Computing Homology Group Generators of Images Using Irregular Graph Pyramids[⋆]

S. Peltier[1], W.G. Kropatsch[1], A. Ion[1], Y. Haxhimusa[1], and G. Damiand[2]

[1] Vienna University of Technology, Faculty of Informatics,
Pattern Recognition and Image Processing Group, Austria
{sam,krw,ion,yll}@prip.tuwien.ac.at
[2] University of Poitiers
SIC, FRE CNRS 2731, France
damiand@sic.univ-poitiers.fr

Abstract. We introduce a method for computing homology groups and their generators of a 2D image, using a hierarchical structure i.e. irregular graph pyramid. Starting from an image, a hierarchy of the image is built, by two operations that preserve homology of each region. Instead of computing homology generators in the base where the number of entities (cells) is large, we first reduce the number of cells by a graph pyramid. Then homology generators are computed efficiently on the top level of the pyramid, since the number of cells is small, and a top down process is then used to deduce homology generators in any level of the pyramid, including the base level i.e. the initial image. We show that the new method produces valid homology generators and present some experimental results.

1 Introduction

Handling 'structured geometric objects' is important for many applications related to geometric modeling, computational geometry, image analysis, etc. One has often to distinguish between different parts of an object, according to properties which are relevant for the application. For image analysis, a region is a (structured) set of pixels or voxels, or more generally a (structured) set of lower-level regions. At the lowest level of abstraction, such an object is a subdivision[3], i.e. a partition of the object into cells of dimension 0, 1, 2, 3 ... (i.e. vertices, edges, faces, volumes ...) [1, 2]. In general, combinatorial structures (graphs, combinatorial maps, nG-maps etc.) are used to describe objects subdivided into cells of different dimensions. The structure of the object is related to the decomposition of the object into sub-objects, and to the relations between these sub-objects: basically, topological information is related to the cells and their adjacency or incidence relations. Further information (embedding information) is associated to these sub-objects, and describe for instance their shapes (e.g. a point, respectively a curve, a part of a surface, is associated with each vertex, respectively each edge, each face), their textures or colors, or other information depending

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[3] For instance, a Voronoi diagram in the plane defines a subdivision of the plane.
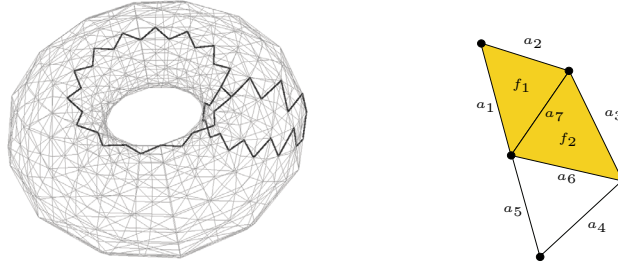
Fig. 1. (a) : a triangulation of the torus. (b) : a simplicial complex made of 1 connected component and containing one $1-$dimensional hole.

on the application. A common problem is to characterize structural (topological) properties of handled objects. Different topological invariants have been proposed, like Euler characteristics, orientability, homology,... (see [3]).

Homology is a powerful topological invariant, which characterizes an object by its "$p-$dimensional holes". Intuitively the $0-$dimensional holes can be seen as connected components, $1-$dimensional holes can be seen as tunnels and $2-$dimensional holes as cavities. For example, the torus (see Fig.1(a)) contains one $0-$dimensional hole, two $1-$dimensional holes (each of them are an edge cycle) and one $2-$dimensional hole (the cavity enclosed by the entire surface of the torus). This notion of $p-$dimensional hole is defined in any dimension. Another important property of homology is that local calculations induce global properties. In other words, homology is a tool to study spaces, and has been applied in image processing for 2D and 3D images analysis [4]. Although we use 2D binary image in this paper to show the proof of concept, we do not encourage usage of homology groups and generators to find connected components in 2D image, since efficient approaches already exist [5]. However, these 'classical' approaches cannot be easily extended for many problems that exist in higher dimensions, since our visual intuition is inappropriate and topological reasoning becomes important. Computational topology has been used in metallurgy [6] to analyze 3D spatial structure of metals in an alloy and in medical image processing [7] in analyzing blood vessels. In higher dimensional problems (e.g. beating heart represented in 4D) the importance of homology groups and generators becomes clear in analyzing objects (its number of connected components, tunnels, holes, etc) in these spaces, because of the nice and clean formulations which hold in any dimension. One can think of other applications as a preprocessing step to speed up recognition of complex shapes in large image databases, e.g. images are first filtered based on their topological invariants and afterward are matched using shapes, appearances, etc.

