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Persistent homology of directed spaces

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Abstract – In this work, we explore links between natural homology and persistent homology for the classification of directed spaces. The former is an algebraic invariant of directed spaces, a semantic model of concurrent programs. The latter was developed in the context of topological data analysis, in which topological properties of point-cloud data sets are extracted while eliminating noise. In both approaches, the evolution homological properties are tracked through a sequence of inclusions of usual topological spaces. Exploiting this similarity, we show that natural homology may be considered a persistence object, and may be calculated as a colimit of uni-dimensional persistent homologies along traces. Finally, we suggest further links and avenues of future work in this direction.

Keywords – Concurrent programs, semantic models, directed homotopy, persistent homology.

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1 Introduction

Geometry, algebraic topology, and homological algebra have now been in the computer science landscape through many significant applications in recent years. In topological data analysis, the shape of point-cloud data can be hinted at through suitable homological invariants, persistence homology (see e.g. [13], and [6] for a survey of the earlier days of persistence). These invariants capture the essential topological features of the point-cloud data, in that these are independent of the metrics used, are robust to noise and compact in their presentation. In the same period, similar ideas appeared in the realm of semantics of programming languages, in particular in concurrency theory [18, 17] and distributed computing [26], see e.g. [23, 16, 27] for surveys.

This article makes a formal bridge between these two approaches and illustrates the interest of applying persistent homology methods to problems such as classification of potential behaviors in concurrency theory and distributed computing through motivational examples.

The semantic models that describe possible executions of concurrent programs are based on the notion of *directed space*, which is a topological space X equipped with a topological space dX of *directed paths*, *i.e.* maps from the unit interval to X which enjoy a number of properties, see Section 4.1 and [22, 16]. For the purpose of this article, we will be exemplifying our results on directed spaces which are generated by *compact partially-ordered spaces*, which will furthermore be (directed) geometric realizations of finite precubical sets, see e.g. [16]. A compact partially-ordered space is a compact topological space X, together with a partial ordering $\leq$ which is a closed subset of $X \times X$ with the product topology. The directed paths in X are continuous and increasing maps from the unit interval, with the standard total order, to X. A particular

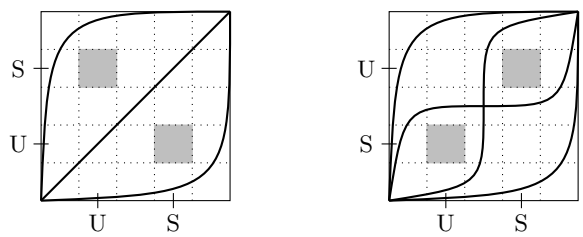


Figure 1: Two essentially different concurrent programs with homeomorphic state space.

class of compact partially-ordered spaces is given by the geometric realization of (loop-free) finite precubical sets, in which all n-cubes are realized by the unit n-cube in $\mathbb{R}^n$, with the componentwise ordering.

Consider now the problem of classifying such directed spaces, meaning determining when two directed spaces are "the same", that is, dihomeomorphic, as defined in Section 4.1, meaning homeomorphic as topological spaces plus some extra condition implying preservation of the directed structure. From the concurrency theory point of view, having dihomeomorphic directed spaces means essentially having the same coordination between concurrent processes [16], whereas non-dihomeomorphic directed spaces are the semantics of different concurrent programs.

As for the classification problem of topological spaces, it is far too hard a problem as such, and we need tractable (directed) topological invariants to give witnesses of the non-existence of dihomeomorphisms. One such invariant called natural homology, is based on homology, as generally done in classical algebraic topology, and has been developed in e.g. [9]. The idea is to observe that a dihomeomorphism f induces, for all points α, β in X, an isomorphism f^* between sub-spaces $dX(\alpha, \beta)$ of dipaths in X from α to β (see Section 4.1) in with sub-spaces $dY(f(\alpha), f(\beta))$ of dipaths in Y from $f(\alpha)$ to $f(\beta)$. The natural homology of directed space X is a diagram (or a "natural system" of groups, [1]) combining all (classical) homology groups of $dX(\alpha, \beta)$ for α and β varying over X, with induced "extension maps" between them.

Consider for instance the two compact partially-ordered spaces within $\mathbb{R}^2$ with the componentwise ordering pictured in Figure 1. They give semantics, for the left one X, to program $U.S \mid\mid U.S$, and for the one on the right Y, to program $U.S \mid\mid S.U$, where S stands for a scan operation and U stands for an update operation in shared memory, see e.g. [21]. As topological spaces, X and Y are homeomorphic spaces, homotopic to a wedge of two circles. Still, they are not dihomeomorphic directed spaces. Indeed, for α, β in X, $dX(\alpha, \beta)$ can only be homotopic to a point, two points or three points, whereas for γ, δ in Y, $dY(\gamma, \delta)$ can only be homotopic to a point, two points or four points. All these points do indeed correspond to traces of executions of the respective concurrent programs. These traces describe distinct coordination properties between two processes, and may give different outcomes. Figure 1 shows the three maximal directed paths up to directed homotopy for the space on the left, and the four maximal ones on the space on the right.

