


Homological Tree-Based Strategies for Image Analysis*

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Abstract. Homological characteristics of digital objects can be obtained in a straightforward manner computing an algebraic map ϕ over a finite cell complex K (with coefficients in the finite field $\mathbb{F}_2 = \{0, 1\}$) which represents the digital object [9]. Computable homological information includes the Euler characteristic, homology generators and representative cycles, higher (co)homology operations, etc. This algebraic map ϕ is described in combinatorial terms using a mixed three-level forest. Different strategies changing only two parameters of this algorithm for computing ϕ are presented. Each one of those strategies gives rise to different maps, although all of them provides the same homological information for K . For example, tree-based structures useful in image analysis like topological skeletons and pyramids can be obtained as subgraphs of this forest.

Keywords: Cell complex, chain homotopy, digital volume, homology, gradient vector field, image pyramid, tree, skeleton.

1 Introduction

A finite cell complex K is a graded set formed of cells, with an operator ∂ describing the boundary of each cell in terms of linear combination of its faces. The finite linear combination (with coefficients in $\mathbb{F}_2 = \{0, 1\}$) of cells form a graded vector space called chain complex associated to K and denoted by $C_*(K; \mathbb{F}_2)$. In [9] the solution to the homology computation problem (calculating n -dimensional holes) of K is described in the following terms: to find a concrete linear map $\phi : C_*(K; \mathbb{F}_2) \rightarrow C_{*+1}(K; \mathbb{F}_2)$, increasing the dimension by one and satisfying that $\phi\phi = 0$, $\phi\partial\phi = \phi$ and $\partial\phi\partial = \partial$. In [10], a map ϕ of this kind is called homology gradient vector field (hgvf). This datum ϕ is, in fact, a chain homotopy operator on K (a purely homological algebra notion) and it is immediate

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to establish a strong algebraic link between the cell complex associate to K and its homology groups ($H_0(K)$, $H_1(K)$, $H_2(K)$).

This approach is followed here as a solution to the homology computation problem. We will codify the deformation process ϕ to a minimal homological expression in terms of graphs. In [9] the input of the algorithm for computing homology information is a filtered finite chain complex. This input filter and the choice of a homological face for each cell-step are the two parameters of this algorithm. Different useful strategies in digital imagery (segmentation, analysis, topological skeleton, multiresolution analysis,...) can be performed running this algorithm. The final result depends on suitable choices of these two factors. Concerning the output, we will express the resulting homology gvfs of the algorithm as a three-level forest data structure which geometrically represent the underlying acyclic submodule $\text{Im } \phi = \{x \in C(K; \mathbb{F}_2) : x = \phi(y), \text{ for some } y\}$. This connectivity encoding method is susceptible to be generalized to any subdivision representation scheme, higher dimension and coefficient ring. Different modalities of this process are presented here showing its versatility.

2 Obtaining Homological Information

Some notions about algebraic topology must be introduced. A q -chain a of a three-dimensional cell complex K is a formal sum of cells of $K^{(q)}$ ($q = 0, 1, 2, 3$). Let us consider the ground ring as the finite field $\mathbf{F}_2 = \{0, 1\}$. The q -chains form a group with respect to the component-wise addition; this group is the q th 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 $\partial_q : C_q(K) \rightarrow C_{q-1}(K)$ 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, and satisfies $\partial_{q-1}\partial_q = 0$. From now on, a cell complex will be denoted by (K, ∂) . 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 q th homology group to be the quotient group of q -cycles and q -boundaries, denoted by $H_q(K)$.

Let (K, d) be a finite cell complex. A linear map of chains $\phi : C_*(K) \rightarrow C_{*+1}(K)$ 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) $\phi^2 = 0$. Removing the first condition, ϕ will be called an *algebraic gradient vector field*. An algebraic gvf satisfying the conditions $\phi d\phi = \phi$ and $d\phi d = d$ will be called a *homology gvf* [9]. If ϕ is a combinatorial gvf which is only non-null for a unique cell $a \in K_q$ and satisfying the extra-condition $\phi\partial\phi = \phi$, then it is called a (combinatorial) *integral operator* [6]. An algebraic gvf ϕ is called *strongly nilpotent* if it satisfies the following property: Given any $u \in K^{(q)}$, if $\phi(u) = \sum_{i=1}^r v_i$ then $\phi(v_i) = 0$ for all $i = 1, \dots, r$. We say that a linear map $f : C_*(K) \rightarrow C_*(K)$ is *strongly null over an algebraic gradient vector field* ϕ if given any $u \in K^{(q)}$, if $\phi(u) = \sum_{i=1}^r v_i$ then $f(v_i) = 0$ for all $i = 1, \dots, r$.

