Directed homotopy and homology theories for geometric models of true concurrency

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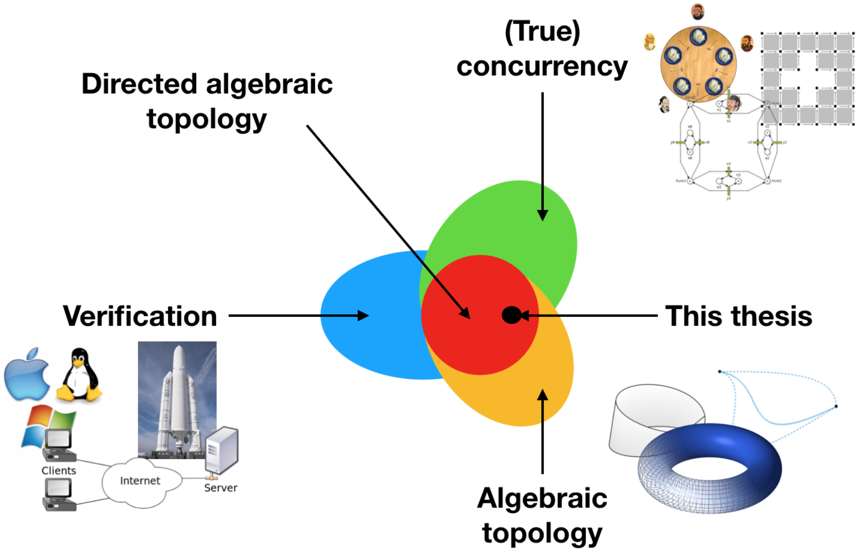

Directed algebraic topology
(True) concurrency
Verification
This thesis
Algebraic topology
Clients
Internet
Server

Applications of directed algebraic topology

Some work done:

- models for true concurrency and distributed tasks **[Pratt, van Glabbeek, Winskel, Nielsen]**,
- state space reduction techniques **[Haucourt, Goubault, Fajstrup, Raussen, Mimram]**,
- verification (deadlocks/unreachable states detection, correctness via serialisability, decomposition of processes) **[Haucourt, Goubault, Fajstrup, Raussen, Mimram, Ninin]**

Work in progress:

- fault-tolerance (possibility and impossibility results) **[Herlihy, Rajsbaum, Kozlov, Goubault, Mimram, Tasson]**,
- higher-order rewriting **[Malbos]**,
- Conley-Morse-Forman theory **[Mrozek]**,
- pursuit-evasion games and max flow-min cut duality **[Krishnan, Grhist]**,
- relativity **[Dodson, Postdon]**.

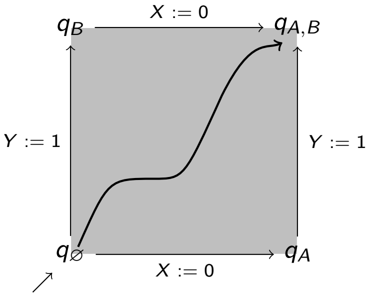
The geometry of true concurrency

Independent actions: interleaving vs true concurrency

$$
\begin{tikzcd}
q_B \arrow[r, "X := 0"] & q_{A,B} \\
q_\varnothing \arrow[u, "Y := 1"] \arrow[r, "X := 0"'] & q_A \arrow[u, "Y := 1"']
\end{tikzcd}
$$

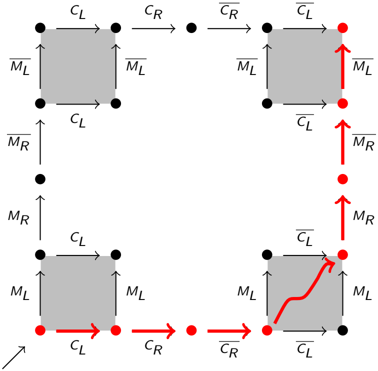
Interleaving behaviors: A then B or B then A

