

Visualisation du calcul de l'homologie

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Structure

- 1 Le problème
 - L'homologie
 - La théorie discrète de Morse
- 2 Notre approche
- 3 Applications
 - Les squelettes et les « jolis » générateurs
 - Le calcul de l'homologie assisté par l'utilisateur
- 4 Conclusion

Les groupes d'homologie

Pour $q \geq 0$,

$$\begin{aligned} H_q &= \ker (d_q) / \text{im} (d_{q+1}) \\ &= \{[x] : x \text{ est un cycle}\} \end{aligned}$$

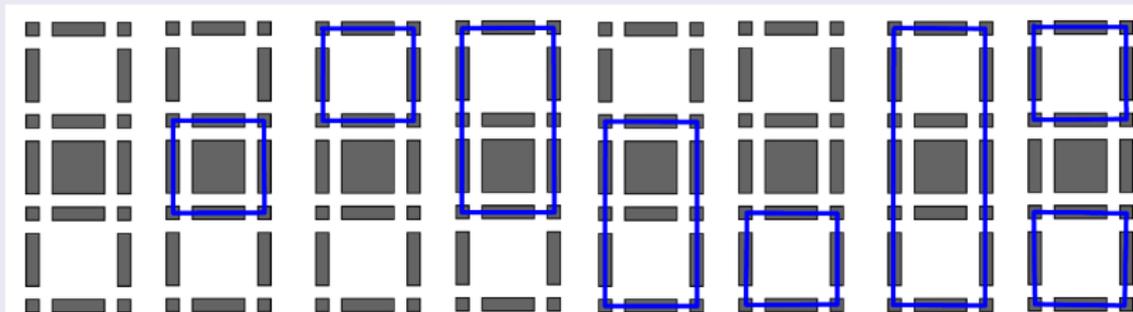
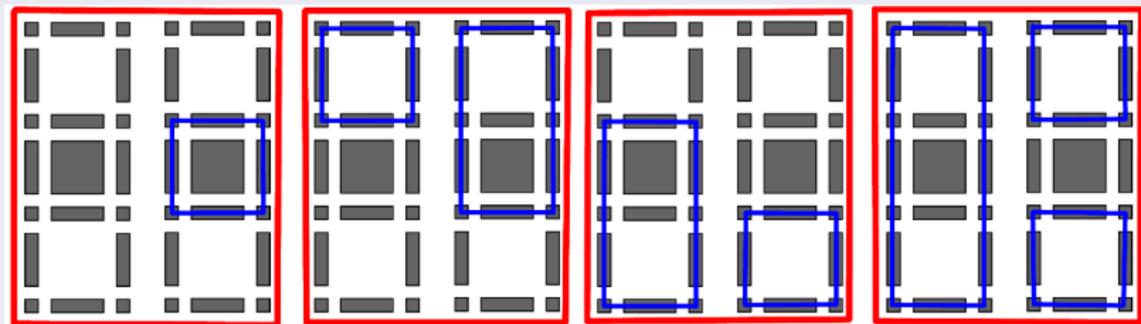
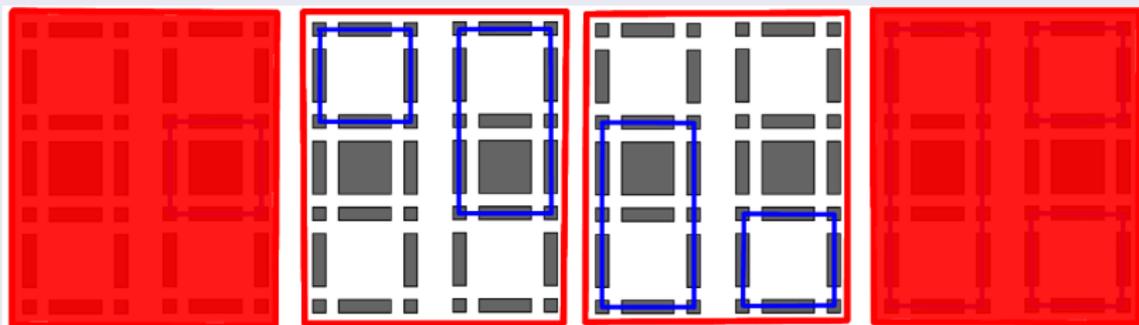
Exemple : groupe d'homologie H_1 

Figure : Cycles de dimension 1

Exemple : groupe d'homologie H_1 Figure : Éléments de H_1

Exemple : groupe d'homologie H_1 Figure : Générateurs de H_1 : il y a deux trous

Les nombres de Betti

- $H_0 \longrightarrow \beta_0 = \dim(H_0) =$ "nombre de composantes connexes"
- $H_1 \longrightarrow \beta_1 = \dim(H_1) =$ "nombre de tunnels ou anses"
- $H_2 \longrightarrow \beta_2 = \dim(H_2) =$ "nombre de cavités"

Comment calculer les groupes d'homologie :

- La Forme Normale de Smith (FNS)
- Théorie discrète de Morse + FNS

DGVF

Un discrete gradient vector field (DGVF) est un couplage "acyclique" sur le diagramme de Hasse du complexe.

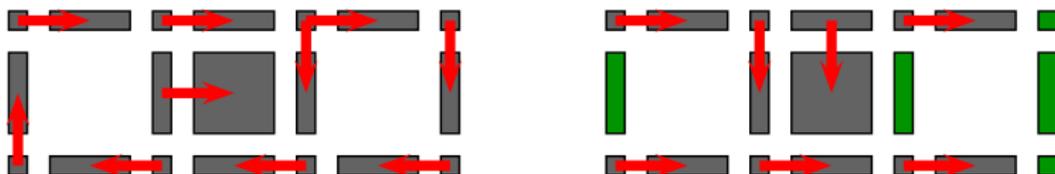


Figure : Gauche : ce n'est pas un DGVF. Droite : c'est un DGVF.

