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Homology of Cellular Structures allowing Multi-Incidence

S. Alayrangues · G. Damiand · P. Lienhardt · S. Peltier

Abstract This paper focuses on homology computation over "cellular" structures whose cells are not necessarily homeomorphic to balls and which allow multi-incidence between cells. We deal here with combinatorial maps, more precisely chains of maps and subclasses as generalized maps and maps. Homology computation on such structures is usually achieved by computing simplicial homology on a simplicial analog. But such an approach is computationally expensive as it requires to compute this simplicial analog and to perform the homology computation on a structure containing many more cells (simplices) than the initial one. Our work aims at providing a way to compute homology directly on the cellular structure. This is done through the computation of incidence numbers. Roughly speaking, if two cells are incident, then their incidence number characterizes how they are attached. Having these numbers naturally leads to the definition of a boundary operator, which induces a homology. We propose hence a boundary operator for chains of maps, and provide optimization for the other structures. It is proved that, under specific conditions, the homology of a combinatorial map as defined in the paper is equivalent to the homology of its simplicial analog.

Keywords homology computation, boundary operator, combinatorial maps

1 Introduction

Characterizing subdivided objects regarding their topological structure is of interest in different domains as computer graphics, discrete geometry or geometric modeling (e.g. [LPR93, NSK+02, VL07]).

Classically, two spaces are topologically equivalent if a *homeomorphism* exists between them. In general, it is very difficult to prove the (in)existence of a homeo-

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morphism between two topological spaces. So topological invariants (i.e. properties that are preserved by homeomorphisms) have been introduced: for instance, the number of connected components, the Euler characteristic, the fundamental group, the homology groups or the orientability. In particular, homology groups contain meaningful topological information (e.g. connected components, orientability of closed manifolds, Betti numbers) and are computable similarly in any dimension [Ago76, Hat02]. Intuitively, these groups describe different kinds of "holes" (e.g. connected components, tunnels, cavities); generators of these groups provide a representation of the homological information. In practice, homology is often computed on combinatorial structures.

Many such structures exist. For some applications, e.g. reconstruction from point clouds, simplicial or cubical meshes generation, computation of Voronoï diagrams, it is sufficient to use structures as abstract simplicial complexes for simplicial complexes, or a subclass of incidence graphs for regular $CW-$complexes [FP90, Mas91, DKMW10]. In such applications, cells are usually convex ones. Thus, multi-incidence between cells does not occur, and cells are homeomorphic to balls. So, operations applied on the structures that could introduce multi-incidence or alter the topology of the cells are forbidden. Under these strong assumptions, the classical definition of homology applies.

Our work takes place in another context. For some applications (e.g. constructive ones, as those addressed by commercial and free $3D$ modeling softwares), both previous properties cannot be taken for granted. Cells are not necessarily convex: this is the case when cells are embedded as parts of free-form curves, surfaces, etc; this can be the case when cells are embedded as parts of straight lines, planes, etc. A very basic construction operation consists in identifying cells (e.g. take a usual four sided sheet of paper and glue together two opposite sides; this consists in identifying the four initial vertices into two resulting vertices, the two opposite edges into one resulting edge). It is thus very easy to construct objects in which a cell is incident several times to another cell (e.g. the face corresponding to the sheet of paper is incident twice to an edge). Several higher-level operations can also produce such objects, which do not correspond to regular CW-complexes: cf. Fig. 1. So, more general structures have been defined to handle such objects, for instance in geometric modeling, algebraic topology, computational geometry, image analysis, etc., e.g.:

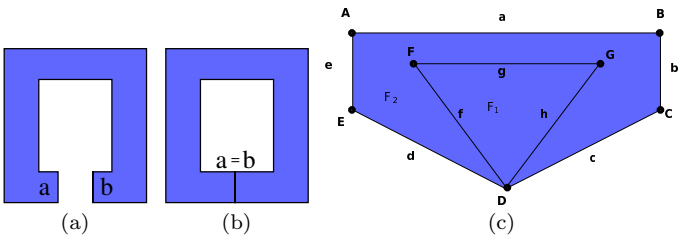


Fig. 1 (a) A polygonal face (b) Identification of edges a and b creates an annulus. The face is incident twice to edge $a = b$ (c) Polygonal faces F_1 and F_2 are glued together by identifying three edges and their boundaries. Subdivisions of surfaces depicted in (b) and (c) are not regular CW-complexes.

– (semi-)simplicial sets, in which cells are simplices [Hu51, May67, ML75, LL96];
– cubical structures and simploidal sets, in which cells are products of simplices [Ser51, NSK+02, KMM04, PFL09];
– cellular structures, in which cells are not so regular, and may not be topologically equivalent to a ball [Bau75, GS85, Wei86, DL89, GP90, Lie91, Spe91, Lie94, CCM97, BDF00, LL01, BDDV03, BSP+05, MK05a, CMP06, DD08].

These many structures have been proved to be equivalent to structures derived from combinatorial maps [Edm60, Jac70, Tut84, Vin83]. Combinatorial maps represent a class of objects much wider than regular CW-complexes as their cells do not need to be homeomorphic to balls; cells in such structures can also be attached more loosely; moreover these structures are able to represent multiply incident cells. Operations on such structures can lead to complex topological changes of the represented object. For instance, even if each cell of the initial cellular subdivision is homeomorphic to a ball, one cannot take for granted that they still are after the application of a sequence of arbitrary operations. It is hence essential to control the topological evolution of an object at each step of its construction process. A partial control can be achieved through the computation of topological properties as homology. The problem is that homology theory is classically defined on CW-complexes and the structures we deal with are not. They are a superset of regular CW-complex. So, no homology theory has so far been defined on such structures. Moreover, we are not even able to characterize the subclass of combinatorial maps which are CW-complexes: as far as we know, no combinatorial characterization of balls exists. There even exist well-known topological spaces which are homologically equivalent to spheres but not homeomorphic to spheres, namely Poincaré homology sphere. The goal of our work is hence to study homology on combinatorial maps. And due to their similarities with them, our results can be straightforwardly transferred to all previously mentioned cellular structures.

More precisely we focus on homology computation for chains of maps [EL94], a cellular structure derived from combinatorial maps. First note that chains of maps have a simplicial interpretation: a semi-simplicial set can be associated with any chain of maps[1] (in a similar way, any incidence graph has a simplicial interpretation, which is an abstract simplicial complex). Note also that when the object associated with the chain of maps is a CW-complex, its simplicial analog is simply the barycentric subdivision of the CW-complex. So, a first approach for computing the homology of a cellular object would be to compute the homology of its associated simplicial object. But this option has the main disadvantage of losing the cellular optimization in terms of number of cells (there are less cells in a chain of maps than simplices in the associated semi-simplicial set)[2].

Our objective is to follow a second approach consisting in taking advantage of the cell structuring. We are looking for optimization (regarding the number of cells), which means that we have to define a homology theory directly on the cellular structure. The main contribution of this work (Theorem 1 page 22) is:

[1] More precisely, given a chain of maps C, it is possible to associate a semi-simplicial set S with C. Since the geometric realization of a semi-simplicial set is a CW-complex, it is possible to associate a CW-complex with S and thus with C. But it is not possible to *directly* associate a CW-complex with C, since cells can exist in C which can not be associated with balls.

[2] The same fact also holds for incidence graphs: they contain less cells than simplices in their associated abstract simplicial complexes.

– to provide a subclass of chains of maps on which homology can be *directly* computed;
– to prove that this homology is equivalent to the simplicial homology of its simplicial analog.

More precisely, two homologies are studied: homology with coefficients over $\mathbb{Z}/2\mathbb{Z}$ and homology with coefficients over $\mathbb{Z}$. The second one is obviously more general than the first one, and the distinction is simply made to clearly introduce the several conditions required to obtain the results. For instance, the first homology can be defined for a subclass of chains of maps which contains the subclass for which the second homology can be defined. Note also that the exhibited subclasses are characterized by combinatorial properties (Condition $C3$ page 21) that can be computed on any chain of maps.

To achieve this goal we first characterize a subclass of chains of maps on which a boundary operator can be constructed. This is also a contribution of this work as only subclasses of generalized maps were previously exhibited [APDL09]. This subclass is still more general than regular CW-complexes. It contains regular CW-complexes, CW-complexes which are not regular and even objects that are no CW-complexes at all. We prove then that under some constraints, the homology of a chain of maps induced by our boundary operator is equivalent to the homology of its simplicial analog.

We perform this work successively in two different frameworks. We first focus on $\mathbb{Z}/2\mathbb{Z}$ homology, and study then homology over $\mathbb{Z}$. It allows us to obtain a progressive presentation of our results in order to clearly identify the conditions for computing a homology[3] and prove its equivalence with the simplicial one. Finally, we optimize our results on two important sub-classes of chains of maps: generalized maps and maps. Generalized maps (resp. maps) describe the topology of manifold-like cellular objects (resp. orientable manifold-like without boundaries). We retrieve here partial results obtained previously for generalized maps, presented in [APDL09].

The paper is organized as follows: Section 2 covers the whole background of the paper. It briefly recalls essential notions about homology theory and associated computation methods (Subsection 2.1). Then it presents the combinatorial structures that are used in this work: semi-simplicial sets in Subsection 2.2, generalized maps and chains of maps in Subsection 2.3. This presentation ends in Subsection 2.4 with the simplicial interpretation that can be associated with generalized maps and chains of maps. In order to obtain a progressive presentation and improve the clarity of the discussion, we first define a subclass of chains of maps on which a boundary operator, and hence a homology, can be defined (Section 3). A more restricted subclass is then defined (Section 4) on which the computed homology is equivalent to the simplicial one. More precisely, in Section 3, the notion of unsigned incidence number is defined and proved to lead to a consistent boundary operator over $\mathbb{Z}/2\mathbb{Z}$ (Subsection 3.1). Afterwards, this notion is extended to signed incidence number and a boundary operator over $\mathbb{Z}$ is obtained (Subsection 3.2). Algorithms for computing incidence numbers are provided in Subsection 3.3. Then, the proof of the equivalence between the cellular homology defined on chains of maps and

[3] The conditions are not exactly the same for $\mathbb{Z}/2\mathbb{Z}$ and $\mathbb{Z}$. Moreover, it suffices to compute the homology over $\mathbb{Z}/2\mathbb{Z}$ for torsion-free objects, in order to get the whole homological information, and the computation can be more efficient with coefficients in $\mathbb{Z}/2\mathbb{Z}$.

the classical simplicial one is detailed in Section 4. It is based on the correspondence between cellular and simplicial chains. We show that this correspondence preserves both cycles and boundaries under specific conditions. Section 5 presents optimizations of our results for more specialized structures: generalized maps in Subsection 5.1 and maps in Subsection 5.2. Finally, we conclude and give some insight into future works in Section 6.

2 Background

2.1 Homology

Among all the existing topological invariants, we focus on homology groups which are classically studied in algebraic topology [Mun84]. For each dimension $i = 0, \ldots, n$, the ith homology group H_i of an $n-$dimensional object (or nD object) characterizes its $i-$dimensional holes (e.g. connected components for H_0, tunnels for H_1, cavities for H_2). From a computational point of view, homology groups are defined in the same way in any dimension from the boundaries of the cells.

2.1.1 Chain complex, cycles, boundaries, homology groups

Homology groups are defined from an algebraic structure called a chain complex, i.e. a sequence $C_n \xrightarrow{\partial_n} C_{n-1} \xrightarrow{\partial_{n-1}} \cdots \xrightarrow{\partial_1} C_0 \xrightarrow{\partial_0} 0$ of (boundary) homomorphisms of abelian groups, called chain groups, satisfying[4] $\partial\partial = 0$. Such a chain complex is denoted by (C_*, ∂), where C_* denotes the family of chain groups. A chain complex can be associated with a subdivided object O in the following way: each chain group C_i is generated by all the i-cells of O. The boundary homomorphisms are defined over chains of cells as linear extensions of the basic boundary operators defined on the cells.

Among all the possible chains, homology consider two particular kinds of chains: cycles and boundaries. A cycle z is a chain satisfying[5] $z\partial = 0$. A chain b is a boundary iff there exists a chain c satisfying $c\partial = b$. The set of $i-$cycles equipped with the addition is a subgroup of C_i, denoted Z_i. The set of $i-$boundaries equipped with the addition is a subgroup of Z_i, denoted B_i (a boundary is a cycle as $\partial\partial = 0$).

Homology groups H_i are defined as the quotient groups Z_i/B_i. So the elements of the homology group H_i are equivalence classes such that two cycles are in the same equivalence class if they differ by a boundary (two such cycles are homologous).

The algebraic notions of chain, cycle, boundary, and homology generator, are illustrated on Fig. 2.

Homology groups are finitely generated abelian groups, so the following theorem describes their structure [Hat02].

[4] Usually, we do not explicitly denote the dimensions of the boundary homomorphisms.

[5] $z\partial$ denotes $\partial(z)$ and $z\partial\partial$ denotes $\partial(\partial(z))$. Similar notations will be used in the whole paper.

