Cell AT-Models for Digital Volumes*

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Abstract. In [4], given a binary 26-adjacency voxel-based digital volume V, the homological information (that related to n-dimensional holes: connected components, "tunnels" and cavities) is extracted from a linear map (called homology gradient vector field) acting on a polyhedral cell complex $P(V)$ homologically equivalent to V. We develop here an alternative way for constructing $P(V)$ based on homological algebra arguments as well as a new more efficient algorithm for computing a homology gradient vector field based on the contractibility of the maximal cells of $P(V)$.

1 Introduction

In [4], a polyhedral cell complex $P(V)$ homologically equivalent to a binary 26-adjacency voxel-based digital volume V is constructed. The former is an useful tool in order to visualize, analyze and topologically process the latter.The continuous analogous $P(V)$ is constituted of contractile polyhedral blocks installed in overlapping $2\times2\times2$ unit cubes. Concerning visualization, the boundary cell complex $\partial P(V)$ (in fact, a triangulation) of $P(V)$ is an alternative to marching-cube based algorithms [7]. The complex $P(V)$ is obtained in [4] suitably extending to volumes the discrete boundary triangulation method given in [8]. Nevertheless, the main interest in constructing $P(V)$ essentially lies in the fact that we can extract from it homological information in a straightforward manner. More precisely, by homological information we mean here not only Betti numbers (number of connected components, "tunnels" or "holes" and cavities), Euler characteristic and representative cycles of homology classes but also homological classification of cycles and higher cohomology invariants. Roughly speaking, for obtaining this homological acuity, we use an approach in which the homology problem is posed in terms of finding a concrete algebraic "deformation process" ϕ (so-called chain homotopy in Homological Algebra language [6] or homology gradient vector field as in [4]) which we can apply to $P(V)$, obtaining a minimal cell complex with exactly one cell of dimension n for each homology generator of dimension n.

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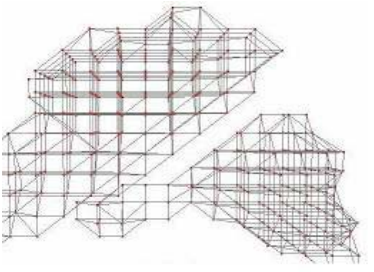

Fig. 1. Zoom of the polyhedral cell complex associated to a digital volume

Collaterally, homology groups can be deduced in a straightforward manner from ϕ. This idea of describing homology in terms of chain homotopies is not new and comes back to Eilenberg-MacLane work [2] on Algebraic Topology and it has been developed later in algebraic-topological methods like Effective Homology and Homological Perturbation Theory and in discrete settings as Discrete Morse [3] and AT-model [5] theories. In this paper, working in the field of general cell complexes embedded in R^3 and using discrete Morse theory notions, we construct a homology gradient vector field starting from any initial gradient vector field on a cell complex and, in the setting of the polyhedral cell complexes associated to digital volumes we design an efficient homology computation algorithm based on addition of contractile maximal cells. We work with coefficients in the finite field $F_2 = 0, 1$, but all the results here can be extended to other finite field or integer homology.

2 Homological Information on Cell Complexes

We deal with here the homology problem for finite cell complexes. Throughout the paper, we consider that the ground ring is the finite field $\mathbf{F}_2 = \{0, 1\}$. Let K be a three-dimensional cell complex. A *q–chain* a is a formal sum of simplices of $K^{(q)}$ $(q = 0, 1, 2, 3)$. We denote $\sigma \in a$ if $\sigma \in K^{(q)}$ is a summand of a. The q–chains form a group with respect to the component–wise addition; this group is the *qth chain complex* of K, denoted by $C_q(K)$. There is a chain group for every integer $q \geq 0$, but for a complex in $\mathbf{R}^3$, only the ones for $0 \leq q \leq 3$ may be non–trivial. The boundary map $\partial_q : C_q(K) \to C_{q-1}(K)$ applied to a q–cell σ gives us the collection of all its $(q-1)$–faces which is a $(q-1)$–chain. By linearity, the boundary operator ∂_q can be extended to q–chains. In the concrete case of a simplicial complex, the boundary of a q-simplex defined in terms of vertices $\sigma = \langle v_0, \ldots, v_q \rangle$ is defined by: $\partial_q(\sigma) = \sum \langle v_0, \ldots, \hat{v}_i, \ldots, v_q \rangle$, where the hat means that vertex v_i is omitted. In our case, taking into account that the 3-cells of our cell complexes can automatically be subdivided into tetrahedra, its boundary map can directly be derived from that of the component tetrahedra. It is clear that $\partial_{q-1}\partial_q = 0$. From now on, a cell complex will be denoted by (K, ∂), being $\partial : C(K) \to C(K)$ its boundary map. A chain $a \in C_q(K)$ is called