Even more importantly, for any directed path u from α' to α in X and any path v from β to β' in X, we have a continuous map $dX\langle u, v\rangle$ from $dX(\alpha, \beta)$ to $dX(\alpha', \beta')$ by pre-composition by u and post-composition by v, and when f is a dihomeomorphism, the graph of the homology of

f^* is a bisimulation between the natural homology of X and the natural homology of Y. We will recap this notion in Section 4. The study of the shape of such spaces of dipaths, when moving α and β, will be the essential ingredient of invariants under directed homeomorphisms.

Now, the idea of persistent homology comes from a different line, but we will see that it is based on similar intuitions. In the classical"uni-dimensional" approach of persistent homology of a point cloud in a space $\mathbb{R}^n$, we construct a filtration, i.e. a sequence of inclusions of simplicial sets. Typically, this starts on the point cloud and develops by adding relationships between the initial points resulting in a $\mathbb{R}$-persistence simplicial complex, from which we extract a sequence of homological invariants. The method of filtration depends on the nature and characteristics of the point cloud , according to which one can consider Čech, Vietoris-Rips, witness filtrations... [6]. In general these filtrations are unidimensional but there exist multidimensional analogues [7], in which multiple parameters can vary, that we will briefly discuss later on.

Similarly to persistent homology, there is a natural notion of birth and death of homological generators within natural homology. It is therefore natural to study the relationship between natural homology and persistent homology. For X a Euclidean cubical complex, which can be embedded as a sub-directed space of $\mathbb{R}^n$ for some high enough $n \in \mathbb{N}$, endowed with the component-wise ordering, it is natural to consider multidimensional persistence on $2n$ parameters, the n coordinates of the start point α and the n coordinates of the end point β and study the evolution of $dX(\alpha, \beta)$. In Section 2, we show that this point of view does not quite work using a simple example.

The objective of this article is to cope with this difficulty, in order to give a meaning to natural homology as persistent homology. The shift of point of view we are going to make is similar to recent approaches in multidimensional persistence [7]. We are going to look at all unidimensional persistent homologies that are compatible with the structure of a directed space, and glue this information together. In many ways, this resembles "probing" approaches in multidimensional homology, see e.g. [8].

In this work, we apply this idea to concurrent programs described by directed spaces. In this context, the data which we want to study via homological persistence are not points, but traces in directed spaces, which correspond to all observable executions of some concurrent program.

The directed structure of the space allows for each trace to define several one-dimensional filtrations of the associated trace space. The objective is to amalgamate all these filtrations to obtain the topological properties of the trace space. Contrary to the classical case, wherein the poset-persistence underlying the filtrations is obtained by external methods, the filtrations in the directed framework are inherent to the object of study.

Apart from the theoretical bridge between seemingly different lines of work, this work is a first step toward providing more tractable ways of computing natural homology (such as rank invariants [7]), as well as giving succinct descriptions of the semantics of concurrent and distributed systems, as some sort of barcodes (see e.g. [30]), an approach which has proven very practical in different areas of engineering, see e.g. [6]. This will be developed elsewhere.

Our first result, namely Proposition 1, provides the basis for this work. Indeed, it states that in the case of a partially ordered space $\mathcal{X}$, which constitute a prevalent example of directed space, there exists an order relation on traces which is isomorphic to the factorisation category

$\mathcal{X}$, which we afterwards call the trace poset $\mathbb{P}(\mathcal{X})$ of $\mathcal{X}$. The latter is the domain of the natural homology functor, so in particular, Proposition 1 states that natural homology is a peristence vector space.

Our next main result, Theorem 2, characterises maximal chains in the trace poset of a partially ordered space, and Proposition 2 shows that parametrisations of (maximal) traces yield unidimensional persistence modules along (maximal) chains by restriction of the natural homology functor.

Finally, in order to link these unidimensional persistence modules to the full natural homology functor, we prove Propositions 3 and 4, stating that an arbitrary poset may be obtained as the colimit of the diagram of its (maximal) chains. We then apply this to functors whose domain is a poset, showing in Proposition 5 that the colimit construction along chains also applies to such functors.