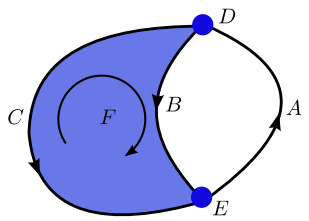


Fig. 2 A cellular subdivision having the following homology groups: $H_0 \simeq H_1 \simeq \mathbb{Z}$, $H_i \simeq 0$ for $i > 1$. $3A - 6B$ and $C + 2B$ are 1−chains. $A + B$ is a 1−cycle as $(A + B)\partial = D - E + E - D = 0$ and $B - C$ is a 1−boundary as $B - C = F\partial$. The 1−chains $A + B$ and $A + C$ are homologous as $A + C + F\partial = A + B$. D is a generator for H_0 and $A + C$ is a generator of H_1.

Every finitely generated abelian group G is isomorphic to a direct sum of the form:

$$\underbrace{\mathbb{Z} \oplus ... \oplus \mathbb{Z}}_{\beta} \oplus \mathbb{Z}/t_1\mathbb{Z} \oplus ... \oplus \mathbb{Z}/t_k\mathbb{Z}.$$

where $1 < t_i \in \mathbb{Z}$ and t_i divides t_{i+1}.

The rank β of an homology group is also called its Betti number, and the t_i are its torsion coefficients.

2.1.2 Computing homology

Depending on what is expected, "computing homology" may have different meanings. For example, the number of i−dimensional holes of a given object is completely defined by the Betti numbers and the torsion coefficients. But in case homology generators are needed, these numbers are not enough: cycles have to be explicitly computed as representatives of each group.

In the previous section, it was implicit that all the chains are considered with coefficients over $\mathbb{Z}$, but homology groups can be computed with any coefficient group (e.g. homology on $\mathbb{Z}/2\mathbb{Z}$ or $\mathbb{Q}$).

The universal coefficient theorem [Hat02] ensures that all the homological information is contained in homology groups with coefficients in $\mathbb{Z}$. But for optimization purposes, it may be useful to compute them with other coefficients. In particular, homology groups over $\mathbb{Z}/2\mathbb{Z}$ are isomorphic to homology groups over $\mathbb{Z}$ for torsion-free objects.

Several algorithms have been designed to compute Betti numbers, torsion coefficients and eventually homology groups generators. The most classical approach is based on reductions of incidence matrices into their Smith Normal Form [Ago76, Mun84, KB79, PAFL06a]. Generally the incidence matrices of the whole object are handled, involving high computational cost and memory issues since huge integers may occur during the computational process [KB79]. Many works aim at optimizing this process [DSV01, Gie96, Sto96]. Others aim at simplifying the structure while preserving its topology [DKMW10, GDJMR09, KMS98, KMM04]. Some works follow an incremental constructive approach [DPF08, DE95]. More recently, persistent homology theory has been introduced [ELZ02] and allows to describe the topology of an object at different scales. In particular, persistent homology led to the notion of localized homology for computing "nice" generators [ZC08].

2.2 Simplicial structures

An *abstract simplicial complex* (V, Δ) is a set of vertices V together with a family Δ of finite non-empty subsets of V, called simplices, such that $\emptyset \neq \tau \subseteq \sigma \in \Delta$ implies $\tau \in \Delta$ [Ago76]. Simplex τ is a *proper face* of simplex σ iff $\tau \subset \sigma$. The *boundary* of σ is the set of its proper faces. The *star* of σ is the set of simplices of which σ is a proper face. σ is a *main* simplex iff its star is empty [6].

Abstract simplicial complexes are widely used in geometric modeling, computational geometry, etc. For instance, the abstract simplicial complex fully defined by its main simplices: $\{\{B\}, \{A, F\}, \{C, D, E\}, \{E, F, G\}\}$ is geometrically represented on Fig. 3(a).

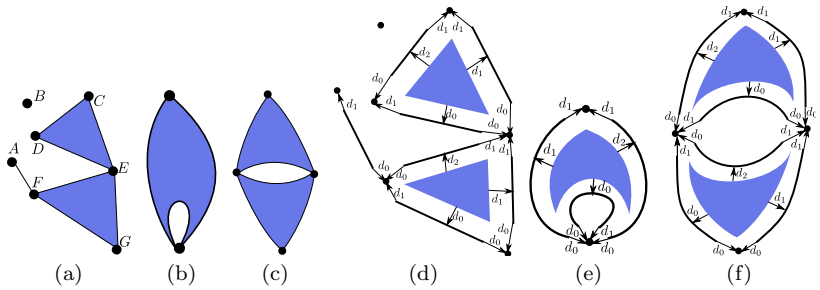


Fig. 3 (a) Representation of an abstract simplicial complex. (b) The triangle is incident to two vertices. (c) Two edges have the same boundary. Subdivisions (b) and (c) can be described by semi-simplicial sets but not by abstract simplicial complexes. (d) Semi-simplicial set associated with (a). (e) Semi-simplicial set associated with (b). (f) Semi-simplicial set associated with (c).

Definition 1 (semi-simplicial set) [May67] An *n-dimensional semi-simplicial set* $S = (K, (d_j)_{j=0,\ldots,n})$ is defined by:

- $K = \bigcup_{i=0,\ldots,n} K_i$, where K_i is a finite set of elements called i-simplices;
- $\forall j \in \{0, \ldots, n\}$, *face operator* $d_j : K \longrightarrow K$ is s.t.[7]:
  - $\forall i \in \{1, \ldots, n\}, \forall j \in \{0, \ldots, i\}$, $d_j : K_i \longrightarrow K_{i-1}$; $\forall j > i$, d_j is undefined on K_i, and no face operator is defined on K_0;
  - *commutation property of face operators*: $\forall i \in \{2, \ldots, n\}$, $\forall j, k \in \{0, \ldots, i\}$, $d_j d_k = d_k d_{j-1}$ for $k < j$.

Simplex τ is a proper face of simplex σ if a non empty sequence of face operators $d_{i_1}, \cdots, d_{i_k}$ exists such that $\tau = \sigma d_{i_1} \cdots d_{i_k}$. All notions of boundary, star, main simplex, etc. are defined in an obvious way.

When a numbering of the vertices exists, such that the vertices of each main i-simplex are numbered from 0 to i, then the semi-simplicial set equipped with such a numbering is called a *numbered semi-simplicial set*: cf. Fig. 8.

[6] These notions will be used for others structures without being formally redefined.

[7] $d_0, \cdots, d_i$ associate its $(i+1)$ $(i-1)-$faces with each $i-$simplex.

Semi-simplicial sets are more "flexible" than abstract simplicial complexes in the sense that they allow multi-incidence [8]: for instance, a k-simplex can be incident to less than $k+1$ vertices (cf. Fig. 3(b) and Fig. 3(e)), distinct simplices can have the same boundary (cf. Fig. 3(c) and Fig. 3(f)). So, it is not always possible to directly associate an abstract simplicial complex with a semi-simplicial set, but the converse is true: given an abstract simplicial complex, we can define an order on the vertices, and associate a sequence of vertices with each simplex (note that this induces an orientation for the simplices). An abstract simplex is then associated with each sequence of vertices, and the boundary operators can directly be deduced from this ordering[9] (cf. Fig. 3(d); let σ be the $2-$simplex corresponding to (C, D, E): then σd_0 (resp. σd_1, σd_2) corresponds to (D, E) (resp. (C, E), (C, D))).

The definition of homology for simplicial objects is well-known: it consists in defining the chain groups (which is straightforward) and the boundary operators. These boundary operators are defined as linear extensions of basic boundary operators which act on simplices. For abstract simplicial complexes, we can define an homology on $\mathbb{Z}/2\mathbb{Z}$ by defining the basic boundary operator in the following way: $\{v_0, \cdots, v_i, \cdots, v_k\}\partial_S = \sum_{0 \leq i \leq k} \{v_0, \cdots, \hat{v_i}, \cdots, v_k\}$ where $\hat{v_i}$ means that vertex v_i is removed. For semi-simplicial sets, as said before, simplices are implicitly oriented, and we can define an homology on $\mathbb{Z}$ by defining the basic boundary operator as: $\sigma\partial_S = \sum (-1)^i \sigma d_i$. Note that the commutation property of face operators has for consequence that $\partial_S \partial_S = 0$.We will follow this idea later for defining a homology for cellular structures: first defining a homology on $\mathbb{Z}/2\mathbb{Z}$, then adding an orientation of the cells for defining a homology on $\mathbb{Z}$.

In the following, ∂_S denotes a simplicial boundary operator: no specific notation will be used to distinguish between boundary operators acting on $\mathbb{Z}/2\mathbb{Z}$ or $\mathbb{Z}$, on abstract simplicial complexes or semi-simplicial sets. The context is sufficient to achieve this distinction.

2.3 Chain of maps

Combinatorial maps based structures are by construction dedicated to the representation of manifold-like "cellular objects".They are used in different applications related to geometrical modeling as well as image analysis [BG88, BDF00, BDDV03, DBF04, BSP+05, MK05b, CMP06, TGM+09, BPA+10, UCB13]. They are also known to be equivalent to other combinatorial structures, such as cell-tuples, facet-edge, quad-edge for instance [Bri93, DL89, GS85, Lie91]. Several families of combinatorial maps have been defined depending on the constraints imposed upon the arrangement of such cells.

Since cells can be multi-incident to each others, these structures are not constructed directly from the cells of the subdivision but from a more elementary object, called a dart (cf. Fig. 4(b)). The set of darts is structured through functions that describe how they are linked to each other (cf. Fig. 4 and Fig. 5). Such

[8] The geometric realization of a semi-simplicial set is a $CW-$complex, and the geometric realization of an abstract simplicial complex is a simplicial complex [May67, Ago76].

[9] For any i, face operator d_i is defined in such a way that it corresponds to remove the ith vertex of the simplex. Note that we thus get the commutation property of face operators.

a representation provides an implicit description of cells as sets of darts and conveys hence a precise description of how the cells of the subdivision are attached together, even when cells are multi-incident to each others.

Chains of maps (*cmaps*), defined below, impose only few constraints on the way cells that are glued together. We first present *generalized maps* (*gmaps*), since they are involved in the definition of cmaps. For more details about gmaps and cmaps, see [Lie94] and [EL94].

2.3.1 gmaps

Definition 2 (gmap) Let $n \geq 0$; an n-dimensional gmap, or n-gmap, is defined by an $(n+2)$-tuple $G = (D, \alpha_0, \cdots, \alpha_n)$ such that:

- D is a finite set of elements called darts;
- $\forall i, 0 \leq i \leq n, \alpha_i : D \to D$ is an involution[10];
- $\forall i, 0 \leq i \leq n-2, \forall j, i+2 \leq j \leq n, \alpha_i \alpha_j$ is an involution.

Examples of gmaps and related subdivisions are presented in Fig. 4 and Fig. 5. When there is no muti-incidence, a dart can be seen as a tuple of incident cells, and involution α_i exchanges the $i-$cells of the corresponding tuples [Bri93] (cf. Fig. 6). Subdivisions encoded by gmaps are precisely what we have called so far *"manifold-like"* subdivisions and are formally known as *"cellular quasi-manifolds"* (see Subsection 2.4.1 and [Lie94]). From a practical point of view, gmaps can be seen as valued graphs, and several notions can be directly adapted (e.g. connected component).

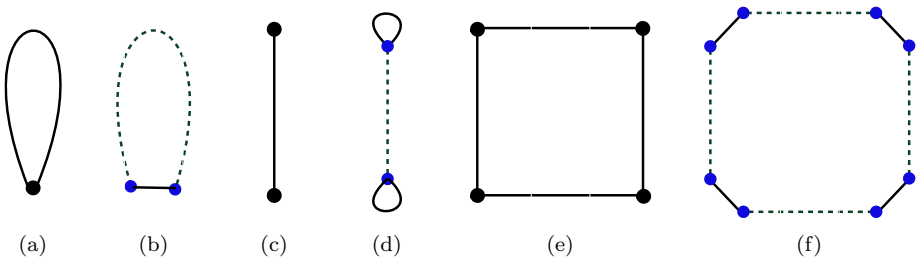
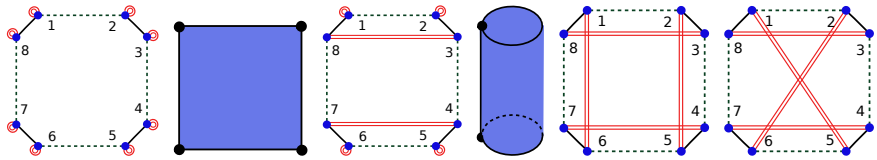


Fig. 4 (a) A loop, i.e. an edge incident twice to a vertex. In order to represent multi-incidence, the two "endpoints" of the edge must be distinguished. (b) Gmap representation of the loop (a). Intuitively, the two darts (represented by points) correspond to the two endpoints of the edge. They are linked by α_0 (dotted line) in order to represent the edge, and by α_1 (full line) in order to represent the vertex. (c) An edge incident to two different vertices, represented by the gmap (d). (e) A cycle of four edges represented by the gmap (f), made of 8 darts. As before, two darts linked by α_0 correspond to an edge and two darts linked by α_1 correspond to a vertex.