Independent actions: interleaving vs true concurrency



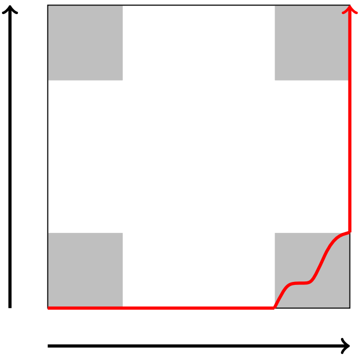
Continuous behaviors: any scheduling of A and B
Refinement **[van Glabbeek, Goltz]**: in reality $X := 0$ and $Y := 1$ are not atomic

Truly concurrent systems



HDA **[Pratt]** = transition system with higher dimensional data that accounts for true concurrency

The geometry of true concurrency



geometry of true concurrency

$$\|$$

form	+	direction
$\uparrow$		$\uparrow$
topological space		partial order

execution

$$\|$$

continuous + directed

path

True concurrency, geometrically

truly concurrent system	directed space
states	points
executions	directed paths
modulo scheduling of independent actions	modulo directed homotopy

The objective of this thesis

- Understand the geometry of those **directed** spaces...

- ...with the study of truly concurrent systems through the prism of geometry as a goal.

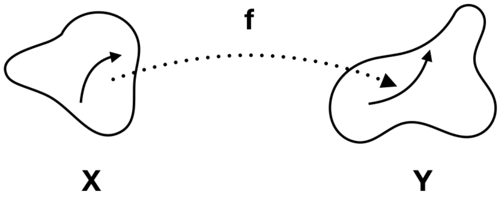
Directed algebraic topology

D-spaces and dipaths **[Grandis]**

A **d-space** is a topological X with a subset $\overrightarrow{P}(X)$ of paths, called **dipaths**, which contains constant paths, and which is closed under concatenation and non decreasing reparametrizations.

Ex: a partially ordered space with monotonic paths

A **dimap** is a continuous function $f : X \longrightarrow Y$ such that for every $\gamma \in \overrightarrow{P}(X)$, $f \circ \gamma \in \overrightarrow{P}(Y)$. We note **dTop** the category of d-spaces and dimaps.

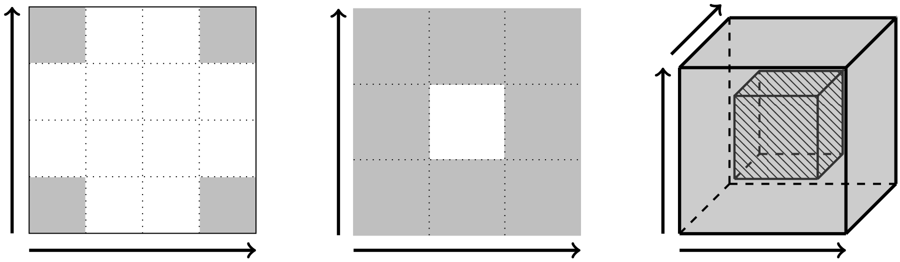


Cubical complexes

Euclidian cubical complex: any subspace of $\mathbb{R}^n$ which is a finite union of cubes of the form

$$[a_1, a_1 + \alpha_1] \times \ldots \times [a_n, a_n + \alpha_n]$$

with $a_i \in \mathbb{Z}$ and $\alpha_i \in \{0, 1\}$.



True concurrency, geometrically

truly concurrent system	directed space
states	points
executions	directed paths
modulo scheduling of independent actions	modulo directed homotopy

True concurrency, geometrically

truly concurrent system	d-space
states	points
executions	dipaths
modulo scheduling of independent actions	modulo directed homotopy ??

Dihomotopy of dipaths

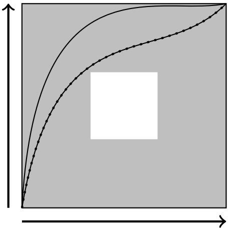
A **dihomotopy** from γ to τ, dipaths from a to b, is a dimap

$$H : \overline{[0,1]} \times \overrightarrow{[0,1]} \longrightarrow X$$

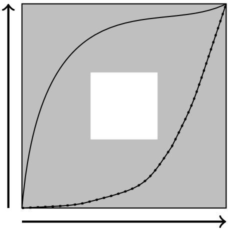
such that:

- for every t, $H(0,t) = a$,
- for every t, $H(1,t) = b$,
- for every t, $H(t,0) = \gamma(t)$
- for every t, $H(t,1) = \tau(t)$.