All of this leads to our main result, Theorem 3. This result shows that natural homology is obtained as the colimit of the unidimensional persistence modules along (maximal) traces, thereby establishing a concrete theoretical link between these two homology theories.

Outline of the article.

The first section presents a motivational example in order to present the relationship between persistent homology and natural homology. In particular, we argue that there is no canonical (multidimensional) filtration of the trace spaces of a given directed space which is solely based on end-points of dipaths. Indeed, we show that one must consider filtrations given by inclusions of trace spaces induced by pre- or post-concatenation by dipaths.

Section 3 deals with basic notions of persistent homology, fixing the notations and making the article self-contained. We recall notions of persistence objects and persistence homology, as well as an algorithm for computing persistent homology, more details on which can be found in [6, 11, 12].

In Section 4, we recall notions from directed topology. In particular, Sections 4.1 and 4.2 recall the notions of directed space and related structure, while the notion of natural homology is recalled in 4.3. Before moving on to the main results of the article, we recall in Section4.4 the notion of bisimulation, which constitutes the appropriate notion of equivalence of natural homology modules.

The first main results of the paper are developed in Section 5. First, we show by way of Proposition 1 that in the case of a partially ordered space $\mathcal{X}$, the domain of the associated natural homology functor is in fact a poset $\mathbb{P}(\mathcal{X})$, thus allowing us to consider it as a persistence object. In Section 5.2, we define a unidimensional persistence module along traces in a pospace, before proving Theorem 2 and Proposition 2, relating (maximal) chains in the poset $\mathbb{P}(\mathcal{X})$ to (maximal) traces in $\mathcal{X}$.

These concepts are illustrated in Section 5.4 on the motivational example from Section 3, the matchbox, for which full calculations are made. The relation to the natural homology of the matchbox is described in Section 5.5.

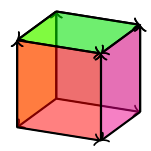
In Section 6, we show how colimit constructions permit us to "glue" together the unidimensional persistence modules obtained along traces in order to recover the entire natural homology diagram of a given pospace. First, in Section 6.1, we recall folkloric results about posets which provide various ways of reconstructing a poset as a colimit of its (maximal) chains. In Section 6.2,

we show via Proposition 5 that these constructions carry over to functors whose domains are posets. Finally, putting this together with results from Section 5, we obtain the main result of this article in Section 6.3, namely Theorem 3, stating that the natural homology of a pospace, or certain subdiagrams thereof, can be obtained from the uni-dimensional persistence modules along traces.

Finally, Section 7 finishes up by giving hints about extensions of these results, further linking natural homology with persistence when the considered partially ordered spaces are equipped with some metric structure in Section 7.1, and giving briefly touching on algorithmic considerations in Section 7.2.

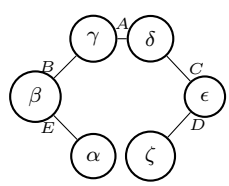
2 A motivational example

To give a glimpse of the intimate relationship between multidimensional persistence and natural homology, let us describe our construction on the following Fahrenberg's matchbox example [14]:



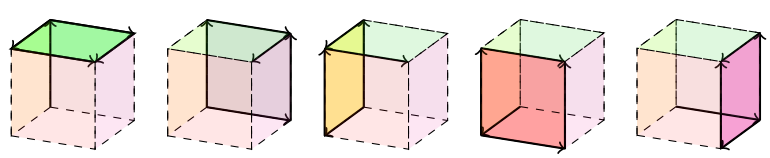
All faces of the unit cube $[0,1] \times [0,1] \times [0,1]$, except the bottom face, constitute the cubical complex, *i.e.* there are 5 squares glued together. A *trace* is the equivalence class $\overline{p}$ of a dipath p modulo monotonic and continuous reparametrization as defined in Section 4.1, and the set of such equivalence classes can be given the structure of a topological space $\mathfrak{T}(K)(a,b)$ for all start (resp. end) points a (resp. b), homotopic to a CW-complex for a large class of geometric realizations of pre-cubical sets.

Using Ziemiański's construction [35], the simplicial set corresponding to its trace space from beginning to end is as follows



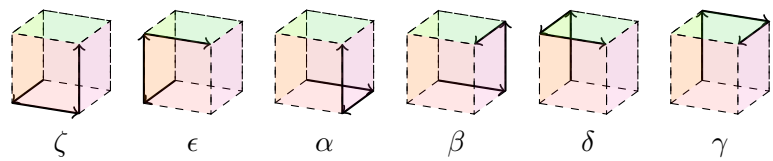
(1)

where the edges A, B, C, D and E correspond to the following five 2-dimensional cubical paths:



A B C D E

and the vertices α, β, γ, δ, ϵ and ζ correspond to the following six 1-dimensional dipaths:



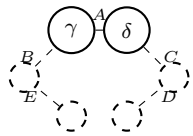
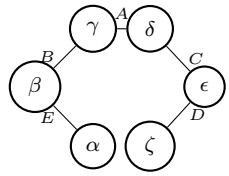
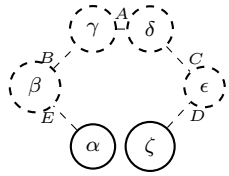
(2)

Note that β is the geometric intersection of B with E, γ is the geometric intersection of B with A and so forth. This leads to the simplicial set pictured in (1).

