Removal Operations in nD Generalized Maps for Efficient Homology Computation

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Abstract. In this paper, we present an efficient way for computing homology generators of nD generalized maps. The algorithm proceeds in two steps: (1) cell removals reduces the number of cells while preserving homology; (2) homology generator computation is performed on the reduced object by reducing incidence matrices into their Smith-Agoston normal form. In this paper, we provide a definition of cells that can be removed while preserving homology. Some results on 2D and 3D homology generators computation are presented.

Keywords: nD Generalized Maps, Cellular Homology, Homology Generators, Removal Operations.

1 Introduction

In this paper, we propose a method for efficiently computing homology generators of subdivided cellular objects. The main idea is to simplify a subdivided object into a smaller one while preserving its homology. This principle is similar to the one used in [10] which is mainly algebraic (i.e. based on reduction of chain complexes), while our approach is mainly combinatorial.

In this work, we define a simplification algorithm based on the cell removal operations defined on generalized maps. Its principle is to simplify as much as possible the number of cells while preserving homology. Then we reduce incidence matrices (used for describing boundary operators) into their Smith-Agoston normal form for computing homology generators [3]. Moreover, generators computed in the reduced object can easily be projected into the original one.

The paper is structured as follows: in Sect. 2 all the necessary background regarding n-Gmaps is recalled. Section 3 presents the main result of the paper: the definition of the simplification algorithm based on the removal of two types of cells, and the proof of the homology preservation. Finally, some experiments are presented in Sect. 4 in order to illustrate that the simplification step widely reduces the number of cells, and also the homology generator computation.

2 Preliminary Works

An n-Gmap is a combinatorial structure devoted to the representation of cellular subdivision of orientable or not orientable nD quasi-manifolds, with or without

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boundaries (see [11,12] for more details). Any polytopal complex can be described by an n-Gmap, while the converse is not true (an i-cell can be non homeomorphic to an i-disk). It is possible to associate a semi-simplicial set with any n-Gmap. An n-Gmap is not constructed directly from the cells of the subdivision but from more elementary objects: *darts*. The set of darts is structured through involutions that describe how they are linked to each other.

Definition 1 (n-Gmap). *An* n-dimensional generalized map*, called* n-Gmap*, with* $0 \leq n$*, is a* $(n+2)$*-tuple* $G = (D, \alpha_0, \ldots, \alpha_n)$ *where:*

1. D *is a finite set of darts;*
2. $\forall i,\ 0 \leq i \leq n$, α_i *is an involution on* D*;*
3. $\forall i : 0 \leq i \leq n-2$, $\forall j : i+2 \leq j \leq n$, $\alpha_i \circ \alpha_j$ *is an involution.*

The cells of the subdivision are defined implicitly as set of darts thank to the orbit notion (see Def. 2). An orbit in an n-Gmap can be seen as the set of darts that we can reach from a given dart and using as many times as possible the given involutions.

Definition 2 (Orbit). *Let* $\Phi = \{\pi_0, \cdots, \pi_n\}$ *be a set of permutations defined on a set* D*.* $\langle \Phi \rangle$ *is 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* $\{\phi(d) \mid \phi \in \langle \Phi \rangle\}$*.*

As we can see in Def. 3, each i-dimensional cell is an n-Gmap is obtained by an orbit using all the involutions except α_i.

Definition 3 (i-cell). *Let* G *be an* n*-Gmap, and* $d \in D$ *be a dart. Given* i*,* $0 \leq i \leq n$*, the* i*-dimensional cell containing* d*, called* i-cell *and denoted by* $c^i(d)$*, is* $\langle \alpha_0, \ldots, \alpha_{(i-1)}, \alpha_{(i+1)}, \ldots, \alpha_n \rangle (d)$*.*

Due to the definition of cells as sets of darts, the incident and adjacency relations on cells can easily be tested. Two distinct cells c_1 and c_2 are *incident* if $c_1 \cap c_2 \neq \emptyset$, and two i-cells c_1 and c_2 are *adjacent* if there is two darts $d_1 \in c_1$ and $d_2 \in c_2$ satisfying $d_1 = \alpha_i(d_2)$. When a dart d belongs to an i-dimensional border, we have $\alpha_i(d) = d$ and we say that d is i-free.