The usage of homology groups and generators in image processing is a new topic and is not widely spread. In this paper we introduce a new method for computing homology groups and their generators using a hierarchical structure

which is build by using two operations: contraction and removal. These two operations are used also in [8] to compute incrementally homology groups and their generators of 2D closed surfaces, but a hierarchy is not build.

The paper is structured as follows. Basic notions on homology and irregular graph pyramids are recalled in Section 2 and Section 3. The proposed method to compute homology groups and their generators is presented in detail in Section 4. Experimental results on 2D images that show the correctness of the new method are found in Section 5.

2 Homology

In this part, the basic homology notions of chain, cycle, boundary, and homology generator are recalled. Interested readers can find more details in [9].

The homology of a subdivided object X can be defined in an algebraic way by studying incidence relations of its subdivision. Within this context, a cell of dimension p is called a $p-$cell and the notion of $p-chain$ is defined as a sum $\sum_{i=1}^{nb\ p-cells} \alpha_i c_i$, where c_i are $p-$cells of X and α_i are coefficients assigned to each cell in the chain. Homology can be computed using any group $\mathfrak{A}$ for the coefficients α_i. But, the theorem of universal coefficients [9] ensures that all homological information can be obtained by choosing $A = \mathbb{Z}$. It is also known [9] that for nD objects embedded in $\mathbb{R}^D$, homology information can be computed considering simply chains with moduli 2 coefficients ($A = \mathbb{Z}/2\mathbb{Z}$). Note that in this case, a cell that appears twice on a chain vanishes, because $c + c = 0$ for any cell c when using moduli 2 coefficients ($i.e.$ if a cell appears even times we discard it otherwise we keep it). In the following, only chains with coefficients over $\mathbb{Z}/2\mathbb{Z}$ will be considered. Note that the notion of chain is purely formal and the cells that compose a chain do not have to satisfy any property. For example, on the simplicial complex illustrated on Fig.1(b) the sums: $a_1 + a_4$, a_3 and $a_2 + a_7 + a_4$ are 1−chains.

For each dimension $p = 0, \ldots, n$, where $n = dim(X)$, the set of $p-$chains forms an abelian group denoted C_p. The $p-$chain groups can be put into a sequence, related by applications ∂_p describing the boundary of $p-$chains as $(p-1)-$chains:

$$ C_n \xrightarrow{\partial_n} C_{n-1} \xrightarrow{\partial_{n-1}} \cdots \xrightarrow{\partial_1} C_0 \xrightarrow{\partial_0} 0, $$

which satisfy $\partial_p \partial_{p-1}(c) = 0$ for any $p-$chain c. This sequence of groups is called a *free chain complex*.

The boundary of a $p-$chain reduced to a single cell is defined as the sum of its incident $(p-1)-$cells. The boundary of a general $p-$chain is then defined by linearity as the sum of the boundaries of each cell that appears in the chain e.g. in Fig.1(b), $\partial(f_1 + f_2) = \partial(f_1) + \partial(f_2) = (a_1 + a_2 + a_7) + (a_7 + a_3 + a_6) = a_1 + a_2 + a_3 + a_6$. Note that as mentioned before, chains are considered over $\mathbb{Z}/2\mathbb{Z}$ coefficients i.e. any cell that appears twice vanishes.