In order to apply persistent homology, we need to obtain a (multidimensional) filtration from this directed space, *i.e.* a map from some poset P such as $\mathbb{N}^2$ to the category of simplicial sets. One could think that such a filtration could be obtained by moving the end-points a and b associated to a trace space $\mathfrak{T}(K)(a,b)$. However, as we illustrate below, there is no canonical way of obtaining such a filtration in general; we must use extensions along traces to define inclusion maps.

There are maps from $\mathfrak{T}(K)(a,b)$ to $\mathfrak{T}(K)(a',b')$, for $a \leq a'$ and $b' \leq b$ that act as restriction maps : they just "cut" the combinatorial dipaths so as to only keep the parts (if any) that go from a' to b'. Hence, we get a decreasing sequence of simplicial sets as soon as any of the three coordinates of a increase or any of the three coordinates of b decrease. Below, we have represented the part of the multidimensional filtration generated, for the vertical coordinate of b (the end point) and of a (the starting point) ; recall also that the 5 squares are here unit squares and the lower coordinates are 0, upper ones are 1. In this filtration, the restriction maps acting on combinatorial dipaths should correspond to inclusion maps from bottom to top, and from left to right, of simplicial sets representing the corresponding trace spaces.

For instance, moving the end point b from vertical coordinate 1 to 0 while keeping vertical coordinate of a at 0 (right column in the table below), the only 1-dimensional paths going through coordinate 0 for b are α and ζ, hence all other vertices (and edges) have to disappear. This induces the upwards inclusion map from the two point simplicial set (α and ζ) into the connected simplicial set above : H_0 of these simplicial sets goes from $\mathbb{Z}^2$ to $\mathbb{Z}$, "killing" one component when extending paths to reach the end point of the matchbox. This corresponds, in the natural homology diagram $\overrightarrow{H}_1(K)$, to part of the diagram being a projection map from $\mathbb{Z}^2$ to $\mathbb{Z}$ when moving b to the endpoint of the matchbox, while keeping the starting point fixed at the initial vertex.

b/a	1	0
1		
0	$\emptyset$	

The reason that we obtain an inclusion map from bottom to top in this case is because there is a unique map from the point $(1,1,0)$ to the point $(1,1,1)$. When there is a choice between maps, we no longer obtain a canonical inclusion map. Indeed, consider the case in which $a=(0,0,0)$, the initial point, $b'=(1,1,0)$ and $b=(1,1,1)$, the terminal point. There are two extension maps from $\mathfrak{T}(K)(b',b)$ to $\mathfrak{T}(K)(a,b)$, one by precomposition by the trace of ζ, and one by precomposition by the trace of α. These will produce different homology maps once the invariant is applied.

Therefore there is no canonical multidimensional filtration of the trace spaces which depends only on start and end points. More generally, it is easily seen that such a multidimensional filtration for studying a directed space X would exist only if we had a way to associate in a continuous manner, to each pair of points α and β, a directed path going from α to β. It is well-known that indeed, such a continuous map will only exist if X is contractible in a directed manner, *i.e.* is trivial, see e.g. [19].

The objective of this article is to cope with this difficulty, in order to give a meaning to natural homology as persistence homology. The shift of point of view we are going to make is similar to recent approaches in multidimensional persistence. We are going to look at all unidimensional persistence homologies that are compatible with our directed space structure, and glue this information together. The non-canonicity of multidimensional filtrations, due to the existence in general of multiple extensions between trace spaces, we will no longer be considering filtrations parametrised by beginning- and end-points, but which are generated by extensions along a given trace. These have a natural interpretation as uni-dimensional persistence modules and are closely related to the structure of the directed space in question.

3 A sketch of persistence

In this section we recall the definitions of persistence homology using the notion of persistence module from [36]. We recall also an algorithm for computing persistent homology based on a structure theorem on persistence [36]. We refer the reader to [6, 11, 12] for complete accounts of persistent homology.

