A Heuristic for Short Homology Basis of Digital Objects

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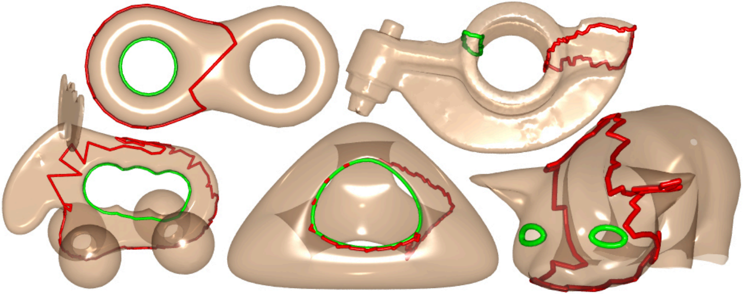
Outline

Outline

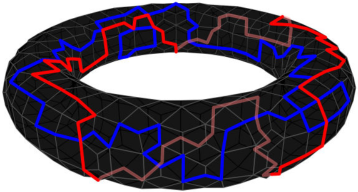
Problem : visualize the holes in a digital object

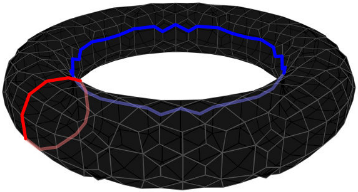


Why ? Identify errors, measure holes

Approach:

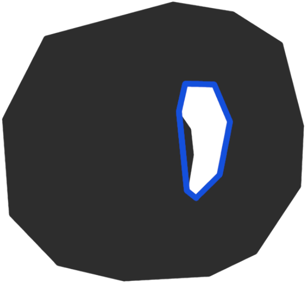
- Visualize holes as homology cyles ($\sim$ discrete manifolds)
- Short cycles are better (tight, well located)





Computing a minimal homology basis

- size of cycle: number of cells
- $q = 1$: $\mathcal{O}(n^{\omega} + n^2 \cdot \beta_1)$[1]
- $q > 1$: NP-hard[2]

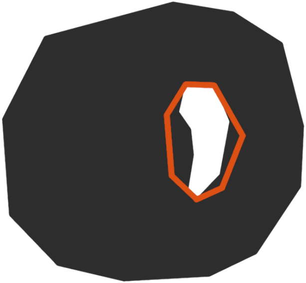


[1] Dey et al: Efficient algorithms for computing a minimal homology basis (2018)

[2] Chen and Friedman: Hardness results for homology localization (2011)

Computing a minimal radius homology basis

- size of cycle: radius of smallest geodesic ball containing it
- $q \geq 1$: $\mathcal{O}(\beta_q \cdot n^4)$ [3], then $\mathcal{O}(n^{\omega+1})$ [4]
- Theoretical algorithm, not implemented



[3] Chen and Friedman: Measuring and computing natural generators for homology groups (2011)

[4] Dey et al: Efficient algorithms for computing a minimal homology basis (2018)

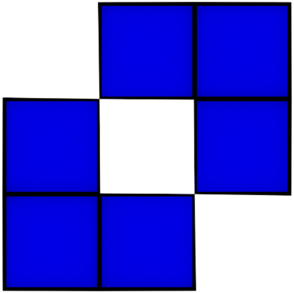
Goal: we want an algorithm that

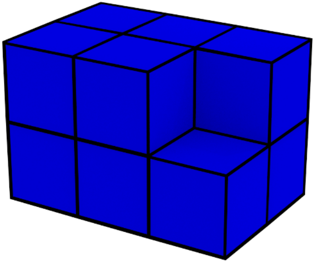
1. can be implemented in practice
2. is faster (even if it is worse)

Outline

Digital object

A nD digital object is a subset of $\mathbb{Z}^n$





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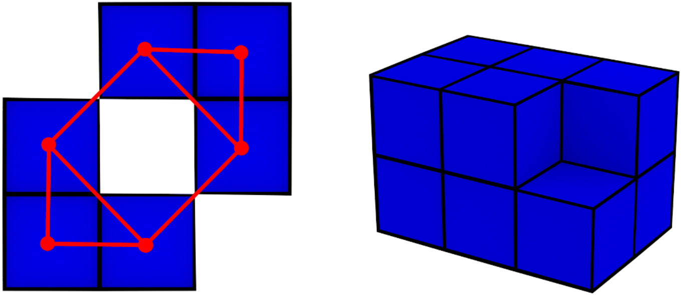


Connectivity relation: $(3^n - 1)$-connectivity (or $2n$).