For each dimension p, the set of p-chains which have a null boundary are called p-*cycles* and are a subgroup of C_p, denoted Z_p e.g. $a_1 + a_2 + a_7$ and $a_7 + a_5 + a_4 + a_3$ are 1−cycles. The set of p-chains which bound a $p+1$-chain are

Table 1. Translation of homology notions to graph theory.

Homology theory	Graph theory
0-cell, 1-cell, 2-cell	vertex, edge, face
0-chain, 1-chain, 2-chain	set of vertices, set of edges, set of faces
0-cycle, 1-cycle, 2-cycle	set of vertices, closed path of edges, closed path of faces

called *p-boundaries* and they are a subgroup of C_p, denoted B_p e.g. $a_1 + a_2 + a_7 = \partial(f_1)$ and $a_1 + a_6 + a_3 + a_2 = \partial(f_1 + f_2)$ are $1-$boundaries.

According to the definition of a free chain complex, the boundary of a boundary is the null chain. Hence, this implies that any boundary is a cycle. Note that according to the definition of a free chain complex, any $0-$chain has a null boundary, hence every $0-$chain is a cycle.

The pth homology group, denoted H_p, is defined as the quotient group Z_p/B_p. Thus, elements of the homology groups H_p are equivalence classes and two cycles z_1 and z_2 belong to the same equivalence class if their difference is a boundary (*i.e.* $z_1 = z_2 + b$, where b is a boundary). Such two cycles are called *homologous* e.g. let $z_1 = a_5 + a_4 + a_3 + a_7$, $z_2 = a_5 + a_4 + a_6$ and $z_3 = a_1 + a_2 + a_3$; z_1 and z_2 are homologous ($z_1 = z_2 + \partial(f_2)$) but z_1 and z_2 are not homologous to z_3. Let H_p be a homology group generated by q independent equivalence classes $\mathcal{C}_1, \cdots, \mathcal{C}_q$, any set $\{h_1, \cdots, h_q \mid h_1 \in \mathcal{C}_1, \cdots, h_q \in \mathcal{C}_q\}$ is called a *set of generators* for H_p. For example, either $\{z_1\}$ or $\{z_2\}$ can be chosen as a generator of H_1 for the object represented in Fig.1(b).

Note that some of the notions mentioned before could be confused with similar notions from graph theory. Tab.1 associates these homology notions with notions classically used in graph theory.

3 Irregular Graph Pyramids

In this part, basic notions of pyramids like receptive field, contraction kernel, and equivalent contraction kernel, are introduced. For more details see [10].

A pyramid (Fig. 2a) describes the contents of an image at multiple levels of resolution. A high resolution input image is at the base level. Successive levels reduce the size of the data by a *reduction factor* $\lambda > 1.0$. The *reduction window* relates one cell at the reduced level with a set of cells in the level directly below. The contents of a lower resolution cell is computed by means of a *reduction function* the input of which are the descriptions of the cells in the reduction window. Higher level descriptions should be related to the original input data in the base of the pyramid. This is done by the *receptive field* (RF) of a given pyramidal cell c_i. The RF(c_i) aggregates all cells (pixels) in the base level of which c_i is the ancestor.

Each level represents a partition of the pixel set into cells, *i.e. connected subsets of pixels*. The construction of an irregular pyramid is iteratively local [11]. On the base level (level 0) of an irregular pyramid the cells represent single pixels and the neighborhood of the cells is defined by the 4(8)-connectivity of the

