



# A Hierarchical Approach to Topological Shape Analysis

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## 1 Motivations

**Our interest** - applying tools from algebraic topology (homology) to the description and analysis of shapes

- ▶ defined by finite sets of points organized to form discrete structures, like cells or simplicial complexes
- ▶ here we use cell complexes

**Issues** both theoretical and computational

- ▶ size of the data sets: often huge collections of unorganized sets of points
- ▶ dimension of the data sets: high-dimensional data

**Computational problems** in using topological tools

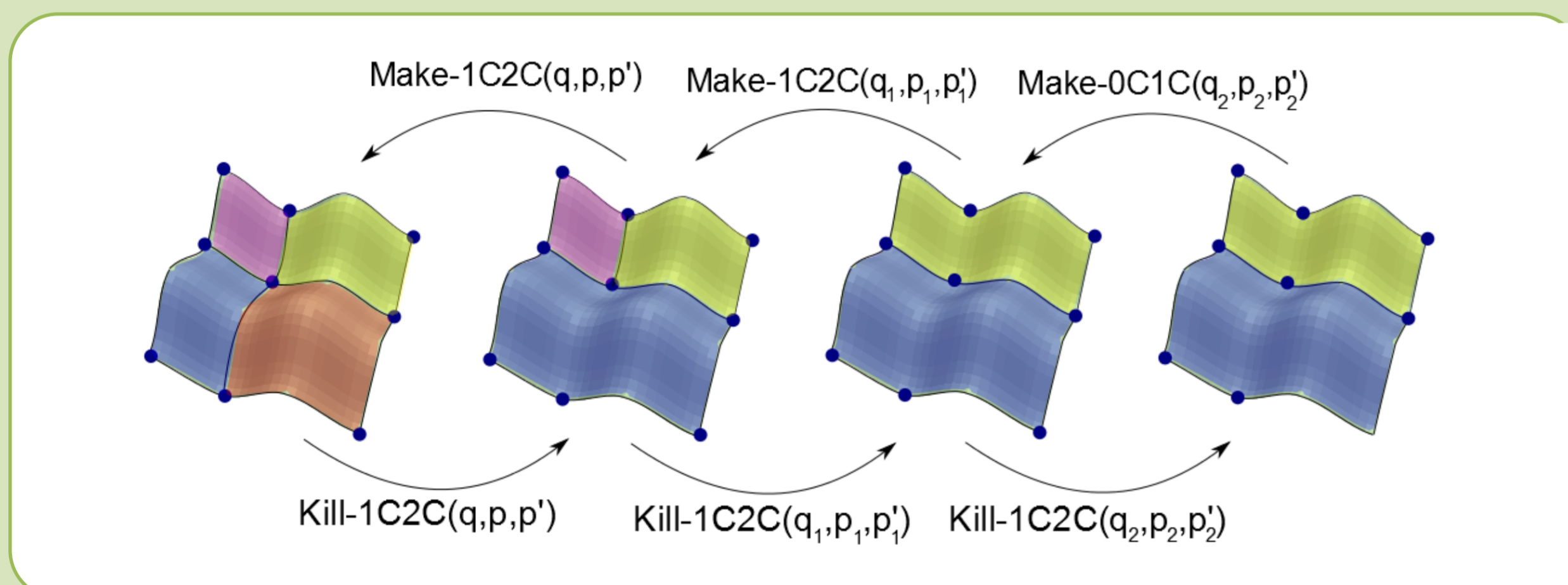
- ▶ high computational costs
- ▶ high storage costs