Dart d is a *fixed point* of involution α_i iff $d\alpha_i = d$. When all involutions are without fixed points, the gmap is *without boundaries*. Two darts d_1 and d_2 are *linked* by α_i iff $d_1\alpha_i = d_2$ (and thus $d_2\alpha_i = d_1$). We retrieve the notions of connected component and cell through the following notion of orbit.

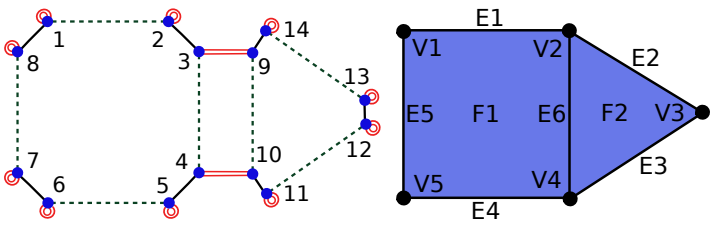
[10] i.e. a one-to-one mapping (a permutation) such that $\alpha_i = \alpha_i^{-1}$.



(a) (b) (c) (d) (e) (f)

Fig. 5 (a) A 2−gmap (α_2 is represented by double lines) representing the face in (b). Orbit $< \alpha_0, \alpha_1 > (1) = \{1, 2, 3, 4, 5, 6, 7, 8\}$ corresponds to the face, incident to 4 edges (corresponding to the four orbits $< \alpha_0, \alpha_2 >$, i.e. $\{1, 2\}$, $\{3, 4\}$, $\{5, 6\}$, $\{7, 8\}$), and to 4 vertices (corresponding to the 4 orbits $< \alpha_1, \alpha_2 >$, i.e. $\{1, 8\}$, $\{2, 3\}$, $\{4, 5\}$, $\{6, 7\}$). (c) A 2−gmap corresponding to the cylinder represented in (d), made of 1 face, 3 edges ($\{1, 2\}$, $\{3, 4, 7, 8\}$, $\{5, 6\}$), and 2 vertices ($\{1, 2, 3, 8\}$, $\{4, 5, 6, 7\}$). (e) A 2−gmap corresponding to a torus (1 face, 2 edges $\{1, 2, 5, 6\}$, $\{3, 4, 7, 8\}$ and 1 vertex). (f) A 2−gmap corresponding to a Klein bottle (1 face, 2 edges $\{1, 2, 5, 6\}$, $\{3, 4, 7, 8\}$ and 1 vertex).

Definition 3 (orbit) Let $\Phi = \{\pi_0, \cdots, \pi_n\}$ be a set of permutations defined on a set D. We denote $\langle \Phi \rangle = \langle \pi_0, \cdots, \pi_n \rangle = \langle \rangle_{[0,n]}$ the permutation group of D generated by Φ. The orbit of an element $d \in D$ relatively to $\langle \Phi \rangle$, denoted $\langle \Phi \rangle (d)$ is the set $\{d\phi \mid \phi \in \langle \Phi \rangle\}$. It denotes also the structure $(D^d = \langle \Phi \rangle (d), \pi_0/D^d, \cdots, \pi_n/D^d)$, where π_i/D^d denotes the restriction of π_i to D^d [11].



(a) (b)

Fig. 6 (a) A 2-gmap corresponding to the subdivision depicted on (b). Dart 5 corresponds to the cell tuple $(V4, E4, F1)$, dart 6 corresponds to the cell tuple $(V5, E4, F1)$, dart 4 corresponds to the cell tuple $(V4, E6, F1)$, dart 10 corresponds to the cell tuple $(V4, E6, F2)$.

The *connected component* of gmap G incident to dart d is the orbit $\langle \alpha_0, \cdots, \alpha_n \rangle (d)$. For example, Figure 6(a) represents a 2-gmap with only one connected component. Figures 10(a) and 10(c) display 1-gmaps with respectively 7 and 2 connected components. The i-dimensional cell (or i−cell) incident to dart d is the orbit $\langle \alpha_0, \cdots, \hat{\alpha}_i, \cdots, \alpha_n \rangle (d)$, where $\hat{\alpha}_i$ denotes that involution α_i is removed[12]. Two cells which share a dart are *incident* one to the other. When α_n is the identity on D, the $(n-1)$−gmap $(D, \alpha_0, \ldots, \alpha_{n-1})$ is the *canonical boundary* of the n−gmap $(D, \alpha_0, \ldots, \alpha_n)$. A connected n−gmap without boundaries is *orientable* if and only if it contains exactly two orbits $\langle \alpha_0\alpha_1, \cdots, \alpha_0\alpha_n \rangle$ (cf. [Lie94] and

[11] We often omit to explicitly indicate the restriction, since it is usually obvious. Due to the relation between gmaps and graphs, an orbit can be seen as a subgraph.

[12] In other words, an i-cell is a connected component of the $(n-1)$-gmap $(D, \alpha_0, \cdots, \hat{\alpha}_i, \cdots, \alpha_n)$.

Subsection 5.2). For instance the torus in Fig. 5(e) contains two orbits $\{1,3,5,7\}$ and $\{2,4,6,8\}$ for $\langle \alpha_0\alpha_1, \alpha_0\alpha_2 \rangle$, but the Klein bottle in Fig. 5(f) contains only one orbit $\{1,2,3,4,5,6,7,8\}$.

2.3.2 Chains of maps

Definition 4 (cmap)
An *n-dimensional cmap* is a tuple $C = ((G^i)_{i=0,\ldots,n}, (\sigma^i)_{i=1,\ldots,n})$ such that:

1. $\forall i,\ 0 \leq i \leq n,\ \ G^i = (D^i, \alpha_0^i, \ldots, \alpha_{i-1}^i, \alpha_i^i = \omega)$ is an i-dimensional gmap such that ω is undefined on D^i;
2. $\forall i,\ 1 \leq i \leq n,\ \ \sigma^i : D^i \longrightarrow D^{i-1}$;
   for $i \geq 2$, σ^i satisfies, for any dart d of D^i:
   (a) σ^i is an isomorphism[13] between any orbit $\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle$ of G^i and an orbit $\langle \alpha_0^{i-1}, \cdots, \alpha_{i-2}^{i-1} \rangle$ of G^{i-1};
   (b) $d\alpha_{i-1}^i \sigma^i \sigma^{i-1} = d\sigma^i \sigma^{i-1}$.

In this definition, any connected component of an i-gmap is an i-dimensional cell, or $i-$cell (that is why $\alpha_i^i = \omega$ is undefined: cf. simplicial interpretation of gmaps in Subsection 2.4.1). The *canonical boundary* of an $i-$cell $(D^{c_i}, \alpha_0^i, \ldots, \alpha_{i-1}^i, \alpha_i^i = \omega)$ is $(D^{c_i}, \alpha_0^i, \ldots, \alpha_{i-1}^i)$. The cells are linked by *face operators* σ^i. Two cells are *incident* if a dart of one cell can be obtained starting from a dart of the other cell by successive applications of face operators. So, a cmap describes the topology of a subdivision in which cells are quasi-manifolds, linked along the cells of their boundaries (cf. Fig. 7). More precisely, any i-cell can be structured into orbits $\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle$; these orbits are linked with $(i-1)$-cells by operator σ^i, defining the boundary of the i-cell. For instance, the $2-$cells of the objects represented Fig. 7 are structured in order to correspond to the $1-$cells of their boundaries, i.e. orbits $\langle \alpha_0^2, \alpha_1^2 \rangle$ can be partitionned into orbits $\langle \alpha_0^2 \rangle$, which are linked with orbits $\langle \alpha_0^1 \rangle$ by σ^2. The fact that $\forall i$, σ^i restricted to an orbit $\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle$ is an isomorphism between this orbit and an $(i-1)$-cell implies that there is a strong correspondence between the structure of the interior of a cell and the structure of its boundary, even when cells are multi-incident ones to the others. This means that there exists some redundancy which can be taken into account in order to reduce the amount of explicit information within a data structure. From a practical point of view, cmaps can be implemented as valued (oriented) graphs.

2.4 Simplicial interpretation of combinatorial maps

2.4.1 Simplicial interpretation of a gmap

It is not possible to associate directly a $CW-$complex with a gmap (or a cmap), since it is not possible to associate a topological ball with any cell[14].

[13] i.e. σ^i is a one-to-one mapping between the darts of the orbits, such that for any $j, 0 \leq j \leq i-2$, $\alpha_j^i \sigma^i = \sigma^i \alpha_j^{i-1}$. This condition is more restrictive than that given in [EL94], where σ^i can be a homomorphism for instance.

[14] For instance, take a $3-$gmap where $\alpha_3 = identity$, containing one connected component, i.e. one $3-$dimensional cell, such that its canonical boundary corresponds to the $2-$gmap of

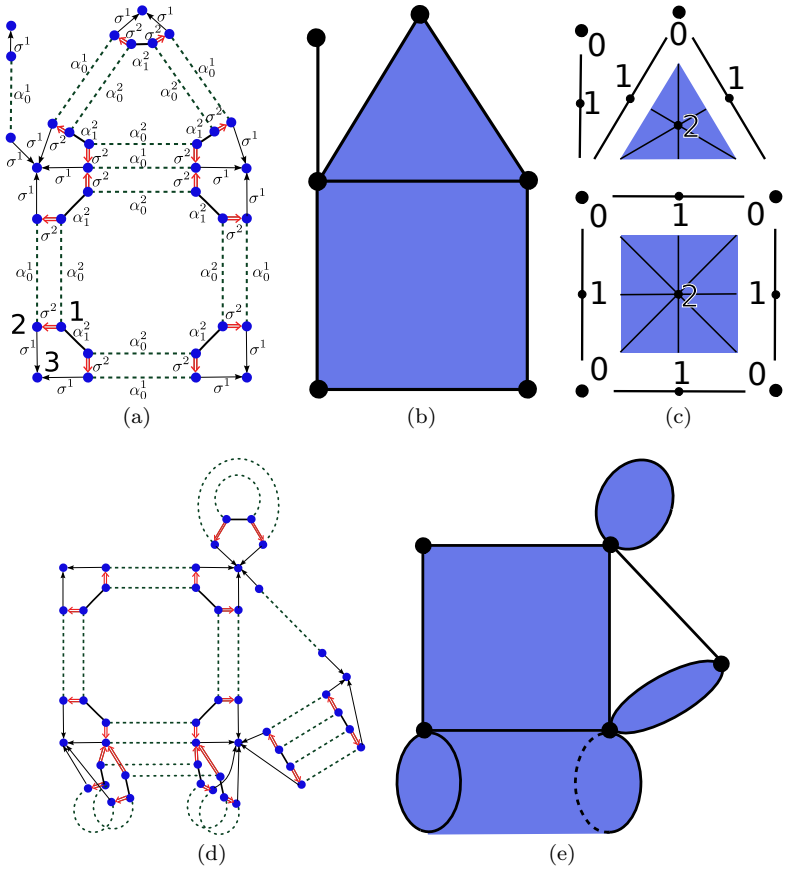


Fig. 7 (a) A 2−cmap corresponding to the subdivision represented in (b). σ^2 (resp. σ^1) is represented by red (resp. black) arrows. Orbit $< \alpha_0^2, \alpha_1^2 >$ (1) corresponds to the square face. Orbit $< \alpha_0^1 >$ (2) corresponds to an edge. Orbit $<>$ (3) corresponds to a vertex. (c) The numbered semi-simplicial set corresponding to the cmap depicted on Fig. 7(a). The simplices of any cell are graphically glued together. (d) A 2−cmap corresponding to the subdivision (e).

But a *numbered semi-simplicial set* $T(G)$ can always be associated with any gmap $G = (D, \alpha_0, \cdots, \alpha_n)$, in the following way (cf. Fig. 8 and [Lie94]):

- *Simplices*. For $0 \leq i \leq n$, an i−dimensional simplex is associated with any orbit $\langle\rangle_{N-\{k_0,\cdots,k_i\}}(d)$, denoted $T(\langle\rangle_{N-\{k_0,\cdots,k_i\}}(d))$, where d is a dart, $0 \leq k_0, \cdots, k_j \leq n$ and $N = \{0, \cdots, n\}$;
- *Face operators* $(d_l)_{l\in[0,\cdots,i]}$, *if* $i \geq 1$; $T(\langle\rangle_{N-\{k_0,\cdots,k_l,\cdots,k_i\}}(d))d_l = T(\langle\rangle_{N-\{k_0,\cdots,\hat{k_l},\cdots,k_i\}}(d))$;
- each 0−simplex $T(\langle\rangle_{N-\{i\}}(d))$ is associated with i.

Note that the 0−simplices are numbered from 0 to n, and, for a given simplex $T(\langle\rangle_{N-\{k_0,\cdots,k_i\}}(d))$, all its incident 0− simplices are associated with distinct in-

Fig. 5(e) (a torus) or Fig. 5(f) (a Klein bottle). Conversely, note that a cmap can be associated with any regular *CW*-complex [ADLP11].