pixels. A cell on level $k + 1$ (parent) is a union of neighboring cells on level k (children). This union is controlled by so called *contraction kernels* (CK) [12], a spanning forest which relates two successive levels of a pyramid. Every parent computes its values independently of other cells on the same level. Thus local independent (and parallel) processes propagate information up and down and laterally in the pyramid. Neighborhoods on level $k + 1$ are derived from neighborhoods on level k. Higher level descriptions are related to the original input by the *equivalent contraction kernels* (ECK). A level of the graph pyramid consists of a pair $(G_k, \overline{G_k})$ of plane graphs G_k and its geometric dual $\overline{G_k}$ (Fig. 2b). The vertices of G_k represent the cells on level k and the edges of G_k represent the neighborhood relations of the cells, depicted with square vertices and dashed edges in Fig. 2b. The edges of $\overline{G_k}$ represent the borders of the cells on level k, solid lines in Fig. 2b, including so called pseudo edges needed to represent neighborhood relations to a cell completely enclosed by another cell. Finally, the vertices of $\overline{G_k}$ (circles in Fig. 2b), represent junctions of border segments of $\overline{G_k}$. The sequence $(G_k, \overline{G_k})$, $0 \leq k \leq h$ is called irregular (dual) graph pyramid. For simplicity of the presentation the dual $\overline{G}$ is omitted afterward.

4 Computing Homology Generators in a Graph Pyramid

There exists a general method for computing homology groups. This method is based on the transformation of incidence matrices [9] (which describe the boundary homomorphisms) into their reduced form called *Smith normal form*. Agoston proposes a general algorithm, based on the use of slightly modified Smith normal form, for computing a set of generators of these groups [3]. Even if Agoston's algorithm is defined in any dimension, the main drawback of this method is directly linked to the complexity of the reduction of an incidence matrix into its Smith normal form, which is known to consume a huge amount of time and space. Another well known problem is the possible appearance of huge integers during the reduction of the matrix. A more complete discussion about Smith normal algorithm complexity can be found in [13]. Indeed, Agoston's algorithm cannot directly be used for computing homology generators and different kinds of optimisations have been proposed.

Based on the work of [14, 15], an optimisation for the computation of homology generators, based on the use of sparse matrices and moduli operations has

a) Discrete levels   b) Image to dual graphs
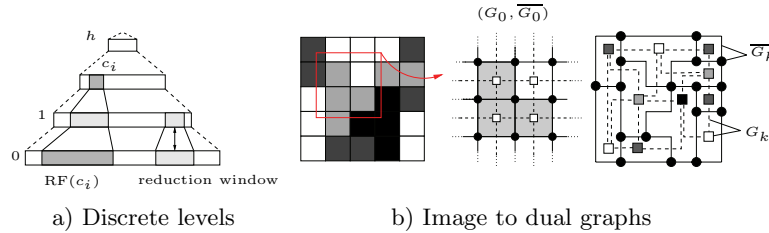
Fig. 2. a) Pyramid concept, and b) representation of the cells and their neighborhood relations by a dual pair of plane graphs at the level 0 and k of the pyramid.

been proposed [16]. This method avoids the possible appearance of huge integers. The authors also observed an improvement of time complexity dropping from $O(n^2)$ to $O(n^{5/3})$, where n is the number of cells of the subdivision.

An algorithm for computing the rank of homology groups *i.e.* the Betti numbers has been proposed in [17]. The main idea of this algorithm is to reduce the number of cells of the initial object in order to obtain a homologically equivalent object, made of less cells. In some special cases (orientable objects), Betti numbers can directly be deduced from the resulting object. However, this method cannot directly provide a set of generators. Based on the previously mentioned work, an algorithm for computing a minimal representation of the boundary of a 3D voxel region, from which homology generators can directly be deduced has been defined in [8].

### 4.1 Description of the new method

The method we propose in this paper has the same philosophy as the methods of Kaczynski and Damiand [19, 18]: reducing the number of cells of an object for computing homology. Moreover, we keep all simplifications that are computed during the reduction process by using a pyramid. In this way, homology generators can be computed in the top level of the pyramid, and can be used to deduce generators of any level of the pyramid. In particular, we show how generators of the higher level can be directly down-projected on the desired level (using equivalent contraction kernels).

Starting from an initial image, we build an irregular graph pyramid. The method we provide here is valid as long as the algorithm used for the construction of the pyramid preserves homology. In particular, we show here that the decimation by contraction kernels, described in section 3 [12], preserves homology of a subdivided object. Indeed, homology of the initial image can thus be computed in any level of the pyramid, and in particular in the top level where the object is described with the smallest number of cells.