In the example of Fig. 1, face f_3 is described by $\langle \alpha_0, \alpha_1 \rangle (1) = \{1,2,3,4,5,6\}$, edge e_1 by $\langle \alpha_0, \alpha_2 \rangle (13) = \{13,14,15,16\}$, and vertex v_1 by $\langle \alpha_1, \alpha_2 \rangle (2) = \{2,3,7,14,15,24\}$. v_1 and e_1 are incident since $\langle \alpha_1, \alpha_2 \rangle (2) \cap \langle \alpha_0, \alpha_2 \rangle (13) = \{14,15\} \neq \emptyset$. f_1 and f_3 are adjacent since $23 \in f_1$, $1 \in f_3$, and $\alpha_2(1) = 23$.

In this paper, the main operations used to simplify an n-Gmap are the *removal operations* (see [7,6] for the definitions). Intuitively, removing a removable cell c merges the two $(i+1)$-cells incident to c, without modifying the other cells.

Definition 4 (Removable cell). *Let* G *be an* n*-Gmap,* c *be an* i*-cell of* G*.* c *is* removable *if one of the two conditions is satisfied:*

$i = n-1$*; or* $0 \leq i < n-1$ *and* $\forall d \in c, \alpha_{i+1} \circ \alpha_{i+2}(d) = \alpha_{i+2} \circ \alpha_{i+1}(d)$*.*

The notion of removable cell c is strongly related to the number of its $(i+1)$ incident cells, called the *degree* of c and denoted $degree(c)$. A direct consequence of Def. 4 is that an $i-$cell c of degree > 2 is not removable.

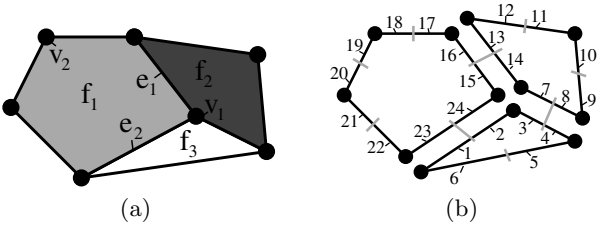


Fig. 1. Example of a 2G-map $G = (D, \alpha_0, \alpha_1, \alpha_2)$. (a) A 2D cellular complex containing 3 faces; 9 edges and 7 vertices. (b) The 2G-map describing this cellular complex, having 24 darts (represented by numbered black segments). Two darts linked by α_0 are drawn consecutively and separated by a gray segment (for example $\alpha_0(19) = 20$), two darts linked by α_1 share a common point (for example $\alpha_1(20) = 21$), and two darts linked by α_2 are drawn parallel, the gray segment over these two darts (for example $\alpha_2(13) = 16$).

In the example of Fig. 1, all the edges are removable (since an $(n-1)$-cell is always removable in an nG-map), vertex v_2 is removable while vertex v_1 not. Removing edge e_1 merges faces f_1 and f_2 in one face having as boundary the boundary of f_1 plus the boundary of f_2 minus edge e_1.

To be able to compute homology of an n-Gmap, we need to have a boundary operator (defined in [5,4]). The boundary operator is defined for n-Gmaps having orientable cells. Note that it is possible to represent a non-orientable object (e.g. a Klein bottle) with a n-Gmaphaving only orientable cells.

In the following we detail the notions of orientable cell and signed cell (cf. Defs. 5 and 6).

Definition 5 (Orientable i-cell). *An i-cell c is* orientable *if $c = e_1 \cup e_2$ such that: $\forall d \in c$, $\forall j$, $0 \leq j \leq n$, $j \neq i$: d is not j-free $\Rightarrow$ d and $\alpha_j(d)$ do not belong to the same set e_1 or e_2. c is* non-orientable *otherwise.*

If c is orientable, then it can be partitioned in two sets of darts representing its two orientations and we can associate a value -1 or $+1$ to each of its dart, called a *sign*. In the following, we only consider n-Gmap having all its cells signed.

Definition 6 (Signed i-cell). *Let c be an orientable i-cell. The corresponding signed i-cell is c together with a sign for each of its dart d, denoted $sg^i(d)$:*

- $sg^i(d) = -sg^i(\alpha_j(d))$ $\forall j$: $0 \leq j < i$ *such that d is not j-free;*
- $sg^i(d) = sg^i(\alpha_j(d))$ $\forall j$: $i < j \leq n$.