**Our approach here:** use of hierarchical, multi-resolution representations

## 2 Hierarchical Cell Complex (HCC)

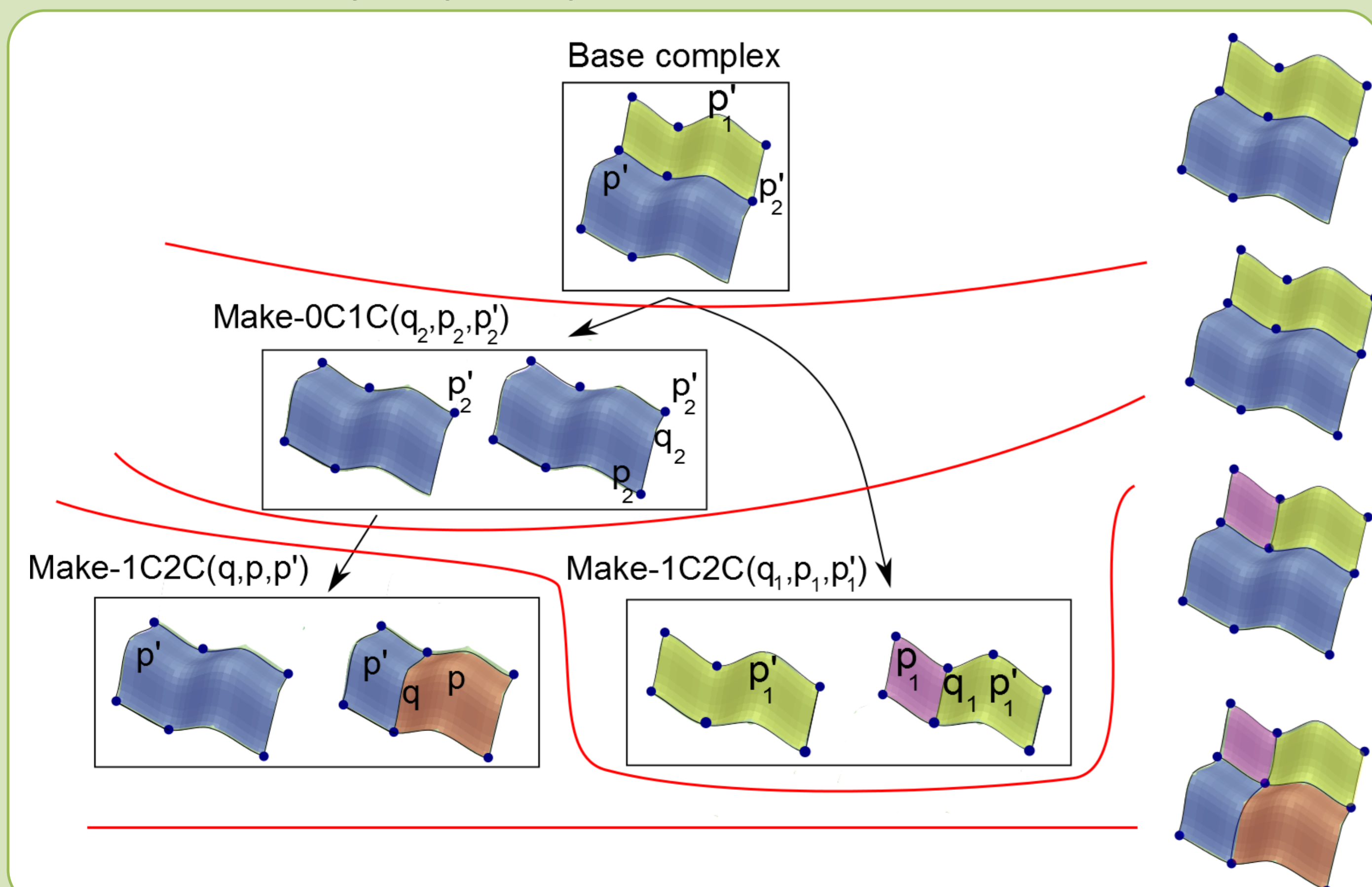
Based on the **simplification** of a given cell complex  $X$  by iteratively applying atomic **homology-preserving** operators ( $Kill-iCell-(i+1)Cell$ )