Moreover, we use the notion of receptive field and equivalent contraction kernel, and show that the generators of homology groups of any level of the pyramid can be deduced from those computed on the higher level. Note that in special cases, the higher level of the pyramid may be reduced to exactly a set of generators of the initial image, as shown in [8].

Our method can be summarized in the following steps :

1 Starting from a labeled image, a graph pyramid $\{G_0, G_1, \ldots, G_k\}$ is built using contraction kernels of cells with the same label.
2 Homology groups generators are computed for G_k, using Agoston's method.
3 Homology generators of any level i can be deduced from those of level $i + 1$ using the contraction kernels. In particular, we obtain the homology generators of the initial image.
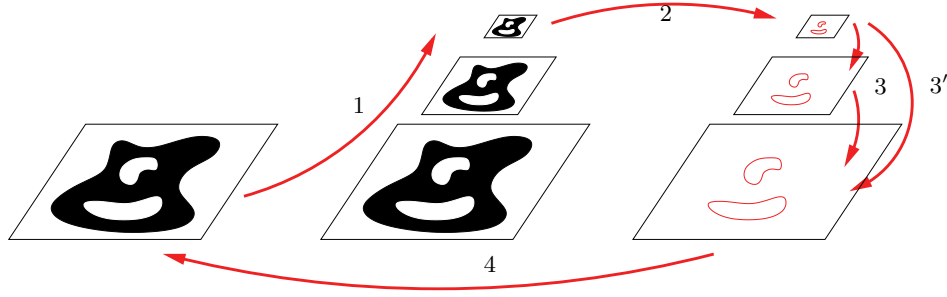
Fig. 3. Computing generators of homology groups using an image pyramid.

Note that homology generators of the lowest level can directly be deduced from the highest level using the notion of equivalent contraction kernel (arrow $3'$ in Fig.3). Fig.3 illustrates the general method that we propose for computing homology generators of an image.

4.2 Preserving homology on irregular graph pyramids

The algorithm described in [17] is based on operations of *interior face reduction* that reduce the number of cells of the subdivision. The main idea is to find a $p-$cell a and a $(p+1)-$cell b, such that a is incident to b. Then a and b are removed and the boundary of the other $p-$cells that were adjacent to a are modified such that the new boundary $\partial(b')$ is defined as its initial boundary added with the boundary of b. Indeed, if a is incident to exactly two $p-$cells b and b', the result of the corresponding interior face reduction can be seen as the removal of a and the merging of b and b'. It is proved in [17] that interior face reduction preserves homology.

Observing the dual graph, the operations of contraction and removal that are used to build each level of the pyramid are interior face reduction: two faces that are merged share a common edge that is removed, and an edge is contracted if one of its endpoints is incident to exactly two different edges. Thus, homology is preserved in every level of the pyramid.

4.3 Delineating Generators

A $1D$ generator in $\overline{G}_k = (\overline{V}_k, \overline{E}_k)$ is a closed path connecting vertices of $\overline{G}_k$ and surrounding at least one hole. Each vertex $\overline{v} \in \overline{G}_k$ is the result of contracting a tree (contraction kernel $\overline{CK}$) of $\overline{G}_{k-1}$. Each edge $(\overline{v}_1, \overline{v}_2) \in \overline{G}_k$ corresponds to a surviving edge $(\overline{w}_1, \overline{w}_2) \in \overline{G}_{k-1}$ with $\overline{w}_1 \in \overline{CK}_{k-1}(\overline{v}_1)$ and $\overline{w}_2 \in \overline{CK}_{k-1}(\overline{v}_2)$ i.e. one that has neither been contracted nor removed[4].