Signed distance transform

Let O be a digital object,

$$sdt_O(x) = \begin{cases} -d(x, O^c) & \text{if } x \in O \\ d(x, O) & \text{if } x \notin O \end{cases}$$

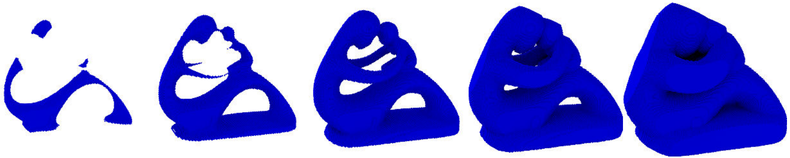
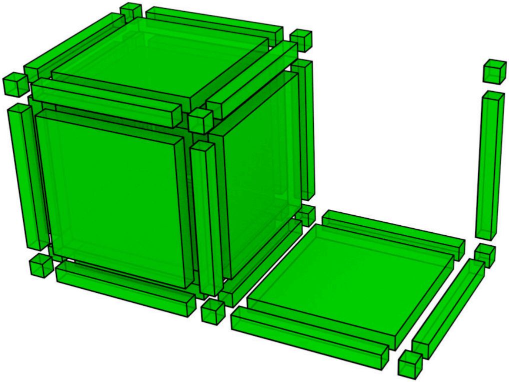


Figure: Sublevel sets of the signed distance transform

Cubical complex

Union of points, edges, squares, cubes, ... (cubes) closed under inclusion



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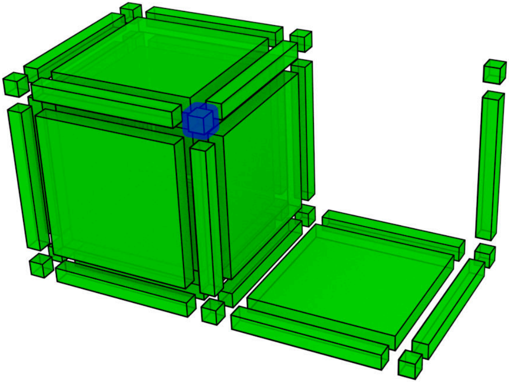

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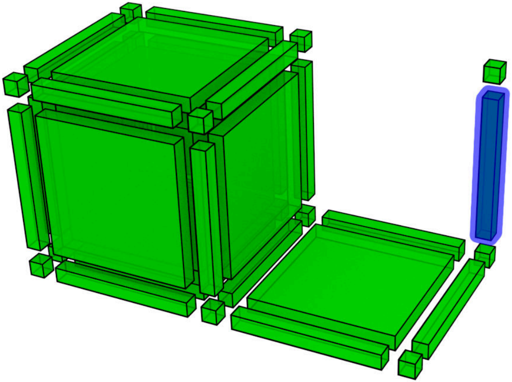

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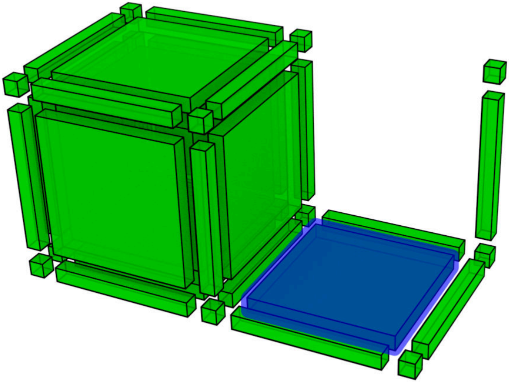

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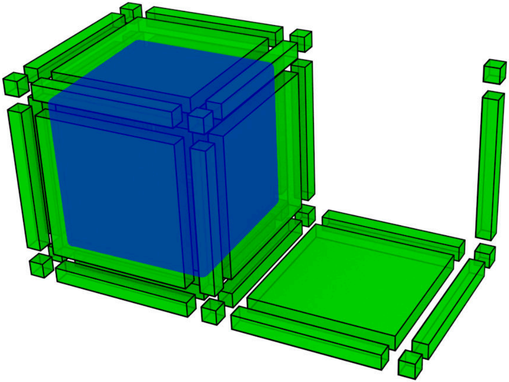
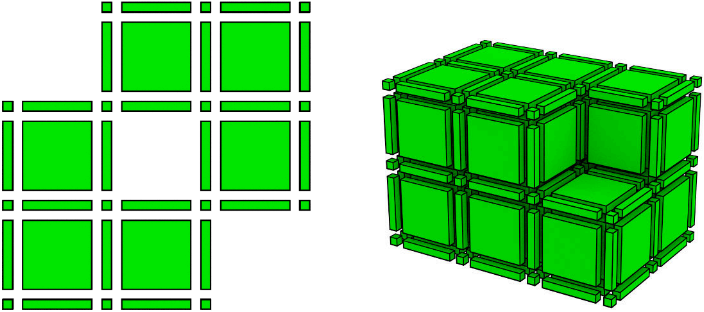
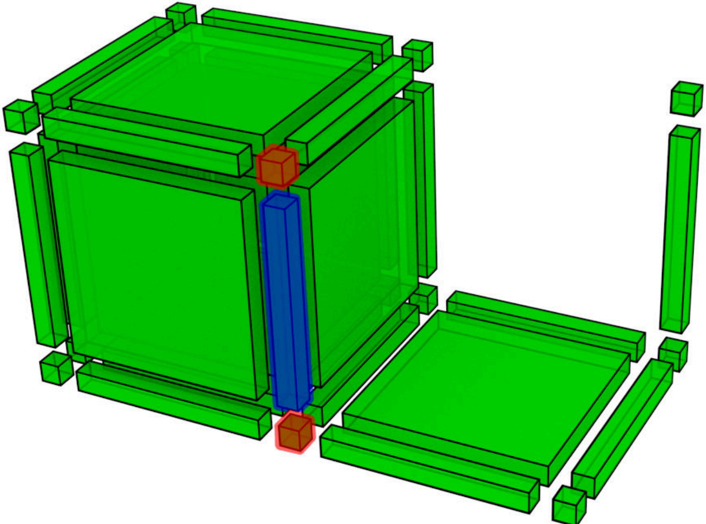


