

Arnau Mas

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- ▶ Extract many **radiomic features** from scans
- ▶ Look for correlations between radiomic features and treatment response

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Benefits

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Drawbacks

- ▶ May be hard to reproduce
- ▶ High dimensional feature spaces
- ▶ Limited number of cases



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TOPiomics



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- ▶ Main aim: early detection of patients with strange radiomic signatures, *outliers*, for whom standard treatments could fail.
- ▶ Use *topological data analysis*, hence TOPiomics (topological radiomics).

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This is persistence

The elevator pitch

Algebraic topology studies topological spaces by computing algebraic invariants, namely with functors

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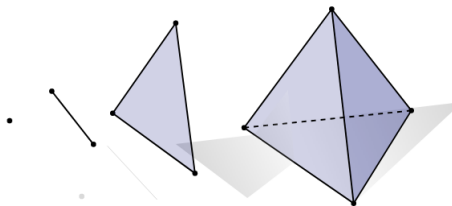
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They come in many flavours, the simplest one is *simplicial homology*, which works for *simplicial complexes*.

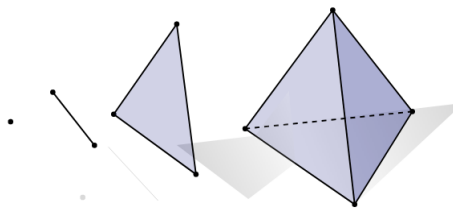
The ingredients of homology

- *Simplex*. The convex hull of a set of points.



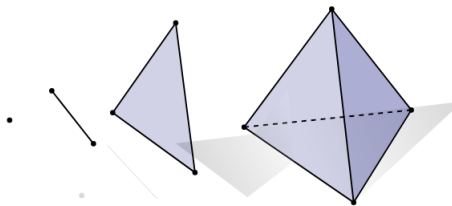
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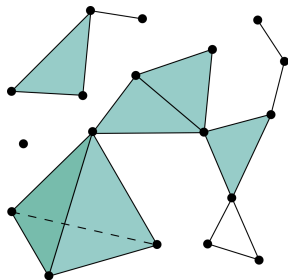
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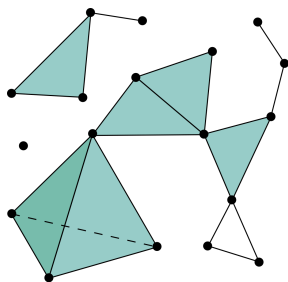
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- ▶ *Simplicial complex, K* . Topological space assembled out of simplices glued along their faces.
- ▶ *Chain groups, $C_n(K)$* . Free abelian groups generated by the n -simplices of a complex.



Remark

In the combinatorial picture, the geometrical requirements are dropped and one speaks of *abstract* simplices, *abstract* simplicial complexes, etc.

The boundary morphism

Orientation

The simplex generated by p_0, \dots, p_n is written $[p_0, \dots, p_n]$. The ordering determines an orientation, and we require that flipping orientation implies a change of sign in $C_n(K)$, e.g.

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The chain groups are not really free!

The boundary morphisms

Define the boundary morphism $\partial_n: C_n(K) \rightarrow C_{n-1}(K)$ by

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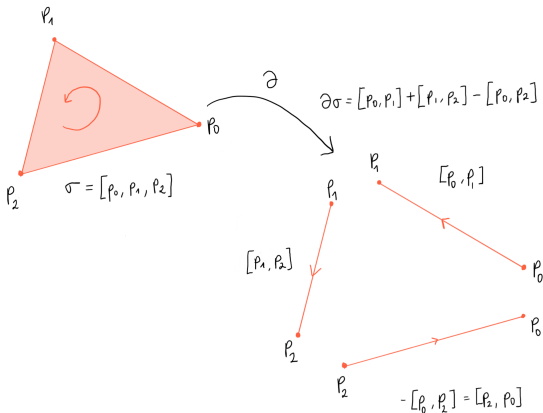
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Fact

$$\partial_n \circ \partial_{n+1} = 0$$

so boundaries are always cycles.

Homology groups

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The key insight: Homology groups measure **cycles which are not boundaries**. They tell us about the number of n -dimensional holes in our space.