Given a generator in $\overline{G}_k$, mapping it to the level below is done by identifying the surviving edges in $\overline{G}_{k-1}$ corresponding to the generator edges in $\overline{G}_k$ and,

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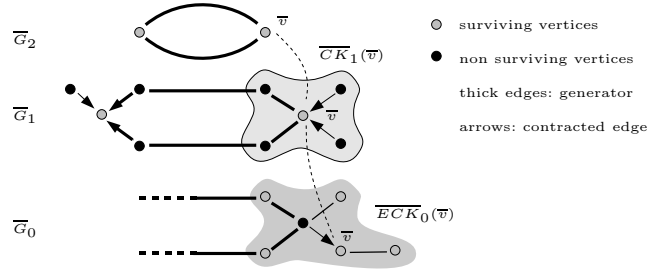[4] Not part of any simplification.

Fig. 4. Top-down delineation of a generator computed in $\overline{G}_2$.

where the generator is disconnected, adding paths to fill in the gaps and reconnect. For every two consecutive edges not having a common vertex in $\overline{G}_{k-1}$ but having one in $\overline{G}_k$, the unique path connecting their disconnected endpoints in the contraction kernel $\overline{CK} \subset \overline{G}_{k-1}$ of their shared vertex in $\overline{G}_k$ is added.

Because each path added in $\overline{G}_{k-1}$ is entirely part of a contraction kernel, with contraction being used in the dual only for boundary simplification purposes, never connecting two different boundaries, and because the building process preserves homology (see Sec. 4.2) the obtained generators will be homologous to the ones in $\overline{G}_k$.

Reiterating this process of mapping the generator cycles of $\overline{G}_k$ from k to $k-1, \dots$ to 0, cycles in $\overline{G}_0$ corresponding to the generators of the top level can be identified. By replacing the contraction kernels, with the equivalent contraction kernels, using the same methodology, the generator cycles of $\overline{G}_k$ can be directly mapped to $\overline{G}_0$. For an example, see Fig. 4.

5 Experiments on 2D Images

We present and discuss initial experiments that have been performed on 2D binary shapes. For each shape, we have computed homology generators directly on the initial image, and on the top level of the pyramid.

Tab.2 shows the number of $0D$, $1D$ and $2D-$cells on the initial image, and on the top level of the pyramid for the shape presented on Fig.5 and Fig.6. One can observe that for each shape the total number of cells is considerably reduced on the higher level of the pyramid. Thus, the computation of homology generators can be done on very smaller matrices on the top level instead of the initial image.

In Fig.5 and Fig.6, it can be seen that our new method provides a valid set of generators in each case.

Moreover, using the classical method, we cannot have any control of the the geometry of the generators computed. More precisely, the aspect of the obtained generators are directly linked to the construction of incidence matrices, which is determined by the scanning of each cell of the initial image. The shape shown on Fig.7 has been obtained from rotating Fig.5. In Fig.7(a), one can observe that the aspect of the generators computed on the initial image "follows" the

(a)   (b)
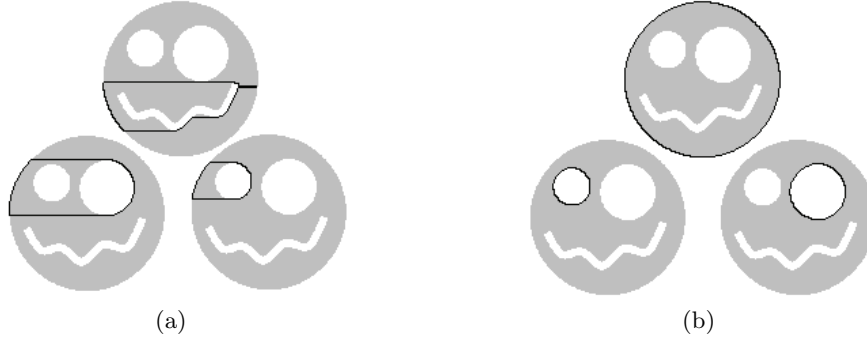
Fig. 5. (*a*): the homology generators computed on the initial image. (*b*): the down-projected generator.

scanning of the cells (from top to bottom, and left to right). The generators obtained in Fig.7(b) always fit on the boundaries of the image. It is proved in [20] that any generator computed with our new method will always fit on some boundaries of the initial image.