Une cellule est critique si elle n'appartient pas au couplage.

Théorème

Soit μ_q le nombre de q -cellules critiques,

$$\mu_q \geq \beta_q, \text{ pour tout } q \geq 0$$

Cela donne une approximation.

Une cellule est critique si elle n'appartient pas au couplage.

Théorème

Soit μ_q le nombre de q -cellules critiques,

$$\mu_q \geq \beta_q, \text{ pour tout } q \geq 0$$

Cela donne une ~~approximation~~ réduction.

Un DGVF induit un complexe réduit :



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Le problème

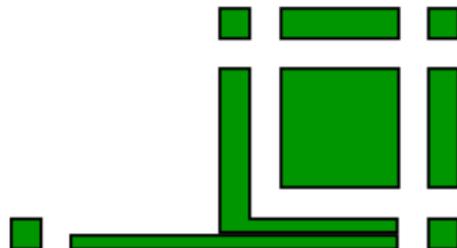
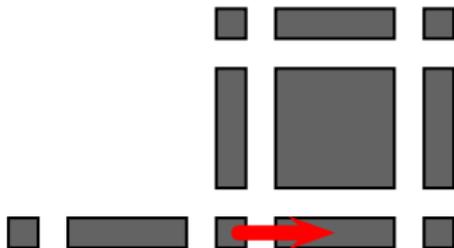
Ne peut-on pas mieux visualiser cela ?

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On peut trouver deux problèmes :

1 Chevauchement de cellules



2 La dissimilarité de la forme du complexe réduit

Algorithm 1 CellClustering

Require: K a CW-complex.**Ensure:** \mathcal{V} a DGVF.

```

1:  $\mathcal{V}, \text{FinalCells} \leftarrow \emptyset$ 
2: for  $q = \dim(K), \dots, 1$  do
3:    $\text{BlockedCells} \leftarrow \{\sigma \in Cr_{q-1} : \#d_{|Cr_{q-1}}^*(\sigma) \neq 2\}$ 
4:   repeat
5:     Take any critical  $q$ -cell  $\gamma$  not in FinalCells
6:      $\text{FinalCells} \leftarrow \gamma$ 
7:      $\mathcal{V} \leftarrow \text{spread}(\mathcal{V}, \gamma, \text{FinalCells}, \text{BlockedCells})$ 
8:   until idempotency
9: end for
10: return  $\mathcal{V}$ 

```

Algorithm 2 spread

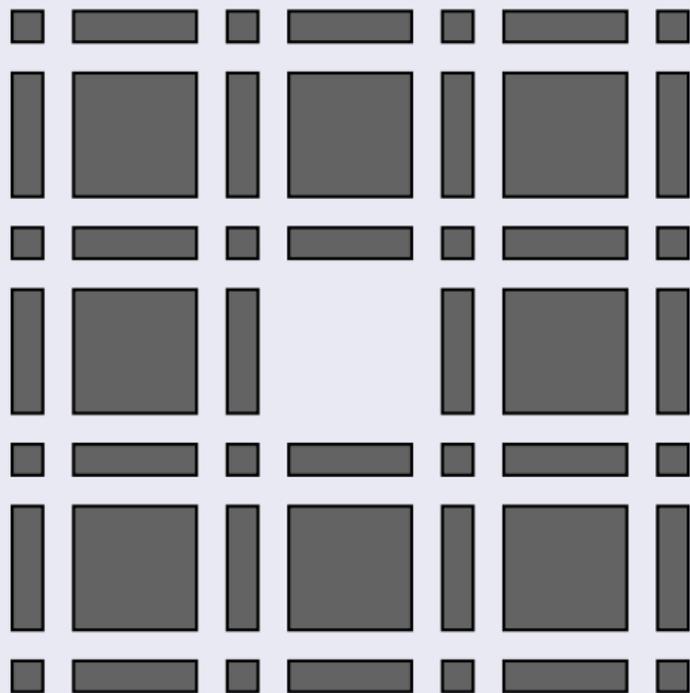
Require: \mathcal{V} a DGVF, $\gamma \in K$, FinalCells, BlockedCells $\subset K$ **Ensure:** \mathcal{V}' an extension of \mathcal{V}

```

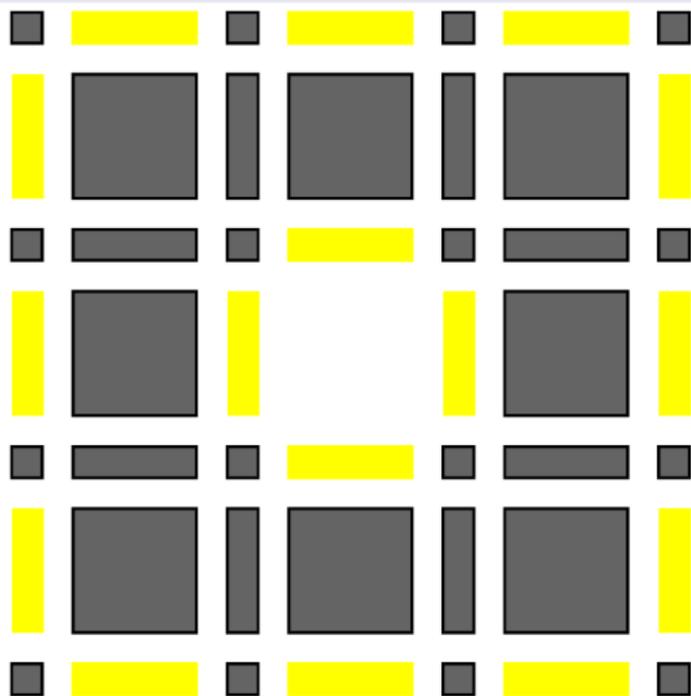
1:  $\mathcal{V}' \leftarrow \mathcal{V}$ 
2:  $Q \leftarrow \{\gamma\}$  queue
3: while  $Q \neq \emptyset$  do
4:    $\sigma \leftarrow Q$ 
5:   if  $\sigma$  is critical and  $\sigma \notin \text{BlockedCells}$  then
6:     if  $\sigma$  has only one critical coface  $\tau$  not in FinalCells then
7:        $\mathcal{V}' \leftarrow (\sigma, \tau)$ 
8:        $Q \leftarrow d_{|Cr}(\sigma), d_{|Cr}(\tau)$ 
9:     end if
10:  end if
11: end while
12: return  $\mathcal{V}'$ 