Two dipaths are **dihomotopic** if there is a dihomotopy between them.

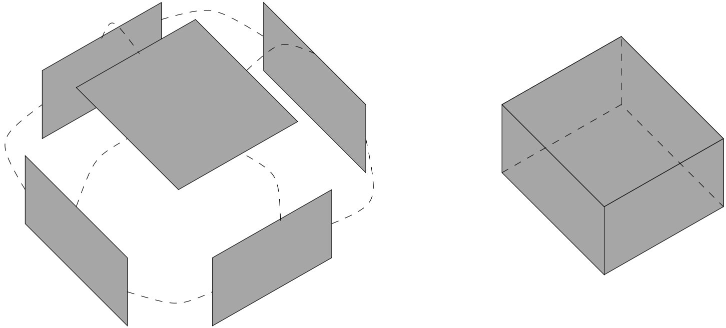


dihomotopic

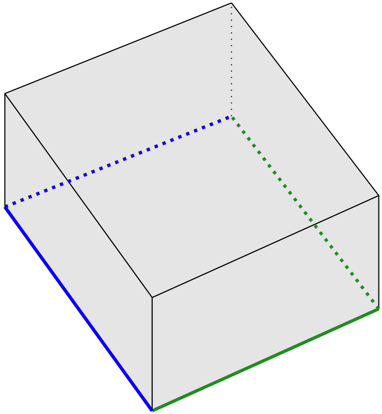


non-dihomotopic

Example: Fahrenberg's matchbox

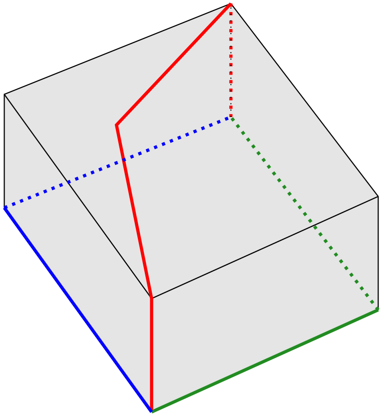


Example: Fahrenberg's matchbox



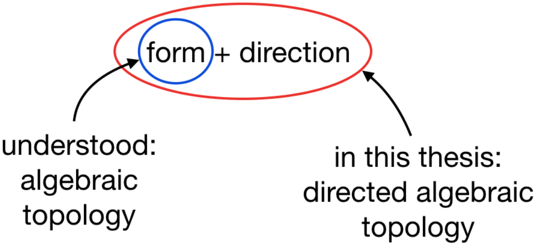
homotopic...

Example: Fahrenberg's matchbox



... but not dihomotopic

Goal of thesis

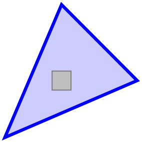


Extend the work from algebraic topology:

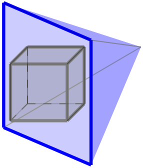
- homology
- homotopy

Homology theories

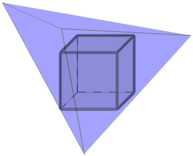
Homology = counting



hole of dimension 1



not a hole of dimension 1 ...



... but a hole of dimension 2

$$H_n(X) \simeq \mathbb{R}^{\text{number of holes of dimension } n}$$
$$H_0(X) \simeq \mathbb{R}^{\text{number of path-connected components}}$$

Properties of homology

- **sound**: invariant of homotopy
- **precise**: do not lose too much information from homotopy **[Hurewicz]**, partially complete **[Whitehead]**
- **modular**: the homology of a space can be expressed from the homology of simpler spaces **[Mayer-Vietoris]**
- **computable**: when the space is finitely presented

Our contribution:
a homology theory for d-spaces with the same kind of properties