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Instead of a single simplicial complex, consider a *filtration*,

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The steps of the filtration can be thought of as time

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Because of functoriality, there are maps between the different steps of homology,

$$f_i^j : H_d^i(K) \rightarrow H_d^j(K).$$

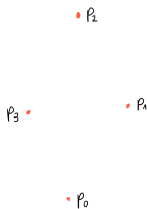
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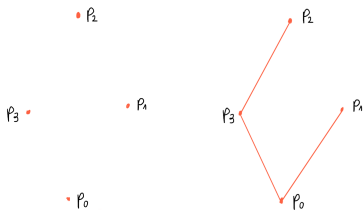
At each step, classes can be born (not in the image of f_i^{i+1}), die (in the kernel of f_i^{i+1}) or merge (have the same image through f_i^{i+1}).

An example



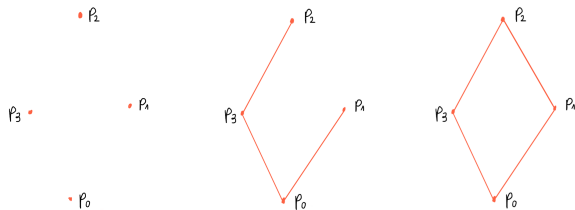
$[p_0], [p_1], [p_2], [p_3]$ are born.

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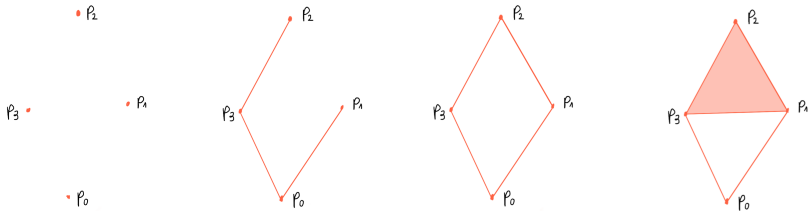
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An example



The cycle $[p_0, p_1] + [p_1, p_2] + [p_2, p_3] + [p_3, p_0]$ is born.

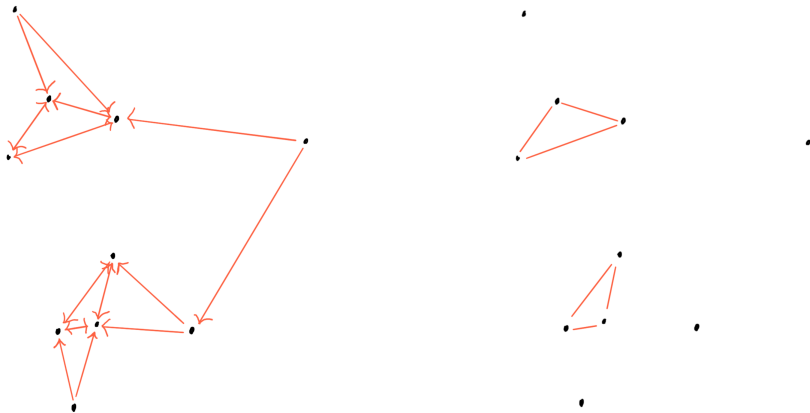
An example



The cycle does not die.

Why the MkNN graph?

It is good for detecting clusters in a data set.



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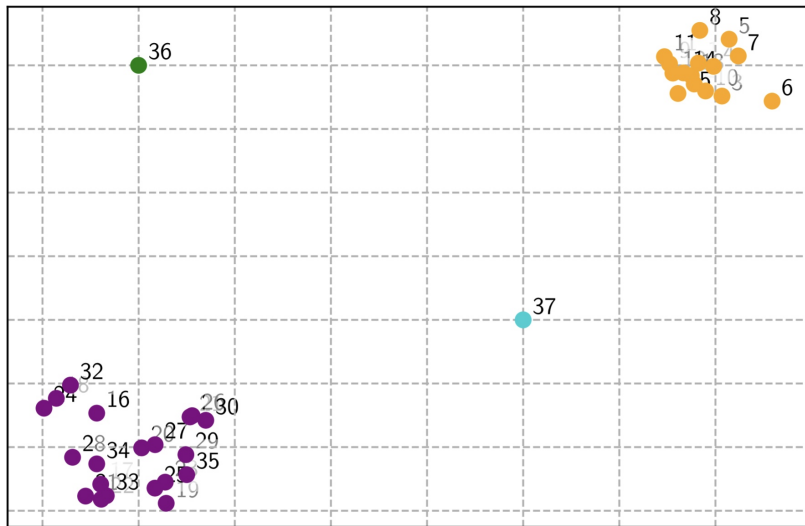
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- ▶ The class `Homology` computes the homology.
- ▶ The persistence data of each class is gathered and plotted to detect the outliers.

The class Cloud

A run with toy data



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