For defining a boundary operator on n-Gmaps, we first define the signed incidence number between two cells c^i and c^{i-1} which describes the number of times that c^{i-1} appears in the boundary of c^i.

Definition 7 (Signed incidence number). *let $\{p_j\}_{j=1\cdots k}$ be a set of darts s.t. the orbits $\{\langle \alpha_0, \cdots, \alpha_{(i-2)} \rangle (p_j)\}_{j=1\cdots k}$ make a partition of $\langle \alpha_0, \ldots, \alpha_{(i-1)} \rangle (d)$. The* signed incidence number *between c^i and c^{i-1} is defined by*

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

Note that this definition is equivalent to the one given in [5]. Now the boundary operator ∂_G of any i-cell c is defined as $\partial_G(c) = \sum_{c'}(c : c')c'$, where c' are $(i-1)-$cells incident to c. The boundary operator ∂_G satisfies $\partial_G \circ \partial_G = 0$ when involutions α_i are without fixed points for $0 \leq i \leq n-1$. Moreover, we have proven in [4] that the homology defined on n-Gmaps by this boundary operator is equivalent to the simplicial homology of the associated quasi-manifolds when the homology of the canonical boundary of each i-cell is that of an $(i-1)$-sphere, and when $\forall d \in D$, $\forall i \in \{0, \ldots, n\}$, d is i-free or $\alpha_i(d) \notin \langle \alpha_0, \ldots, \alpha_{i-2}, \alpha_{i+2}, \ldots, \alpha_n \rangle (d)$. In the following, all the considered n-Gmaps satisfied these conditions.

3 Removal Operations Preserving Homology

In this section, we prove that removing a degree two cell or a dangling cell preserves the homology of the n-Gmap.

3.1 Chain Complexes and Chain Contractions

Let $S = \{S_q\}_q$ be a graded. A q-chain is a finite formal sum of elements of S_q with coefficients in $\mathbb{Z}$. Let $C_q(S)$ denote the group of q-chains of S. The *chain complex* $(C_*(S), \partial)$ is the chain group $C_*(S) = \{C_q(S)\}_q$ together with a boundary operator ∂. Given an n-Gmap G, let S_G be the set of all the cells of G. $(C_*(S_G), \partial_G)$ is the chain complex associated to G.

A *chain contraction* [13] of $(C_*(S), \partial)$ *to* $(C_*(S'), \partial')$ is a triple ($f = \{f_q : C_q(S) \to C_q(S')\}_q$, $g = \{g_q : C_q(S') \to C_q(S)\}_q$ and $\phi = \{\phi_q : C_q(S) \to C_{q+1}(S)\}_q$) such that: (i) f and g are chain maps; i.e. $f_q \circ \partial_q = \partial'_q \circ f_q$ and $g_q \circ \partial_q = \partial'_q \circ g_q$ for all q; (ii) ϕ is a chain homotopy of $id_{C_*(S)} = \{id_q : C_q(S) \to C_q(S)\}_q$ to $g \circ f = \{g_q \circ f_q : C_q(S) \to C_q(S)\}_q$; i. e. $\phi_{q-1} \circ \partial_q + \partial'_{q+1} \circ \phi_q = id_q - g_q \circ f_q$ for all q; (iii) $f \circ g = id_{C_*(S')}$. If a chain contraction of $(C_*(S_G), \partial_G)$ to $(C_*(S_{G'}), \partial_{G'})$ exists, then the n-Gmaps G and G' have isomorphic homology groups.

3.2 Degree Two Cells

Proposition 1. *Let c be an i-cell in an n-Gmap. If c is removable and degree two cell, then there are two $(i+1)$-cells a and b satisfying: $|(a : c)| = |(b : c)| = 1$ and for all other $(i+1)$-cells c', $(c' : c) = 0$.*

Proof. Since c is degree two, there are two $(i+1)$-cells a and b that are incident to c. For these two cells, we have $c \in \partial_G(a)$ and $c \in \partial_G(b)$. So, $(a : c) \neq 0$ and $(b : c) \neq 0$. If $|(a : c)| > 1$, contradiction with removal property, thus $|(a : c)| = 1$ (and the same for $|(b : c)| = 1$). For all other $(i+1)$-cells c', c' is not incident to c otherwise the degree was greater than two. Thus $(c' : c) = 0$. □