- ▶ this generates a **sequence  $S$**  of simplifications



An **HCC** consists of **three components** ( $X', M, R$ ):

- ▶ **base complex  $X'$**  obtained from  $X$  by applying the sequence  $S$  of simplifications
- ▶ set  $M$  of **refinements** ( $Make-iCell-(i+1)Cell$ ), inverse of the operators in sequence  $S$
- ▶ **direct dependency relation  $R$**  between pairs of refinements, described as a *Directed Acyclic Graph (DAG)*:
  - ▶ a **refinement  $\mu = Make-iCell-(i+1)Cell(q,p)$**  directly depends on a refinement  $\mu^*$  if and only if  $\mu^*$  creates a cell that will be in the immediate boundary or co-boundary of  $p$  or  $q$



- ▶ The transitive closure of the direct dependency relation can be shown to be a **partial order**

In an  $HCC(X', M, R)$ , there is a **one-to-one correspondence** between

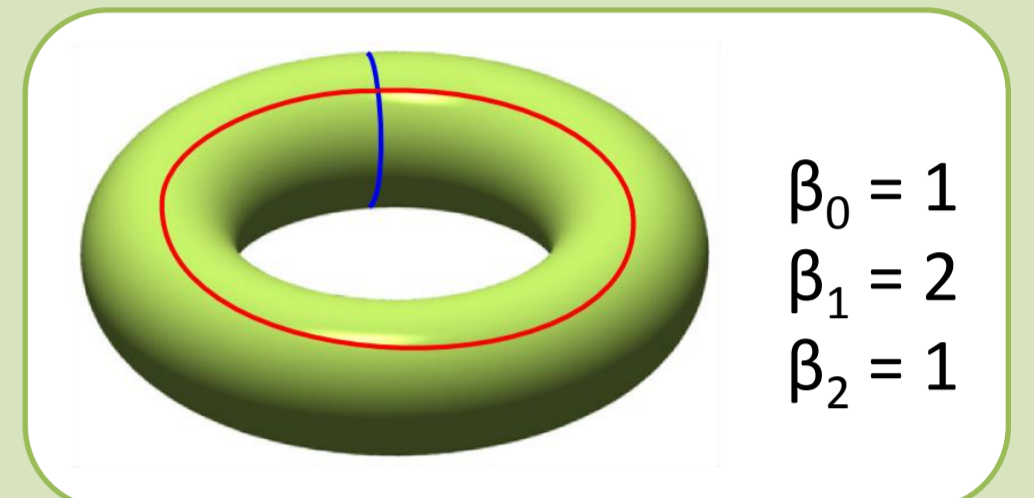
- ▶ the subsets of refinements in  $M$ , which are **closed** w.r.t. respect to the dependency relation, and the complex which can be extracted from it

Extraction process (**selective refinement**):

- ▶ top-down traversal of the DAG with iterative application of  $Make-iCell-(i+1)Cell$  refinements to the base complex  $X'$

## 3 Homology Computation on the HCC

We are interested in computing the **homology groups**  $H_i(X; \mathbb{Z}_2)$  of a cell complex  $X$  with coefficients in  $\mathbb{Z}_2$