a *q–cycle* if $\partial\_q\ (a) = 0$. If $a = \partial\_q + 1(a')$ for some $a' \in C_{q+1}(K)$ then a is called a *q–boundary*. Define the *qth homology group* to be the quotient group of q–cycles and q–boundaries, denoted by $H_q(K)$. The homology class of a chain $a \in C_q(K)$ is denoted by $[a]$. It is clear that the Homology Problem for cell complexes (K, ∂) can be reduced to solving up to boundary the equation $\partial = 0$. Two main approaches can be used:

The differential approach. Classically, in Algebraic Topology, this last question has mainly been understood in terms of obtaining the different equivalence classes $(H_0(K), H_1(K), H_2(K))$. In an informal way, the homology groups describe in an algebraic way the maximal different disjoint set of cycles such that two cycles belonging to the same set can be deformed (using a boundary) to each other. For a $3D$ object, the ranks of the free part of the groups $H_0(K)$, $H_1(K)$ and $H_2(K)$, called Betti numbers, measure the corresponding number of connected components, "holes" or "tunnels" and cavities of this object. The homology groups are "computable" (up to isomorphism) global properties for the most of object representation models, they are strongly linked to the object structure (they do not depend on the particular subdivision you use), they are free groups up to dimension three and the main topological characteristics exhaustively used at to now in Digital Imagery (Euler characteristic and Betti numbers) can directly be obtained from them. There are two main strategies for computing homology groups for cell complexes: (a) the classical matrix "reduction algorithm" [9], mainly based on the Smith normal form diagonalization of the incidence matrices corresponding to the boundary map in each dimension; (b) the incremental technique of Delfinado-Edelsbrunner [1] in which homology is updated in each one-cell processing step, until the object is completely covered.

The integral approach. The solution to the Homology Problem can also be described in the following terms: to find a concrete map $\phi : C_*(K) \to C_{*+1}(K)$, increasing the dimension by one and satisfying that $\phi\phi = 0$, $\phi\partial\phi = \phi$ and $\partial\phi\partial = \partial$. In [4], a map ϕ of this kind have been called homology gradient vector field. This datum ϕ is, in fact, a chain homotopy operator on K (a purely homological algebra notion) and it is immediate to establish a strong algebraic link between the cell complex associate to K and its homology groups ($H_0(K)$, $H_1(K)$, $H_2(K)$), such that it is possible to "reconstruct" the object starting from its homology. For example, we need to specify a homological integral operator in order to homologically classifying any cycle or computing cohomology ring numbers. An algorithms using this integral approach can be classified into one of these two main groups: (a) starting from a zero integral operator, the idea is to save more algebraic information for constructing a homology gradient vector field ϕ (cost negligible in time but not in space) during the execution of the previous homology computation algorithms (matrix and incremental); (b) processes generating first a non-zero initial gradient vector field ϕ_0 (using, for example, Discrete Morse Theory techniques via Morse functions), constructing a reduced cell complex K' resulting from the application of the deformation ϕ_0, and finally applying algorithms of kind (a) to K'. Let us emphasize that this

description of "homology" as a pure algebraic deformation process is classical and comes from Eilenberg-Mac Lane work on Algebraic Topology in the sixties of the last century. Nevertheless, its use in the context of Digital Imagery is relatively recent [4,5,10].