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* $(f, g, \phi) : (C, \partial) \Rightarrow (C', \partial')$ between two chain complexes as a triple of linear maps such that $f : C_* \rightarrow C'_*$, $g : C'_* \rightarrow C_*$ and $\phi : C_* \rightarrow C_{*+1}$ and they satisfy the following conditions: (a) $id_C - gf = \partial\phi + \phi\partial$; (b) $fg = id_{C'}$; (c) $f\phi = 0$; (d) $\phi g = 0$; (e) $\phi\phi = 0$. Given a chain contraction (f, g, ϕ) , elementary homological algebra results are: (a) $\text{Ker } \phi = \text{Img } \bigoplus \text{Im } \phi$ (direct sum); (b) $\text{Im } \phi$ is acyclic (i.e., it has null homology); (c) $\text{Ker } \partial = \text{Img } \bigoplus \text{Im } \partial$ (direct sum).

Proposition 1 (see [9]). *Let (K, ∂) be a finite cell complex. A homology gvf $\phi : C_*(K) \rightarrow C_{*+1}(K)$ over K gives rise to a chain contraction (π, ι, ϕ) from $C(K)$ onto its chain subcomplex isomorphic to the homology of K , where $\pi = id_{C(K)} + \phi\partial + \partial\phi$ is a projection and ι is the inclusion map. Reciprocally, if (f, g, ϕ) is a chain contraction from $C(K)$ to its homology $H(K)$, then ϕ is a homology gvf.*

Given a cell complex (K, ∂) , an ordered set of cells $\mathcal{K} = \langle c_1, \dots, c_m \rangle$ is called a *filter* for K if $\{c_1, \dots, c_m\} = \bigcup_{q \in \mathbb{Z}} K^{(q)}$, and for each $j = 1, \dots, m$, all the faces of c_j are contained in the subset $\{c_1, \dots, c_{j-1}\}$. A straightforward filter for K can be consider all the 0-cells, then all the 1-cells, and so on. Another important example is to consider a spanning tree strategy as a filter for a one-dimensional cell complex or a topological graph $G = (V, E)$. It is a classical result that the edges of $E \setminus E'$ determine the homologically different 1-cycles for G . A generalization of a spanning tree technique for higher dimensional cell complexes [11] can be applied for determining filters with interesting homological properties. The algorithm proposed in [10,9] for calculating in an incremental way a \mathbb{F}_2 -homology gvf is the following one:

Algorithm 1 (see [10,9]). *Let (K, ∂) be a finite cell complex with the filter $\mathcal{K}_m = \langle c_0, \dots, c_m \rangle$. For each $i = 0, \dots, m$, we represent the cell subcomplex of K by the filter $\mathcal{K}_i := \langle c_0, \dots, c_i \rangle$, with the boundary map ∂_i . Let \mathcal{H} be the homology chain complex (that is, a chain complex with the zero boundary map) associated to (K, ∂) .*

$\phi_0(c_0) := 0$.

For $i := 1$ to m do

 define $\bar{c}_i := c_i + \phi_{i-1}\partial_i(c_i)$

$\forall e_{s_j} \in \mathcal{K}_{i-1}$ such that $\partial_i(c_i) = \sum_{j=1}^r \lambda_j e_{s_j}$

 define $\bar{e}_{s_j} := (id_{C(\mathcal{K}_{i-1})} - \phi_{i-1}\partial_{i-1} - \partial_{i-1}\phi_{i-1})(e_{s_j}) \quad \forall j = 1, \dots, r$

$\phi_i(c_i) := 0$,

 If $\partial_i\bar{c}_i = 0$ then

 For $j := 0$ to $i - 1$ do

$\phi_i(c_j) := \phi_{i-1}(c_j)$.

 Otherwise choose an element $\bar{e}_{s_k} \neq 0$ and define $\tilde{\phi}(\bar{e}_{s_k}) := \bar{c}_i$

 and zero otherwise.

