Computation of Natural Homology

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Introduction

The objective of directed algebraic topology is to compare spaces **with a notion of order** up to continuous deformations **that preserve this order**. This problem originally comes from geometric semantics of truly concurrent systems : PV-programs **[Dijkstra 68]** ; scan/update **[Afek et al. 90]** ; higher dimensional automata **[Pratt 91]** and has applications in various fields like rewriting **[Malbos 03]** and the theory of relativity **[Dodson, Poston 97]**.

Its purpose is to provide tools for the study of those directed spaces mimicking those that exist in algebraic topology, which studies topological spaces up to continuous deformation (**homotopy**). One of these tools is **homology**:

- **sound invariant of homotopy** : if two spaces are equal up-to continuous deformations then they have the same homology.
- **partially complete** : if two simple spaces have the same homology then they are homotopically equivalent.
- **computable** : if a space is finitely presented, then we can compute its homology.
- **modular** : homology can be expressed from homology of simpler spaces.

In directed algebraic topology, we consider spaces equipped with a collection of **directed paths**, i.e., **increasing** continuous functions from $[0, 1]$ to the space. We say that two dipaths are **dihomotopic** if you can continuously deform one into the other **while staying a dipath**.

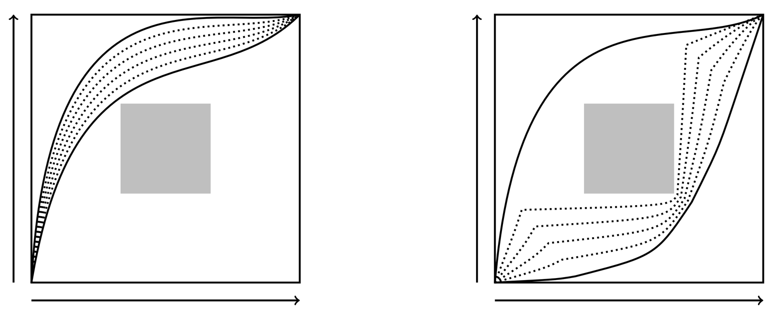


Figure 1: (a) (di)homotopic (b) non-(di)homotopic

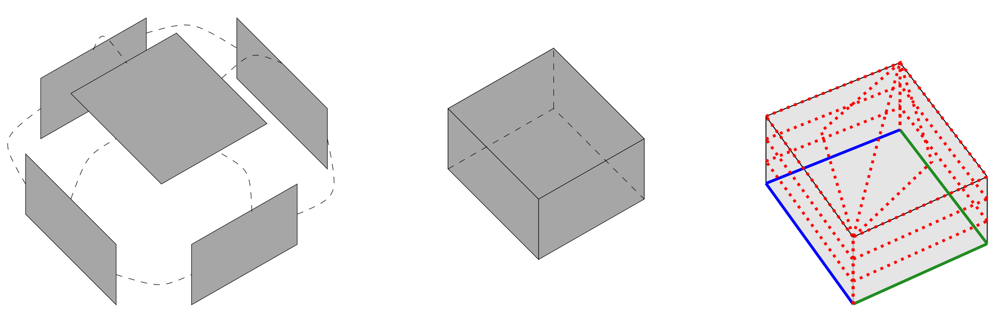


Figure 2: Fahrenberg's matchbox - blue and green dipaths are homotopic but not dihomotopic

One important thing is that **homotopy and dihomotopy may be different**. This is a real problem when we design a directed homology : such a homology must detect a default of dihomotopy even if there is no default of homotopy. In particular, Fahrenberg's matchbox must have a directed homology different from the one of a point.

Problem : this is not the case of the candidates of directed homology in the literature.
Our main contribution : a definition of a computable directed homology, which is fine-grained enough.

Natural homology

For the geometric realization of a cubical set (glueing of cubes), a first natural definition of a directed homology could be the **classical homology of the space of traces** (i.e., dipaths modulo increasing reparametrizations **[2]**) from the initial state to the final state. The idea is that n-directed loops are $(n-1)$-loops of a space of traces. However, that is not sufficient to classify programs.