Digital object $\longrightarrow$ cubical complex ($(3^n - 1)$-connectivity)



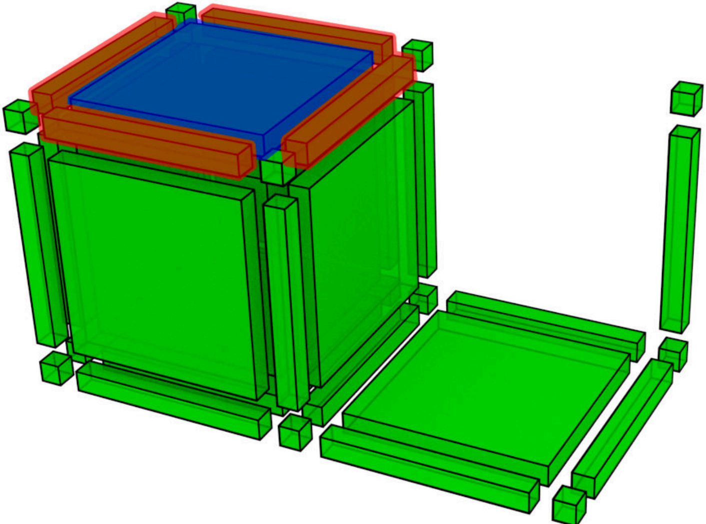
Blue: 1-cube

Red: its boundary (faces)



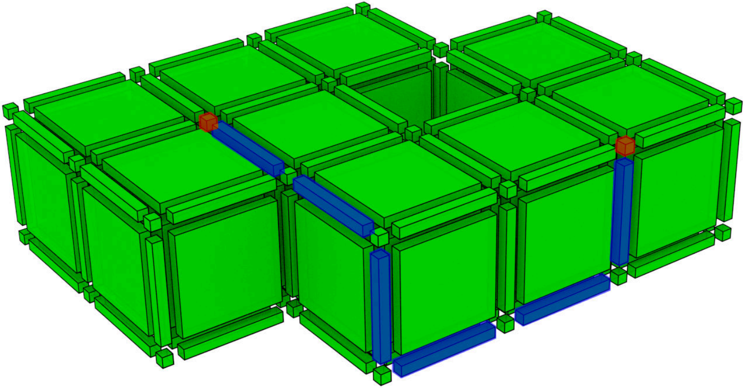
Blue: 2-cube

Red: its boundary (faces)