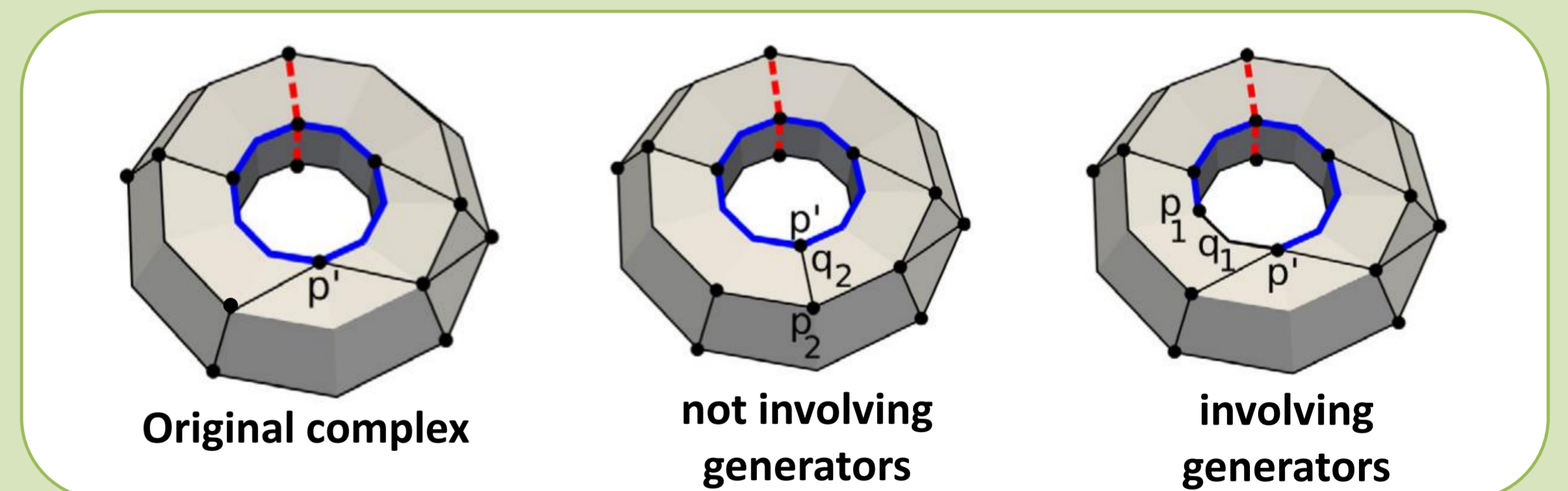
- ▶ the Betti numbers  $\beta_i$ 's of  $X$ 
  - ▶  $\beta_i$  measures the number of independent non-bounding  $i$ -cycles in  $X$  ( $i$ -holes)
- ▶ the homology generators of degree  $i$ : generators of the  $\mathbb{Z}_2$ -vector space  $H_i(X; \mathbb{Z}_2)$

All complexes, which can be extracted from an  $HCC(X', M, R)$ , have the same homology of the original complex  $X$

- ▶ **Smith Normal Form (SNF)** reduction used to compute homology on the base complex  $X'$ .

**Computing generators** during selective refinement

- ▶ application of  $Make-iCell-(i+1)Cell$  only affects generators of degree  $i+1$