 For $j := 0$ to $i - 1$ do

$\phi_i(c_j) := (\phi_{i-1} + \tilde{\phi}(id_{C(\mathcal{K}_i)} + \phi_{i-1}\partial_i + \partial_{i-1}\phi_{i-1}))(c_j)$,

OUTPUT: a homology gradient vector field ϕ_m for K .

The key idea of this algorithm is the same as in [4]: in the i th step, the element c_i of the filter is added and a homology class is created or destroyed. Let us note that the homology of (K, ∂) is given by the set $\mathcal{H} := \text{Im}(1_{\mathcal{K}_m} + \phi_m \partial_m + \partial_m \phi_m)$.

Algorithm 1 essentially depends on two parameters (framed in the algorithm): the filter and the choice of a homological face for each cell step. Concerning the filter parameter, different orders of the cells as an input of the algorithm give rise to different homology gradient vector fields, although they all provide the same homological results. The homological face choice parameter involves the selected cell $e_{\bar{s}_k}$ used to define $\tilde{\phi}$, in order to “kill” the cell \bar{c}_i .

Focussing our interest in the output of the Algorithm 1 and based on experimental results, it can be conjectured that the underlying structure of the homology gvf ϕ_m is a suitable generalization to cell complexes of the notion of the spanning forest for a topological graph [11]. The following result is the key for determining the graph-based nature of a homology gradient vector field. This can be easily proved using induction on i .

Proposition 2. *In Algorithm 1, the homology gradient vector field ϕ_m is strongly nilpotent and the map $\pi_m = 1 + \partial\phi_m + \phi_m\partial$ is strongly null over ϕ_m . Moreover, if $\phi_m(c) = \sum_{j=1}^t \bar{c}_j$ (\bar{c}_j being a cell of K), then $\bar{c}_j = \phi_m(\bar{e}_j)$, for some $\bar{e}_j \in C(K)$ and $\forall j = 1, \dots, t$.*

In fact, these properties establishing the combinatorial nature of ϕ_m and the fact that $\text{Im}\phi_m$ is a acyclic vector subspace guarantee that ϕ in each level (levels 0,1 and 2) can be represented as a kind of spanning forest $(T(\phi_m)_0, T_1(\phi_m), T_2(\phi_m))$ for the cell complex K called homological forest of the homology gvf ϕ_m . This structure is a mixed graph in each level (that is, some edges are undirected and others are arcs). We use here the notation $e \in h(v)$, whenever the element e appears as a summand of the linear map h applied to v .

1. Let us form the forest $T_0(\phi_m) = (V_0, E_0)$ (called the vertex homological forest), in which $V_0 = V_0^0 \cup V_0^1$ (red and blue vertices of $T_0(\phi_m)$), with $V_0^0 = K_0$, $V_0^1 = \{e \in K_1 / e \in \phi(v), \text{ for some } v \in K_0\}$ and E_0 is composed of all the unordered pairs $\{v, e\}$, where v is a vertex of K appearing as a summand in the boundary of e (that is, $v \in \partial e$).
2. Let us form the forest $T_1(\phi_m) = (V_1, E_1)$ (called the edge homological forest), in which $V_1 = V_1^0 \cup V_1^1$ (red and blue vertices of $T_1(\phi_m)$), with $V_1^0 = (K_1 \setminus V_0^1)$, $V_1^1 = \{e \in K_2 / e \in \phi(v), \text{ for some } v \in V_1^0\}$ and E_1 is composed of all the unordered pairs $\{v, e\}$, where v is an edge of $V_1^0 \subset K_1$ appearing as a summand in the boundary of the 2-cell e .
3. Let us form the forest $T_2(\phi_m) = (V_2, E_2)$ (called the face homological forest), in which $V_2 = V_2^0 \cup V_2^1$ (red and blue vertices of $T_2(\phi_m)$), with $V_2^0 = (K_2 \setminus V_1^1)$, $V_2^1 = \{K_3\}$ and E_2 is composed of all the unordered pairs $\{v, e\}$, where v is a 2-cell belonging to $K_2 \setminus V_1^1$ appearing as a summand in the boundary of the 3-cell e .