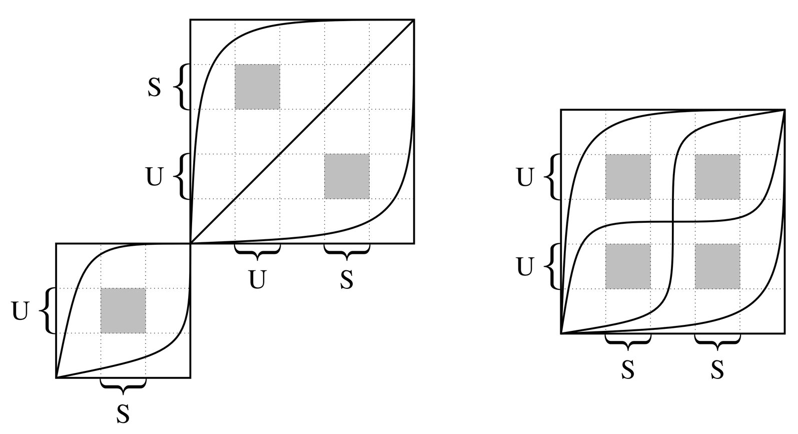
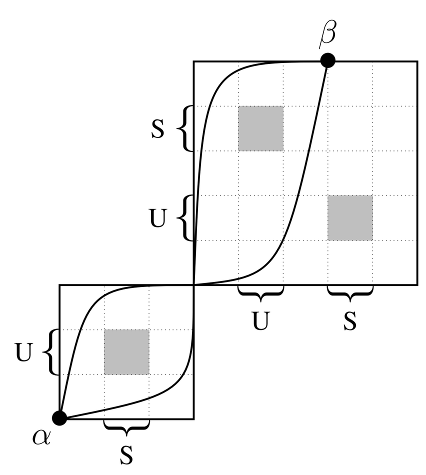


Figure 3: geometric semantics of scan/update programs $(S|U) \bullet (U.S|U.S)$ and $S.S|U.U$

Let us consider the spaces on the left (coming from the geometric semantics of scan/update). Their trace spaces from their bottom-left point to their top-right point are homotopically equivalent to a 6 point space (i.e., there are 6 equivalence classes of total executions). Consequently, this first definition of directed homology does not distinguish these programs that have very different behaviors. **Our idea is to replace this homology of a trace space by the collection of homologies of all trace spaces between two accessible points and the way they vary when we extend the traces.**

It will be enough to distinguish those two spaces. Indeed, in the left one, the trace space between α and β is homotopically equivalent to a 4 point space, but there is no pair of points in the right one between which the trace space is of this homotopy type. Thus, in the first homology system of the left program, there will be a group isomorphic to $\mathbb{R}^4$ but not in the one of the right space. Also, the **natural homology of the matchbox is not trivial** because, since there are non-dihomotopic paths, there is a trace space with two path-connected components.



Concretely, the n**th natural homology system** of a directed space will be the functor defined as follow **[6]**:

trace of p with p dipath from a to b	$\longmapsto$	classical homology of the space of traces from a to b
extension (α, β) α from a' to a, β from b to b'	$\longmapsto$	morphism induced in homology by concatenation with α on the left and β on the right

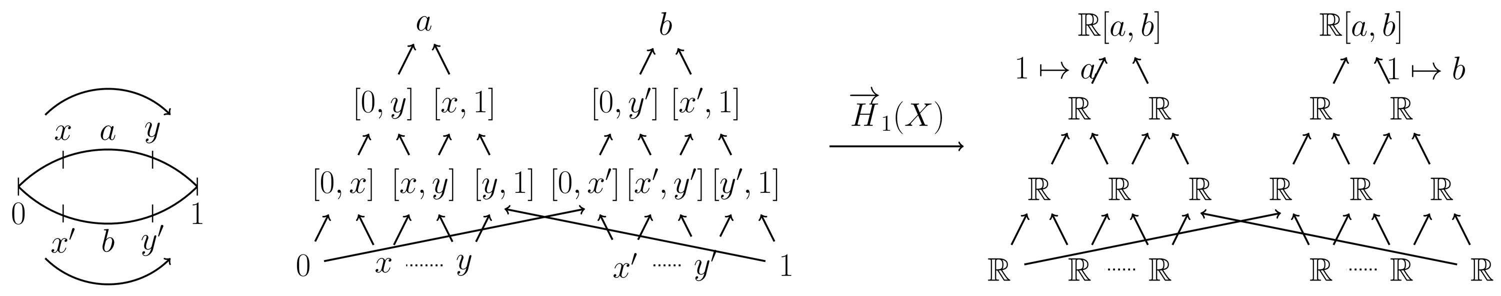


Figure 4: example of a first natural homology

Bisimulation of functors

The natural homology of a directed space is incredibly **fine-grained**: it not only records local homology groups of all the trace spaces but also for which traces they occur. If we wish to compare the natural homology of two directed spaces, the latter should be unimportant. It is the **patterns of change** when we extend traces that count, not the value at each trace. **We have introduced a notion of bisimulation of functors that smoothes this out [1].** This comes from the theory of open maps **[5]**.