Summing up, differential approach can be seen as a sort of minimal (and classical) solution in the sense that only the final result is considered while integral approach is a "maximal" solution in which all the homological deformation process is codified in an efficient way.

We are here now ready for defining *homological information* for an object K: any feature or characteristic extracted in a straightforward manner from a (non necessarily homological) gradient vector field for K. In that way, homological information includes not only Euler characteristic, Betti numbers, topological skeletons, Reeb graphs, representative cycles of homology generators and relative homology groups but also homological classification of cycles, homology and cohomology operations, cohomology ring, induced homomorphisms in homology.

Our choice within the context of Digital Imagery between differential or integral approach for the Homology Problem will mainly depend on the concrete application we are involved and can be "modulated" (from minimal-differential to maximal-integral approach) mainly in terms of the input, output and the homological elementary process for gradually constructing an homology gradient vector field on a cell complex.

In order to be understandable, the following definitions are needed.

Definition 1. *[3] Let (K, d) be a finite cell complex. A linear map of chains $\phi : C_*(K) \to C_{*+1}(K)$ is a* combinatorial gradient vector field *(or, shortly, combinatorial gvf) on K if the following conditions hold: (1) For any cell $a \in K_q$, $\phi(a)$ is a $q+1$-cell b; (2) $\phi^2 = 0$.*

If we remove the first condition, then ϕ will be called an *algebraic gradient vector field*. If ϕ is a combinatorial gvf which is only non-null for a unique cell $a \in K_q$ and satisfying the extra-condition $\phi d \phi = \phi$, then it is called a (combinatorial) *integral operator* [10]. An algebraic gvf satisfying the condition $\phi d \phi = \phi$ is called an *algebraic integral operator*. An algebraic gvf satisfying the conditions $\phi d \phi = \phi$ and $d \phi d = d$ will be called a *homology gvf* [4]. A gvf is called *strongly-nilpotent* if it satisfies the following property: given any $u \in K_q$, and being $\phi(u) = \sum_{i=1}^{r} v_i$, then $\phi(v_i) = 0$, $\forall i$. We say that a linear map $f : C_*(K) \to C_*(K)$ is strongly null over an algebraic gradient vector field ϕ if given any $u \in K_q$, and being $\phi(u) = \sum_{i=1}^{r} v_i$, then $f(v_i) = 0$, $\forall i$.

Using homological algebra arguments, it is possible to deduce that a homology gvf ϕ determines a strong algebraic relationship connecting $C(K)$ and its homology vector space $H(K)$. Let us define a *chain contraction* $(f, g, \phi) : (C, \partial) => (C', \partial')$ between two chain complexes as a triple of linear maps such that $f : C_* \to C'_*$, $g : C'_* \to C_*$ and $\phi : C_* \to C_{*+1}$ and they satisfy the following conditions: (a) $id_C - gf = \partial\phi + \phi\partial$; (b) $f\, g = id_{C'}$; (c) $f\, \phi = 0$; (d) $\phi\, g = 0$; (e) $\phi\, \phi = 0$.

Proposition 1. *Let (K, ∂) be a finite cell complex. A homology gvf $\phi : C_*(K) \to C_{*+1}(K)$ give raise to a chain contraction $(\pi, incl, \phi)$ from $C(K)$ onto a chain*

subcomplex of it isomorphic to the homology of K. Reciprocally, given a chain contraction (f, g, ϕ) from $C(K)$ to its homology $H(K)$, then ϕ is a homology gvf.