The edges of the set E_i ($i = 0, 1, 2$) connect a red vertex with a blue one. Moreover, we establish an arc in $T_i(\phi_m)$ ($i = 0, 1, 2$) from the red vertex v to the blue vertex e , if $e \in \phi_m(v)$.

Proposition 3. *The filter and the homological face choice at each cell step in Algorithm 1, can be determined in order to obtain as an output a homological forest of the homology $\text{guf } \phi_m$.*

3 Homological Strategies

The versatility of Algorithm 1 is shown throughout this section. Taking into account different variations of the two parameters, useful results for segmentation, analysis, recognition, compression, etc. are presented here.

3.1 Topological Skeleton

The aim of topological thinning is to reduce the image content to its essentials. Thinning an image consists in eliminating border voxels until only a skeleton of the original image remains. We consider a border point of one direction if its adjacent point in this direction is white.

Considering a filter over the cells in a way that each step of Algorithm 1 takes a border cell c_i and one of its faces \bar{e}_{sk} satisfying some conditions: we are performing a topological thinning of the initial object. The main idea is to apply the chain homotopy operator ϕ corresponding to cell collapsing [6] on each direction of the 3D volume, reducing the initial cell complex. Applying this operator to border points satisfying some requirement, we obtain a medial axis skeleton of the 3D initial volume. This requirements can be seen as a selection of those border cells \bar{e}_{sk} which belong to a higher dimension cell c_i , being \bar{e}_{sk} a free face of c_i (non-shared with other cells). In that case we will assign $\tilde{\phi}(\bar{e}_{sk}) = c_i$.

In fact cell collapse operations are seen here from a purely algebraic point of view. Each one of them is a chain homotopy equivalence algebraically connecting the object, before and after the collapsing process. The complete thinning will be considered as a composition of these chain homotopies. In order to preserve the shape of the object, we need additional criteria for deleting points which prevent excessive shrinking.

A special kind of skeleton called Reeb graph can be also obtained using Algorithm 1. Reeb graphs are skeleton graphs that provide a way to understand the intrinsic topological structure of a shape. If we proceed filtering the volume by subdividing it into 2 dimensional slices, the minimum homological representation of each connected component in the slice will be the result of applying the

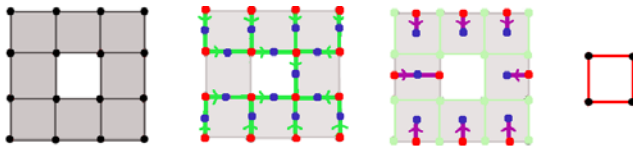


Fig. 1. Topological skeleton strategy showing the T_0 and T_1 forests and the skeleton

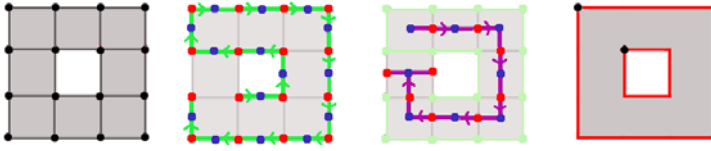


Fig. 2. Segmentation-based strategy showing the T_0 and T_1 forests and the final result

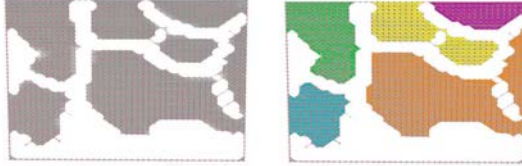


Fig. 3. Segmentation based on connected components of a trabecular bone volume (courtesy of the Institute of Biomechanics, Zurich, Swiss)

algorithm to this 2D images. After processing all the cells belonging to each slice, cells joining different slices will be taken into account. These cells will join each graph with its correspondences (same connected component) in the slices above and below. The result is the Reeb graph with loops codifying the topological structure of the volume.

3.2 Segmentation Strategy

The goal of segmentation is to partition the image into regions with homogeneous properties. A segmentation of an initial volume V can be achieved using the homology gvf algorithm. The filter restrictions used for this aim, is completely different to the one used in Section 1. In this case inner cells of the complex will be included in the algorithm before the ones in the border. Selecting a shared-face \bar{e}_{s_k} of an inner cell c_i and considering $\tilde{\phi}(\bar{e}_{s_k}) = c_i$, the resultant complex after this iteration will contain a cell which is the merge of both cells sharing u_s .