```

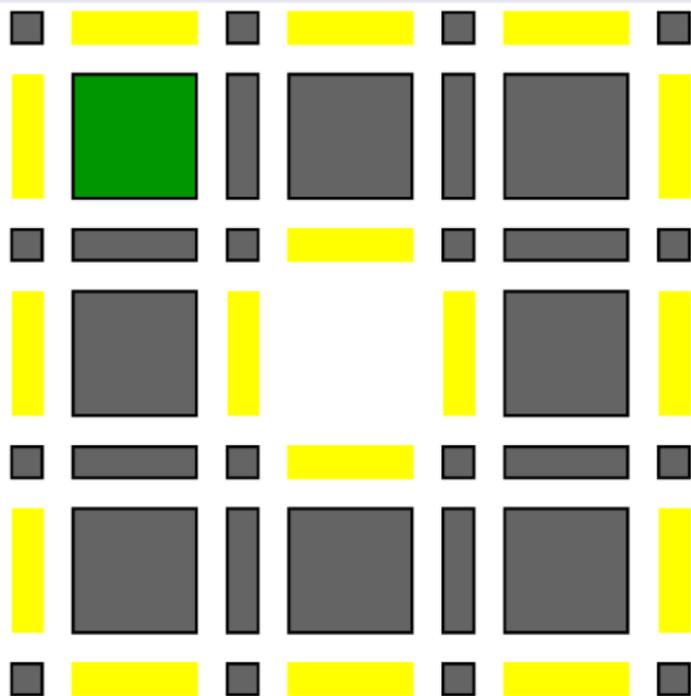
Exemple : CellClustering



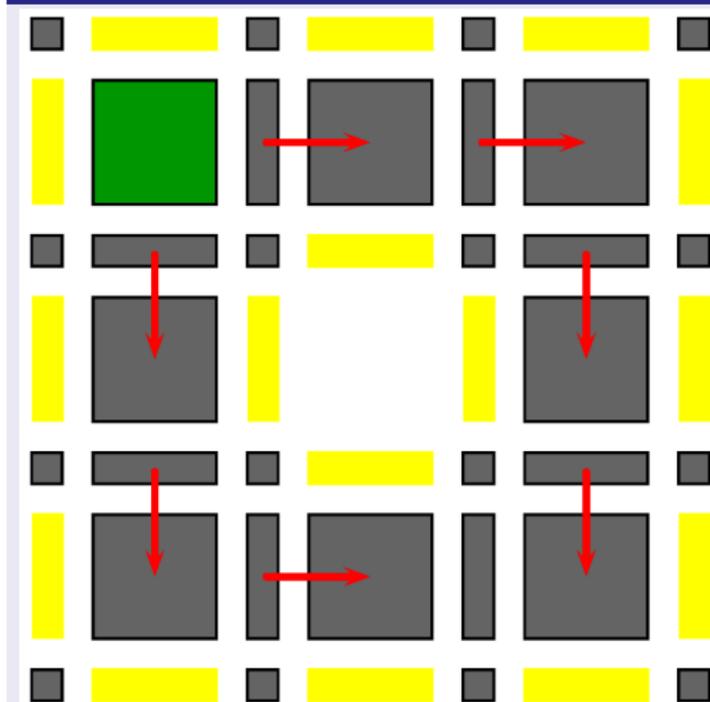
Exemple : CellClustering



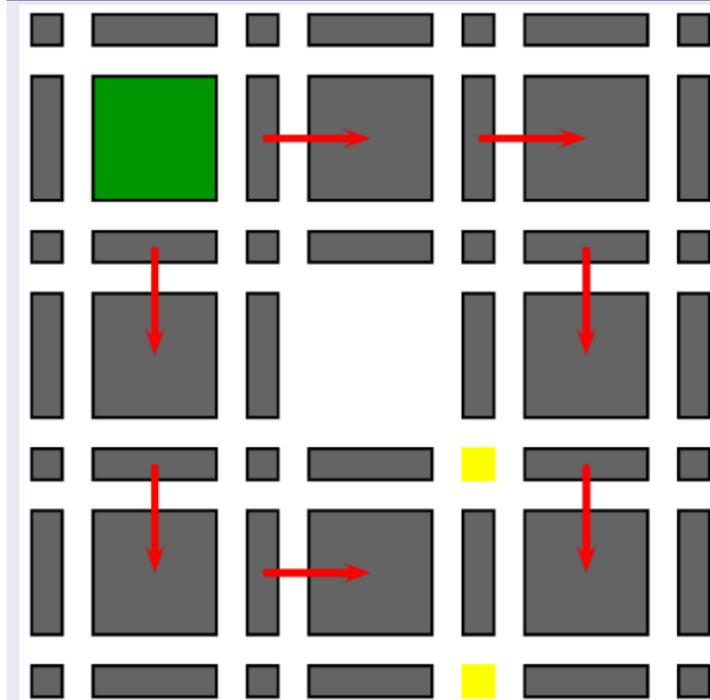
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