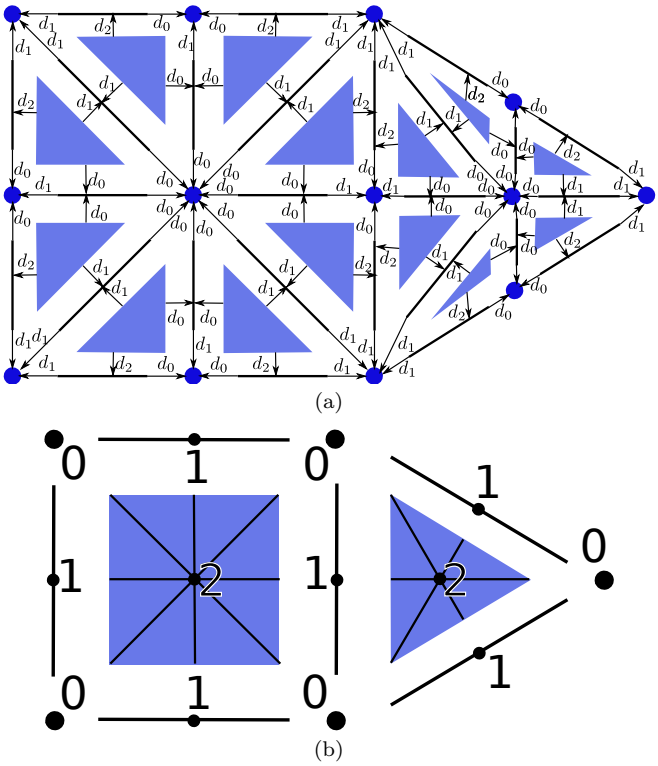


Fig. 8 (a) A numbered semi-simplicial set (the numbers of the vertices are depicted on (b)) which corresponds to the $2-g$map of Fig. 6(a). (b) The corresponding cells.

tegers $k_0, \cdots, k_i$. This numbering induces a notion of cell: an $i-$cell is defined by a $0-$simplex σ numbered i and all the simplices of dimension 1 to i incident to σ which are numbered by integers lower than i. The cells make a partition of the numbered semi-simplicial set. A numbered semi-simplicial set associated with a gmap is a *cellular quasi-manifold*. Note that a cellular quasi-manifold may not be a manifold (see Fig. 9(c)), but it is a pseudo-manifold: for more precisions about manifolds, pseudomanifolds and quasi-manifolds, see [Ago76] and [Lie94].

Cellular quasi-manifolds can also be characterized constructively (cf. Fig. 10): a 0-dimensional cellular quasi-manifold is a collection of sets of one or two vertices. An n-dimensional cellular quasi-manifold containing isolated n-cells is obtained from an $(n-1)$-dimensional cellular quasi-manifold by cone operations over each connected component. The n-cells can then be glued together by identifying $(n-1)-$cells (and their boundaries) in such a way that there is at most two n-cells around an $(n-1)$-cell[15].

[15] We then come up to the definition of gmaps: the fact that at most two $i-$cells share an $(i-1)-$cell in the boundary of an $(i+1)-$cell is ensured by the first condition over the α_i, i.e. α_i is an involution, for all i s.t. $0 \leq i \leq n$; the fact that cells are cellular quasi-manifolds is ensured by the second condition over the α_i, i.e. $\alpha_i\alpha_j$ is an involution for all i, j s.t. $0 \leq i \leq j-2 < j \leq n$.

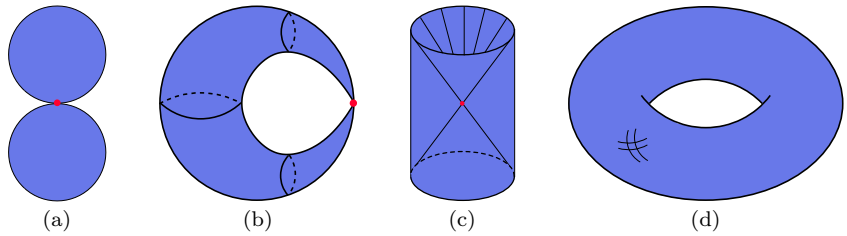


Fig. 9 (a) A non manifold. (b) A pseudo-manifold (non quasi-manifold). (c) A quasi-manifold (non-manifold). This object can be obtained by gluing two opposite triangular faces of a square based pyramid. (d) A manifold.

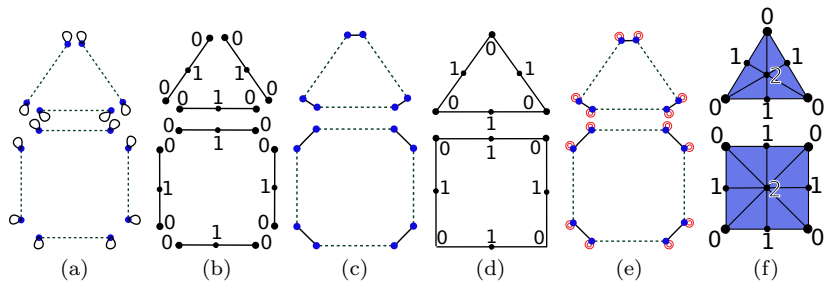


Fig. 10 (a) A $1-$gmap (D, α_0, id) and its corresponding numbered semi-simplicial set. Each edge is a cone on a $0-$sphere (i.e. two vertices, corresponding to two darts linked by α_0). (c) After identifications of $0-$cells, we obtain a new $1-$gmap (D, α_0, α_1). Its corresponding numbered semi-simplicial set is represented in (d). (e) A $2-$gmap $(D, \alpha_0, \alpha_1, id)$ and its corresponding numbered semi-simplicial set on (f). Each $2-$cell is a cone over a $1-$sphere. Then, by identifying one edge of the square and one edge of the triangle, we obtain the $2-$gmap represented in Fig. 6(a). Note that a simplified graphical representation of numbered semi-simplicial sets is used for (b), (d) and (f), i.e. the boundary of a cell is glued with the cell.

2.4.2 Simplicial interpretation of a chain of maps

A numbered semi-simplicial set $T(C)$ can be associated with any cmap C in the following way (cf. Fig. 7(c) and [EL94]). Let c^i be an i-cell of C, d be a dart of c^i, and $I = [0, i]$:

- For $0 \leq j \leq i$, a j-dimensional simplex numbered $\{k_0, \cdots, k_{j-1}, i\}$ is associated with the orbit $\langle\rangle_{I-\{k_0,\cdots,k_{j-1},i\}}(d)$, denoted $T(\langle\rangle_{I-\{k_0,\cdots,k_{j-1},i\}}(d))$;
- if $j \geq 1$;
  - for any $l, 0 \leq l \leq j-1$, $T(\langle\rangle_{I-\{k_0,\cdots,k_l,\cdots,k_{j-1},i\}}(d))d_l = T(\langle\rangle_{I-\{k_0,\cdots,\hat{k_l},\cdots,k_{j-1},i\}}(d))$;
  - $T(\langle\rangle_{I-\{k_0,\cdots,k_{j-1},i\}}(d))d_j = T(\langle\rangle_{K_{j-1}-\{k_0,\cdots,k_{j-1}\}}(d\sigma^i \cdots \sigma^{k_{j-1}+1}))$, where $K_{j-1} = [0, \cdots, k_{j-1}]$.
- $0-$simplex $T(\langle\rangle_{I-\{i\}}(d))$ is numbered i.

Note that α_i is never taken into account for an $i-$cell: this is consistent with the fact that α_i is undefined (cf. Definition 4).

3 Boundary operator

Definition 5 (chain groups associated with a cmap)
Let $C = ((G^i)_{i=0,\ldots,n}, (\sigma^i)_{i=1,\ldots,n}))$ be a cmap. $C_* = \{C_i\}_{i=0,\ldots,n}$ is a family of chain groups associated with C, such that each C_i is an additive group generated by the connected components of G^i (i.e. the i-cells of the cmap).

In the sequel, such groups are defined with coefficients over $\mathbb{Z}/2\mathbb{Z}$ (unsigned case) or $\mathbb{Z}$ (signed case).

Notation: c^i generally denotes an i-cell and when necessary, $c^i(d^i)$ specifies that c^i is incident to dart d^i.

Definition 6 (∂_M operator on chain groups)
Let $C = ((G^i)_{i=0,\ldots,n}, (\sigma^i)_{i=1,\ldots,n}))$ be a cmap on which a function acts, that associates with each pair of cells (c^i, c^{i-1}) its "incidence number" denoted by $(c^i : c^{i-1})$. Let $C_* = \{C_i\}_{i=0,\ldots,n}$ be the family of chain groups associated with C. Operator ∂_i is the linear extension of the operator acting on the i-cells of G^i, which is defined by:

$$c^i\partial_i = \sum_{c^{i-1}\in G^{i-1}} (c^i : c^{i-1})c^{i-1}$$

∂_M denotes $\{\partial_i : C_i \longrightarrow C_{i-1}\}_{i=0,\ldots,n}$.

In this section, we study under which conditions ∂_M is a boundary operator, i.e. $\partial_M\partial_M = 0$. This implies to restrict the set of cmaps which are taken into account (cf. Fig. 11). We also distinguish between homology over $\mathbb{Z}$ and homology over $\mathbb{Z}/2\mathbb{Z}$, since the corresponding subsets are distinct.

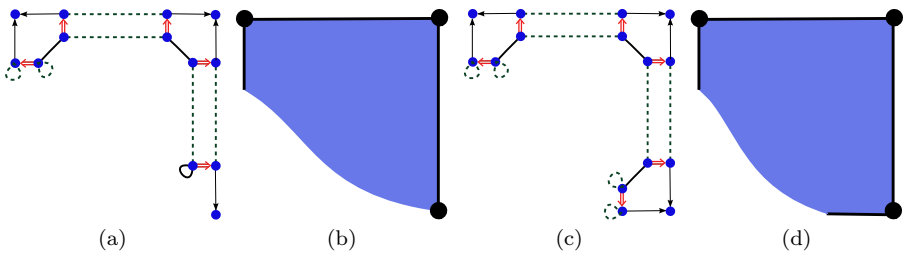


Fig. 11 (a) A cmap having some involutions with fixed points. (b) Its corresponding subdivision, made of 1 face, 3 edges and 3 vertices. The boundary of the face is not a cycle of edges, nevertheless, this cmap has a topological interpretation (see Subsection 2.4.2). Note that $f\partial_M\partial_M \neq 0$, where f denotes the face, since a vertex exists which is incident to only one edge. (c) A cmap satisfying the condition $f\partial_M\partial_M = 0$ where f denotes the face. (d) The corresponding subdivision.

3.1 Unsigned boundary operator

Definition 7 (unsigned incidence number) Let $i \in \{1, \ldots, n\}$. Let c^i and c^{i-1} be two cells of the cmap C. The *unsigned incidence number* is

$$(c^i : c^{i-1}) = (c^i(d^i) : c^{i-1}(d^{i-1})) = \texttt{card}((\sigma^i)^{-1}(d^{i-1}) \cap c^i(d^i)) \ mod\ 2$$

where d^i and d^{i-1} are darts of respectively c^i and c^{i-1}, and $(\sigma^i)^{-1}(d^{i-1})$ denotes the set of darts which have d^{i-1} as image by σ^i.

In other words, the number of times an $(i-1)$-cell c^{i-1} appears in the boundary of an i-cell c^i is, given a dart d^{i-1} of c^{i-1}, the number of darts of c^i which have d^{i-1} as image by σ^i. Since σ^i restricted to an orbit $\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle$ is an isomorphism between this orbit and an $(i-1)$-cell (cf. Property 2a of Definition 4), this number is the same whereas the chosen dart d^{i-1} is[16]. So the definition is consistent.

Also due to Property 2a of Definition 4, this number is equal to the number of orbits $\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle$ of c^i which have c^{i-1} as image (since each dart which image by σ^i is d^{i-1} identifies such an orbit). An alternative definition of the incidence number is then the following: let $\{p_j\}_{j=1\cdots k}$ be a set of darts such that the orbits $\{\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle (p_j)\}_{j=1\cdots k}$ make a partition of c^i, then

$$(c^i : c^{i-1}) = card(\{p_j, j = 1 \cdots k | p_j\sigma^i \in c^{i-1}\}) mod 2.$$

Let ∂_M be the corresponding operator, according to Definition 6. So we have the following property:

Property 1 Let $i \in \{1, \ldots, n\}$. Let c^i be a cell of the cmap C. Let $\{p_j\}_{j=1\cdots k}$ be a set of darts such that the orbits $\{\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle (p_j)\}_{j=1\cdots k}$ make a partition of c^i,

$$c^i \partial_M = \sum_{p_j, j=1\cdots k} c^{i-1}(p_j\sigma^i),$$

and the sum is done upon $\mathbb{Z}/2\mathbb{Z}$. Operator ∂_M is extended upon any sum of cells by linearity.

We prove that under condition $C1$ below, ∂_M is a boundary operator, i.e. $\partial_M\partial_M = 0$. So, this boundary operator defines a homology on the corresponding set of cmaps, with coefficients in $\mathbb{Z}/2\mathbb{Z}$, which will be referred to as *cellular homology.*

Condition** $C1$**: C is a cmap such that all involutions are without fixed points.

The fact that all involutions are without fixed points implies that the boundary of each cell is "complete" (cf. couterexample in Fig. 11(a); note that the property is still satisfied under less restrictive conditions: cf. Fig. 11(c)). The cost of checking condition $C1$ is linear in the number of darts of the cmap times its dimension.