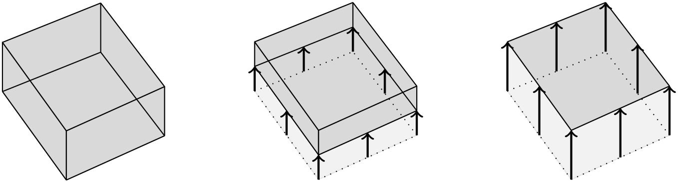
Previous proposals of directed homology

- past and future homologies **[Goubault 95]**
- ordered homology groups **[Grandis 04]**
- directed homology via ω-categories **[Fahrenberg 04]**
- homology graph **[Kahl 13]**
- and some others

The matchbox, a litmus test

ordered homology groups **[Grandis 04]** = classical homology + partial order

Not precise enough : do not distinguish matchbox from a point



The main ingredients of our directed homology [D.&G.G. ICALP'15]

1. Consider trace spaces **[Raussen]** ($\simeq$ spaces of dipaths).
2. Look at how they evolve with time (extensions).
3. Apply classical homology on those data.
4. Look at the evolution (using bisimulation techniques).

Basic block: space of dipaths ?

$\overrightarrow{P}(X)(a,b) =$ the set of $\gamma \in \overrightarrow{P}(X)$ with $\gamma(0) = a$ and $\gamma(1) = b$

$\overrightarrow{P}(X)(a,b)$ can be equipped with a topology: its path-connected components are the dihomotopy class of dipaths

Problem: concatenation of dipaths is not associative

$$\begin{array}{c} (\alpha \star \beta) \star \gamma \\ || \\ \xrightarrow{\alpha}\ \xrightarrow{\beta}\ \xrightarrow{\quad\quad\gamma\quad\quad} \end{array} \qquad\qquad \begin{array}{c} \alpha \star (\beta \star \gamma) \\ || \\ \xrightarrow{\quad\quad\alpha\quad\quad}\ \xrightarrow{\beta}\ \xrightarrow{\gamma} \end{array}$$

Basic block: trace spaces **[Raussen]**

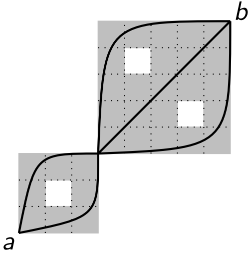
Concatenation is associative modulo reparametrization

Trace = dipath modulo reparametrization

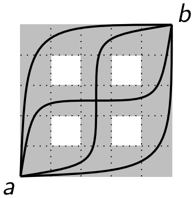
We can also define the **trace space** $\overrightarrow{T}(X)(a, b)$ as the quotient space of $\overrightarrow{P}(X)(a, b)$ modulo reparametrization.

Directed homology = classical homology of a trace space ?

homology of X = classical homology of $T(X)(a,b)$



$(S \mid\mid U) \bullet (S.U \mid\mid S.U)$



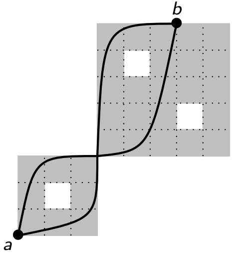
$S.S \mid\mid U.U$

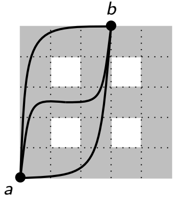
$$T(A)(a,b) \simeq 6 \textit{ point space} \simeq T(B)(a,b)$$

$$\text{homology of } A \simeq \mathbb{R}^6 \simeq \text{homology of } B$$

Directed homology = evolution of classical homology of trace spaces with time

How to distinguish those two d-spaces ?





make a, b vary

$\overrightarrow{T}(A)(a, b) \simeq 4$ *point space*

directed homology of $A \simeq \mathbb{R}^4$

for every a, b,

$\overrightarrow{T}(B)(a, b)$ is either a

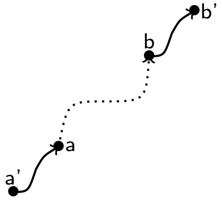
1, 2, 3 or 6 point space

Natural homology

directed homology = collection of modules of homology of the trace spaces indexed by pairs of points, and of linear maps indexed by extensions

$\mathcal{E}_X$ = category whose:

- objects are pairs (a, b) of points such that there is a dipath from a to b
- morphisms are extensions



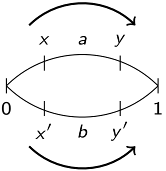
Natural homology [D.&G.G. ICALP'15]:

