Spectral sequences for computing persistent homology of digital images

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Málaga, 3th July 2013

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Definition

Let K be a simplicial complex. A *filtration* of K is a sequence of subcomplexes: $\emptyset = K^0 \subseteq K^1 \subseteq K^2 \subseteq \cdots \subseteq K^m = K$.

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The filtration produces a sequence of groups and homomorphisms:

$$0 = H_n(\mathcal{K}^0) \stackrel{f_n^{0,1}}{\to} H_n(\mathcal{K}^1) \stackrel{f_n^{1,2}}{\to} \cdots \stackrel{f_n^{m-1,m}}{\to} H_n(\mathcal{K}^m) = H_n(\mathcal{K})$$

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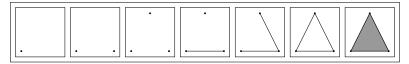
If γ is born at K^i and dies entering K^j , we denote pers $(\gamma) = j - i$.

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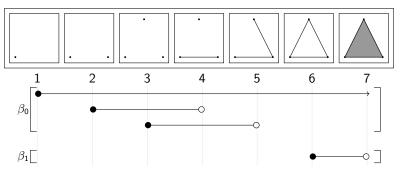


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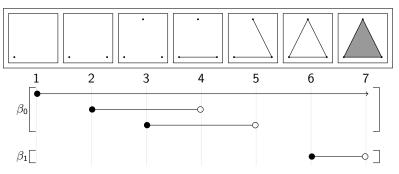


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Example:



Roughly speaking:

- Homology detects topological features (connected components, holes, and so on).
- Persistent homology describes the evolution of topological features looking at consecutive thresholds.

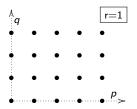
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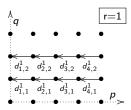
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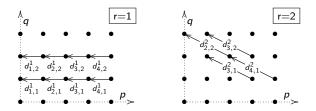
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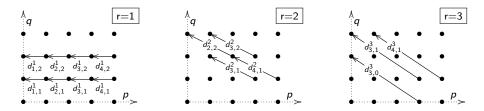


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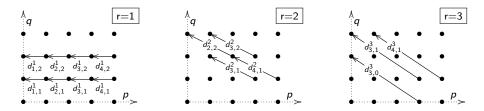
A spectral sequence $E = (E^r, d^r)_{r \ge 1}$ is a family of bigraded \mathbb{Z} -modules $E^r = \{E_{p,q}^r\}$, each provided with a differential $d^r = \{d_{p,q}^r : E_{p,q}^r \to E_{p-r,q+r-1}^r\}$ of bidegree (-r, r-1) and with isomorphisms $H(E^r, d^r) \cong E^{r+1}$ for every $r \ge 1$.



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Since $E_{p,q}^{r+1}$ is a subquotient of $E_{p,q}^r$ for each $r \ge 1$, one can define the *final* groups of the spectral sequence as $E_{p,q}^{\infty} = \bigcap_{r\ge 1} E_{p,q}^r$.

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Theorem

Let C be a chain complex with a filtration. There exists a spectral sequence with

$$E_{p,q}^{r} = \frac{Z_{p,q}^{r} + C_{p+q}^{p-1}}{d_{p+q+1}(Z_{p+r-1,q-r+2}^{r-1}) + C_{p+q}^{p-1}}$$

where $Z_{p,q}^r$ is $Z_{p,q}^r = \{a \in C_{p+q}^p | d_{p+q}(a) \in C_{p+q-1}^{p-r}\} \subseteq C_{p+q}^p$, and $d_{p,q}^r : E_{p,q}^r \to E_{p-r,q+r-1}^r$ is the morphism induced by $d_{p+q} : C_{p+q} \to C_{p+q-1}$. This spectral sequence converges to $H_*(C)$, that is, there are natural isomorphisms

$$E_{p,q}^{\infty} \cong rac{H_{p+q}^{p}(C)}{H_{p+q}^{p-1}(C)}$$

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The total rank of the groups of dimension p + q in the level $r \ge 1$ of the associated spectral sequence equals the number of points in the (p + q)-th persistence diagram whose persistence is r or larger, that is,

$$\sum_{p=1}^m \operatorname{\mathsf{rank}} E_{p,q}^r = \operatorname{\mathsf{card}} \{a \in \operatorname{\mathsf{Dgm}}_{p+q}(f) | \operatorname{\mathsf{pers}}(a) \geq r \}$$

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A. Romero, J. Heras, J. Rubio and F. Sergeraert. Defining and computing persistent \mathbb{Z} -homology in the general case. Preprint, 2013.