Repeating this process until no more inner cells exists on the complex, the final result will be a big cell which is the result of merging all the cells belonging to the same region. This segmentation can be done in terms of different criterions, like connected components, color segmentation, etc. An example of this algorithm segmenting a 3-dimensional image is shown in Fig. 3.

3.3 Topological Pyramids

Image Pyramids are hierarchical structures widely used in Image Analysis [1]. They are made of multiple copies of the same cellular structure, in which the number of cell is reduced from copy to copy (levels of the pyramid). Irregular

graph pyramids are defined as a stack of successively reduced graphs [8] where each level represents an arbitrary partition of the pixel set into cells. An image is transformed into a graph such that, for each pixel a vertex is associated, and pixels that are neighbors are joint by an edge. The graph which represent the pixels is denoted by $G = (V, E)$. It is called *primal graph* and it divides the plane into faces. Let denote each face by a new vertex and connect the faces that are neighbors (sharing the same edge) by a new edge. These vertices and edges added, compose a new graph \overline{G} , which is the *dual graph* of G . The edges of \overline{G} represent the borders of the cells of G , including so called pseudo edges needed to represent neighborhood relations to a cell completely enclosed by another cell. A level of a dual graph pyramid consists of a pair (G_k, \overline{G}_k) of plane graphs, in order to represent the embedding of the graph in the plane. A cell on level $k + 1$ (parent) is a union of neighboring cells on level k (children). Every parent computes its values independently of other cells on the same level. The union of cells is controlled by so called contraction kernels and the only operations used are removal and contraction [8]. The contraction operation is defined informally as the removal of the i -cell and the merging of two $(i - 1)$ -cells, effectively removing one of these $(i - 1)$ -cells. E.g. when contracting an edge, the two bounding vertices of this edge are merged into a single vertex, removing one of the vertices. The connecting edge is also removed in the process. Because a contraction operation merges two $(i - 1)$ -cells, only cells of dimension $i \geq 1$ may be contracted. Intuitively and in a general way for an n -dimensional space, the removal of an i -cell consists in removing this cell and in merging its two incidents $(i + 1)$ -cells: so removal can be defined for $0 \dots (n - 1)$ -cells. According to [2],[3] the removal operation is the dual counterpart to a contraction.

As mentioned in [5], the two operations used to construct an irregular graph pyramid are integral operators satisfying the chain-homotopy property. Following this lemma, an irregular graph pyramid can be directly built using Algorithm 1. We can combine one of the existing algorithms for constructing an image pyramid [7], but updating at each step the resulting gvf following Algorithm 1. For example, given two cells c_i and c_j sharing a face u_s , and defining $\tilde{\phi}(u_s) = c_i$, the cell u_s will be removed and c_i and c_j will be merged, performing in that way a removal operation. Similar situation occurs with cell contractions. The advantage of using this algorithm for building a pyramid is the complete topological control during the whole process, and the possibility of directly compute topological invariants at each level of the pyramid.

4 Conclusions and Future Work

Roughly speaking, in order to progress in homological knowledge for a finite cell complex, we determine here two operators on $C_*(K; \mathbb{F}_2)$: a boundary operator, $\partial : C_*(K; \mathbb{F}_2) \rightarrow C_{*-1}(K; \mathbb{F}_2)$, decreasing the dimension by one and measuring in algebraic terms the boundary of any set of cells; and a ‘‘coboundary’’ operator $\phi : C_*(K; \mathbb{F}_2) \rightarrow C_{*+1}(K; \mathbb{F}_2)$, increasing the dimension by one and measuring in some sort the degree of acyclicity (a space is acyclic is it has the same homology than a point) of any set of cells. In particular, we have seen that the

map $1_K + \partial\phi + \phi\partial$ applied to every cell provides us representative cycles for all the homology generators of K . In fact, having this information at hand, it is possible to compute finer topological invariants for K (relations between the homology generators, cohomology algebra, (co)homology operations, ...) as well as partially or full homologically equivalent graph features (topological skeletons, Reeb graphs, contraction kernels, ...). In combinatorial terms, we specify for the acyclicity operator ϕ a homological forest. As future work, we plan to explore the possibilities of this forest for 3D and 4D geo-topological (saving essential geometric and topological information) representation as well as its robustness with regards to small changes (deformation, noise,...) in the object.

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