3.1 Persistence complexes

Given a poset P, considered as a category, a *P-persistence object* in a category $\mathcal{C}$ is a functor $\Phi : P \to \mathcal{C}$. Explicitly, it is given by a collection $\{C_x\}_x$ of objects in $\mathcal{C}$ indexed by the elements of P, and such that for all $x \leq y$ in P, there exists a unique map $\phi_{x,y} : C_x \to C_y$, such that $\phi_{y,z} \circ \phi_{x,y} = \phi_{x,z}$ whenever $x \leq y \leq z$. We denote by $P_{pers}(\mathcal{C})$ the functor category of P-persistence objects in $\mathcal{C}$. When $\mathcal{C}$ is the category of simplicial complexes, chain complexes, groups, respectively, the objects of $P_{pers}(\mathcal{C})$ are called P-persistence simplicial complexes, chain complexes, groups respectively.

In particular, considering the poset $\mathbb{N}$ of natural numbers with the usual order, a *positive $\mathbb{N}$-persistence complex*, or *persistence complex* for short, over a ground ring R is a family of chain complexes $C = \{C^i_*\}_{i\geq 0}$ over R, together with chain map $f^i : C^i_* \to C^{i+1}_*$, giving the following

diagrams in the category of R-modules:

$$C_*^0 \xrightarrow{f^0} C_*^1 \xrightarrow{f^1} \dots \longrightarrow C_*^i \xrightarrow{f^i} C_*^{i+1} \longrightarrow \dots$$

A *persistence module* M is a persistence complex concentrated in degree zero, *i.e.* a family of R-modules $\{M^i\}_{i\geq 0}$, together with maps $f^i : M^i \to M^{i+1}$.

The persistence complex C is called of *finite type* if each R-module C_k^i is finitely generated, and if there exists some N such that the maps f^i are isomorphisms for $i \geq N$.

3.2 Persistent homology

A *simplical complex* is a set K, together with a collection $\mathcal{K}$ of subsets of K, satisfying the following two conditions:

i) for every $v \in K$, $\{v\} \in \mathcal{K}$, and $\{v\}$ is called a *vertice* of K;

ii) $\sigma \in \mathcal{K}$ and $\sigma' \subseteq \sigma$ implies $\sigma' \in \mathcal{K}$.

A *k-simplex of* K is an element σ of $\mathcal{K}$ whose cardinal $|\sigma|$ is equal to $k+1$. An *orientation* of a k-simplex $\sigma = \{v_0, \dots, v_k\}$ is an equivalence of orderings of the v_i in σ; two orderings are equivalent if they can be obtained from an even permutation. A simplex with an orientation is called an oriented simplex, and we write $[v_0, \dots, v_k]$ or $[\sigma]$ to denote the equivalence class.

Denote by $C_k(K)$ the *kth chain module* of K defined as the free R-module on oriented k-simplices of K. The boundary operator $\partial_k : C_k(K) \to C_{k-1}(K)$ is the map defined on any simplex $\sigma = \{v_0, \dots, v_k\}$ by setting

$$\partial_k(\sigma) = \sum_i (-1)^i [v_0, \dots, \widehat{v_i}, \dots, v_k],$$

where in the right side $\widehat{v_i}$ indicates that the vertex v_i is eliminated from the simplex. Denote by $Z_k(K) = \ker \partial_k$, $B_k(K) = \operatorname{Im} \partial_{k+1}$, and $H_k(K) = Z_k(K)/B_k(K)$ the *cycle*, *boundary*, and *homology* modules respectively.

A *subcomplex* of K is a simplicial complex L such that $L \subseteq K$. A *filtered complex* is a complex K together with a *filtration*, that is a nested sequence of subcomplexes:

$$K^0 \subseteq K^1 \subseteq K^2 \subseteq \dots \subseteq K^n = K.$$

Given such a filtration, we define the persistence complex $C(K) = \{C_*(K^i)\}_{i\in\mathbb{N}}$, in which the chain maps $f^{i,i+1} : C_*(K^i) \to C_*(K^{i+1})$ are induced by the inclusions $K^i \to K^{i+1}$. Applying the kth homology functor H_k to each complex, we obtain $H_k(C(K)) := \{H_k(C(K_i)_*)\}_{i\in\mathbb{N}}$, which has the structure of persistence module over the ground ring R. Denoting by $\eta_k^{i,i+p} : H_k(K^i) \to H_k(K^{i+p})$ the map induced by the inclusion $K^i \to K^{i+p}$, we define the *p-persistent* k^{th} *homology group of* K^i as $im(\eta_k^{i,i+p})$, which we denote by $H_k^{i,p}(K)$, see [13].

Finally, note that if K is finite, then the persistence complex $C(K)$ is of finite type, and thus the persistent homology $H_k(C(K))$ is also of finite type.