A Kenzo module for spectral sequences

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- These algorithms were implemented in Common Lisp as a new module for the Kenzo system. Kenzo implements the *effective homology* method and the notion of *reduction* from one (big) chain complex to a smaller one, such that the homology groups of the two complexes are explicitly isomorphic and one can compute homology of infinite spaces.
- The new programs use the effective homology technique and allow the Kenzo user to determine the different components of spectral sequences of filtered complexes even in some cases where the chain complex has infinite type.

• Using our programs for spectral sequences, and thanks to our theorem expressing the relation between spectral sequences and persistent homology, one can determine the ranks of the groups $H_n^{i,j}$.

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- In fact a small modification of our programs for spectral sequences is sufficient to determine the groups $H_n^{i,j}$, which can be expressed as a quotient:

$$H_n^{i,j} = \frac{\operatorname{Ker} d_n \cap C_n^i}{d_{n+1}(Z_{j,n-j+1}^{j-i})} = \frac{Z_{i,n-i}^i}{d_{n+1}(Z_{j,n-j+1}^{j-i})}$$

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- Our programs can also be applied in the infinite case, where the effective homology method can be used to determine the groups $H_n^{i,j}$ by means of a *reduction* of the initial chain complex C to an auxiliary chain complex of finite type.

Digital Algebraic Topology

Digital Image

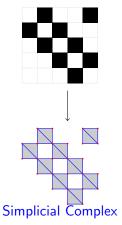


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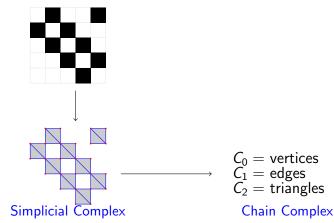
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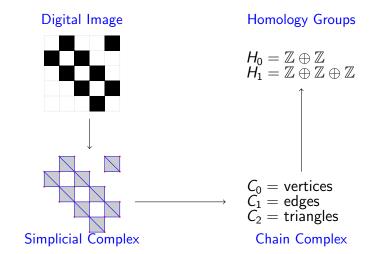


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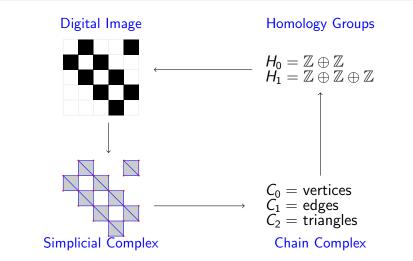
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Persistent Homology H^{1,4}_0
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> (prst-hmlg-group K 2 4 1)
Persistent Homology H^{2,4}_1
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Discrete Vector Fields

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Discrete Vector Fields

Definition

Let $C_* = (C_p, d_p)_{p \in \mathbb{Z}}$ be a free chain complex with distinguished \mathbb{Z} -basis $\beta_p \subset C_p$. A discrete vector field on C_* is a collection of pairs $V = \{(\sigma_i, \tau_i)\}_{i \in \beta}$ satisfying the conditions:

- **()** Every σ_i is some element of β_p , in which case the other corresponding component $\tau_i \in \beta_{p+1}$. The degree p depends on i and in general is not constant.
- 2 Every component σ_i is a *regular face* of the corresponding component τ_i .
- **(3)** A generator of C_* appears at most one time in V.

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- A generator of C_{*} appears at most one time in V.