Let $incl : \mathrm{Im}\pi \to C(K)$ be the inclusion map. Let $\pi = id_{\mathcal{C}(\mathcal{K})} - \partial\phi - \phi\partial$. This chain map describe for each cell a representative cycle of the homology class associated to this cell and satisfies that $\pi^2 = \pi$. If $\mathrm{Im}\pi = \{x \in C(K),$ such that $x = \phi(y)$ for some $y\}$ and $\mathrm{Ker}\pi = \{x \in C(K)$ such that $\phi(x) = 0\}$, then $\mathcal{C}(\mathcal{K}) = \mathrm{Im}\pi \oplus \mathrm{Ker}\pi)$. Let $f : C(K) \to \mathrm{Im}(\pi)$ be the corestriction of π to $\mathrm{Im}(\pi)$ (that is, $\pi : C(K) \to \mathrm{Im}(\pi)$) and $g : \mathrm{Im}(\pi) \to C(K)$ be the inclusion. Let $\tilde{d}$ be the boundary operator of $\mathrm{Im}(\pi)$. We now prove that $\tilde{d} = 0$. Taking into account that $id_{C(K)} + gf = \phi\partial + \partial\phi$, $\partial\partial = 0$ and $\partial\phi\partial = \partial$, we then obtain $\partial - \partial gf = \partial$. Therefore, $\partial gf = g\tilde{d}f = 0$. Since f is onto and g is one-to-one, we deduce that $\tilde{d} = 0$. That means that the Morse complex $M_\phi = Im\pi$ is a graded vector space with null boundary operator isomorphic to the homology $H(K)$.

The homology computation process we apply in this paper is that given in [4], in which the incremental homology algorithm of [1] is adapted for getting a homology gradient vector field.

Given a cell complex (K, ∂), the ordered set of cells $\mathcal{K} = \langle c_1, \ldots, c_m\rangle$ is a filter if c_i is a face of c_j for $i < j$. It is possible to "filter" K by first considering all the 0-cells in a certain order, then an order on all the 1-cells, and so on.

Algorithm 1. *Let (K, ∂) be a filtered finite cell complex with filter $\mathcal{K}_m = \langle c_0, \ldots, c_m\rangle$. We represent the cell complex K up to filter level i by $\mathcal{K}_i = \langle c_0, \ldots, c_i\rangle$, with boundary map ∂_i. Let $\mathcal{H}_i$ the homology chain complex (with zero boundary map) associated to $\mathcal{K}_i$.*

$\mathcal{H}_0 := \{c_0\}$, $\phi_0(c_0) := 0$, $\pi_0(c_0) := c_0$.
`For` $i = 1$ `to` m `do`
  $\pi_i(c_i) = \overline{c}_i = c_i + \phi_{i-1}\partial_i(c_i)$,
  $\mathcal{H}_i := \mathcal{H}_{i-1} \cup \{\overline{c}_i\}$, $\phi_i(c_i) := 0$,
  `If` $(\partial_i + \partial_{i-1}\phi_{i-1}\partial_i)(c_i) = 0$, `then`
    `For` $j = 0$ `to` $i - 1$ `do`,
      $\phi_i(c_j) := \phi_{i-1}(c_j)$.
  `If` $(\partial_i + \partial_{i-1}\phi_{i-1}\partial_i)(c_i)$ `is`
  `a sum of a kind` $\sum_{j=1}^{r} \pi_{i-1}(e_{s_j}) = \sum_{j=1}^{r} u_j \neq 0$ $(u_i \in \mathcal{H}_{i-1})$, `then:`
    `Let us choose a summand` u_k `and define` $\tilde{\phi}(u_k) := c_i$
    `and zero for the rest of elements of` $\mathcal{H}_{i-1}$.
    `then For` $j = 0$ `to` $i - 1$ `do`,
      $\phi_i(c_j) = (\phi_{i-1} + \tilde{\phi}(1_{\mathcal{K}_i} + \phi_{i-1}\partial_{i-1} + \partial_{i-1}\phi_{i-1})(c_j)$,
      $\pi_i(c_j) = [1_{\mathcal{K}_i} - \phi_i\partial_i + \partial_i\phi_i](c_j)$
  $\mathcal{H}_i := \mathcal{H}_i \setminus \{u_k, \overline{c}_i\}$
OUTPUT: `a homology gradient vector field` ϕ_m `for` K.

Sketch of the proof
It can be proved by induction on i that ϕ_m is a homology gvf and, in consequence, it naturally produces a chain contraction $(\pi_m, incl, \phi_m)$ from $C(K)$ to its homology $H(K)$. The number of elementary operations involved in this process is $O(m^3)$.