3.3 Classification of persistence module and algorithm for persistence

Given a persistence R-module $(M^i, \phi_{i,i+1})_i$, we define a graded module over $R[t]$ by setting

$$\alpha(M) = \bigoplus_{i=0}^{\infty} M^i,$$

where the R-module structure is induced by the direct sum of its components, and the action of t is defined by

$$t \cdot (m_0, m_1, \dots, m_k, \dots) = (0, \phi_{0,1}(m_0), \phi_{1,2}(m_1), \dots, \phi_{n,n+1}(m_k), \dots).$$

The correspondence α is functorial and establishes an equivalence between the category of persistence R-modules of finite type and the category of finitely generated graded $R[t]$-modules. When the ground ring is a field $\Bbbk$, combining this with the structure theorem of finitely generated graded modules, we know that a persistence module has a decomposition

$$\left(\bigoplus_{i=1}^{n} \Sigma^{k_i} \Bbbk[t]\right) \oplus \left(\bigoplus_{j=1}^{m} \Sigma^{l_j} \Bbbk[t]/(t^{h_j})\right) \tag{3}$$

for some n, m and families of natural numbers $(k_i)_i$, $(l_j)_j$ and $(h_j)_j$, where Σ^k denotes a k-shift in grading.

From this classification of persistant modules one derives an algorithm for computation of persistence homology over a field [36]. This algorithms is defined as follows. Denote by $\{e_j\}$ and $\{\hat{e}_i\}$ to represent homogenous bases for the persistence $\Bbbk$-modules C_k and Z_{k-1}. Denote by M_k the matrix of ∂_k in these bases. The usual procedure for calculating homology is to reduce the matrix to Smith normal form and read off the description of H_k from the diagonal elements. We compute these bases and matrix representations by induction on k. For $k = 1$, the standard basis of $C_0 = Z_0$ is homogenous and we may proceed as usual.

Suppose now that we have a representation M_k of ∂_k relative to the standard basis $\{e_j\}$ of C_k and a homogeneous basis $\{\hat{e}_i\}$ of Z_{k-1}. For induction, we must compute a homogeneous basis for Z_k and represent ∂_{k+1} relative to the computed basis for Z_k and the standard basis of C_{k+1}.

We begin by sorting the basis $\{\hat{e}_i\}$ in reverse degree order and then transform the matrix M_k into *column-echelon form* $\tilde{M}_k$. This is a lower staircase form, the general form of which is depicted below, in which each landing is of width one, the steps have variable height. A *pivot* is the first non-zero value in a column and a row (resp. column) with a pivot is called a *pivot row* (resp. *column*). The diagonal elements in Smith normal form are the same as the pivots in column-echelon form and that the degrees of the corresponding basis elements are also the same in both cases [36]. Zomorodian and Carlsson prove in [36] that each row contributes to the persistent homology H_{k-1} of $\mathcal{C}_*$ in the following way:

i) If row i is a pivot row with pivot t^n, then it contributes $\Sigma^{\deg \hat{e}_i} \Bbbk[t]/t^n$.

ii) If row i is not a pivot row, it contributes $\Sigma^{\deg \hat{e}_i} \Bbbk[t]$.

where these contributions correspond to factors in the characterization (3), see [36] for details.

4 Natural homology of directed spaces

In this section, we recall definitions and constructions involving directed spaces and natural homology, an invariant thereof. In Sections 4.1 and 4.2, we recall the definition of directed space and associated categorical constructions, as well as the notion of natural system and composition pairings. Finally, Section 4.3 recalls the definition of natural homology from [9], an invariant of directed spaces encoded by natural systems. In this final subsection, we also recall the notion of bisimulation and provide, see Lemma 1, the link between dihomemorphisms between directed spaces and bisimulation equivalence of their associated natural homology diagrams.

4.1 Directed spaces

Recall from [22] that a *directed space*, or *dispace*, is a pair $\mathcal{X} = (X, dX)$, where X is a topological space and dX is a set of paths in X, *i.e.* continuous maps from $[0,1]$ to X, called *directed paths*, or *dipaths*, satisfying the three following conditions:

i) Every constant path is directed,

ii) dX is closed under *monotonic reparametrization*, *i.e.*, for any continuous map $\varphi : [0,1] \to [0,1]$ such that $\varphi(0) = 0$, $\varphi(1) = 1$ and φ is monotonic, then $f \circ \varphi$ belongs to dX for every f in dX,

iii) dX is closed under concatenation.