Proposition 2. *Let c be an i-cell in an n-Gmap. If c is a removable degree two cell, and if each j-cell e incident to c, is after the removal of c a j-cell equal to $e \setminus c$, then homology is preserved after the removal of c.*

Note that the removal of a cell may induce removal of other cells (for example, it is possible to build a sphere made of one vertex, one degree two edge and two faces. Removing the edge would supress all the darts and so the vertex and the two faces). The second condition ensures that only one cell is removed

Proof. Let $(C_*(S_G), \partial_G)$ be the chain complex associated to G. Since c is degree two, there are two $(i+1)$-cells a and b that are incident to c. The set $S_{G'}$ of the cells of the n-Gmap G' obtained after removing the cell c consists in $S_G \setminus \{a, b, c\} \cup \{a'\}$ where a' is the resulting $(i+1)$-cell from merging the two cells a and b. Since, by Prop. 1, $|(a : c)| = |(b : c)| = 1$ and for all other $(i+1)$-cells c', $(c' : c) = 0$, we can construct a chain contraction (f, g, ϕ) of $(C_*(S_G), \partial_G)$ to $(C_*(S_{G'}), \partial_{G'})$ as follows:

$$f(x) = \begin{cases} c - (b : c)\partial_G(b), & \text{if } x = c, \\ a', & \text{if } x = a, \\ 0, & \text{if } x = b, \\ x, & \text{otherwise;} \end{cases} \qquad g(x) = \begin{cases} a - (a : c)(b : c)b, & \text{if } x = a', \\ x, & \text{otherwise;} \end{cases}$$

$$\phi(x) = \begin{cases} (b : c)b, & \text{if } x = c, \\ 0, & \text{otherwise.} \end{cases}$$

To check that (f, g, ϕ) is a chain contraction is left to the reader. Moreover, we know that each j-cell incident to c is preserved by the removal operation. Then G and G' have isomorphic homology groups. □

3.3 Dangling Cells

Let $(C_*(S), \partial)$ be a chain complex. Let $s, t \in S$ such that $|(s : t)| = 1$ and $(s' : t) = 0$ for any $s' \in S$, $s' \neq s$. If we remove s and t from S to get S', we obtain another chain complex $(C_*(S'), \partial')$ which is called an *elementary collapse* of S. A chain contraction of $(C_*(S), \partial)$ to $(C_*(S'), \partial')$ is given by

$$f(x) = \begin{cases} 0, & \text{if } x = s, \\ t - (s : t)\partial(s), & \text{if } x = t, \\ x, & \text{otherwise;} \end{cases} \qquad g(x) = x; \quad \phi(x) = \begin{cases} (s : t)t, & \text{if } x = t, \\ 0, & \text{otherwise.} \end{cases}$$

Therefore an elementary collapse preserves homology. A subset of S is *collapsible* if they can all be removed from S in a sequence of elementary collapses.

Let c be a k-cell, the *closure* of c, denoted $\overline{c}$, is the set made of c plus all the j-cells, $0 \leq j < k$ that are incident to c. The closure of a set S of cells, denoted $\overline{S}$, is the union of the closures of all the cells of S.

Definition 8 (Dangling cell). *Let c be an i-cell. We denote C the set of $(i-1)$-cells of $\partial_G(c)$, and $B = \{c' \in \partial_G(c) | degree(c') > 1\}$. c is* dangling *if c is orientable, its degree is 1, $\{c\} \cup \overline{C} \setminus \overline{B}$ is collapsible, and each j-cell $e \in \bar{B}$, is after the removal of c a j-cell equal to $e \setminus c$.*

Proposition 3. *Let c be an i-cell in an n-Gmap. If c is removable and dangling cell, then its removal preserves the homology of the n-Gmap.*

Proof. Removing c will remove also all the cells in $\overline{C} \setminus \overline{B}$ because these cells are included in c (i.e. their set of darts is included in the set of darts of c). As $\{c\} \cup \overline{C} \setminus \overline{B}$ is collapsible, and as all the other cells are preserved, the homology of the n-Gmap is preserved by the definition and property of collapsible. □

3.4 Simplification Preserving Homology

The main principle of the simplification algorithm consists in removing successively all the degree two cells and all the dangling cells for all the dimensions starting from $(n-1)$-cells to 0-cells. For that, we start to define Algo. 1 which simplifies all the i-cells of a given n-Gmap for a given dimension i.

Algorithm 1. Simplification of i-cells.