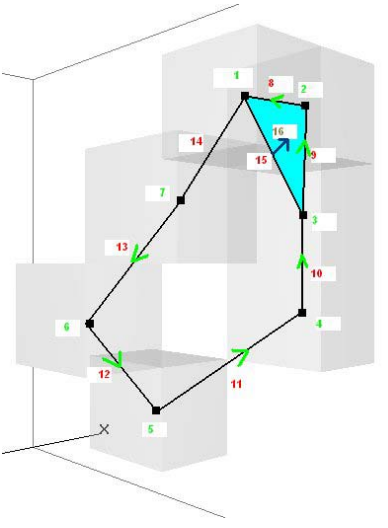

Fig. 2. Figure showing a 3D digital object V, an simplicial continuous analogous $K(V)$, and an homology gradient vector field ϕ on $K(V)$ using the filter $\{1, 2, 3, 4, ...\}$. For example, $\phi(5) = (11) + (10) + (9) + (8)$, $\phi(14) = 0$, $\phi(15) = (16)$.

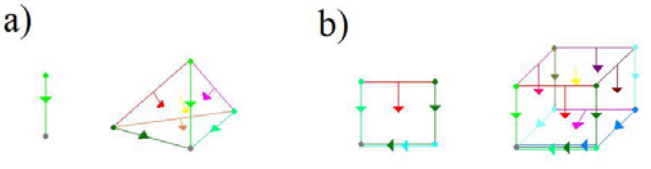

Fig. 3. Combinatorial gvf (a) and algebraic gvf (b)

Morevoer, it is not difficult to prove in that the resulting homology gvf ϕ_m of Algorithm 1 is a strongly nilpotent algebraic gvf and π_m is a strongly null map over ϕ_m.

Using Discrete Morse Theory pictorial language, combinatorial gvfs can be described in terms of directed graphs on the cell complex. For example, let us take an integral operator ϕ such that $\phi(a) = c$, $a \in K_0$ and being a and b the vertices of the 1-cell c. It is clear that ϕ can be represented by a directed tree consisting in the edge c together with its vertices, such that the arrow on c goes out from vertex a. Of course, the previous properties of a homology gvf $\phi_i : C_i(K) \to C_{i+1}(K)$ $(i = 0, 1, 2)$ help us to suitably express all the ϕ_i in terms of graphs.

Proposition 2. *If $\phi : C(K) \to C(K)$ is a homology gvf for a cell complex (K, ∂) and we denote by $H^{\partial}(K)$ and $H^{\phi}(K)$ the homology groups of K taking respectively ∂ and ϕ as boundary maps on K (both satisfy the 2-nilpotency*

condition). Then, $H^{\partial}(K)$ *and* $H^{\phi}(K)$ *are isomorphs. The maps* $h : H^{\partial}(K) \to H^{\phi}(K)$ *defined by* $h([c]^{\partial}) = [c + \partial\phi(c)]^{\phi}$ *and* $k : H^{\phi}(K) \to H^{\partial}(K)$ *defined by* $h([c]^{\phi}) = [c + \phi\partial(c)]^{\phi}$ *specify this isomorphism.*

3 Polyhedral AT-Model for a Digital Volume

Let V be a binary 26-adjacency voxel-based digital volume. A *cell AT-model* for V is a pair $((P(V), \partial), \phi)$, such that $(P(V), \partial)$ is a polyhedral cell complex (for example, that specified in [4]) homologically equivalent to V and $\phi : C(P(V)) \to C(P(V))$ is a homology gvf for $P(V)$. To obtain the cell complex $P(V)$ we do as follows. Each black voxel can be seen as a point (0-cell) of our complex. The algorithm consist of dividing the volume into overlapped (its intersection being a "square" of four voxels mutually 26-adjacent) unit cubes formed by eight voxels mutually 26-adjacent, and to associate each unit cube configuration with its corresponding cell. We scan the complete volume, always taking as elementary step a unit cube.