We will denote by $f \star g$ the concatenation of dipaths f and g. A morphism $\varphi : (X, dX) \to (Y, dY)$ of dispaces is a continuous function $\varphi : X \to Y$ that preserves directed paths, *i.e.*, for every path $p : [0,1] \to X$ in dX, the path $p \circ \varphi : [0,1] \to Y$ belongs to dY. The category of dispaces is denoted dTop. An isomorphism in dTop from (X, dX) to (Y, dY) is a homeomorphism from X to Y that induces a bijection between the sets of dipaths dX and dY.

Given two directed spaces X and Y, a dihomeomorphism from X to Y is a continuous map $f : X \to Y$ which respects directed paths, *i.e.* $f^*(p) = p \circ f \in dY$ for all $p \in dX$, such that there exists a continuous map $g : Y \to X$ respecting directed paths as well, with $f \circ g = Id$ and $g \circ f = Id$. Equivalently, for the sub-class of compact partially-ordered spaces, f and g must be continuous, respect the respective partial orders, and be inverses to one another. It is clear that having dihomeomorphic directed spaces is a fine semantic equivalence, when it comes to applications in concurrency theory.

Two dipaths f and g are *reparametrization equivalent* if there exist reparametrizations φ, ψ such that $f \circ \varphi = g \circ \psi$. The *trace* of a dipath f in $\mathcal{X}$, denoted by $\overline{f}$, or f if no confusion is possible, is the equivalence class of f modulo monotonic reparametrization. The concatenation of dipaths of $\mathcal{X}$ is compatible with this quotient, inducing a concatenation of traces defined by $\overline{f} \star \overline{g} := \overline{f \star g}$, for all dipaths f and g of $\mathcal{X}$. The sub-topological space of dX of dipaths in X from $\alpha \in X$ to $\beta \in X$ is denoted by $dX(\alpha, \beta)$.

Note that in the case of the geometric realization of finite geometric precubical sets without loops, it is known [20] that we have a complete metric space and that we can define the l_1-arc length $l_1(p)$ of a directed path p. In that context, traces $\overline{f}$ always have a representative f such that the length of the sub-path from $f(0)$ to $f(t)$ along f is t.

For a dispace $\mathcal{X} = (X, dX)$ and $x, y \in X$, we denote by $\overrightarrow{Di}(\mathcal{X})(x, y)$ the space of dipaths f in X with source $x = f(0)$ and target $y = f(1)$, equipped with the compact-open topology. For $x, y \in X$, the *trace space* of the dispace $\mathcal{X}$ from x to y, denoted by $\mathfrak{T}(\mathcal{X})(x, y)$, is the quotient of $\overrightarrow{Di}(\mathcal{X})(x, y)$ by monotonic reparametrization, equipped with the quotient topology.

4.2 Trace category and trace diagrams

Recall that the *category of factorizations* of a category $\mathcal{C}$, denoted by $F\mathcal{C}$, is the category whose 0-cells are the 1-cells of $\mathcal{C}$, and a 1-cell from f to f' is a pair (u, v) of 1-cells of $\mathcal{C}$ such that $ufv = f'$ holds in $\mathcal{C}$. Composition is given by

$$(u, v)(u', v') = (u'u, vv'),$$

whenever the pairs u', u and v, v' are composable in $\mathcal{C}$, and the identity on $f : x \to y$ is the pair $(1_x, 1_y)$. A *natural system on $\mathcal{C}$ with values in a category* $\mathbf{V}$ is a functor $D : F\mathcal{C} \to \mathbf{V}$. We will denote by D_f (resp. $D(u, v)$) the image of a 0-cell f (resp. 1-cell (u, v)) of $F\mathcal{C}$.

A directed space may be seen as a category using the notion of traces, and this association is functorial. Indeed, consider the functor

$$\overrightarrow{\mathbf{P}} : \mathsf{dTop} \to \mathsf{Cat}$$

with values in the category of small categories which associates to a dispace $\mathcal{X}$ the *trace category of* $\mathcal{X}$, whose 0-cells are points of X, 1-cells are traces of $\mathcal{X}$, and composition is given by concatenation of traces. The *trace diagram* of a dispace $\mathcal{X}$ in the category Top of topological spaces is the natural system

$$T(\mathcal{X}) : F\overrightarrow{\mathbf{P}}(\mathcal{X}) \to \mathsf{Top},$$

sending a trace $\overline{f} : x \to y$ of $\mathcal{X}$ to the topological space $\mathfrak{T}(\mathcal{X})(x, y)$, and a 1-cell $(\overline{u}, \overline{v})$ of $F\overrightarrow{\mathbf{P}}(\mathcal{X})$ to the continuous map

$$\overline{u} \star _ \star \overline{v} : \mathfrak{T}(\mathcal{X})(x, y) \to \mathfrak{T}(\mathcal{X})(x', y'),$$

which sends a trace $\overline{f}$ to $\overline{u} \star \overline{f} \star \overline{v}$.

