

### Introduction

The objective of directed algebraic topology is to compare spaces **with a notion of order** up to continuous deformation **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 what exists in algebraic topology, a well developed field in mathematics, which studies topological spaces up to continuous deformation (**homotopy**). One of these tools is **homology**. In algebraic topology, homology is :

- a **sound invariant of homotopy** : if two spaces are equal up to continuous deformations (homotopically equivalent) then they have the same homology
- **partially complete** : if two simply-connected CW-complexes have the same homology then they are homotopically equivalent
- **computable** : if a space is finitely presented (finite simplicial set, precubical set, ...), then we can compute its homology (via matrixes algebra)
- **modular** : homology can be expressed from homology of simpler spaces (for example, Mayer-Vietoris theorem)

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**.

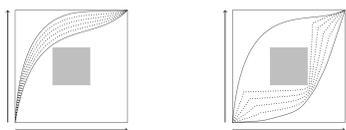


Figure 1: (di)homotopic non-(di)homotopic

One important thing is that **homotopy and dihomotopy may be different** :

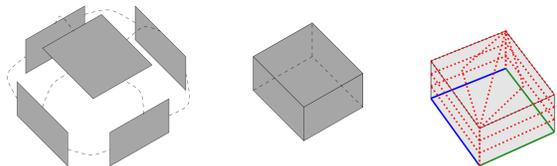


Figure 2: Fahrenberg's matchbox - blue and green dipaths are homotopic but not dihomotopic

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 directed homology fine enough to detect default of dihomotopy.**

### Natural homology

For the geometric realization of a cubical set (gluing 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 reparametrization [Raussen 09]) between the initial state to the end 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 !

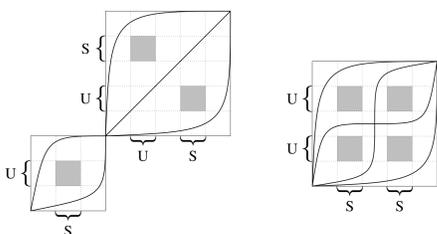


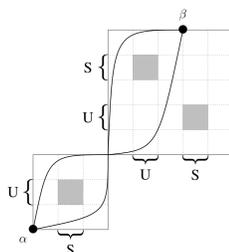
Figure 3: geometric semantics of scan/update programs  $(S|U) \bullet (U.S|U.S)$  and  $S.S|U.U$

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. in those two programs, they are 6 equivalence classes of total executions). And so, 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 a natural system [Baues, Wirsching 85] of homologies of all trace spaces between two accessible points and the way they vary when**

**we extend the traces.**

It will be sufficient to distinguish those two spaces. Indeed, in the left one, the trace space between  $\alpha$  and  $\beta$  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  $\mathbb{Z}^4$  but not in the one of the right space. Also, the first homology system of the matchbox is not trivial because the trace space between  $s$  and  $t$  is homotopically equivalent to a 2 point space.

More concretely, the  $n$ th homology system of a directed space will be the functor defined this way [Raussen 07] :



trace  $p$   $\mapsto$   $H_{n-1}$ (space of traces from  $a$  to  $b$ )  
 $p$  dipath from  $a$  to  $b$

extension  $(\alpha, \beta)$   $\mapsto$  morphism induced in homology by concatenation  
 $\alpha$  from  $a'$  to  $a$ ,  $\beta$  from  $b$  to  $b'$  with  $\alpha$  on the left and  $\beta$  on the right

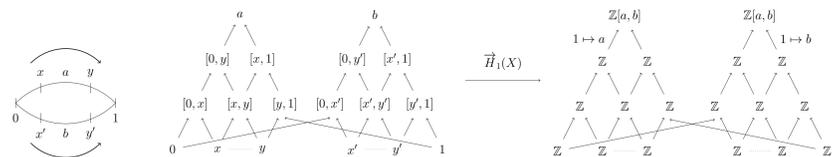


Figure 4: example of a first natural homology

### 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 trace 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 natural systems that smoothes this out [Dubut et al. 15].

This comes from the theory of open maps [Joyal et al. 96]. In our case, an open map between small **Ab**-valued functors  $F : X \rightarrow \mathbf{Ab}$  and  $G : Y \rightarrow \mathbf{Ab}$  is a pair of:

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

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

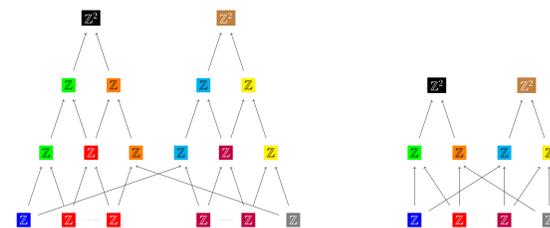


Figure 5: example of bisimilar functors

### 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 than 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. With each point of the geometric realization, we associate a cube of the precubical set as the biggest one to which this point belongs. This is the **carrier** of the point [Fajstrup 05]. Then with each trace, we can associate the sequence of cubes crossed by this trace and from this sequence of cubes we can construct a trace by joining the center of consecutive cubes. We can then restrict our natural homology systems to those traces and call these new systems **discrete** natural homology systems.



Figure 6: trace, sequence of carriers, combinatorial trace

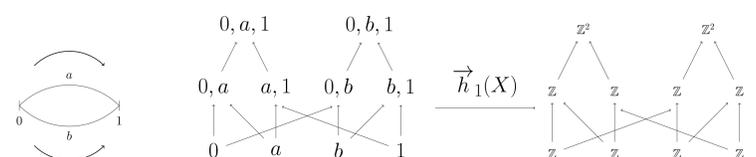


Figure 7: example of a first discrete natural homology

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

- Theorem [Dubut et al. 15]:** If  $X$  is the geometric realization of a simple precubical set, then
- there exists an open map from  $\vec{H}_n(X)$  to  $\vec{h}_n(X)$  (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  $\vec{H}_n(X)$  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 dihomeomorphism and

**subdivision**

- has long exact sequences (natural homology lives in a homological category [Grandis 91])
- verifies a Hurewicz-like theorem