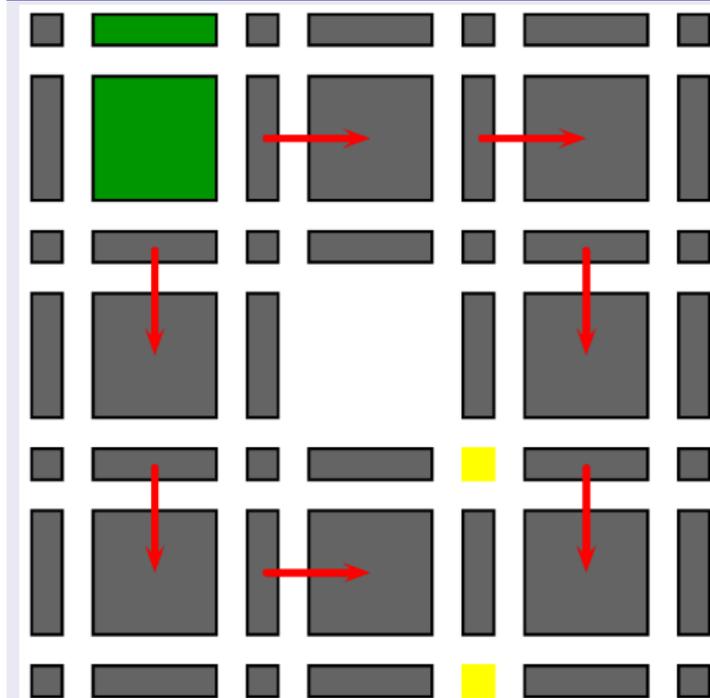
Exemple : CellClustering



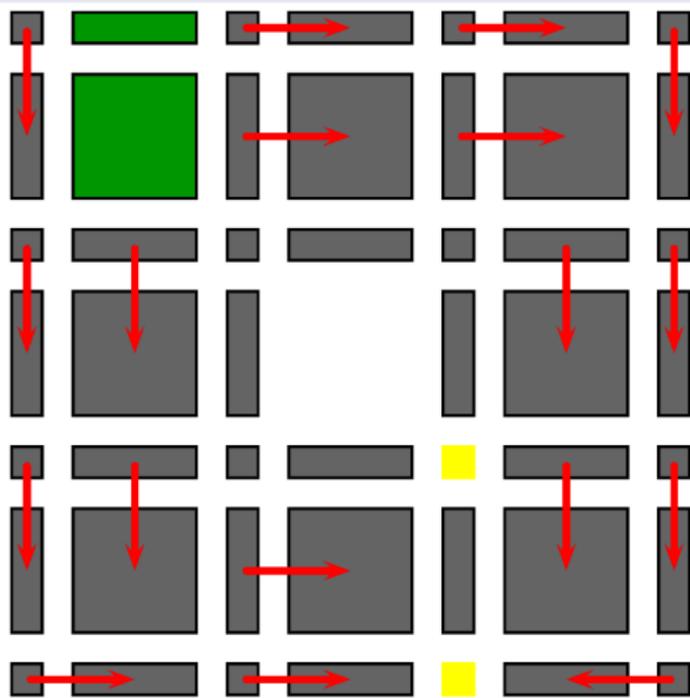
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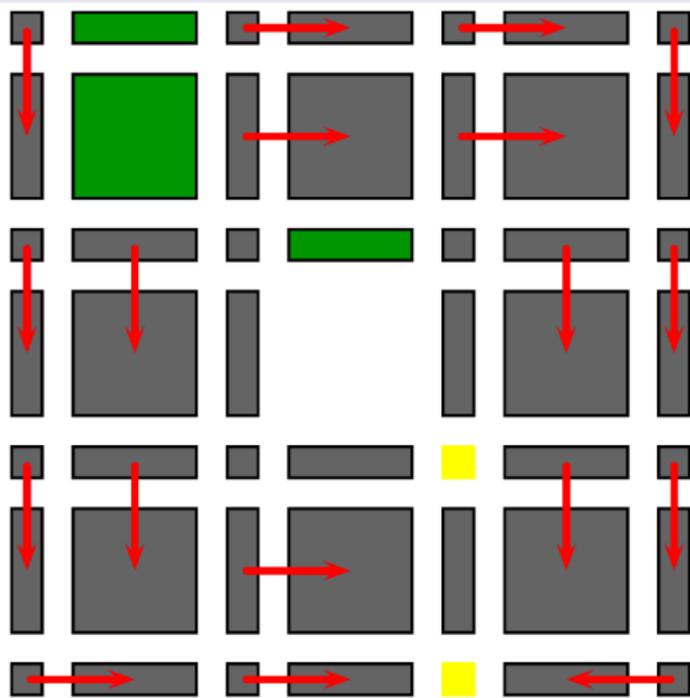
Exemple : CellClustering