We restrict here to cmaps satisfying condition $C1$. A chain of simplices can be associated with any cell in the following way:

Definition 8 Let $C = ((G^i)_{i=0,\ldots,n}, (\sigma^i)_{i=1,\ldots,n})$ be a cmap, S be its associated semi-simplicial set, C_* be the chain groups associated with C and (S_*, ∂_S) be the chain complex associated with S.

$\tau : C_* \to S_*$ is defined by:

$$\forall i, 0 \leq i \leq n, \forall c^i \in G^i, c^i\tau = \sum_{d \in c^i} T(\langle\rangle(d)),$$

extended by linearity with coefficients in $\mathbb{Z}/2\mathbb{Z}$ to the chains of C_*.

[16] In fact, the property still holds when σ^i is an homomorphism.

Such a sum is an *unsigned chain of cells.*

Lemma 1 *τ satisfies:*

$$x\tau\partial_S = x\partial_M\tau$$

for any unsigned chain of cells x of dimension greater than or equal to 1.

Proof We prove that any i-dimensional cell c^i, with $1 \leq i$, satisfies $c^i\tau\partial_S = c^i\partial_M\tau$, and the lemma is deduced by linearity. $c^i\tau$ is a chain of $i-$simplices; since all involutions of the cmap are without fixed points, all $(i-1)-$simplices "internal" to c^i are incident to exactly two distinct $i-$simplices (cf. Fig. 7(c)). So, when taking the simplicial boundary of $c^i\tau$, all internal $(i-1)-$simplices vanish and we get the chain of $(i-1)-$simplices associated with $c^i\partial_M$.

Lemma 2 *τ associates a simplicial cycle (resp. boundary) with any cellular cycle (resp. boundary).*

Proof Let z be a cellular cycle, i.e. $z\partial_M = 0$. So $z\partial_M\tau = 0 = z\tau\partial_S$, and $z\tau$ is a simplicial cycle.

Let b, c^{i+1} be such that $b = c^{i+1}\partial_M$. Then $b\tau = c^{i+1}\partial_M\tau = c^{i+1}\tau\partial_S$, and $b\tau$ is a simplicial boundary.

Property 2 ∂_M is a boundary operator, i.e. $\partial_M\partial_M = 0$, and (C_*, ∂_M) is a chain complex.

Proof First, we can show that, for any chain of cells x, $x\tau = 0 \Rightarrow x = 0$, since the simplicial chain associated with a cell is not null, and the chains associated with two distinct cells are generated by sets of simplices the intersection of which is empty. Second, we can deduce from Lemma 1 that $x\partial_M\partial_M\tau = x\tau\partial_S\partial_S = 0$, since ∂_S satisfies $\partial_S\partial_S = 0$. Thus $x\partial_M\partial_M = 0$ (see also [ADLP11] in which a direct proof is provided, which does not use the equivalence between cmaps and semi-simplicial sets).

3.2 Signed boundary operator

We restrict here to cmaps satisfying the following condition denoted $C2$:

Condition $C2$: C is a cmap such that:

- ***C satisfies $C1$;***
- ***For all i, all i-cells are orientable***[17]***.***

The orientability condition corresponds to the fact that all darts of any cell can be partitioned into two distinct subsets, such that if dart d belongs to one of these subsets, all darts $d\alpha_j^i$ belong to the other subset. A possible way for representing this property consists in associating a sign (+1 or −1) with any dart d, denoted

[17] cf. Subsection 2.3. Note that we don't take involutions α_i^i into account, since they are undefined. Formally, this means that an $i-$cell $(D, \alpha_0^i, \ldots, \alpha_{i-1}^i, \alpha_i^i = \omega)$ is orientable iff its canonical boundary $(D, \alpha_0^i, \ldots, \alpha_{i-1}^i)$ is orientable. There exists non orientable cells, for instance a 3-cell which boundary corresponds to the 2−gmap of Fig. 5(f), i.e. corresponding to a Klein bottle. At last, note that the fact that all cells are orientable does not involve that the whole cmap is orientable.

$sg(d)$, such that $sg(d) \neq sg(d\alpha_j^i)\forall j$. Let c^i be the i-cell incident to d: choosing an orientation for c^i consists in choosing a sign for d, the signs of the other darts of the cell are deduced from $sg(d)$. In practice, this can be done easily during a traversal of the whole cmap, i.e. in linear time according to the number of darts. So, the cost of checking condition $C2$ is the cost of condition $C1$, linear in the number of darts times the dimension of the cmap.

Definition 9 (signed incidence number) Let C be a cmap, and let $i \in \{1, \ldots, n\}$. Let $c^i(d^i)$ and $c^{i-1}(d^{i-1})$ be two cells of C. The *signed incidence number*, $(c^i(d^i) : c^{i-1}(d^{i-1}))$, is equal to $n_+ - n_-$, where:
n_+ is the number of preimages (related to σ^i) of d^{i-1} in c^i whose sign is equal to $sg(d^{i-1})$;
n_- is the number of preimages (related to σ^i) of d^{i-1} in c^i whose sign is different from $sg(d^{i-1})$.

The signed incidence number $(c^i : c^{i-1})$ is well defined, independently from the chosen darts: since c^i is orientable, any orbit $\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle$ of c^i is orientable. Since σ^i restricted to an orbit $\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle$ is an isomorphism, we can show that for any darts d and d' of this orbit, $sg(d).sg(d\sigma^i) = sg(d').sg(d'\sigma^i)$.

As for the unsigned boundary operator, we can provide an alternative definition: let $\{p_j\}_{j=1\cdots k}$ be darts of c^i such that $\{\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle (p_j)\}_{j=1\cdots k}$ makes a partition of c^i. Then

$$(c^i : c^{i-1}) = \sum_{p_j, j=1\cdots k | p_j\sigma^i \in c^{i-1}} sg(p_j).sg(p_j\sigma^i).$$

This alternative definition is equivalent to the original one, due to Property 2a of Definition 4. The corresponding operator ∂_M acts on any i-cell c^i in the following way:

Property 3 Let $i \in \{1, \ldots, n\}$. Let c^i be a cell of the cmap C. Let $\{p_j\}_{j=1\cdots k}$ be a set of darts such that the orbits $\{\langle \alpha_0^i, \cdots, \alpha_{i-2}^i \rangle (p_j)\}_{j=1\cdots k}$ make a partition of c^i,

$$c^i\partial_M = \sum_{p_j, j=1\cdots k} sg(p_j).sg(p_j\sigma^i)c^{i-1}(p_j\sigma^i).$$

Operator ∂_M is extended on any sum of cells taken with any integer coefficients, by linearity.

We will prove below that under condition $C2$ above, ∂_M is a boundary operator, i.e. $\partial_M\partial_M = 0$. So, this boundary operator defines a homology on the corresponding set of cmaps, with coefficients in $\mathbb{Z}$, which will be referred to as *cellular homology*, as for the unsigned case, since no ambiguity will be induced.

We restrict here to cmaps satisfying condition $C2$.

Definition 10 Let $C = ((G^i)_{i=0,\ldots,n}, (\sigma^i)_{i=1,\ldots,n}$ be a cmap, S be its associated semi-simplicial set, C_* be the chain groups associated with C and (S_*, ∂_S) be the chain complex associated with S.

$\tau : C_* \to S_*$ is defined by:

$$\forall i, 0 \leq i \leq n, \forall c^i \in G^i, c^i\tau = \sum_{d \in c^i} sg(d)T(\langle\rangle(d)),$$

extended by linearity with integer coefficients to the chains of C_*.

Such a sum is a *signed chain of cells.*

Lemma 3 *τ satisfies:*

$$x\tau\partial_S = (-1)^i x\partial_M\tau$$

for any signed chain of cells x of dimension i greater than or equal to 1.

Proof The proof is similar to that of Lemma 1, by taking also into account:

- in any $i-$cell, two $i-$simplices sharing an $(i-1)-$simplex are oriented in opposite ways, since cells are orientable; so, when taking the boundary of the simplicial chain associated with an $i-$cell, the $(i-1)-$simplices "internal" to the cell vanish;
- cellular face operator σ^i corresponds to simplicial face operator d_i, involving a $(-1)^i$ coefficient (cf. definition of simplicial boundary operator in Subsection 2.2).

See also [ADLP11] for a more detailed proof.

Lemma 4 *τ associates a simplicial cycle (resp. boundary) with any cellular cycle (resp. boundary).*

Property 4 ∂_M is a boundary operator, i.e. $\partial_M\partial_M = 0$, and (C_*, ∂_M) is a chain complex.

The proofs of Lemma 4 and Property 4 are similar to the unsigned case (cf. also [ADLP11]).

3.3 Algorithm

We present now Algorithm 1 which computes the ith incidence matrix E^i, i.e. incidence numbers between all i-cells and $(i-1)$-cells, for any cmap satisfying condition $C2$. Remember that cells in cmaps are linked together by the σ^i operator. When only σ^i operators are represented in data structures, it is more efficient to run through darts in c^i and to count the number of times a dart belonging to c^{i-1} is found than to run through darts in c^{i-1} and finding its number of preimages in c^i by σ^i.

For this reason, we use in our algorithm the formulation of the boundary operator as stated in Property 3.

This algorithm takes as input a signed cmap C, i.e. each dart d of C is marked with $sg(d)$, and computes the ith incidence matrix E^i.

Notation: given a gmap G, let $card(G)$ denote the number of connected components of G.

The case $i = 0$ is specific since there is no (-1)-cell thus the 0th incidence matrix is a zero matrix having card(G^0) columns and one line.

Otherwise, the incidence matrix E^i is initialized to a zero matrix having card(G^i) columns and card(G^{i-1}) lines. Then we run through all the darts $d \in G^i$. If d is not marked, its i-cell $c^i(d)$ is not yet processed. Thus we enter in the second loop to compute all the incidence numbers between $c^i(d)$ and its incident $(i-1)$-cells. For that we only run through the darts $d' \in c^i(d)$ and consider each $(i-1)$-cell

Algorithm 1: Computation of the ith incidence matrix

Data: $C = ((G^i)_{i=0,\ldots,n}, (\sigma^i)_{i=1,\ldots,n})$: a signed n-dimensional cmap
i: a dimension, $0 \leq i \leq n$

Result: The incidence matrix E^i

```
if i=0 then
    E^i ← zeroMatrix(card(G^0),1);
else
    E^i ← zeroMatrix(card(G^i),card(G^{i-1}));
    foreach dart d ∈ G^i do
        if d is not marked treated then
            foreach dart d' ∈ c^i(d) do
                if d' is not marked treated then
                    E^i(c^i(d), c^{i-1}(d'σ^i)) ← E^i(c^i(d), c^{i-1}(d'σ^i)) + sg(d').sg(d'σ^i);
                    mark treated all the darts of ⟨α^i_0, ··· , α^i_{i-2}⟩ (d');
    return E^i;
```

$c^{i-1}(d'\sigma^i)$. Indeed, other $(i-1)$-cells do not belong to the boundary of $c^i(d)$, and thus the incidence number between these cells and $c^i(d)$ is zero.

For each $(i-1)$-cell, we mainly add or subtract 1 depending if d' and $d'\sigma^i$ have the same sign or not. After having considered all the darts of $c^i(d)$, all the $(i-1)$-cells incident to $c^i(d)$ have been treated, thus all the incidence numbers involving $c^i(d)$ have been computed. At the end of Algorithm 1, all the i-cells of the cmap have been treated, and thus the matrix E^i is the ith incidence matrix.

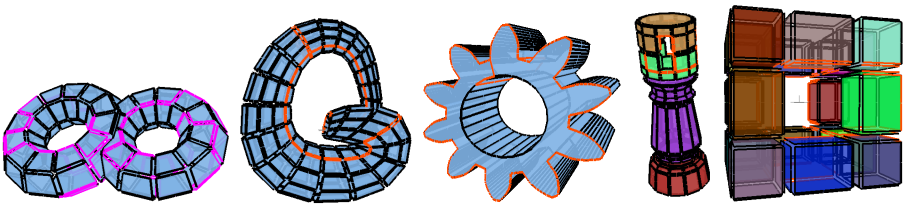
The complexity of Algorithm 1 is linear in the number of darts of G^i. Indeed, each dart is considered exactly once during the second loop thanks to the *treated* mark, and for each dart, we have a direct access to each value used to compute the incidence number (i.e. $d'\sigma^i$, $sg(d')$ and $sg(d'\sigma^i)$).

Note that we can define in a similar way an algorithm to compute the signed incidence number $(c^i(d) : c^{i-1}(d'))$ for any cells $c^i(d)$ and $c^{i-1}(d')$.

To compute all the incidence matrices for a given $n-$dimensional cmap, we need first to orient each cell of the cmap; second to run Algorithm 1 for each i, $0 \leq i \leq n$. The complexity of the overall process is thus linear in the number of darts, i.e. in the size of the cmap.