Input: An n-Gmap G.
Output: Simplify all the i-cells of G while preserving the same homology.

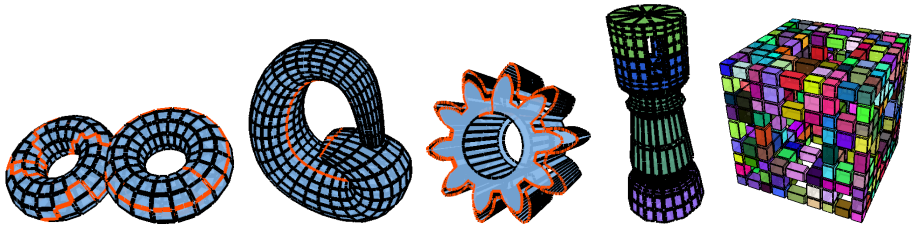
```
foreach i-cell c of G do
    if c is removable and the degree of c is 2 then
        Remove f;
    else if c is removable and c is a dangling cell then
        push(P, c);
        repeat
            c ← pop(P);
            push in P all the dangling i-cells adjacent to c;
            Remove c;
        until empty(P);
```

In this algorithm, we consider successively each i-cell c, and there are three possible cases. First, if c is not removable, then we are sure that c cannot be removable in a future step of the algorithm. Indeed, we only remove i-cells and this does not modify the $(i+1)$-cells incident to c. Second, if c is removable and its degree is two, we remove c. Third, if c is removable and dangling, we also remove c, but now we have to reconsider all the i-cells adjacent to c. Indeed, these cells can possibly become dangling due to the removal of c. At the end of the loop, we have considered all the i-cells and removed all the degree 2 cells and the dangling cells that were removable.

Now the global simplification method consists only in simplifying all the i-cells of the n-Gmap for all the cells by decreasing dimensions. We have to work in decreasing dimensions because the removal of an i-cell modifies the degree of all the incident $(i-1)$-cells. At the end of the global simplification algorithm, we have removed all the removable cells of degree 2 or dangling. By using Props. 2 and 3, we know that the final n-Gmap obtained after all the removals has the same homology than the initial n-Gmap.

4 Experiments

In order to illustrate the interest of our simplification algorithm, we show results on homology generator computation for the five objects shown in Fig. 2. Objects (a), (b) and (c) are described by 2-Gmaps; objects (d) and (e) are described by 3-Gmaps.



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

Fig. 2. (a) 2-torus. (b) Klein bottle. (c) pinion. (d) tower. (e) Menger sponge.

Table 1. Results of our experiments. We give the number of cells (columns *# cells*) for initial objects, and after the simplification algorithm. The last column gives the time of the simplification step. The two columns *Homology computation* give the memory space and the time of the homology generators computation (0s means less than 10^{-6}s).

Object	Initial						Simplified						
	# cells				Homology		# cells				Homology		Simplif.
Cell dim.	0	1	2	3	computation		0	1	2	3	computation		time
2-torus	404	802	396	-	14Mb	5.76s	6	9	1	-	2.36Kb	0s	0s
Klein	900	1800	900	-	74Mb	128.47s	2	3	1	-	0.41Kb	0s	0s
Pinion	470	701	231	-	11Mb	3.56s	2	3	1	-	0.41Kb	0s	0s
Tower	906	1856	952	4	85Mb	140.97s	10	15	4	1	6.53Kb	0s	0s
Menger	896	2304	1728	400	159Mb	372.50s	189	365	97	1	2938.00Kb	0.81s	0.03s

To compute the homology generators, we iterate through all the cells of the n-Gmap and we compute incidence matrices (which describes the boundary of the cells) using the incidence number definition. Then we reduce incidence matrices into their Smith-Agoston normal form for computing homology generators [3]. Compared to the classical Smith normal form, the specificity of the Agoston reduced normal form is that for a given dimension d, the basis of the boundaries B_p is a subset of the basis of cycles Z_p, thus the quotient group $H_p = Z_p/B_p$ can directly be obtained by simply removing from Z_p the boundaries of infinite order. Note that several optimizations exists for the reduction of incidence matrices [15,8]. Even if they can be used, we do not use them here as we focus on showing the improvement obtained with the simplification process.