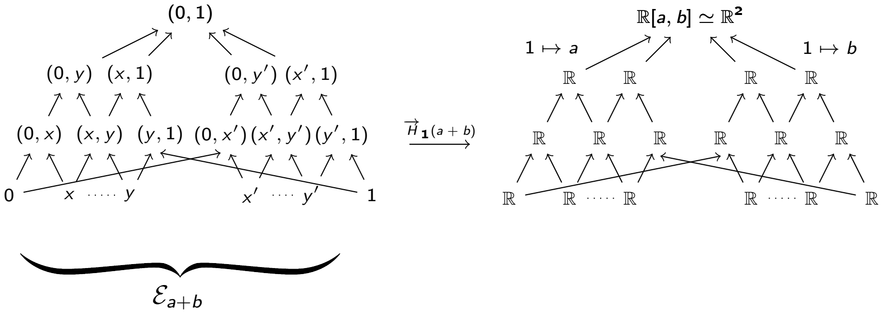
diagram $\overrightarrow{H}_n(X) : \mathcal{E}_X \longrightarrow \mathbf{Mod}(\mathcal{R})$

$$(a, b) \longmapsto H_{n-1}(\overrightarrow{T}(X)(a, b))$$

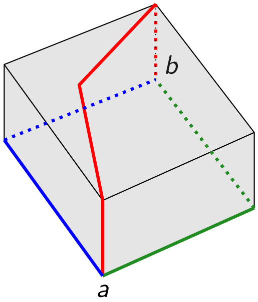
(H_{n-1} = classical singular homology)

Example : first natural homology of $a + b$





Natural homology on the litmus test



Natural homology detects failure of dihomotopy in the matchbox.

2 dipaths non dihomotopic

$\Rightarrow \overrightarrow{T}(X)(a,b) \simeq$ 2 point space

$\Rightarrow H_0(\overrightarrow{T}(X)(a,b)) \simeq \mathbb{R}^2$

$\Rightarrow \overrightarrow{H}_1(X)$ not trivial

Properties of natural homology

Properties of homology

- **sound**: invariant of homotopy
- **precise**: do not lose too much information from homotopy **[Hurewicz]**, partially complete **[Whitehead]**
- **modular**: the homology of a space can be expressed from the homology of simpler spaces **[Mayer-Vietoris]**
- **computable**: when the space is finitely presented

Two ways of computing homology

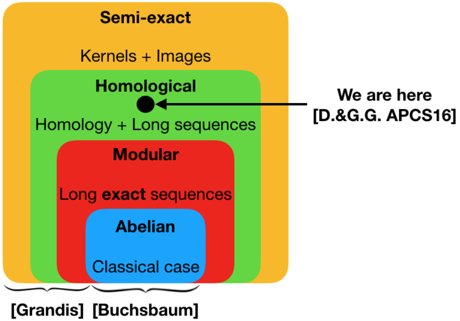
- Direct computation:
  - from a finite presentation of the space, compute a finite presentation of the homology (good for automatization)
- Modular computation:
  - from a description of a space using simpler spaces, compute the homology of the space from the homology of the spaces involved in the description (ex: spheres)
  - uses the theory of exact sequences

Non-Abelian exactness theory (modularity)

Modularity rely on the possibility to produce long exact sequence:

$$\cdots \longrightarrow H_n(V) \xrightarrow{f_n} H_n(W) \xrightarrow{g_n} H_{n-1}(U) \xrightarrow{h_{n-1}} H_{n-1}(V) \longrightarrow \cdots$$

with $\operatorname{Im} f_n = \operatorname{Ker} g_n$, ...

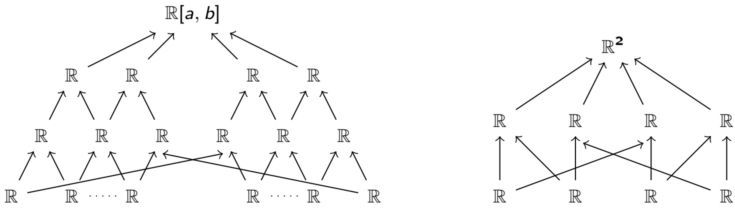


Sequences of order two:
in general $\operatorname{Im} f_n \subseteq \operatorname{Ker} g_n$.