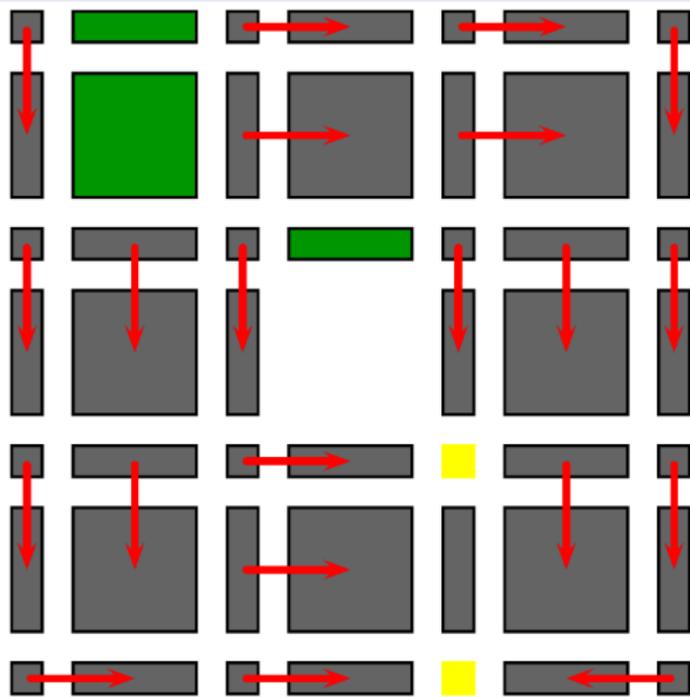
Exemple : CellClustering



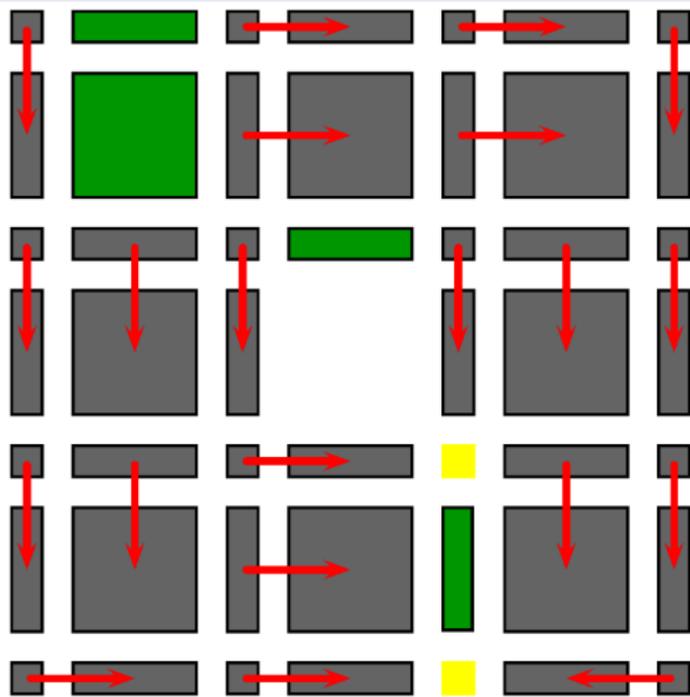
Exemple : CellClustering



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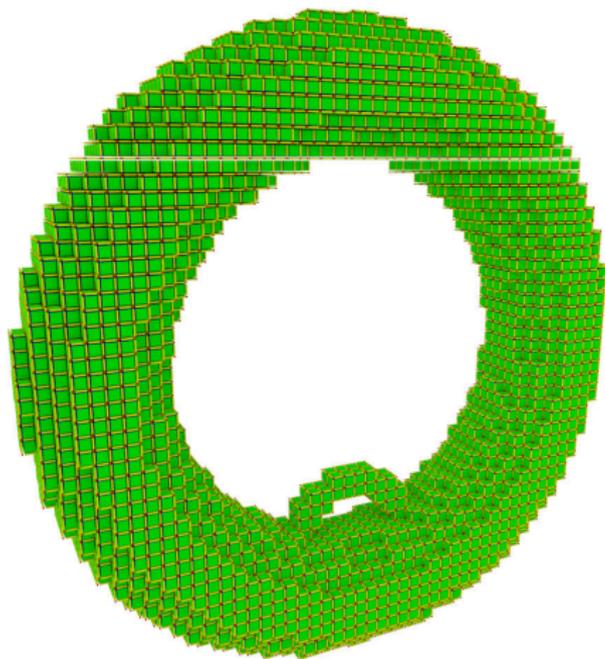
Théorème

Pour toute $\sigma \in K$ maximale ($d^(\sigma) = 0$), il existe une et seulement une cellule critique γ telle que $\langle g(\gamma), \sigma \rangle = 1$*

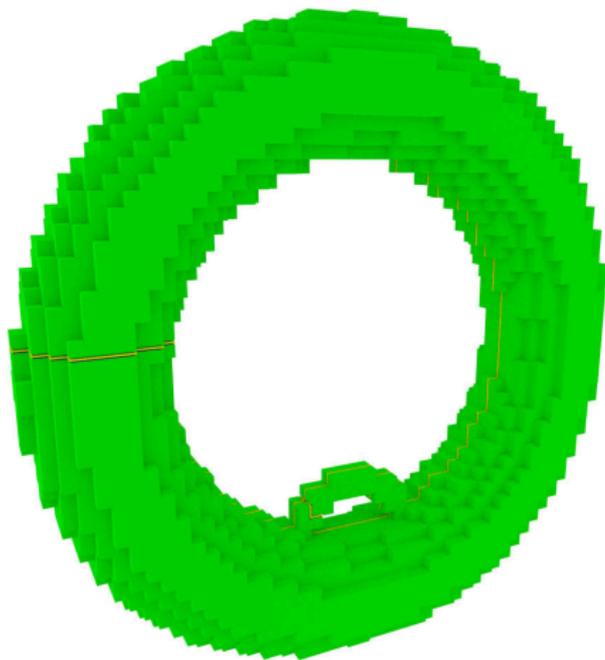
En français :

le complexe réduit peut être visualisé sans chevauchement et avec la même forme que l'original.