## 4 Experimental Evaluation

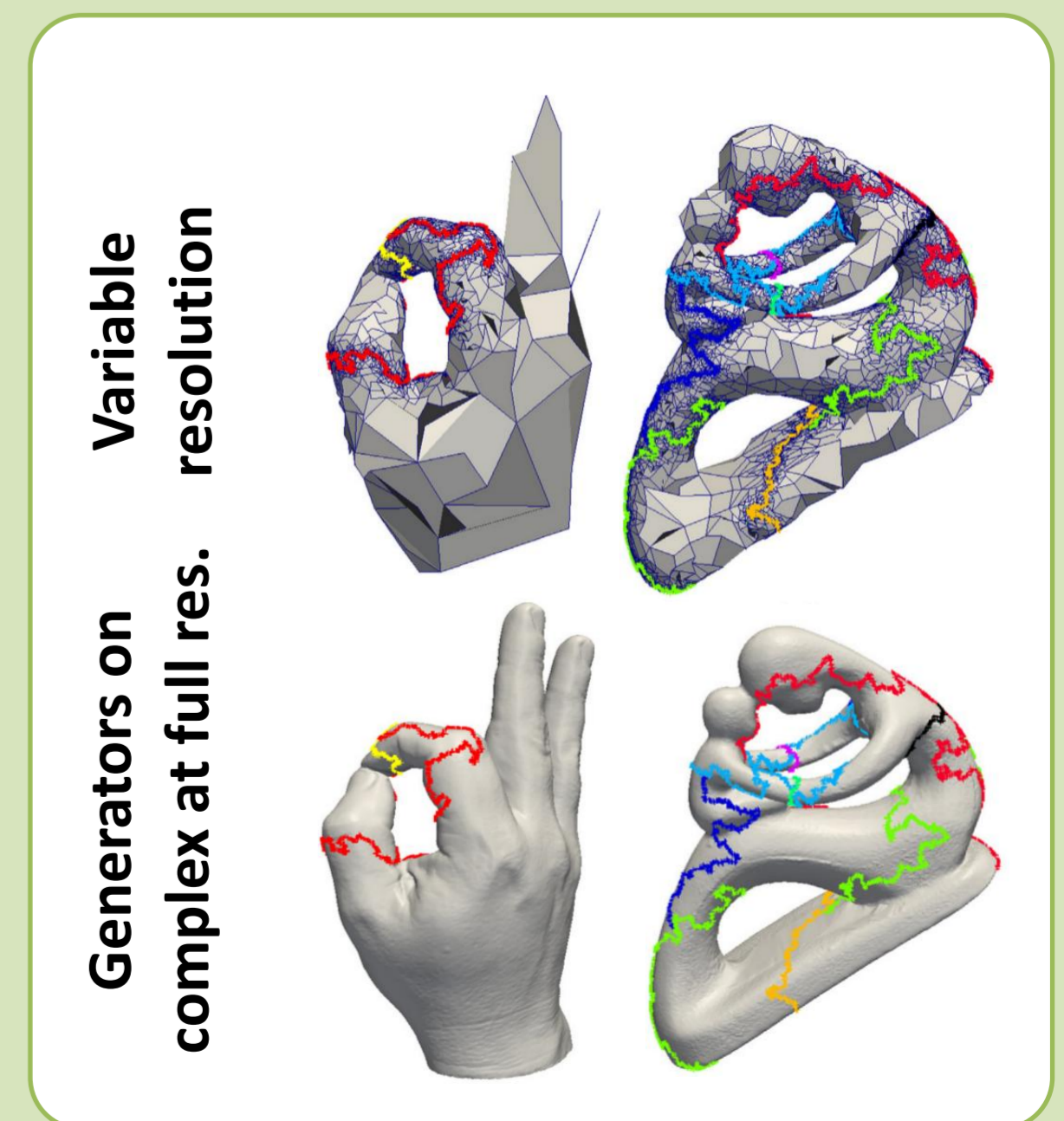
**Computation** of homology on the base complex plus refining all the generators to full resolution:

- ▶ min 0.15 seconds – max 83.3 seconds
- ▶ on the smallest complex (*Genus3*- 40K cells) 2.6 hours for homology computation

**Extraction at uniform and variable resolutions:**

- ▶ variable resolution: maximum detail only in the neighborhood of specific homology generators

Dataset	SNF Time	Tot Ref Time	Uniform Ref. Time	Generators Ref. Time
Genus3	$9.2 \times 10^{-5}$ s	0.15s	4K	0.03s
			10K	0.07s
			16K	0.12s
Fertility	$8.3 \times 10^{-5}$ s	9.31s	144K	1.8s
			362K	4.6s
			579K	7.52s
Hand	$9.8 \times 10^{-5}$ s	14.9s	200K	2.6s
			500K	6.8s
			800K	11.2s
Buddha	0.02s	23.7s	320K	0.5s
			800K	4.3s
			1.2M	19.2s
Skull	0.007s	6.4s	75K	1.0s
			187K	2.9s
			299K	5.0s
Fert-Solid	8.8s	74.5s	1.2M	7.5s
			3.1M	29.1s
			4.9M	69.3s



**Datasets** – triangle and tetrahedral complexes (between 40K and 6.2M cells); storage cost between 4.8 and 980 MB.