One can note that the set of cycles obtained in Fig.5(a) and Fig.5(b) do not surround the same (set of) $1D-$holes of the shape S. Indeed, these two sets are two different basis of the same group $H_1(S)$: let a, b and c denote the equivalence class of cycles that surround respectively the left eye, the right eye, and the mouth. The set of generators in Fig.5(a) describe $H_1(S)$ in the basis $\{a+b, c, a\}$ whereas in Fig.5(b), $H_1(S)$ is described in the basis $\{a, a+b+c, b\}$.

6   Conclusion

We have presented a new method for computing homology groups of images and their generators, using irregular graph pyramids. The homology generators are computed efficiently on the top level of the pyramid, since the number of

Table 2. The number of cells on the initial image and on the top of the pyramid.

	Initial image			Top of the pyramid		
	0D-cells	1D-cells	2D-cells	0D-cells	1D-cells	2D-cells
Fig.5.	8153	15785	7630	7	10	1
Fig.6	10352	20148	9793	9	13	1
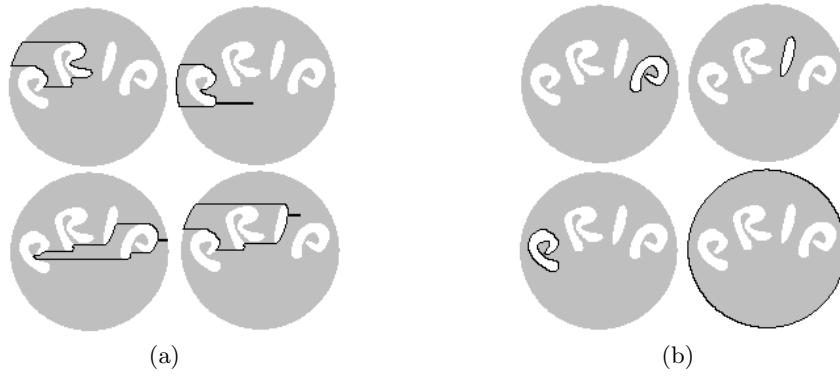
Fig. 6. (*a*): the homology generators computed on the initial image. (*b*): the down-projected generator.
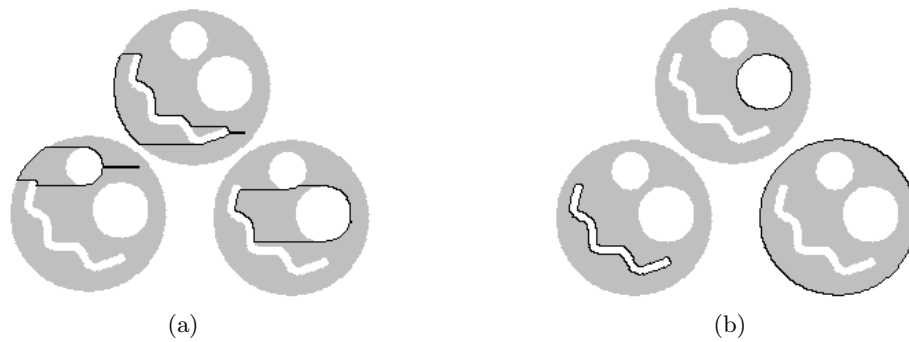
Fig. 7. Influence of the scanning.

cells is small, and a top down process (down-projection) delineates the homology generators of the initial image. Some preliminary results have been shown for 2D binary images. We have also observed that the generators computed with this new method seem to stay on boundaries.

In a future work, we plan to extend this method to 3D and nD images, using the (already existing) structures of 3D and nD irregular pyramids. We also plan to use the property that down-projected generators always fit on boundaries in order to use homology generators for object matching and object tracking.

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