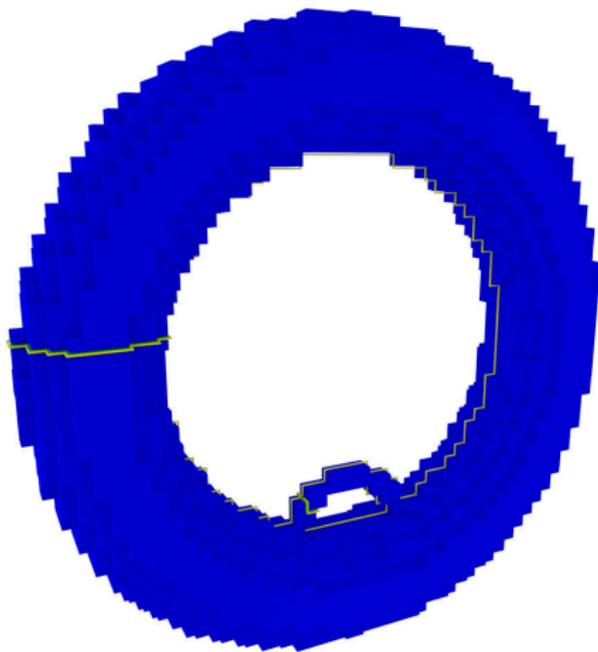
Exemple : CellClustering sur un complexe plus grand



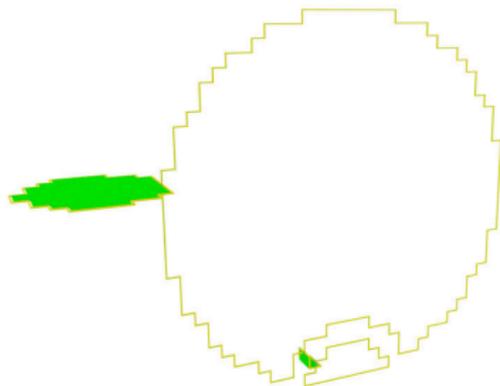
Exemple : CellClustering sur un complexe plus grand



Exemple : CellClustering sur un complexe plus grand



Exemple : CellClustering sur un complexe plus grand



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Cellular skeletons or: how to combine topological skeletons with homology computation

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Motivation

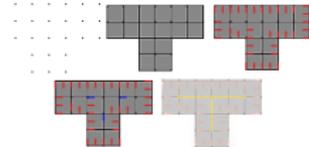


HC → TS: Betti numbers, which measure the number of holes in an object, give the number of pieces (cells) necessary to build a homotopically equivalent object

HC ← TS: Existing methods for skeletonization can be used for obtaining well-shaped homology generators

Objective

Given a 3D binary volume with its connectivity relation (6 or 26), we obtain a reduction (fg,h) which encodes a topological skeleton preserving its geometric features. This algebraic object can be reused for computing the exact homology information of the original object

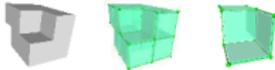


Method

There are three steps:

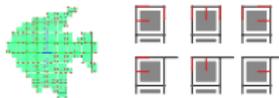
1.- Construction of the cubical complex: choosing the connectivity

We can build the cubical complex by substituting each point by a cube (26-connectivity) or a point (6-connectivity)



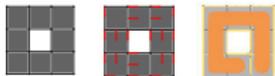
2.- Homotopic thinning algorithm

We perform a homotopic thinning by elementary collapses. There are different methods [Liu10, Couprie13, Dlotko14] for keeping the geometrical features

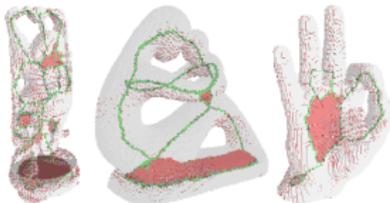


3.- Cell clustering: minimizing the number of cells

We extend the reduction given by the previous step, reducing the number of cells in the complex but maintaining the shape of the skeleton.



Validation



Conclusion

- A new kind of skeleton for binary volumes which is a chain complex together with a reduction
- It works for different connectivity relations and it does not make use of look-up tables
- It can be extended for further homology computations

References

- [Liu10] L. Liu, E. W. Chambers, D. Letscher, and T. Ju. A simple and robust thinning algorithm on cell complexes. *Computer Graphics Forum*, 2010.
- [Dlotko14] P. Dlotko and R. Specogna. Topology preserving thinning of cell complexes. *Image Processing, IEEE Transactions on Image Processing*, 2014.
- [Couprie13] Michel Couprie. Topological maps and robust hierarchical euclidean skeletons in cubical complexes. *Computer Vision and Image Understanding*, 2013.

Acknowledgement

The hand and the statue datasets are courtesy of Michel Couprie, and the Happy Buddha is courtesy of the Stanford University Computer Graphics Laboratory. We thank Mahatsanga for the assistance with the graphical design (www.mahatsang.wordpress.com).

Additional info

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Cellular Skeletons: a New Approach to Topological Skeletons with Geometric Features

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Abstract. This paper introduces a new way of skeletonizing objects. The skeleton is the union of small S^1 spheres and a curve graph. The critical points in the curve graph are the only singularities for the original complex. Starting from the binary volume and both a vertex complex which represents a simplifying topological structure. This structure is then used to get the abstract skeleton based on the set of spheres which represent singular geometric features. This method allows the analysis of skeletonizing binary objects. The resulting skeleton is a structure that preserves the topology of the original complex and a geometric approximation of the original object.