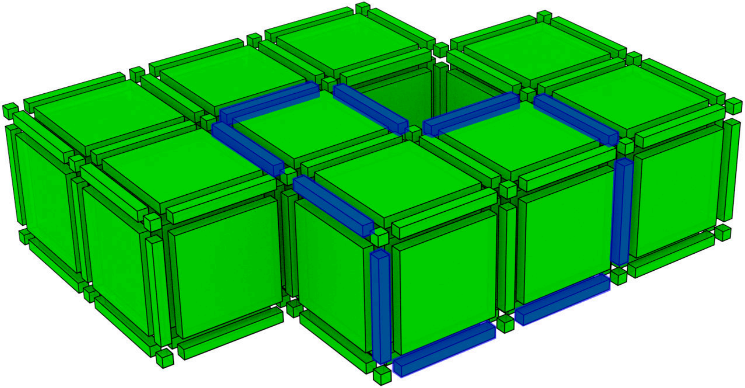


Blue: 1-chain

Red: its boundary

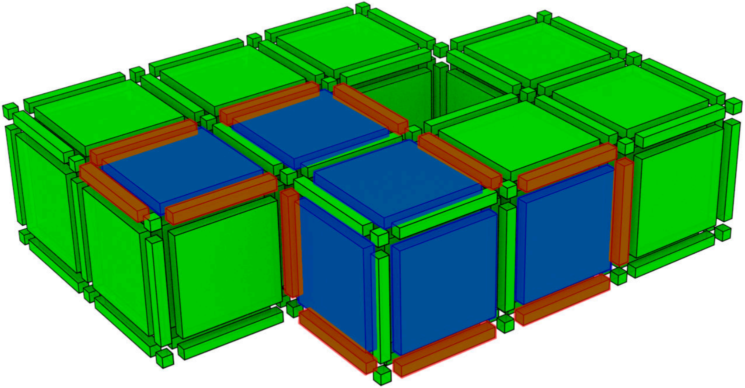


Blue: 1-chain (1-cycle)
Red: its boundary ($= \emptyset$)



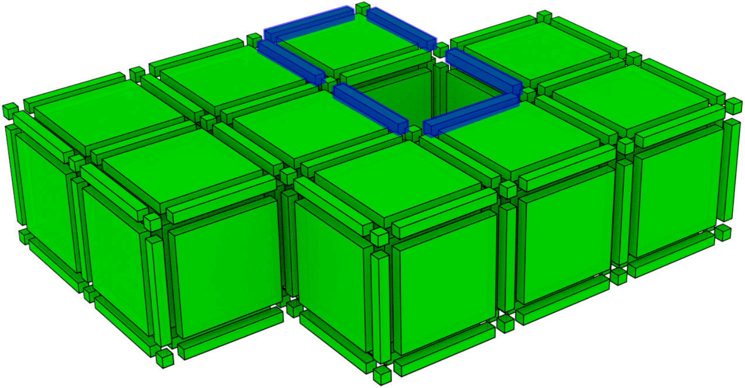
Blue: 2-chain

Red: its boundary (1-cycle)



Blue: 1-chain (1-cycle, but not boundary)

Red: its boundary ($= \emptyset$)



- K cubical complex
- Chain complex of K

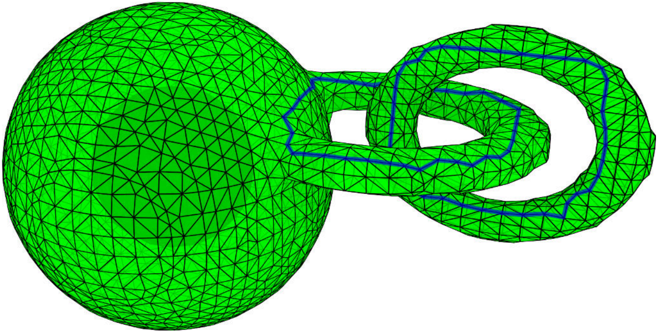
$$\cdots C_3 \xrightarrow{d_3} C_2 \xrightarrow{d_2} C_1 \xrightarrow{d_1} C_0 \xrightarrow{d_0} 0$$

where $d_q d_{q+1} = 0 \Rightarrow \mathrm{im}(d_{q+1}) \subset \ker(d_q)$

- q-dimensional homology group (vector space) $H_q(K) := \ker(d_q)/\mathrm{im}(d_{q+1})$[5] $= (\mathbb{F}_2)^{\beta_q}$

[5] $\forall x, y \in \ker(d_q), x \sim y \Leftrightarrow x + y \in \mathrm{im}(d_{q+1})$

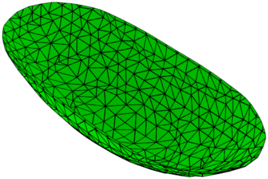
- $\beta_q := \dim(H_q(K))$: number of holes (connected components, tunnels, cavities...)
- Homology basis: set of independent classes $\rightarrow$ cycles

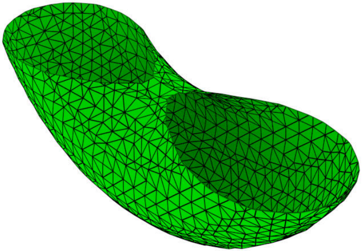


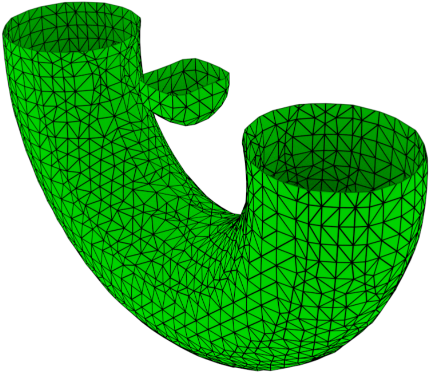
- Filtration F: $K_1 \subset K_2 \subset K_3 \subset \cdots$