In our case, an **open map** between small **Vect**($\mathbb{R}$)-valued functors $F : X \longrightarrow$ **Vect**($\mathbb{R}$) and $G : Y \longrightarrow$ **Vect**($\mathbb{R}$) is a pair of:

- a fibration $\Phi : X \longrightarrow Y$, i.e., a functor such that:
  - Φ is surjective on objects
  - for every object x of X, and every morphism $f : \Phi(x) \longrightarrow y$ of Y, there exists a morphism $g : x \longrightarrow x'$ of X such that $\Phi(g) = f$
- a natural isomorphism: $\sigma : F \Longrightarrow G \circ \Phi$

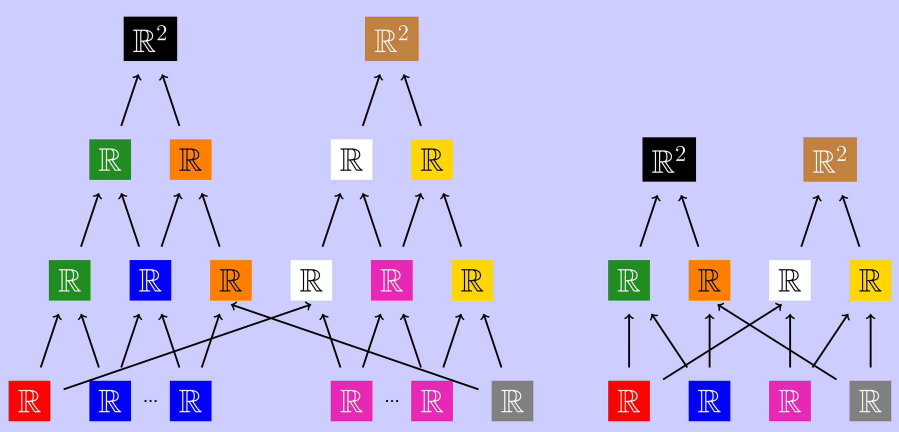


Figure 5: example of an open map between functors

We say that two functors F and G are **bisimilar** if there exists a span of open maps between them.

Discrete natural homology

When X is the geometric realization of a non-looping precubical set, we can define discrete natural systems that intuitively will have the same information as the natural homology systems of X and that will be finite when the precubical set is. This will be done by considering a sub-category of the category of traces, **restricted to some combinatorial traces**, similar to **[3]**. This produces what is called **discrete natural homology systems**.

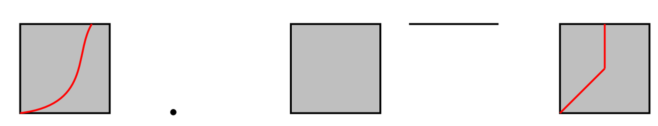


Figure 6: trace, sequence of carriers, combinatorial trace

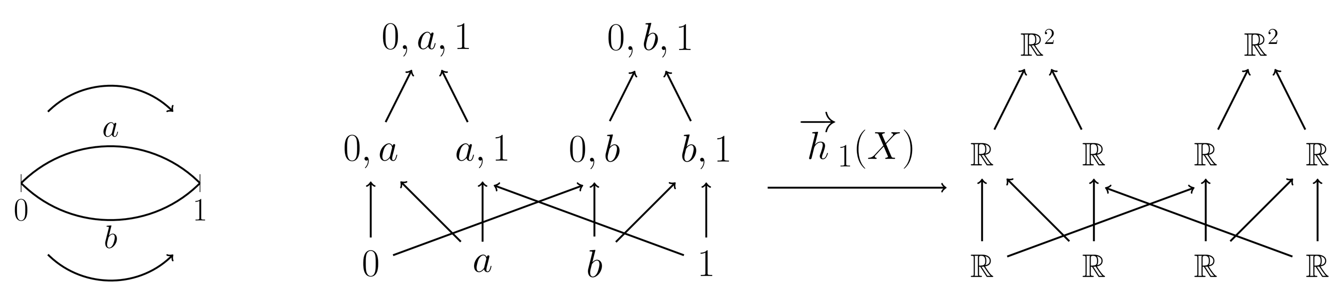


Figure 7: example of a first discrete natural homology

The function that maps each trace to the combinatorial trace constructed like in Figure 6, can always be extended to a fibration, but in general we cannot construct an open map between the natural homology systems and the discrete ones. But it can be done in simple cases:

Theorem [1]: If X is the geometric realization of a simple precubical set, then
- there exists an open map from $\overrightarrow{H}_n(X)$ to $\overrightarrow{h}_n(X)$ (in particular, they are bisimilar).
- the bisimulation type of discrete natural homology systems is invariant under subdivision
- if the precubical set is finite, the bisimulation type of $\overrightarrow{H}_n(X)$ is computable when homology is taken in $\mathbb{R}$ or $\mathbb{Q}$.

Conclusion

Definition of a directed homology which :

- **is computable on finite simple precubical sets,**
- **classifies the matchbox correctly,**
- **is invariant under subdivision and directed deformation retracts,**
- **has long exact sequences (homological category [4]),**
- **verifies a Hurewicz-like theorem.**

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