Definition

- A V-path of degree p is a sequence $\pi = ((\sigma_{i_k}, \tau_{i_k}))_{0 \le k < m}$ satisfying:
 - **()** Every pair $((\sigma_{i_k}, \tau_{i_k}))$ is a component of V and the cell τ_{i_k} is a p-cell
 - **(2)** For every 0 < k < m, the component σ_{i_k} is a face of $\tau_{i_{k-1}}$, non necessarily regular, but different from $\sigma_{i_{k-1}}$

Definition

A discrete vector field V is admissible if for every $p \in \mathbb{Z}$, a function $\lambda_p : \beta_p \to \mathbb{Z}$ is provided satisfying the property: every V-path starting from $\sigma \in \beta_p$ has a length bounded by $\lambda_p(\sigma)$.

Example: an admissible discrete vector field

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Example: an admissible discrete vector field





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Discrete Vector Fields and effective homology

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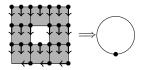
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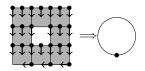
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$${f 1} \ 1 \le a_i \le m$$
 and $1 \le b_i \le n$

2 The entry $M[a_i, b_i]$ of the matrix is 1 or -1

The indices a_i (resp. b_i) are pairwise different

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Input: A matrix M Output: An admissible discrete vector field for M

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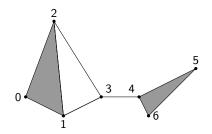
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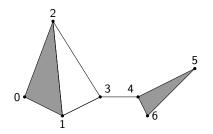
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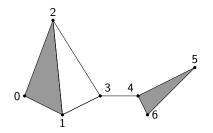


Vector fields and matrices



	$\{0, 1\}$	$\{0, 2\}$	$\{1, 2\}$	$\{1, 3\}$	{2, 3}	$\{3, 4\}$	$\{4, 5\}$	$\{4, 6\}$	$\{5, 6\}$
{0}	/ 1	1	0	0	0	0	0	0	0 \
$\{1\}$	1	0	1	1	0	0	0	0	0)
{2}	0	1	1	0	1	0	0	0	0
{3}	0	0	0	1	1	1	0	0	0
{4}	0	0	0	0	0	1	1	1	0
{5}	0	0	0	0	0	0	1	0	1
{6}	(0	0	0	0	0	0	0	1	1 /

Vector fields and matrices



	$\{0, 1\}$	$\{0, 2\}$	$\{1, 2\}$	$\{1, 3\}$	{2, 3}	$\{3, 4\}$	$\{4, 5\}$	$\{4, 6\}$	$\{5, 6\}$
{0}	(1	1	0	0	0	0	0	0	0 \
$\{1\}$	1	0	1	1	0	0	0	0	0
{2}	0	1	1	0	1	0	0	0	0
{3}	0	0	0	1	1	1	0	0	0
{4}	0	0	0	0	0	1	1	1	0
{5}	0	0	0	0	0	0	1	0	1
{6}	\ 0	0	0	0	0	0	0	1	1 /

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- If we want to determine persistent homology groups, we need a discrete vector field which is compatible with the filtration (such that the obtained reduction is compatible with the filtration).
- To obtain such a *filtered* discrete vector field, we apply our algorithm separately to the differential submatrices corresponding to each filtration index.

- Given an admissible discrete vector field on a digital image, a reduction is obtained from the big chain complex to the critical (small) chain complex, such that the homology groups of both chain complexes are isomorphic.
- If we want to determine persistent homology groups, we need a discrete vector field which is compatible with the filtration (such that the obtained reduction is compatible with the filtration).
- To obtain such a *filtered* discrete vector field, we apply our algorithm separately to the differential submatrices corresponding to each filtration index.
- This allows us to compute persistent homology groups of big digital images by means of a reduced chain complex.

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	Big chain complex	Reduced chain complex
Vertices	9082	150
Edges	20364	86
Triangles	11352	6



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Edges	20364	86
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	Big chain complex	Reduced chain complex
$H_0^{1,1}$	57sec	0, 5sec
$H_0^{1,2}$	33min	10sec
$H_0^{1,3}$	-	0, 4 <i>sec</i>
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Conclusions

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Conclusions

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Conclusions

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- The relation between persistent homology and spectral sequences allows us to reuse our previous programs for spectral sequences to compute persistent homology groups. The programs are valid for the integer case and for infinite simplicial sets with effective homology. In particular they can be used for digital images.
- Discrete vector fields and effective homology can be used to reduce the size of digital images before computing persistent homology.