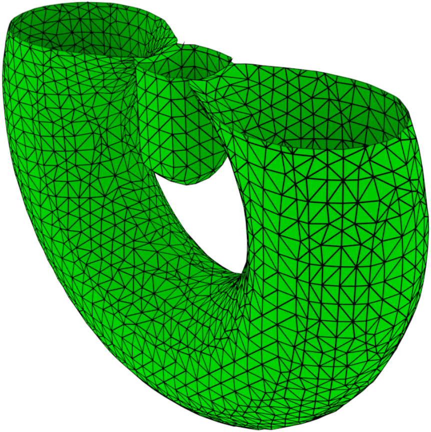
$$\begin{array}{ccccccc} K_1 & \xrightarrow{\iota} & K_2 & \xrightarrow{\iota} & K_3 & \xrightarrow{\iota} & \cdots \\ \downarrow & & \downarrow & & \downarrow & & \\ H(K_1) & \xrightarrow{\iota_*} & H(K_2) & \xrightarrow{\iota_*} & H(K_3) & \xrightarrow{\iota_*} & \cdots \end{array}$$

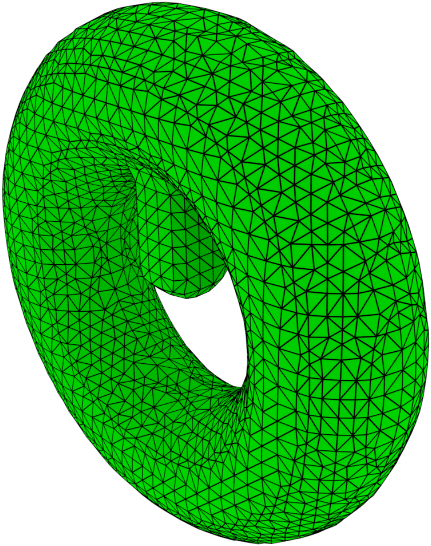
- Usually defined by a function $f : K \to \mathbb{R}$
- $\beta_{i,j} = \dim(\iota : H(K_i) \to H(K_j))$
  number of holes in K_i still in K_j
- $\mu_{i,j} = \beta_{i,j} - \beta_{i,j+1} - \beta_{i-1,j} + \beta_{i-1,j+1}$
  number of holes born in K_i and dying in K_j











Sketch of persistent homology computation:

- Sort cells according to the filtration
- For each cell, associate it with one of the previous ones
- Each of these pairs makes a persistence pair

Persistence pairs

$PD(F) = \{(i, j) \text{ with multiplicity } \mu_{i,j}\}$

We also obtain:

- A partial matching of cells
- A cycle associated to each pair ($\simeq$ hole)

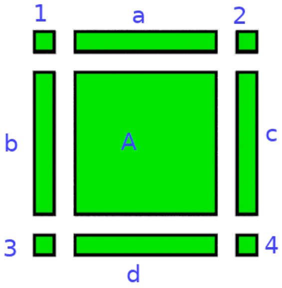
Homological Discrete Vector Field

Let K be a cubical complex and $P, S \subset K, P \cap S = \emptyset$.
(P, S) is a HDVF if $j_P \circ \partial \circ i_S$ is an isomorphism.

where

- $i_S : S \to K$ inclusion
- $j_P : K \to P$ projection

$(j_P \circ \partial \circ i_S)$ is an invertible submatrix of the boundary matrix



$$\partial_1 = \begin{bmatrix} 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 \end{bmatrix} \quad \partial_2 = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}$$

$P = \{1, 2, 3, 4\}, S = \{a, b, c, d\}$ is not a HDVF (not invertible)
$P = \{1, 2, 3, a\}, S = \{a, b, c, A\}$ is not a HDVF ($P \cap S \neq \emptyset$)
$P = \{1, 2, 3, d\}, S = \{a, b, c, A\}$ is a HDVF

A maximal HDVF provides:

- A homology basis
- A cohomology basis
- Check if a cycle is trivial
- Check if two cycles are homologous
- ...