Still enough to do some modularity and have the homotopy axiom from **[Eilenberg, Steenrod]**.

How to compare natural homologies ?

Isomorphism of diagrams is the wrong notion to compare diagrams of natural homology (because of the category $\mathcal{E}_X$)



Key notion [D.&G.G. ICALP'15]:

Compare natural homologies up-to evolution with time.
Idea similar to bisimulations in concurrent systems.

Bisimulation of diagrams **[D.&G.G. ICALP'15]**

Bisimulation between $F : C \longrightarrow \mathbf{Mod}(\mathcal{R})$ and $G : D \longrightarrow \mathbf{Mod}(\mathcal{R})$
$=$ set R of triples (c, η, d) such that :

- c is an object of C,
- d is an object of D,
- $\eta : F(c) \longrightarrow G(d)$ is an isomorphism of modules

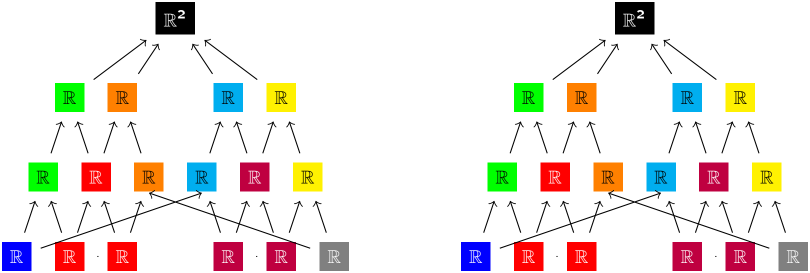
satisfying :

- for every object c of C, there exists d and η such that $(c, \eta, d) \in R$
-
$$(c, \eta, d) \in R$$
$$\begin{tikzcd}
c \arrow[d, "i"'] & Fc \arrow[rr, "\eta"] \arrow[d, "Fi"'] & & Gd \arrow[d, dotted, "Gj"] & d \arrow[d, dotted, "j"] \\
c' & Fc' \arrow[rr, dotted, "\eta'"'] & & Gd' & d'
\end{tikzcd}$$
$$(c', \eta', d') \in R$$

and symmetrically

Similar to bisimulations of event structures **[Rabinovitch, Trakhtenbrot 88]**.

Examples



the first natural homology of the matchbox is not bisimilar to the one of a point space

Deciding bisimilarity

Theorem [D. submitted]:

It is decidable in EXPSPACE wether two finitary diagrams are bisimilar.

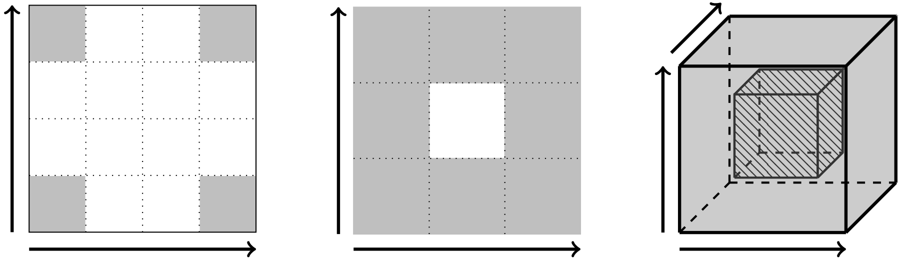
Proof (sketch):

in the finite dimensional case: bisimilarity = problem of matrices in reals.
$\rightarrow$ can be encoded in the existential theory of the reals (decidable).

Corollary (soon):

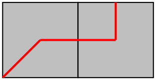
It is decidable wether two finitely presented d-spaces have the same natural homology, up-to bisimilarity.