This process can be compared with the "simplicial homology computation", which consists in:

- compute the simplicial analog of the given cmap. So, it is necessary to compute all possible orbits of the cmap (cf. Subsection 2.4.2), for any combination of involutions. Since the cost is 2^n times the number of darts for a n-dimensional gmap, it is easy to deduce that the cost of computing an orientation for each cell of a cmap is less than the cost of computing its simplicial analog;
- then compute the incidence matrices: this is linear in the number of simplices times the dimension of the cmap. It is clear that there are less cells in the cmap than simplices in its simplicial analog. See for instance the five objects shown in Fig. 12 plus the Poincaré homology sphere (not shown). The first three objects are surfacic (i.e. they are 2D combinatorial objects embedded in 3D space) while the last three ones are topologically 3-dimensional ones.



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

Fig. 12 Cellular objects. (a) A torus with two holes (surfacic). (b) A Klein bottle (surfacic). (c) A pinion (surfacic). (d) A tower (volumic). (e) A Menger sponge (volumic).

Object	Cellular object				Simplicial analog			
Cell dimension	0	1	2	3	0	1	2	3
2-torus	151	294	142	-	588	1,770	1,180	-
Klein bottle	324	648	324	-	1,296	3,888	2,592	-
Pinion	470	701	231	-	1,402	4,206	2,804	-
Tower	228	452	226	4	910	3,824	4,928	2,016
Menger sponge	64	144	96	20	324	1,576	2,208	960
Poincaré sphere	5	10	6	1	22	142	240	120

Table 1 Numbers of cells of the objects shown in Fig. 12, and of Poincaré sphere.

We give in Table 1 the number of cells of each object for each dimension, and compare these numbers with the number of simplices of the corresponding simplicial object: it is thus possible to compare the sizes of the incidence matrices associated with the cellular objects and their simplicial analogs.

So, we can easily deduce that it is more efficient to compute the homology of a cmap with the method presented in this paper, when it is possible, than to compute the homology of its simplicial analog.

At last, note that we can also deduce an algorithm for computing the unsigned incidence number, the only difference being that the considered cmap is no more signed:

- so, it is useless to orient the cells before computing the incidence matrices;
- the incidence number can be represented by a Boolean initialized to false, and negated at each time the condition *d is not marked treated* ***and*** $d\sigma^i \in c^{i-1}(d')$ is satisfied (since the computation is done over $\mathbb{Z}/2\mathbb{Z}$).

4 Conditions and proof of the equivalence between cellular and simplicial homology on chains of maps

We restrict here to cmaps satisfying the following condition denoted $C3$:

Condition $C3$: C is a cmap such that:

- ***C satisfies condition $C1$ (homology over $\mathbb{Z}/2\mathbb{Z}$) or condition $C2$ (homology over $\mathbb{Z}$);***

– ***for each $i-$cell, the cmap corresponding to its canonical boundary***[18] ***has the homology of an $(i-1)$-dimensional sphere (i.e. $H_0 = \mathbb{Z}, H_j = 0, 1 \leq j \leq i-2, H_{i-1} = \mathbb{Z}$).***

The cost of checking condition $C1$ or $C2$ has been discussed in the previous section. The cost related to condition $C3$ is mainly the cost of checking that the canonical boundary of each cell has the homology of a sphere. As said in introduction, it is important to check the constructed object during a construction process: so, checking the homology of the boundary of a cell can naturally be done when the cell is constructed or modified.

We prove that under condition $C3$, the defined homology of a cmap is equivalent to the homology of its simplicial analog. Otherwise stated:

Theorem 1 *Let C be a cmap satisfying condition $C3$, S be its associated semi-simplicial set, (C_*, ∂_M), (S_*, ∂_S) and $\tau : C_* \to S_*$ be their associated chain complexes and morphism. Let $H_*(C)$ and $H_*(S)$ be the corresponding homology groups.*

τ induces an isomorphism $\tau_* : H_*(C) \to H_*(S)$.

The following lemma[19] is needed for the proof of Theorem 1:

Lemma 5 *Let z_s be a simplicial cycle (resp. boundary), i.e. a cycle (resp. boundary) in the semi-simplicial set associated with a cmap. Then a cellular cycle (resp. boundary) z exists in the cmap, such that $z\tau$ is homologous to z_s.*

Its proof uses the following lemma illustrated in Fig. 14:

Lemma 6 *Let x_s be a simplicial chain, such that:*

- *all simplices of x_s belong to $T(cel)$, where cel is a cell which dimension is strictly greater than that of x_s;*
- *the simplices of the boundary of x_s belong to the semi-simplicial subset associated with the boundary of cel.*

Then a simplicial chain x'_s exists, which is homologous to x_s (and thus which has the same boundary as x_s), such that all simplices of x'_s are in the semi-simplicial subset associated with the boundary of cel.

Proof of Theorem 1

A consequence of lemmas 2, 4 and 5 is the existence of a one-to-one mapping between the classes of cellular cycles (resp. boundaries) of a cmap and the classes of simplicial cycles (resp. boundaries) of the associated semi-simplicial set.

Note that a particular boundary operator ∂_M depends on the chosen cell orientations when considering homology over $\mathbb{Z}$. The theorem shows that the corresponding homology is equivalent to the simplicial homology of the semi-simplicial set associated with the cmap, independently of the cell orientations. The cellular homology defined by a particular operator ∂_M is thus independent of the cell orientations which have been chosen for defining this operator.

[18] A cmap can be associated with any gmap: see [EL94], proof of Lemma 6 and Subsection 5.1.

[19] We do not distinguish between the signed and the unsigned cases, since the proofs are quite similar.

4.1 Proof of Lemma 5

We first prove Lemma 5, assuming Lemma 6 is true.

Correspondence of cycles.

Let z_s be a k-dimensional simplicial cycle (i.e. $z_s\partial_S = 0$, where ∂_S denotes the simplicial boundary operator with coefficients in $\mathbb{Z}/2\mathbb{Z}$ or in $\mathbb{Z}$). We can define a partition of the simplices of z_s according to the cells which triangulations produce these simplices, i.e. $z_s = \sum_{c_i}\sum_j \nu_{i_j} s_{i_j}$, where s_{i_j} is a simplex of $T(c_i)$ and ν_{i_j} is its coefficient (in $\mathbb{Z}/2\mathbb{Z}$ or in $\mathbb{Z}$).

- Assume that $\forall i$, the dimension of c_i is equal to the dimension of z_s. Then $\forall i$, $\sum_j \nu_{i_j} s_{i_j} = \nu_i c_i \tau$. If it is not the case, it is easy to prove that the boundary of this "subchain" contains simplices of $T(c_i)$, which cannot be removed by the boundary of an other "subchain", involving that the boundary of z_s is not null: contradiction.
- Assume that cells exist which dimension is strictly greater than that of z_s. Let c_i be such a cell, such that its dimension is maximal. The simplices of $(\sum_j \nu_{i_j} s_{i_j})\partial_S$ are in the semi-simplicial set associated with the boundary of c_i: otherwise, and due to the definition of face operators of the semi-simplicial set associated with a cmap, the boundary of this "subchain" contains simplices of $T(c_i)$, which cannot be removed by the boundary of an other "subchain": as before, we get a contradiction. Using the lemma, a chain z_i exists, such that its simplices are in the semi-simplicial set associated with the boundary of c_i, and which is homologous to $\sum_j \nu_{i_j} s_{i_j}$. We can thus replace this subchain by z_i in z_s. By iterating the process, we can replace z_s by an homologous cycle which satisfies the conditions of the first case.

Correspondence of boundaries.

Let b_s be a simplicial boundary: since a boundary is a cycle, a cellular cycle z exists, such that $z\tau$ is homologous to b_s; $z\tau$ is thus a simplicial boundary, i.e. a simplicial chain x_s exists, such that $z\tau = x_s\partial_S$. As before, we can define a partition of the simplices of x_s according to the cells which triangulations produce these simplices, i.e. $x_s = \sum_{c_i}\sum_j \nu_{i_j} s_{i_j}$, where s_{i_j} is a simplex of $T(c_i)$. We prove that x_s is homologous to the image by τ of a cellular chain as before, i.e. by distinguishing the cases:

- assume that $\forall i$, the dimension of c_i is equal to the dimension of x_s. Then $\forall i$, $\sum_j \nu_{i_j} s_{i_j} = \nu_i c_i \tau$. If it is not the case, this leads to a contradiction, since the boundary of c_k is associated by τ with a cellular chain;
- assume that cells exist which dimension is strictly greater than that of x_s. Let c_i be such a cell, such that its dimension is maximal. Using the lemma Lemma 6, a chain z_i exists, such that its simplices are in the semi-simplicial

set associated with the boundary of c_i, and which is homologous to $\sum_j \nu_{i_j} s_{i_j}$.

We can thus replace this subchain by z_i in x_s. By iterating the process, we can replace x_s by an homologous chain which satisfies the conditions of the first case.

4.2 Proof of Lemma 6

We now prove Lemma 6. We use the fact that any cmap can be constructed in the following way [EL94] (see Fig. 13):

- create any main i-dimensional cell[20] [Lie94] and its boundary (this boundary is a cmap equivalent to the canonical boundary of the i-cell). We restrict here this operation to the creation of cells which boundaries have the homology of an $(i-1)$-dimensional sphere;
- identify j-dimensional cells $(0 \leq j \leq i-1)$ which share a same boundary (we assume that the boundary of a vertex is null).

We will show for each operation that if the lemma is satisfied before applying the operation, it is still satisfied after.

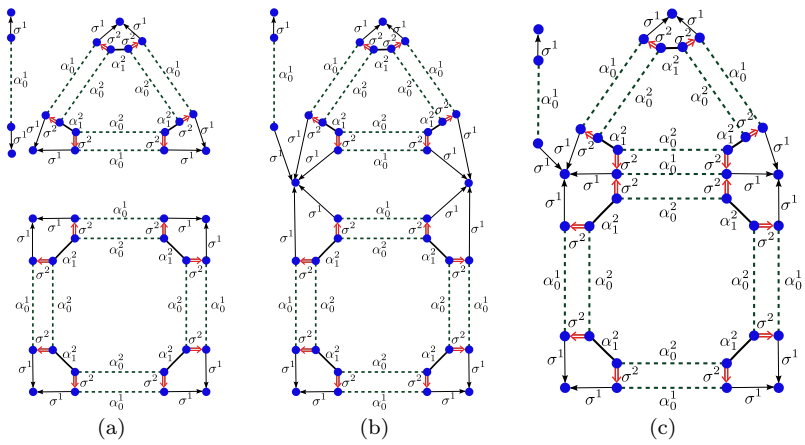


Fig. 13 (a) First step for building a cmap of dimension 2: each cmap, corresponding to a main cell and its boundary, is built. (b) Second step: vertex identifications. (c) The resulting cmap after edge identification.

Creating an i-cell and its boundary.

A connected gmap $G = (D, \alpha_0, \cdots, \alpha_n)$ such that $\alpha_n = identity$ defines an n-cell and its boundary, and it is possible to associate an equivalent cmap with it. More generally, given a gmap $G = (D, \alpha_0, \cdots, \alpha_n)$, we can associate with it a cmap $C = ((G^i = (D^i, \alpha_0^i, \cdots, \alpha_{i-1}^i, \omega))_{i=0\cdots n}, (\sigma^i)_{i=1\cdots n})$, such that the corresponding

[20] Note that it is a generalized map

quasi-manifolds are isomorphic (cf. [EL94] and Subsection 5.1). There is a one-to-one mapping B between the orbits $\langle \alpha_{i+1}, \cdots, \alpha_n \rangle$ of G and the darts of D^i. Moreover, $\forall d \in D$:

- $B(\langle \alpha_{i+1}, \cdots, \alpha_n \rangle (d))\alpha_j^i = B(\langle \alpha_{i+1}, \cdots, \alpha_n \rangle (d\alpha_j))$, $\forall 0 \leq j \leq i-1 < n$;
- $B(\langle \alpha_{i+1}, \cdots, \alpha_n \rangle (d))\sigma^i = B(\langle \alpha_i, \alpha_{i+1}, \cdots, \alpha_n \rangle (d))$, $\forall 1 \leq i \leq n$.

Creating an i-dimensional cell and its boundary consists in creating a cell c^i defined by $(D, \alpha_0, \cdots, \alpha_{i-1}, \omega)$, a cmap corresponding to its canonical boundary $(D, \alpha_0, \cdots, \alpha_{i-1})$, and σ^i is defined by: $\forall d \in D, d\sigma^i = B(\langle\rangle(d))$. The resulting cmap corresponds to the gmap $(D, \alpha_0, \cdots, \alpha_{i-1}, \alpha_i = \mathit{identity})$, and it is shown in [Lie94] that the corresponding semi-simplicial set is a cone (cf. Fig. 10). Its simplicial homology is thus trivial (i.e. $H_0 = \mathbb{Z}, H_j = 0, \forall j \geq 1$). Moreover, as said before, we restrict here the construction to gmaps such that the cmap associated to $(D, \alpha_0, \cdots, \alpha_{i-1})$ has the cellular homology of a sphere. By the recursion hypothesis, the simplicial homology of the associated semi-simplicial set is also that of a sphere. c^i is the unique i-dimensional cell, and the cells of $c^i\partial_M$ (where ∂_M is the cellular boundary operator defined on chains of maps, with coefficients in $\mathbb{Z}/2\mathbb{Z}$ or in $\mathbb{Z}$) are $(i-1)$-dimensional cells. Since a boundary is a cycle, $c^i\partial_M$ is an element of the unique class of the $(i-1)$-dimensional cycles, and it is now a boundary. The cellular homology of c^i and its boundary is thus the homology of a cone, equal to the simplicial homology of the corresponding semi-simplicial set.