The computation of homology generators was implemented in `Moka` [16], a 3D topological modeler based on 3-Gmap. For this reason, the computation of homology generators is limited to 2D and 3D cases, but all the functions are generic in any dimension. The results are presented in Table 1, where the simplification step widely reduces the number of cells. On the last column one can see that the simplification step is very fast. Memory space is also reduced as the size of incidence matrices are directly linked to the number of cells.

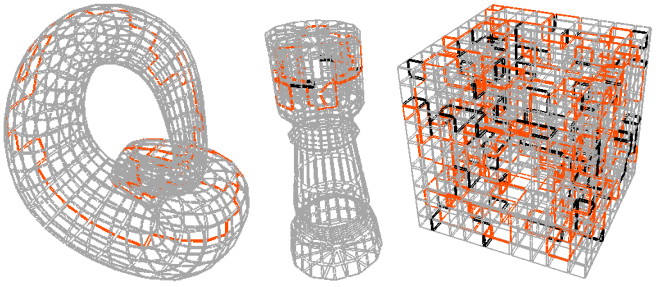


Fig. 3. The generators of H_1 (in red) computed on simplified objects, and projected on initial objects (drawn in grey). (a) Klein bottle. (b) Tower. (c) Menger sponge.

Lastly, we can see in Fig. 3 the different generators of H_1 obtained for some objects. By using the definition of removal operations, we are able to project the generators of the simplified object on the initial one (by using a similar technique as in [14,9]).

We have made a second type of experiments in order to compare our approach with other existing methods. To our knowledge there is no other general method which compute homology generator of cellular objects. Thus we compare our solution with `Chomp` and `RedHom` [1,2] which compute homology generators of cubical complexes. We chose these two methods since the two softwares are publicly available. However, it must be noticed that representing a cubical complex by a n-Gmaps is not efficient since a cube is described by 48 darts; the interest of cellular model is precisely to represent non regular subdivisions. In order to test the scale up property of the three methods, we chose three objects (see in Fig. 4(a), (b) and (c)), and multiply the size of each voxel by 4 to 9 for the first two objects, and by 2 to 7 for the last object which contains more voxels.

We can see in Fig. 4 the time required to compute homology generators of each object by the three compared methods. These results are really encouraging for our method which obtain the best computation time for the first two objects, with an important gain for the second one. For the third object, `Chomp`, and `Moka` performances are very similar (even if `Chomp` is a little bit quicker), while `RedHom` is really faster. In this last case, `Chomp`, and `Moka` have similar computation time than for the two first objects, while `RedHom` is extremely fast. We suppose there is an optimization allowing to remove directly some block of voxels. Indeed, the upper part of the last object is composed by a full block of voxels. This kind of improvement can also be made for our method.

These experiments show that our method is very competitive since it is not optimized for a specific type of subdivision but it is generic for any cellular complex. Thus its main interest is its genericity and we can conclude from this comparison that this is not to the detriment of the efficiency. Moreover, we can improve our results by adding a thinning pre-processing step that reduces the number of voxels while preserving the homology.