The cell associated to a unit cube configuration is a 0-cell if there is a single point. If there are two points, the complex is a 1-cell which is the edge connecting both of them. With three or four coplanar points on the set, the 2-cell associated is a polygon. If there are four non coplanar points or more, the 3-cell is a polyhedra. In other words, the cell associated to a unit cube configuration is just the convex hull of the black points and all its lower dimension faces. Note that for 3-cells, their 2-dimension faces are either triangles or squares.

Once we have covered all the volume and joined all the cells, we build the complete cell complex without incoherences.

The idea here is to design an incremental algorithm for computing the homology of $P(V)$ taking into account the contractibility of the cells (that is, the fact that they are homologically equivalents to a point). First at all, we develop a method for determining a homology gvf for any cell or polyhedral block R for $P(V)$ installed in a $2 \times 2 \times 2$ unit cube Q, which also provides an alternative method for constructing $P(V)$.

Let us start by describing the contractibility of a unit cube Q by a particular homology gvf. In the figure 4, it is visualized this vector field $\phi_Q : C(Q) \to C(Q)$ by colored arrows. For example, $\phi_Q(< 3, 4, 5, 6 >) =< 1, 2, 3, 4, 5, 6, 7, 8 >$

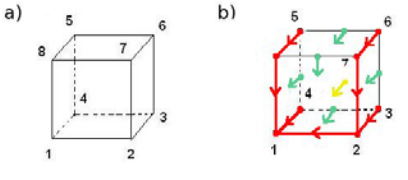

Fig. 4. A unit cube with labeled vertices (a) and arrows describing the contractibility of the cube (b)

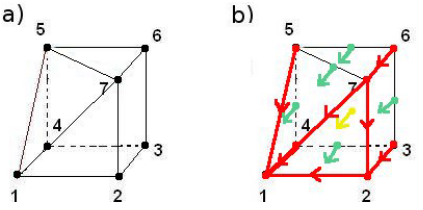

Fig. 5. The maximal cell R' (a) and its corresponding homology gvf (b)

(shown in yellow), $\phi_Q(< 5,6 >) =< 5,6,7,8 > + < 1,2,7,8 >$ (shown in green) and $\phi_Q(< 6 >) =< 1,2 > + < 2,7 > + < 6,7 >$ (shown in red). Obviously, the boundary map $\partial_Q : C(Q) \to C(Q)$ is defined in a canonical way (no problems here with the orientation of the cells, due to the fact we work over $\mathbf{F}_2$). For instance, $\partial_Q(< 1,2,3,4 >) =< 1,2 > + < 2,3 > + < 3,4 > + < 4,1 >$ and $\partial_Q(< 1,8 >) =< 1 > + < 8 >$.

Now, an alternative technique to the modified Kenmochi et al. method [8] for constructing $P(V)$ is sketched here. In order to determine a concrete polyhedral configuration R as well as a concrete homology gvf for it (to determine its boundary map is straightforward in $\mathbf{F}_2$), we use a homological algebra strategy which amounts to take advantage of the contractibility of Q for creating a homology gvf for R, by means of integral operators acting on Q. For avoiding to overburden with too much notation, we only develop the method in one concrete cases.

First, let us take the convex hull of eight black points showed in figure 4. Applying the integral operator given by $\psi(< 8 >) =< 1,8 >$, the final result R' and its homology gvf appears in figure 5. The face $< 1,5,,67 >$ need to be subdivided into two triangular faces: $< 1,5,7 >$ and $< 1,6,7 >$ for getting the configuration R. For connecting R and R', we applied to R the integral operator given by the formula $\psi(< 5,7 >) =< 1,5,7 >$.

In consequence, a homology gvf for R appears in Figure 5.

In fact, all this homology gvfs are obtained by transferring the homology gvf of Q via chain homotopy equivalences.

All these techniques are valid for any finite field or integer coefficients, and additional difficulties about orientation of the cells can be easily overcome.

We are now able for designing an incremental algorithm for computing the homology of V via the cell complex $P(V)$, based on the reiterated use of homology gvfs for polyhedral cells inscribed in the unit cube Q, we face to the problem of computing the homology of an union of a polyhedral cell complex $P(V')$ and a polyhedral cell R.