Let x_s be a k-dimensional simplicial chain, such that $1 \leq k \leq i-1$, the simplices of x_s are simplices of $T(c^i)$, and the simplices of $x_s\partial_S$ are simplices of the semi-simplicial set associated with the boundary of c^i: cf. Fig. 14. $x_s\partial_S$ is thus a cycle made with simplices contained in the semi-simplicial set associated with the boundary of c^i. Since the simplicial homology of the boundary of c^i is the homology of a sphere, any $(k-1)$-cycle is a boundary, and a k-dimensional chain x'_s exists, which simplices are contained in the semi-simplicial set associated with the boundary of c^i, and such that $x'_s\partial_S = x_s\partial_S$. Thus $x_s - x'_s$ is a cycle, and since any k-dimensional cycle is a k-dimensional boundary (the homology of the cmap is the homology of a cone), a simplicial chain x''_s exists, which simplices are contained in $T(c^i)$ and in the semi-simplicial set associated with its boundary, such that $x'_s = x_s + x''_s\partial_S$. So, if the lemma is satisfied before creating a cell and its boundary, it is still satisfied after.

Identifying two cells.

The identification of two cells corresponds to the following operation: let c^i and c'^i be two distinct isomorphic i-dimensional cells (having the same boundary if $i \geq 1$), i.e. an isomorphism ϕ exists, such that $\forall d \in c^i, \forall j, 0 \leq j \leq i-1, d\alpha_j^i\phi = d\phi\alpha_j^i$, and $d\sigma^i = d\phi\sigma^i$. The cmap is then modified by dividing it by ϕ, i.e. by identifying d with $d\phi$ for all darts d of c^i. Let us denote $\overline{c^i}$ the cell resulting from the identification of c^i and c'^i. Due to the definition of the identification operation, a morphism exists between the initial cmap and the cmap resulting from the identification operation: this morphism can be extended onto a morphism between the associated semi-simplicial sets, and finally onto a morphism Φ between the associated simplicial chain complexes. By definition of a morphism, we have the following property: let x_s be a simplicial chain, the simplices of which belong to the initial cmap, then $x_s\partial_S\Phi = x_s\Phi\partial_S$.

Assume that Lemma 6 is satisfied before an identification operation. After operation, let x'_s be a simplicial chain which simplices are contained in $T(cel)$, where cel is a cell of the cmap, and such that the simplices of $x'_s\partial_S$ are contained in the semi-simplicial set associated with the boundary of cel. We are now going to show that Lemma 6 is still satisfied. For this we are considering the following three possible cases of identification.

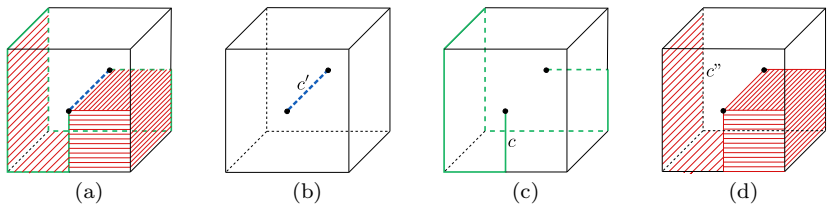


Fig. 14 (b) A $1d-$chain x' having all its simplices in a $3d-$cell, such that the simplices of its boundary are in the boundary of the $3d$-cell. (c) A $1d-$chain x homologous to x' having all its simplices in the boundary of the $3d-$cell. (d) $2d-$chain x" such that $x' = x + x"\partial_S$. (a) x', x and x" on the same figure.

case 1*:* $\overline{c^i} = cel$. The chain x' corresponds thus to a chain x'_1 and to a chain x'_2, such that the simplices of x'_1 (resp. x'_2) are contained in $T(c^i)$ (resp. $T(c'^i)$), and they are isomorphic to each other (by ϕ extended to $T(c^i)$ and to the associated chains of simplices). Since $x'_1\partial_S = x'_2\partial_S$, and the corresponding simplices are contained in $T(c^i)\partial_S = T(c'^i)\partial_S$, by the recursion hypothesis, a chain x_1 exists, which simplices are contained in $T(c^i)\partial_S$, a chain $x"_1$ exists, which simplices are contained in $T(c^i)$ and in $T(c^i)\partial_S$, such that $x'_1 = x_1 + x"_1\partial_S$, and $x'_2 = x_1 + x"_1\Phi\partial_S$. The identification operation results in identifying x'_1 with x'_2 into x', $x"_1$ with $x"_1\Phi$ into x", and we get: $x' = x_1 + x"\partial_S$, where the simplices of x_1 are contained in $T(cel)\partial_S$, and the simplices of x" are contained in $T(cel)$ and in $T(cel)\partial_S$.

case 2*:* $\overline{c^i}$ *is in the boundary of* cel. First, we show that x' satisfied the lemma conditions before identification. We know that cel was not affected by the identification, so before identification, x' was a simplicial chain the simplices of which are contained in $T(cel)$. Moreover, the fact that Φ is a morphism ensures that the simplices of $x'\partial_S$ were in $T(cel)\partial_S$. So, before identification, x' satisfied the lemma conditions, and $x' = x + x"\partial_S$, where the simplices of x (resp. x") belong to $T(cel)\partial_S$ (resp. to $T(cel) \cup T(cel)\partial_S$). More precisely, the chain x' can be decomposed as follow:

$$x' = (x_1 + x_2 + x_3) + (x"_1 + x"_2 + x"_3 + x"_4)\partial_S$$

where:

- the simplices of x_1 (resp. x_2, x_3) belong to $T(cel)\partial_S - T(c^i) - T(c'^i)$ (resp. $T(c^i)$, $T(c'^i)$);
- the simplices of $x"_1$ (resp. $x"_2$, $x"_3$, $x"_4$) belong to $T(cel)$ (resp. $T(c^i)$, $T(c'^i)$, $T(cel)\partial_S - T(c^i) - T(c'^i)$).

After identification, we get:

$$\begin{aligned} x' = x'\Phi &= (x_1 + x_2 + x_3)\Phi + (x"_1 + x"_2 + x"_3 + x"_4)\partial_S\Phi \\ &= (x_1 + x_2 + x_3)\Phi + (x"_1 + x"_2 + x"_3 + x"_4)\Phi\partial_S \\ &= x_1 + x_2\Phi + x_3\Phi + x"_1\partial_S + x"_2\Phi\partial_S + x"_3\Phi\partial_S + x"_4\partial_S \end{aligned}$$

As Φ is a morphism, the simplices of $x_i\Phi$ belong to the boundary of $T(cel)$, for $i = 1..3$; the simplices of $x"_1$ belong to $T(cel)$ and the simplices of $x"_j\Phi$ belong to the boundary of $T(cel)$, for $j = 2..4$, and the lemma is satisfied.

case 3: $\overline{c^i} \neq cel$ and $\overline{c^i} \notin cel\partial_M$. x' is not affected by the identification, and the lemma remains true for x'.

5 Optimizations

5.1 Generalized Maps

5.1.1 Definition

Definitions of boundary operators have been proposed in [APDL09] in order to optimize the computation of the homology groups for gmaps. We recall here these definitions, and we show that the so-defined homology of a gmap is equivalent to the simplicial homology of the associated quasi-manifold under conditions equivalent to $C3$. The proof of this equivalence is based upon the relations between a cmap corresponding to a quasi-manifold and the associated gmap, which can be explained in the following way.

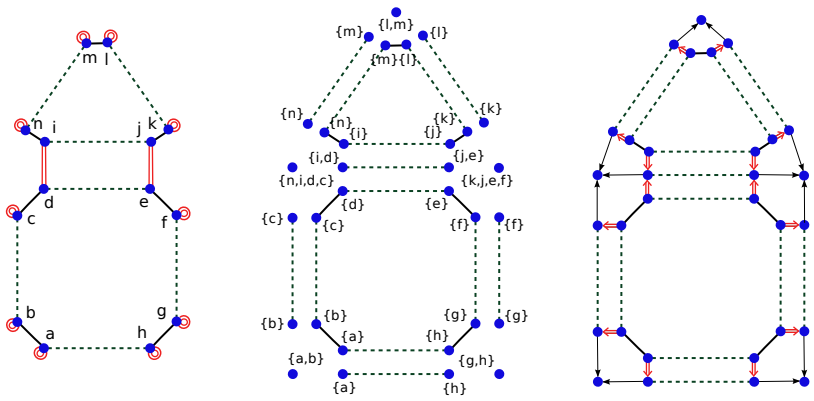
An homogeneous (or pure) n-dimensional cmap $C = ((G^i)_{i=0,\ldots,n}, (\sigma^i)_{i=1,\ldots,n})$ is such that any i-cell is incident to an n-cell, for $0 \leq i \leq n-1$ [EL94] (in others words, the dimension of any main cell is n). We can then define an equivalent structure $C' = (G^n, (R^i)_{i=0,\ldots,n-1})$, where $(R^i)_{i=0,\ldots,n-1}$ are equivalence relations between the darts of G^n, such that two darts d and d' satisfy relation R^i if and only if they have the same image $d\sigma^n \ldots \sigma^{i+1} = d'\sigma^n \ldots \sigma^{i+1}$, for $0 \leq i \leq n-1$. In fact, relations $(R^i)_{i=0,\ldots,n-1}$ implicitly represent the i-cells, and they satisfy properties which can be deduced from the definition of the cmaps.

When the cmap corresponds to a quasi-manifold, this structure can again be simplified: it is sufficient to explicitly represent n-cells and relation R^{n-1}, since n-cells are glued along $(n-1)$-cells; each equivalence class of R^{n-1} contains at most two darts, since at most two n-cells share an $(n-1)$-cell. R^{n-1} can thus be represented by an involution, namely α_n, and we get the definition of gmaps.

Moreover, since we consider cmaps in which σ^{i+1}, for $0 \leq i \leq n-1$, is an isomorphism between orbits $\langle \alpha_0^{i+1}, \ldots, \alpha_{i-1}^{i+1} \rangle$ and orbits $\langle \alpha_0^i, \ldots, \alpha_{i-1}^i \rangle$ (cf. Definition 4), we get the subclass of *gmaps without self-bending*: note that it is easy, during the construction of a gmap, to control the fact that it is without self-bending [ADLL08, CMP06]. A 2−gmap and a cmap encoding the same quasi-manifold are respectively displayed on Figure 15(a) and Figure 15(c).

Gmaps without self-bending satisfy Property 5 below.

Property 5 A gmap without self-bending $G = (D, \alpha_0, \ldots, \alpha_n)$, equivalent to a cmap as defined in Definition 4, satisfies, $\forall d \in D$, $\forall i, 0 \leq i \leq n$:



(a) (b) (c)

Fig. 15 (a) A 2-gmap. (b) Using the notion of compacted cells (see Property 5, point 2), an $i-$gmap can be associated with each $i-$cell of the gmap. (c) The corresponding cmap.

1. $\langle\alpha_0,\ldots,\alpha_{i-1}\rangle(d)\cap\langle\alpha_{i+1},\ldots,\alpha_n\rangle(d)=\{d\}$;
2. the *simple* cell $(\langle\alpha_0,\ldots,\alpha_{i-1}\rangle(d),\alpha_0,\ldots,\alpha_{i-1})$ is isomorphic to the *compacted* cell $(c^i(d)/\langle\alpha_{i+1},\ldots,\alpha_n\rangle,\alpha_0,\ldots,\alpha_{i-1})$, where $c^i(d)=\langle\alpha_0,\ldots,\alpha_{i-1},\alpha_{i+1},\ldots,\alpha_n\rangle(d)$. More precisely, $c^i(d)/\langle\alpha_{i+1},\ldots,\alpha_n\rangle$ means that a dart is associated with each orbit $\langle\alpha_{i+1},\ldots,\alpha_n\rangle$ of $c^i(d)$; since $\alpha_k\alpha_l=\alpha_l\alpha_k$ for $k\leq l-2$, we get (by abuse of notations) that $(\langle\alpha_{i+1},\ldots,\alpha_n\rangle(d))\alpha_k=\langle\alpha_{i+1},\ldots,\alpha_n\rangle(d\alpha_k)$ for $0\leq k\leq i-1$.

This property is a direct consequence of similar properties of cmaps detailed and proved in [ADLP11]. An important consequence of this property is the following. Let $C=((G^i)_{i=0,\ldots,n},(\sigma^i)_{i=1,\ldots,n})$ be a cmap satisfying condition $C1$ and corresponding to a quasi-manifold, and let $G=(D,\alpha_0,\ldots,\alpha_n)$ be the equivalent gmap. All involutions α_i are without fixed points for $0\leq i\leq n-1$. For $0\leq i\leq n$, there is a one-to-one mapping between the i-cells of C and orbits $(D/\langle\alpha_{i+1},\ldots,\alpha_n\rangle,\alpha_0,\ldots,\alpha_{i-1})$ of G (see Fig. 15). More precisely, each dart of G^i corresponds to an orbit $\langle\alpha_{i+1},\ldots,\alpha_n\rangle$, and $\langle\alpha_{i+1},\ldots,\alpha_n\rangle(d)\sigma^i=\langle\alpha_i,\ldots,\alpha_n\rangle(d)$ [APDL09].

