalized maps using a constructive approach is to keep tracks for each step of the construction process of an homological equivalence of each cell (more precisely each cell's interior) and of each connected components of the new object.



(a)

Figure 6: Effective homology diagram of an elementary identification.

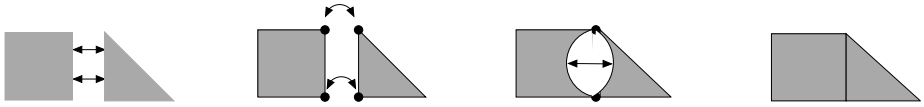
$$\underset{(B,\alpha_0,\ldots,\alpha_{n-1})}{G_1} \xrightarrow{Cone} \underset{(B,\alpha_0,\ldots,\alpha_{n-1},id)}{G_2} \xrightarrow{Identification} \underset{(B,\alpha_0,\ldots,\alpha_{n-1},\alpha_n)}{G_3}$$

(a)

Figure 7: Construction process for generalized maps

(a) (b)

Figure 8: Illustration of a cone construction process



(a) (b) (c) (d)

Figure 9: Illustration of an identification process

Note that the computation on simplicial structures only requires to memorize the evolution of an homological equivalence of the whole object.

Such a process can be defined for cone and identification operations. The evolution of homology equivalences under both operations are described below.

Let G be an $(n-1)$-generalized map, such that homology equivalences for each cell's interior and for each connected component have been computed and stored during its construction. The cone operation which builds an n-generalized map from G consists in adding for each connected

component a new vertex v and to attach each $(n-1)$-cell of the connected component to v with a new n-cell (see an example on Fig. 8). Cells of dimensions 0 to $(n-1)$ remain the same. Thus, the corresponding homology equivalences do not change. Each new cell of dimension n has been constructed from a connected component of dimension $(n-1)$, so that an homology equivalence of this cell can be deduced from the homology equivalence of the corresponding connected component of G. Finally, each connected component is reduced onto one vertex so that it has the homology of a cone, i.e. the trivial homology.

Identifying two $(n-1)$-cells (having isomorphic boundaries) consists in merging both cells. The identification operation is achieved by recursively identifying cells of dimension 0 to $n-1$ (see an illustration of an identification process of two 1-cells on Fig. 9). Homology equivalences of cells of dimension 0 to $n-1$, which are not involved in any identification, are preserved. If two cells of dimension 0 to $n-1$ are merged into a single cell then this cell has the same homology as both merged cells and only one homology equivalence has to be kept (any homology equivalence is accurate since both initial cells have the same homology). Cells of dimension n are not modified by any identification, thus their homology equivalences remain the same. The computation of an homology equivalence for each connected component is trickier and needs to go back to the effective homology theorem. When a new connected component is created due to the identification of a pair of isomorphic i-cells, a diagram as the one displayed on Fig. 5 has to be constructed where the new connected component corresponds to the object C. The object A is an i-cell isomorphic to both i-cells that shall be merged. The object B represents the components that are going to be connected by the identification process, i.e. the two distinct components of the current subdivision containing the two cells to be identified. Note that the homology equivalence of B has already been computed. The morphism j is the identification operation. Morphisms i,r and s can be straightforwardly deduced as an homology equivalence for A. Then Theorem 3.1 grants that it is possible to compute the morphisms $\widehat{i}$ and Ei and then to deduce an homology equivalence for C.

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