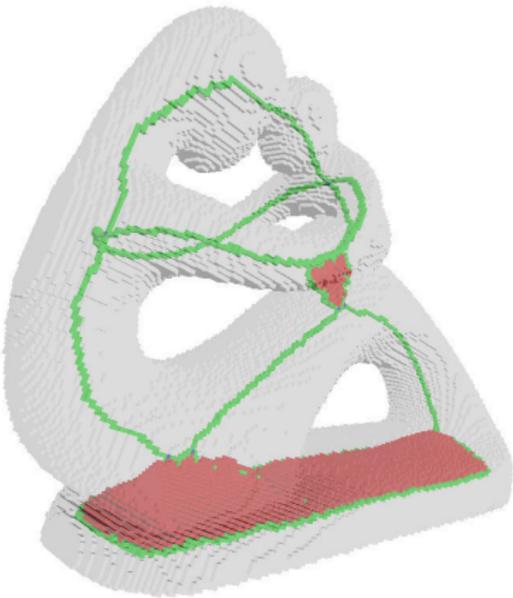
Key words. Cellular skeleton, binary skeletonization, critical points, topological structure, geometric approximation.

1 Introduction

The notion of skeleton (or medial axis) was introduced by H. Blum in 1967 [Blu67] (Gauss circle, S. 27). It could be considered as the union of all the points in \mathbb{R}^2 that are contained in the object in such a way that if it is a good enough approximation, then it is not the convex type of boundary, and it gives the best approximation of the boundary in terms of area, and it is the medial axis of the object. It is the distance of each point to the boundary.

Skeletons are valuable tools for various applications such as object tracking [Bou03], shape recognition [Wong04], image skeletonization [Wang04], and many others.

In a discrete context there is a natural way of thinking to the continuous details. A discrete skeleton gives a skeletonization of the object, which is a set of points in the discrete object. There are several ways to define the skeleton of the object: center of mass of each neighborhood of pixels [Gonzalez and Woods 1992], shape of points [RipS], center of mass [Ch04]. The given approach is a set of spheres and a curve graph, which is a topological structure and a geometric approximation of the original object and its features. There is another way of thinking to the skeletonization: medial axis, which is the set of points that are equidistant to the boundary [Ch04, RipS].



On propose deux opérations pour réduire un complexe

| | CellClustering | Elementary collapse |
|------------------------------|----------------|---------------------|
| réduit le nombre de cellules | oui | oui |
| garde la forme du complexe | oui | non |
| idempotent | oui | non |

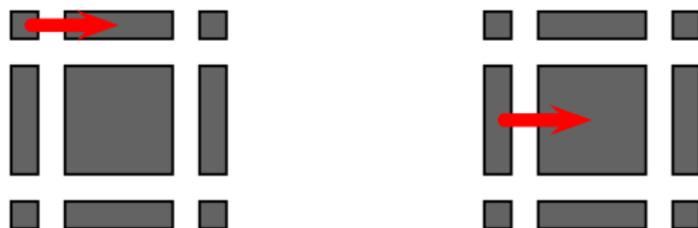
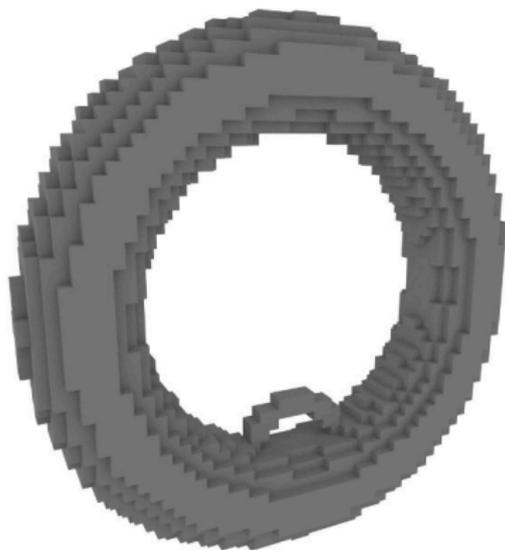
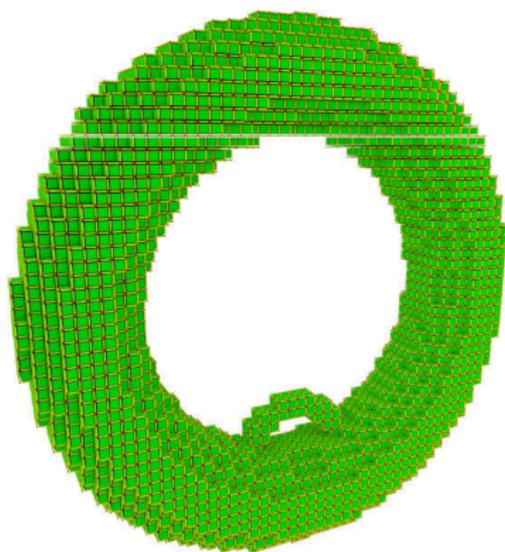


Figure : Gauche : ce n'est pas un *elementary collapse*. Droite : c'est un *elementary collapse*