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Simplest case: only one hole

1. Get some candidate (non trivial) cycles
2. Keep the shortest one

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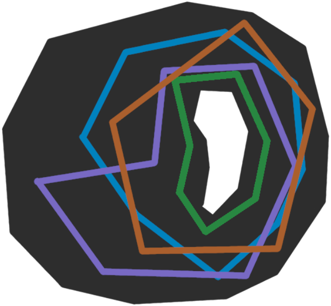

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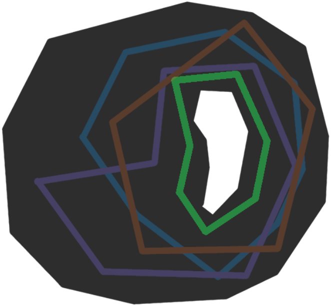

General case: more than one hole

1. Get some candidate (non trivial) cycles
2. Keep the shortest cycles that make a homology basis

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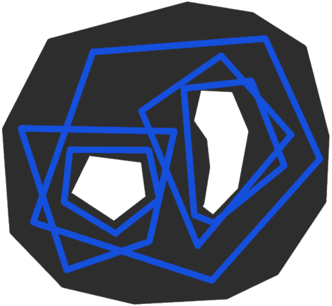

General case: more than one hole

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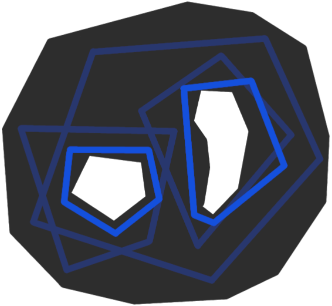


Pitfalls:

1. How to find good candidate cycles?
2. A cycle is trivial or not?
3. A set of cycles is a homology basis ?

Our algorithm has 4 steps

1. Breadth balls (good starting points)
2. Compute filtrations (candidate cycles)
3. Sort and annotate (cycles to classes)
4. Earliest basis (shortest homology basis)

Notation :

- K is the cubical complex of a digital object O
- We fix $q \geq 1$ and we look for a short homology basis for $H_q(K)$
- $g := \dim(H_q(K))$

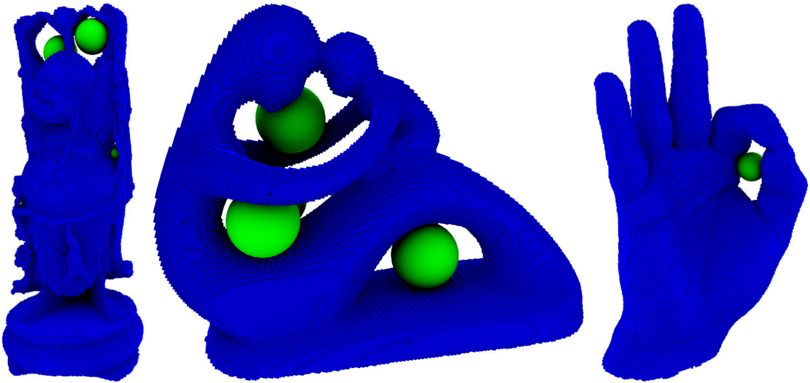
Step 1 - Breadth balls

- Full[6] cubical complex + signed distance function f_{sdt} = filtration
- Compute partial matching $M = \{(\sigma_1, \tau_1) \ldots\}$
- Get $\mathcal{B}$ = cells τ such that
  1. $(\sigma, \tau) \in M$
  2. $f_{sdt}(\sigma) < 0 < f_{sdt}(\tau)$
  3. $\dim(\sigma) = q$

These are the centers of the breadth balls of the digital object O

[6] Other approaches: convex hull, homotopical closing

Step 1 - Breadth balls



Step 2 - Compute filtrations

For each $\tau \in \mathcal{B}$ ($\tau \notin K$), we compute a discrete geodesic transform:

Discrete geodesic transform

Let K be a cubical complex, $\tau_0 \in K$ a 0-cube,

$$f_{K,\tau_0}(\sigma) = \begin{cases} \text{size of shortest path to } \tau_0 & \text{if } \dim(\sigma) = 0 \\ \max\{f_{K,\tau_0}(\sigma') : \sigma' \subset \sigma, \dim(\sigma') = 0\} & \text{if } \dim(\sigma) > 0 \end{cases}$$

Step 2 - Compute filtrations

Then, for each $\tau \in \mathcal{B}$

- Let $\tau_0 \in K$ be a closest 0-cube to τ
- f_{K,τ_0} is a filtration over K
- Persistent homology computation $\rightarrow \{x_1 \ldots x_g\}$ a homology basis for K
- $|\mathcal{B}| = q \Rightarrow$ we compute g homology bases $= g^2$ cycles

Step 3 - Sort and annotate

We sort the g^2 cycles by size: $\{x_1 \ldots x_{g^2}\}$

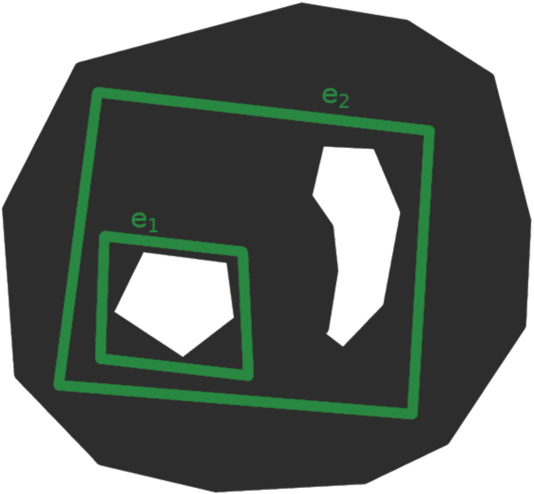
To find a basis, we have to write these cycles in a homology basis: an *annotation*