5.1.2 Boundary operators

With this equivalence, we can thus extend the results presented above for chains of maps onto gmaps. First, we define the unsigned incidence numbers:

Definition 11 (unsigned incidence number) Let $i\in\{1,\ldots,n\}$. Let $c^i(d)$ and $c^{i-1}(d')$ be two cells of G. The *unsigned incidence number*, $(c^i(d):c^{i-1}(d'))$, is:
$\mathrm{card}(\{\langle\alpha_{i+1},\ldots,\alpha_n\rangle(d'')\subseteq\langle\alpha_i,\ldots,\alpha_n\rangle(d')\ s.t.\ \langle\alpha_{i+1},\ldots,\alpha_n\rangle\left(d''\right)\subseteq c^i(d)\})$.

This definition is a direct translation of the unsigned incidence numbers on chains of maps. We can simplify the definition in the following way :

$$(c^i(d):c^{i-1}(d'))=\mathrm{card}(\{\langle\alpha_{i+1},\ldots,\alpha_n\rangle(d'')|d"\in\langle\alpha_i,\ldots,\alpha_n\rangle(d'),d"\in c^i(d)\})$$

As for cmaps, we can provide the following alternative definition:

Property 6 Let $\{p_j\}_{j=1\ldots k}$ be a set of darts such that the orbits $\{\langle\alpha_0,\ldots,\alpha_{i-2}\rangle(p_j)\}_{j=1\ldots k}$ make a partition of $\langle\alpha_0,\ldots,\alpha_{i-1}\rangle(d)$; then

$$(c^i(d):c^{i-1}) = card(\{p_j, j=1\ldots k | p_j \in c^{i-1}\})$$

Then we define the signed incidence numbers, for gmaps whose cells are orientable, i.e. satisfying: for any i-cell $c^i = \langle\alpha_0,\ldots,\alpha_{i-1},\alpha_{i+1},\ldots,\alpha_n\rangle(d)$, there are two distinct orbits $\langle\alpha_0\alpha_1,\ldots,\alpha_0\alpha_{i-1},\alpha_0\alpha_{i+1},\ldots,\alpha_0\alpha_n\rangle(d)$ and $\langle\alpha_0\alpha_1,\ldots,\alpha_0\alpha_{i-1},\alpha_0\alpha_{i+1},\ldots,\alpha_0\alpha_n\rangle(d\alpha_0)$ (cf. [Lie94] and Subsection 5.2). We then choose an orientation for the associated compacted cell, i.e. each dart d of the i-cell is marked with a sign ($+1$ or -1) denoted $sg^i(d)$ such that $sg^i(d) \neq sg^i(d\alpha_j)$ $\forall j$: $0 \leq j < i$, and $sg^i(d) = sg^i(d\alpha_j)$ $\forall j$: $i < j \leq n$ [21]. Note that, as for cmaps, the gmap itself can be non orientable.

Definition 12 (signed incidence number) Let $i \in \{1,\ldots,n\}$. Let $c^i(d)$ and $c^{i-1}(d')$ be two cells of G. The *signed incidence number*, $(c^i(d):c^{i-1}(d'))$, is:

$$\sum_{\substack{\langle\alpha_{i+1},\ldots,\alpha_n\rangle(d'')\subseteq\langle\alpha_i,\ldots,\alpha_n\rangle(d') \\ s.t.\ d''\in c^i(d)}} sg^i(d'').sg^{i-1}(d')$$

It has been shown in [APDL09] that the incidence number does not depend on the chosen darts, and thus that the definitions are consistent. As for unsigned incidence numbers, we will use the following alternative definition:

Property 7 Let $\{p_j\}_{j=1\ldots k}$ be a set of darts such that the orbits $\{\langle\alpha_0,\ldots,\alpha_{i-2}\rangle(p_j)\}_{j=1\ldots k}$ make a partition of $\langle\alpha_0,\ldots,\alpha_{i-1}\rangle(d)$; then

$$(c^i(d):c^{i-1}) = \sum_{p_j, j=1\ldots k | p_j \in c^{i-1}} sg^i(p_j).sg^{i-1}(p_j)$$

Let ∂_M be the corresponding boundary operator, according to Definition 6: we can easily prove that ∂_M satisfies $\partial_M\partial_M = 0$ when involutions α_i are without fixed point for $0 \leq i \leq n-1$. Moreover, we have:

Theorem 2 *The homologies defined on gmaps by these boundary operators are equivalent to the simplicial homologies of the associated quasi-manifolds when the homology of the canonical boundary of each i-cell is that of an $(i-1)$-sphere.*

Proof We have mentioned above the equivalence between cmaps such that all involutions are without fixed point, and gmaps without self-bending, such that all involutions except α_n are without fixed point. This equivalence still holds when the cells are orientable. We can also show easily that a gmap and its corresponding cmap correspond to the same quasi-manifold, and that the incidence numbers defined for the gmap are the same as those defined for the associated cmap. The result comes from the fact that the homology of the cmap is equivalent to the homology of the quasi-manifold.

[21] This definition is equivalent to the one given in [APDL09].

5.1.3 Algorithm

It is easy to propose an algorithm to compute the incidence matrix E^i given a signed gmap. The only difference with the same algorithm for chains of maps (cf. Algorithm 1) is the way that we now consider cells. Indeed, contrary to cmaps, the darts of all the cells in relation by σ are now represented by only one dart in the gmap. Thus we use the same dart d' to represent both the i-cell and the $(i-1)$-cell, $\forall i : 0 \leq i \leq n$. The second difference is that we iterate through all the darts of $\langle \alpha_0, \ldots, \alpha_{i-1} \rangle (d)$ instead of iterating through all the darts $d' \in c^i(d)$ for cmaps. Indeed, when considering gmap G^i in a cmap, we do not consider α_j for $j \geq i$.

The complexity of the algorithm computing the incidence matrix E^i given a signed gmap is linear in number of darts of the gmap.

Let us recall that such an algorithm requires that the gmap has all its cells oriented. Orienting an i-cell can be achieved locally, the complexity being linear in the number of darts of the cell. Thus, the algorithm which orients each cell for each dimension of the gmap is linear in number of darts of the gmap times its dimension.

The algorithm computing all the incidence matrices consists in first orienting all the cells for all dimensions, and second computing all the incidence matrices E^i for $1 \leq i \leq n$. Its overall complexity is thus also linear in the number of darts of the gmap times its dimension.

5.2 Maps

Maps are defined in order to represent orientable quasi-manifolds without boundaries (cf. [Lie94]).

Definition 13 (n-map) Let $n \geq 0$, an n-map is defined by an $(n+1)$-tuple $M = (D, \beta_1, \cdots, \beta_n)$ such that:

- D is a finite set of darts;
- $\beta_1 : D \to D$ is a permutation; $\forall i, 2 \leq i \leq n, \beta_i : D \to D$ is an involution;
- $\forall i, 1 \leq i \leq n-2, \forall j, i+2 \leq j \leq n, \beta_i\beta_j$ is an involution.

The inverse of $M = (D, \beta_1, \beta_2, \cdots, \beta_n)$ is $M^{-1} = (D, \beta_1^{-1}, \beta_2, \cdots, \beta_n)$.

The link with gmaps is the following. Let $G = (D, \alpha_0, \cdots, \alpha_n)$ be a connected gmap without boundaries, i.e. such that α_i is without fixed points for any $0 \leq i \leq n$. Let $O = (D, \alpha_0\alpha_1, \cdots, \alpha_0\alpha_n)$ be the *map of the orientations* of G. O has at most two connected components; G is orientable if and only if O has exactly two connected components; in this case, each connected component is the inverse of the other one (cf. Fig. 16).

Conversely, let $M = (D, \beta_1, \cdots, \beta_n)$ be a connected map, and $M' = (D', \beta'_1, \cdots, \beta'_n)$ be a map isomorphic to M^{-1} by ϕ. Then we can define the corresponding gmap $G = (D \cup D', \alpha_0, \cdots, \alpha_n)$ with:

- for $1 \leq i \leq n$, $\alpha_i/D = \phi\beta'_i$, $\alpha_i/D' = \phi^{-1}\beta_i$;
- $\alpha_0/D = \phi$, $\alpha_0/D' = \phi^{-1}$.

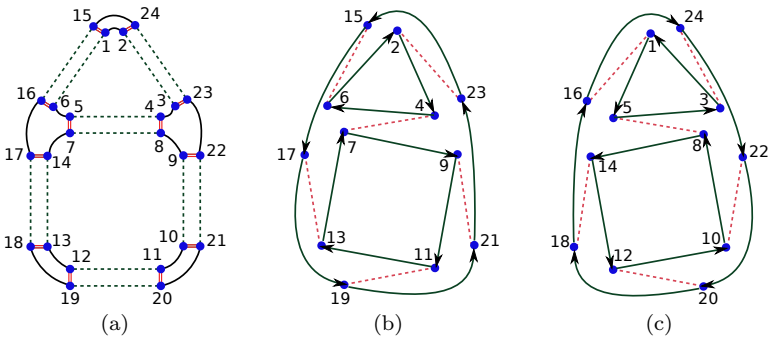


Fig. 16 (a) A 2-gmap representing a decomposition of S^2 with 3 faces. (b)-(c) Its two corresponding oriented maps. Note that the points corresponding to two darts d and d' such that $d\beta_1 = d'$ (resp. $d\beta_2 = d'$) are linked by a black arrow (resp. a red dashed line). Note also that $d\beta_1$ (resp. $d\beta_2$) corresponds to $d\alpha_0\alpha_1$ (resp. $d\alpha_0\alpha_2$).

Note that the two connected components of the map of the orientations of G are M and M'.

We have not found a simple direct characterization of the self-bending condition that maps have to fulfill in order to define an homology which is equivalent to the homology of their simplicial interpretation. Given a map, we think the most easy way consists in computing the associated gmap, and in checking the conditions. The cost of the conversion map-gmap is linear in the size of the map, so it doesn't change the complexity of the whole computation. In practice, it is more efficient to control the construction of the map, in order to get a map without self-bending; as for gmaps, it is easy and not costly.

Maps correspond to oriented quasi-manifolds without boundary. So, all cells are orientable, and the cmap associated with any map without self-bending satisfies condition $C2$. Moreover, main cells are oriented; but it remains necessary to define an orientation for non main cells, in order to compute incidence numbers. Here again, it seems that the most easy way for computing incidence matrices consists in computing the associated gmap and in applying the results obtained for gmaps[22].

6 Conclusion and perspectives

We have provided in this paper a direct definition of "cellular" homology for cmaps, gmaps and maps, i.e. where the chain groups are generated by the cells of the corresponding structure. The present study is, to our knowledge, the first one that tackles the problem of the definition and computation of a consistent cellular homology on quite generic and purely combinatorially defined cellular structures which allow multi-incidence between cells. Though it is always possible to compute

[22] Note that a similar phenomenon arose when studying the definition of cartesian product for cellular structures derived from the notion of combinatorial map [LSB04]. It was possible to optimize the definition for cmaps relatively to semi-simplicial sets, for gmaps relatively to cmaps, but the best way we found for defining the cartesian product of maps was to simulate the computation of the cartesian product of the associated gmaps.

the simplicial homology of a cellular structure on its simplicial analog, we take here advantage of the structuration into cells in order to improve the complexity of the homology computation (a cellular structure contains less cells than its simplicial analog contains simplices).

To achieve this objective, we have defined for cmaps the notions of (unsigned and signed) incidence numbers, and studied the combinatorial conditions under which a homology is defined over $\mathbb{Z}/2\mathbb{Z}$ and over $\mathbb{Z}$. The two cases are distinguished since the corresponding conditions are distinct, but also for optimization issues. We prove that the "cellular" homology is equivalent to the simplicial one when (mainly) the boundary of each cell is homologically equivalent to a sphere, which is also a purely combinatorial constraint. A similar equivalence for gmaps is also proved as a consequence of well-known relations between gmaps and cmaps. We didn't found how to optimize the computation for maps relatively to gmaps, and we think the best way for computing the homology of maps is to compute the homology of the corresponding gmaps.

Algorithms are provided for computing the incidence matrices, which are linear in the size of the corresponding structure. We have implemented the computation of incidence matrices for gmaps, and use these matrices to compute homology of 2D and 3D objects by using the method presented in [PAFL06b]. The dimension is for the moment restricted to 3 because the software used to develop these methods is `Moka` [VD03], which is a 3D modeling software. But all the functions which compute incidence matrices and homology are generic in any dimension.

We plan to improve the complexity of cellular homology computation by adapting techniques proposed for the simplicial framework or for regular $CW-$complexes (e.g. optimization of matrices reductions [Sto96], elementary reductions [KMS98, DKMW10]). We also study the conversions between structures derived from combinatorial maps and incidence graphs: they make it possible for instance to apply our results for the definition and the computation of the homology of cellular structures without multi-incidence [ADLP11, ALP12].

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