Definition 2. *Let (K, ∂) be a finite cell complex and $\phi_1, \phi_2, \ldots, \phi_r$ a sequence of integral operators $\phi_i : C_*(K) \to C_{*+1}(K)$ involving two cells $\{c_1^i, c_2^i\}$ of different dimension and such that $\{c_1^i, c_2^i\} \bigcap \{c_1^k, c_2^k\} = \emptyset$, $\forall 1 \leq i,k \leq r$. Then, an algebraic gvf $\bigoplus_{i=1}^r \phi_i$ for $C(K)$ onto a chain subcomplex having $n-2r$ cells can be constructed. The sum $\bigoplus_{i=1}^r \phi_i$ applied to a cell u is c_2^k is $u = c_1^k$ $(k = 1, \ldots, r)$ and zero elsewhere.*

σ	$\Phi(\sigma)$	$\varphi(\sigma)$
$<1>$	$<1,3>$	$<1,3>+<3,9>+<8,9>$
$<1,2>$	$<1,2,3>$	$<1,2,3>+<2,3,8,9>$
$<4>$	$<4,6>$	$<4,6>+<6,10>+<9,10>+<8,9>$
$<1,4>$	$<1,3,4,6>$	$<1,3,4,6>$
$<5>$	$<5,7>$	$<5,7>+<7,10>+<9,10>+<8,9>$
$<4,5>$	$<4,5,6,7>$	$<4,5,6,7>+<6,7,10>$
$<2>$	$<2,8>$	$<2,8>$
$<3>$	$<3,9>$	$<3,9>+<8,9>$
$<9>$	$<8,9>$	$<8,9>$
$<2,3>$	$<2,3,8,9>$	$<2,3,8,9>$
$<6>$	$<6,10>$	$<6,10>+<9,10>+<8,9>$
$<10>$	$<9,10>$	$<9,10>+<8,9>$
$<7>$	$<7,10>$	$<7,10>+<9,10>+<8,9>$
$<6,7>$	$<6,7,10>$	$<6,7,10>$

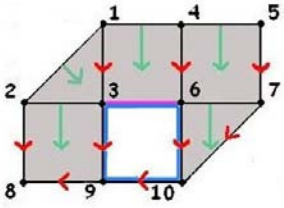

Fig. 6. An example showing the representative generator of the 1-cycle (in blue) and the resulting Φ and φ. Notice that $\Phi(<3,6>)=0$ and $<3,6>\notin Im(\Phi)$ ($<3,6>$ is a critical simplex in terms of Discrete Morse Theory).

σ	$\Phi(\sigma)$	$\varphi(\sigma)$
$<1>$	$<1,3>$	$<1,3>+<3,9>+<8,9>$
$<1,2>$	$<1,2,3>$	$<1,2,3>+<2,3,8,9>$
$<4>$	$<4,6>$	$<4,6>+<6,10>+<9,10>+<8,9>$
$<1,4>$	$<1,3,4,6>$	$<1,3,4,6>+<3,6,9,10>$
$<5>$	$<5,7>$	$<5,7>+<7,10>+<9,10>+<8,9>$
$<4,5>$	$<4,5,6,7>$	$<4,5,6,7>+<6,7,10>$
$<2>$	$<2,8>$	$<2,8>$
$<3>$	$<3,9>$	$<3,9>+<8,9>$
$<9>$	$<8,9>$	$<8,9>$
$<2,3>$	$<2,3,8,9>$	$<2,3,8,9>$
$<6>$	$<6,10>$	$<6,10>+<9,10>+<8,9>$
$<10>$	$<9,10>$	$<9,10>+<8,9>$
$<7>$	$<7,10>$	$<7,10>+<9,10>+<8,9>$
$<6,7>$	$<6,7,10>$	$<6,7,10>$
$<3,6>$	$<3,6,9,10>$	$<3,6,9,10>$
$<11>$	$<11,12>$	$<11,12>+<7,12>+<9,10>+<8,9>$
$<12>$	$<7,12>$	$<7,12>+<7,10>+<9,10>+<8,9>$
$<5,11>$	$<5,7,11,12>$	$<5,7,11,12>$