Finite structure of a Euclidian cubical complex



The trace spaces of a Euclidian cubical complex can be finitely presented, and their homology can be computed **[Raussen, Ziemianski]**

$\mathcal{E}_X$ can also be describe finitely using discrete traces = traces which are a glueing of segments joining centers of cubes

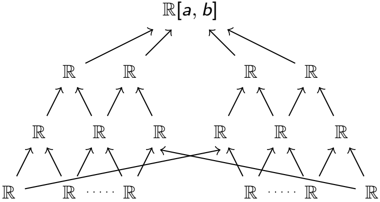


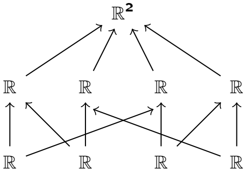
except that everything works only modulo bisimilarity.

Computability

Theorem [D.G.G-L. ICALP'15]:

When X is (finite) Euclidian cubical complex, we can compute a finitary diagram bisimilar to $\overrightarrow{H}_n(X)$. It is then decidable wether two such complexes have the same natural homology (up-to bisimilarity).





Homotopy theories and soundness

Soundness in classical algebraic topology

Homotopy equivalence = maps which is a homeomorphism up-to continuous deformations

Classical invariance: homology is an invariant of homotopy equivalence, i.e., a homotopy equivalence induces isomorphisms $H_n(f) : H_n(X) \longrightarrow H_n(Y)$ for all n.

Can we define a notion of dihomotopy equivalence, i.e., of isomorphism of d-spaces up-to continuous deformations that preserve the directed structure, that makes sense and that is compatible with natural homology ?

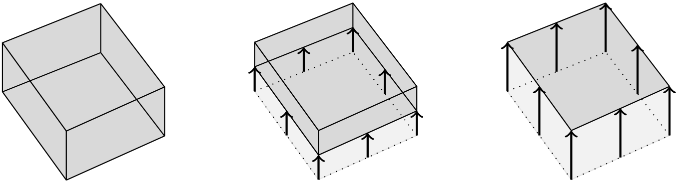
Dihomotopy of dimaps and dihomotopy equivalence à la Grandis

A di**homotopy** from $f : X \longrightarrow Y$ to $g : X \longrightarrow Y$ is a continuous function $H : X \longrightarrow \overrightarrow{P}(Y)$ with $H(\_)(0) = f$ and $H(\_)(1) = g$, and such that for every t, $H(\_)(t)$ is a dimap.

Two dimaps are di**homotopic** if there is a zig-zag of dihomotopies between them.

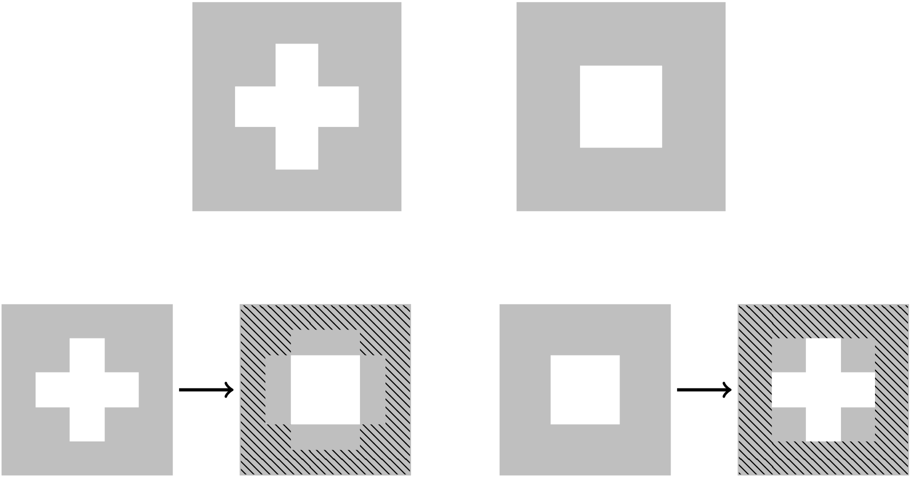
A **dihomotopy equivalence** à la Grandis is a dimap $f : X \longrightarrow Y$ such that there is $g : Y \longrightarrow X$ with $f \circ g$ and $g \circ f$ dihomotopic to identities.