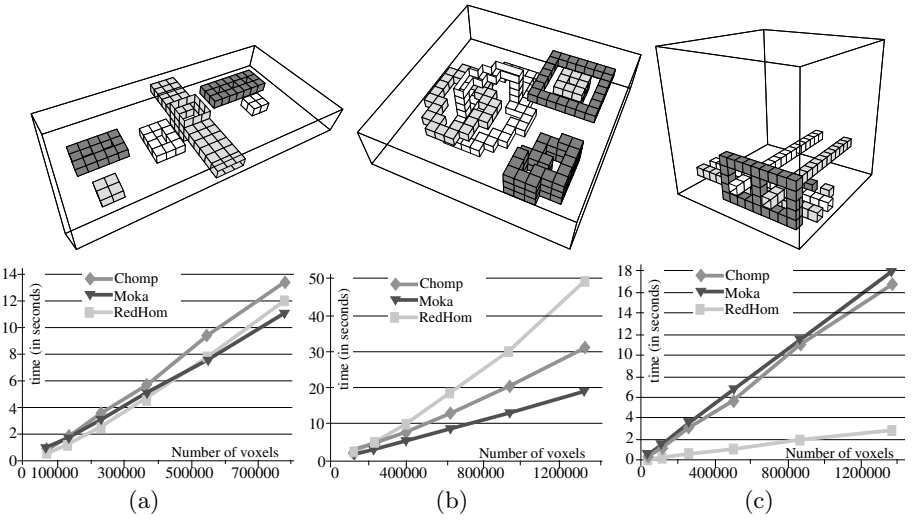


Fig. 4. Homology computation time comparison for `Chomp`, `RedHom` and `Moka`. Objects are made of voxels filling the bounding box (in wireframe), the filled surfaces being borders of cavities or tunnels. (a) `Cub1`: 1067 voxels; 1 connected components; 9 tunnels; 5 cavities. (b) `Cub2`: 1828 voxels; 1 connected components; 7 tunnels; 4 cavities. (c) `Cub3`: 4003 voxels; 1 connected components; 6 tunnels; 3 cavities.

5 Conclusion

In this paper, we have presented an algorithm that simplifies an n-Gmap while preserving its homology. For that, it removes degree two cells and dangling cells. Then we can compute homology on the reduced n-Gmap and project the generator on the original object. Some results show the interest of the simplification step, both in memory space and in computation time.

Some questions are still open. The first question is about the conditions on removed cells. Is it possible to remove some other type of cells while preserving the homology? The answer is no in 2D and 3D, but still open in higher dimension. This question is related to the definition of the minimal generalized map having the same homology. In 3D, to obtain this minimal map, we need to use another type of operation (fictive edge shifting). Thus we would like to study the extension of this operation in higher dimension to define the minimal n-Gmap.

References

1. Chomp, `http://chomp.rutgers.edu/`
2. Redhom, `http://redhom.ii.uj.edu.pl/`
3. Agoston, M.K.: Algebraic Topology, a first course. In: Dekker, M. (ed.) Pure and Applied Mathematics (1976)

4. Alayrangues, S., Damiand, G., Lienhardt, P., Peltier, S.: A boundary operator for computing the homology of cellular structures. Discrete & Computational Geometry (under submission)
5. Alayrangues, S., Peltier, S., Damiand, G., Lienhardt, P.: Border Operator for Generalized Maps. In: Brlek, S., Reutenauer, C., Provençal, X. (eds.) DGCI 2009. LNCS, vol. 5810, pp. 300–312. Springer, Heidelberg (2009)
6. Damiand, G., Dexet-Guiard, M., Lienhardt, P., Andres, E.: Removal and contraction operations to define combinatorial pyramids: Application to the design of a spatial modeler. Image and Vision Computing 23(2), 259–269 (2005)
7. Damiand, G., Lienhardt, P.: Removal and Contraction for n-Dimensional Generalized Maps. In: Nyström, I., Sanniti di Baja, G., Svensson, S. (eds.) DGCI 2003. LNCS, vol. 2886, pp. 408–419. Springer, Heidelberg (2003)
8. Dumas, J.-G., Heckenbach, F., Saunders, B.D., Welker, V.: Computing simplicial homology based on efficient smith normal form algorithms. In: Algebra, Geometry, and Software Systems, pp. 177–206 (2003)
9. Gonzalez-Diaz, R., Ion, A., Iglesias-Ham, M., Kropatsch, W.G.: Invariant representative cocycles of cohomology generators using irregular graph pyramids. Computer Vision and Image Understanding 115(7), 1011–1022 (2011)
10. Kaczynski, T., Mrozek, M., Slusarek, M.: Homology computation by reduction of chain complexes. Computers & Math. Appl. 34(4), 59–70 (1998)
11. Lienhardt, P.: Topological models for boundary representation: a comparison with n-dimensional generalized maps. CAD 23(1), 59–82 (1991)
12. Lienhardt, P.: N-dimensional generalized combinatorial maps and cellular quasi-manifolds. Computational Geometry & Applications 4(3), 275–324 (1994)
13. MacLane, S.: Homology. Classic in Mathematics. Springer (1995)
14. Peltier, S., Ion, A., Kropatsch, W.g., Damiand, G., Haxhimusa, Y.: Directly computing the generators of image homology using graph pyramids. Image and Vision Computing 27(7), 846–853 (2009)
15. Storjohann, A.: Near optimal algorithms for computing smith normal forms of integer matrices. In: Lakshman, Y.N. (ed.) Proceedings of the 1996 Int. Symp. on Symbolic and Algebraic Computation, pp. 267–274. ACM (1996)
16. Vidil, F., Damiand, G.: Moka (2003), `http://moka-modeller.sourceforge.net/`