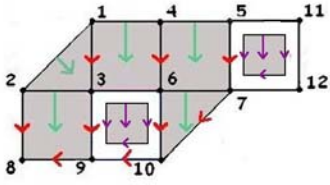

Fig. 7. An example showing the filling of the "hole" and an attachment of a 2-cell

In general $\Phi=\bigoplus_{i=1}^{r}\phi_i$ does not satisfy the condition $\Phi d\Phi=\Phi$. Applying Algorithm 1 to (K,∂) (previously filtered) to a partial filtering affecting only to the cells c_j^i ($1\leq i\leq r$ and $j=1,2$) in its sub-cells and specifying at each cell-step concerning the cell c_2^i that $\tilde{\phi}(f_i(c_1^i)):=c_2^i$, the final result will be a (non necessarily homological) algebraic integral operator $\varphi: C(K)\to C(K)$. Applying Proposition 1 to the algebraic integral operator φ and assuming that K has n cells, we obtain a chain contraction (f,g,φ) from $C(K)$ to a chain subcomplex $C(M(K))$ having $M(K)$ (also called, Morse complex of K associated to the sequence $\{\phi_i\}_{i=1}^{r}$) $n-2r$ cells. Algorithm 1 applied to $M(K)$ gives us a homology gvf ϕ for $M(K)$. Finally, the map $\varphi+\phi(1-d\varphi-\varphi d)$ gives us a homology gvf for the cell complex K.

Using these arguments, it is straightforward to design an algorithmic process of homology computation (over $\mathbf{F}_2$) for a binary 26-adjacency voxel-based digital volume V based on the contractibility of the maximal cells (in terms

of a homology gvf) constituting the continuous analogous $P(V)$. All is reduced to find a sequence of elementary integral operators acting as internal topological thinning operators on $P(V)$. Our candidates are the arrows describing the contractibility of all the maximal polyhedral cell configurations forming the objects.In order to suitably choose these integral operators, we use a maximal cell incremental technique.

References

1. Delfinado, C.J.A., Edelsbrunner, H.: An Incremental Algorithm for Betti Numbers of Simplicial Complexes on the 3–Sphere. Comput. Aided Geom. Design 12, 771–784 (1995)
2. Eilenberg, S., MacLane, S.: Relations between homology and homotopy groups of spaces. Ann. of Math. 46, 480–509 (1945)
3. Forman, R.: A Discrete Morse Theory for Cell Complexes. In: Yau, S.T. (ed.) Geometry, Topology & Physics for Raoul Bott. International Press (1995)
4. Molina-Abril, H., Real, P.: Advanced homology computation of digital volumes via cell complexes. In: Proceedings of the Structural and Syntactic Pattern Recognition Workshop, Orlando, Florida, USA (December 2008)
5. Gonzalez-Diaz, R., Real, P.: On the Cohomology of $3D$ Digital Images. Discrete Applied Math. 147, 245–263 (2005)
6. Hatcher, A.: Algebraic Topology. Cambridge University Press, Cambridge (2001)
7. Kenmochi, Y., Kotani, K., Imiya, A.: Marching cube method with connectivity. In: Proceedings of International Conference on Image Processing. ICIP 1999, vol. 4(4), pp. 361–365 (1999)
8. Kenmochi, Y., Imiya, A., Ichikawa, A.: Boundary extraction of discrete objects. Computer Vision and Image Understanding 71, 281–293 (1998)
9. Munkres, J.R.: Elements of Algebraic Topology. Addison–Wesley Co., London (1984)
10. Real, P., Gonzalez-Diaz, R., Jimenez, M.J., Medrano, B., Molina-Abril, H.: Integral Operators for Computing Homology Generators at Any Dimension. In: Ruiz-Shulcloper, J., Kropatsch, W.G. (eds.) CIARP 2008. LNCS, vol. 5197, pp. 356–363. Springer, Heidelberg (2008)
11. Zomorodian, A., Carlsson, G.: Localized Homology. Computational Geometry: Theory and Applications archive 41(3), 126–148 (2008)