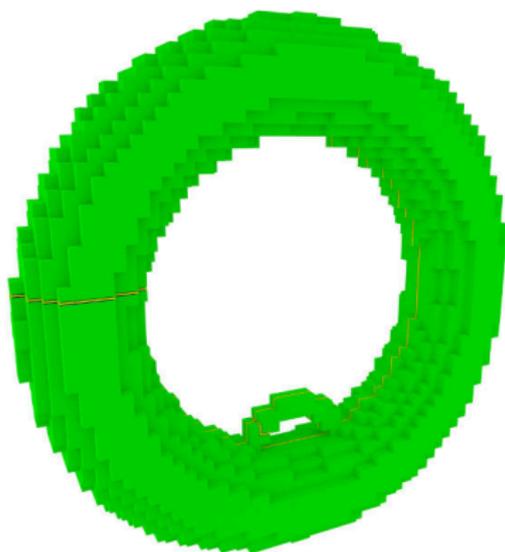
Exemple : calcul de l'homologie assisté par l'utilisateur



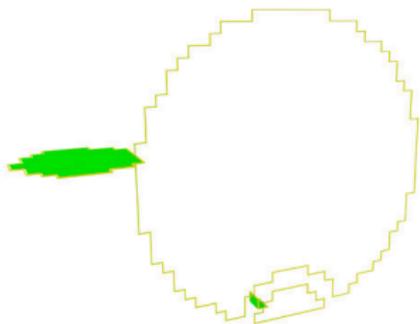
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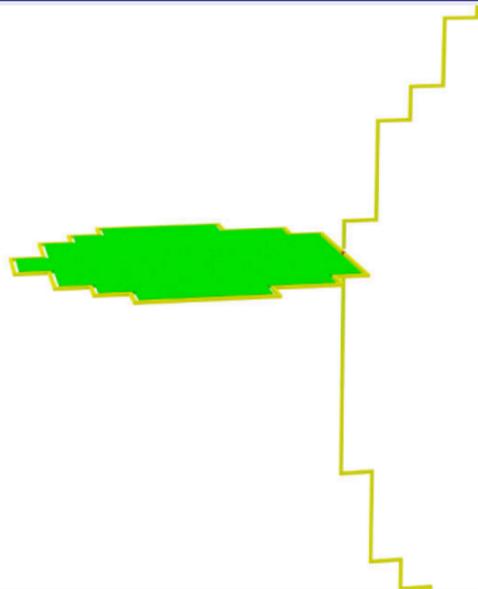
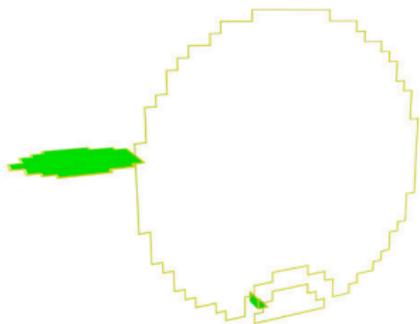
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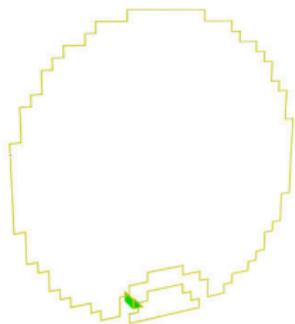
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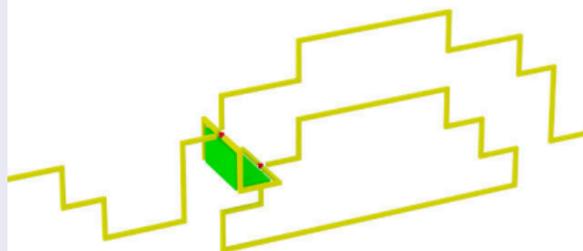
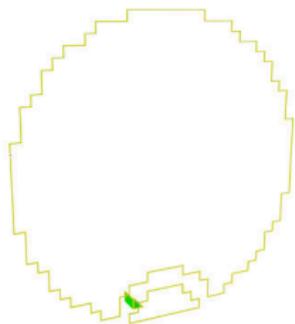
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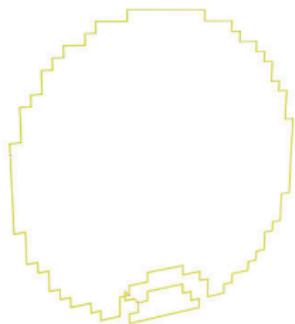
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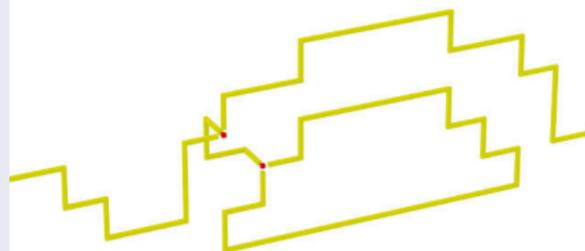
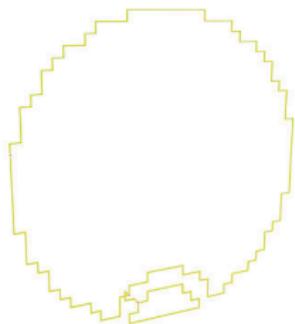
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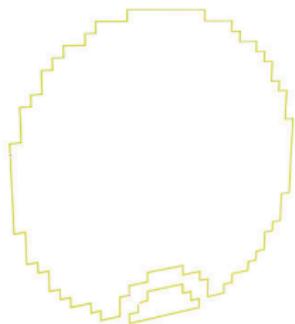
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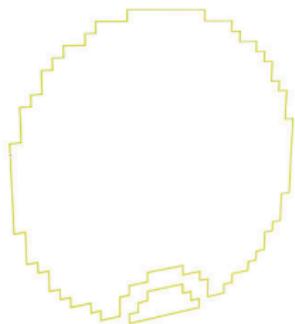
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- CellClustering donne un complexe réduit et visualisable
- Il peut être utilisé pour un calcul assisté de l'homologie
- D'autres théorèmes ou applications ?

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Merci ! Questions ?