Problem n°1: the matchbox

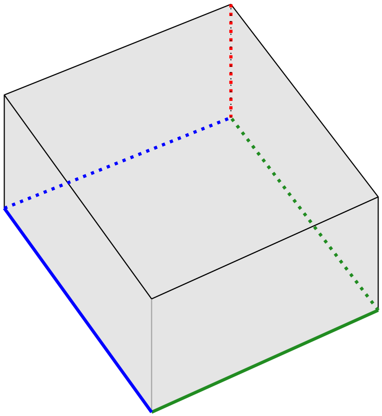


The matchbox is equivalent à la Grandis to a point

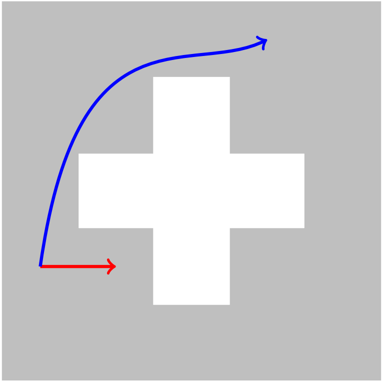
Problem n°2: deadlocks/unreachable states



Solution n°1: do not follow this path !



Solution n°2: do not follow this path either !



Inessential dipaths **[D.&G.G. CSL'16]**

The set $\mathfrak{I}(X)$ of inessential dipaths of X is the largest set of dipaths such that :

- it is closed under concatenation and dihomotopy;
- for every $\gamma \in \mathfrak{I}(X)$ from x to y, for every $z \in X$ such that $\overrightarrow{P}(X)(z,x)$, the map $\gamma \star \_ : \overrightarrow{P}(X)(z,x) \longrightarrow \overrightarrow{P}(X)(z,y) \ \ \delta \mapsto \gamma \star \delta$ is a homotopy equivalence;
- symmetrically for $\_ \star \gamma$;
- $\mathfrak{I}(X)$ has the right and left Ore condition modulo dihomotopy:

$$\begin{tikzcd} w \arrow[r, dotted, "g'"] \arrow[d, dotted, "f' \in \mathfrak{I}(X)"'] \arrow[dr, phantom, "\text{mod. dihomot.}"] & x \arrow[d, "f \in \mathfrak{I}(X)"] \\ z \arrow[r, "g"'] & y \end{tikzcd} \qquad \begin{tikzcd} z \arrow[r, "g"] \arrow[d, "f \in \mathfrak{I}(X)"'] \arrow[dr, phantom, "\text{mod. dihomot.}"] & y \arrow[d, dotted, "f' \in \mathfrak{I}(X)"] \\ x \arrow[r, dotted, "g'"'] & w \end{tikzcd}$$

Idea similar to the construction of the category of components of a d-space **[Goubault, Haucourt]**

Inessential dihomotopy equivalence **[D.&G.G. CSL'16]**

A **future inessential deformation retract** (FIDR) of X on a sub-d-space A is a continuous map

$$H : X \longrightarrow \mathfrak{I}(X)$$

such that :

- for every $x \in X$, $H(x)(0) = x$;
- for every $a \in A$, $t \in [0,1]$, $H(a)(t) = a$;
- for every $x \in X$, $H(x)(1) \in A$;
- for every $t \in [0,1]$, the map $H_t : x \mapsto H(x)(t)$ is a dmap;
- + technical conditions

Definition :

Two d-spaces are inessentially homotopically equivalent iff there is a zigzag of FIDR and PIDR between them.

Soundness

Theorem [D.&G.G. CSL'16]:

Natural homology is an invariant of inessential equivalence: if two Euclidian cubical complexes are inessentially equivalent, then their natural homologies are bisimilar.

Conclusion

We have produced a homology theory of d-spaces:

- using trace spaces and their evolution as a basic block,
- using a notion of **bisimulation** to compare the objects in a smoother way,
- and which have directed analogues of properties of the classical homology theory:
  - precise enough to detect non-cancellative default of dihomotopy (matchbox),
  - is compatible with a non-Abelian theory of exactness,
  - is computable in the case of Euclidian cubical complexes,
  - is an invariant of a dihomotopy equivalence (inessential equivalence).

Perspectives

- Is the computation of natural homology can be related to techniques from persistency ?
- What is the precise complexity of the bisimilarity problem ?
- Do we have model structures (or similar structures) for d-spaces up-to dihomotopy equivalences ?