Annotation

Homomorphism $a : K_q \rightarrow H_q(C)$ such that for any two q-cycles x, y, $a(x) = a(y)$ iff $[x] = [y]$.

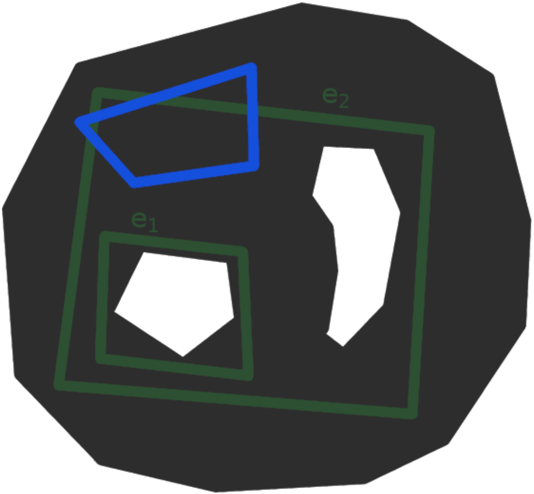
This is simply a linear map that projects each cycle onto the homology group, a $g \times |K_q|$ matrix.

Step 3 - Sort and annotate



$$H_1(K) = \langle e_1, e_2 \rangle$$

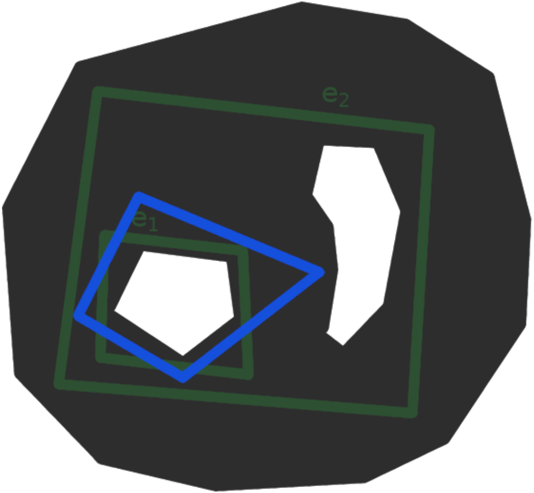
Step 3 - Sort and annotate



$$H_1(K) = \langle e_1, e_2 \rangle$$

$$a(x) = 0$$

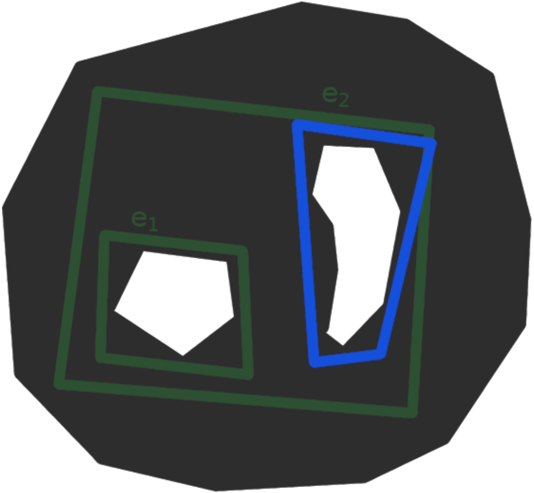
Step 3 - Sort and annotate



$$H_1(K) = \langle e_1, e_2 \rangle$$

$$a(x) = e_1$$

Step 3 - Sort and annotate



$$H_1(K) = \langle e_1, e_2 \rangle$$

$$a(x) = e_1 + e_2$$

Step 3 - Sort and annotate

We compute an annotation with a HDVF:

1. Let $M = \bigcup_{i \in I} \{(\sigma_i, \tau_i)\}$ be the partial matching of cells computed by any of the filtrations in step 2
2. Define $P := \{\sigma : (\sigma, \tau) \in M, \dim(\sigma) = q\}$ and $S := \{\tau : (\sigma, \tau) \in M, \dim(\tau) = q + 1\}$
3. (P, S) is a HDVF and the linear map (matrix)

$$a = (j_C \circ \partial_{q+1} \circ i_S) \circ (j_P \circ \partial_{q+1} \circ i_S)^{-1} \circ j_P + j_C$$

   is an annotation
4. Computation: get $A = (j_C \circ \partial_{q+1} \circ i_S)$, $B = (j_P \circ \partial_{q+1} \circ i_S)$, and compute $A \cdot B^{-1}$

Step 4 - Earliest basis

- Let Y be the $g \times g^2$ matrix with columns $a(x_1) \dots a(x_{g^2})$
- Get the first columns to make a basis with gaussian elimination
- Return the corresponding cycles

$$\begin{bmatrix} 0 & 1 & 1 & 0 & 1 & 0 & 0 & 1 & 1 \\ 1 & 0 & 1 & 1 & 0 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 1 & 0 & 1 & 1 & 0 \end{bmatrix}$$

col:

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col: 2

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col: 6

Short homology basis: $\{x_1, x_2, x_6\}$

Focus on the algorithm by Dey et al (2018):

1. Compute one filtration per 0-cube (fast matrix multiplication)
2. Sort all $|K_0| \cdot g$ cycles
3. Compute annotation (LSP-decomposition, fast matrix multiplication)
4. Earliest basis using (LSP-decomposition)

This is a theoretical algorithm using fast matrix multiplication

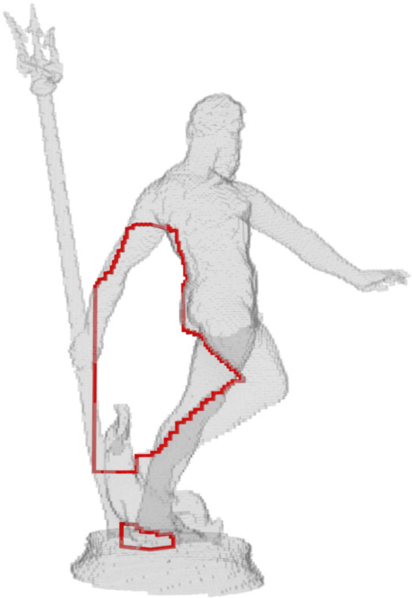
We simplify it to compare it with ours:

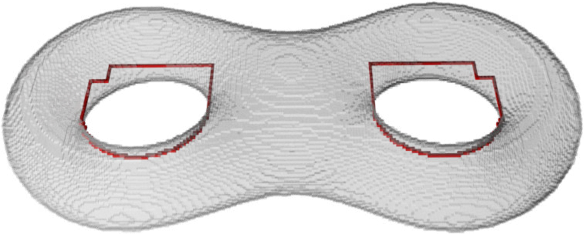
1. Compute g filtrations from random 0-cubes
2. Sort all $g \cdot g$ cycles
3. Compute annotation (with a HDVF)
4. Earliest basis (with gaussian elimination)

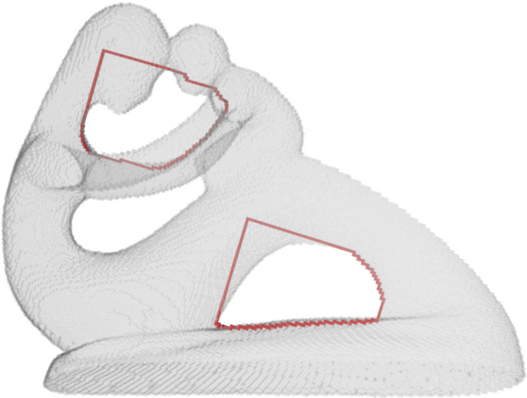
This adaptation can be computed and has a similar time complexity

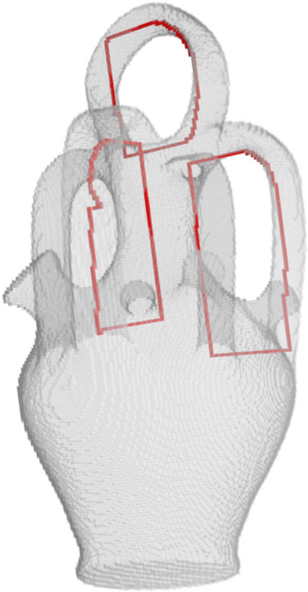
Table: Average sizes of the homology bases produced by both algorithms

Object	Us	Dey et al*
Amphora	930	1068.0
Dancing	902	1042.6
Eight	356	417.0
Fertility	962	999.8
Neptune	640	663.0
Pegasus	1032	1182.8









Outline

Conclusion:

- Heuristic for short homology generators
- Dey et al is not that bad
- $\mathcal{O}(m^3 + g \cdot n^3)$ time complexity
- Easy to implement, check our code

Perspectives:

- Two step algorithm: initial solution + optimization
- Improve length (area, volume. . .) estimation
- Faster algorithm for the annotation

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Thanks! Questions?