Recall from [5], that the *category of natural systems with values in* Top, denoted by $\mathsf{opNat}(\mathsf{Top})$, is defined as follows:

i) its objects are pairs $(\mathcal{C}, D)$ made of a category $\mathcal{C}$ and a natural system $D : F\mathcal{C} \to \mathsf{Top}$,

ii) its morphisms are pairs

$$(\Phi, \tau) : (\mathcal{C}, D) \to (\mathcal{C}', D')$$

consisting of a functor $\Phi : \mathcal{C} \to \mathcal{C}'$ and a natural transformation $\tau : D \to \Phi^* D'$, where the natural system $\Phi^* D' : F\mathcal{C} \to \mathsf{Top}$ is defined by

$$(\Phi^* D')(f) = D'(\Phi f),$$

for every 1-cell f in $\mathcal{C}$, and $\Phi^* D'(u, v) = D'(\Phi(u), \Phi(v))$, for all 1-cells u, v in $\mathcal{C}$,

iii) composition of morphisms $(\Psi, \sigma) : (\mathcal{C}', D') \to (\mathcal{C}'', D'')$ and $(\Phi, \tau) : (\mathcal{C}, D) \to (\mathcal{C}', D')$ is defined by

$$(\Psi, \sigma) \circ (\Phi, \tau) := (\Psi \circ \Phi, (\Phi^* \sigma) \circ \tau),$$

where $\Psi \circ \Phi$ denotes composition of functors and where the component of the natural transformation $(\Phi^* \sigma) \circ \tau$ at a 1-cell f of $\mathcal{C}$ is $\tau_f \sigma_{\Phi(f)}$.

The family of functors $T(\mathcal{X})$ indexed by dispaces $\mathcal{X}$ extends to a functor

$$T : \mathsf{dTop} \to \mathsf{opNat}(\mathsf{Top})$$

sending a dispace $\mathcal{X}$ to the pair $(\overrightarrow{\mathbf{P}}(\mathcal{X}), T(\mathcal{X}))$. Note that a morphism of dispaces $\varphi : \mathcal{X} \to \mathcal{Y}$ induces continuous maps

$$\varphi_{x,y} : \mathfrak{T}(\mathcal{X})(x, y) \to \mathfrak{T}(\mathcal{Y})(\varphi(x), \varphi(y)),$$

for all points x, y of X, and thus a natural transformation between the corresponding trace diagrams:

$$\overrightarrow{\varphi} : T(\mathcal{X}) \Rightarrow T(\mathcal{Y}).$$

4.3 Natural homology

Recall from [10], that for $n \geq 1$, the nth *natural homology functor of* $\mathcal{X}$

$$\overrightarrow{H}_n(\mathcal{X}) : F\overrightarrow{\mathbf{P}}(\mathcal{X}) \to \mathsf{Ab}$$

is the functor defined as the composite

$$F\overrightarrow{\mathbf{P}}(\mathcal{X}) \xrightarrow{T(\mathcal{X})} \mathsf{Top} \xrightarrow{H_{n-1}} \mathsf{Ab},$$

where $T(\mathcal{X})$ is the trace diagram and H_{n-1} is the $(n-1)^{th}$ singular homology functor. The functors $\overrightarrow{P}_n(\mathcal{X})$ and $\overrightarrow{H}_n(\mathcal{X})$, for $\mathcal{X}$ in dTop, extend to functors

$$\overrightarrow{P}_n : \mathsf{dTop} \longrightarrow \mathsf{opNat}(\mathsf{Act}), \quad \text{and} \quad \overrightarrow{H}_n : \mathsf{dTop} \longrightarrow \mathsf{opNat}(\mathsf{Ab}),$$

sending a dispace $\mathcal{X}$ to $(\overrightarrow{\mathbf{P}}(\mathcal{X}), \overrightarrow{P}_n(\mathcal{X}))$ and $(\overrightarrow{\mathbf{P}}(\mathcal{X}), \overrightarrow{H}_n(\mathcal{X}))$ respectively.

The natural homology $\overrightarrow{H}_n(\mathcal{X})$ of a directed topological space $\mathcal{X}$ is very fine-grained: it not only records local homology groups $\overrightarrow{H}_n(\mathcal{X})_f$ for a trace f of $\mathcal{X}$, but also for which traces they occur. Just as with persistent homology, see Section 3, what counts is the patterns of change between groups $\overrightarrow{H}_n(\mathcal{X})_f$ and $\overrightarrow{H}_n(\mathcal{X})_g$ when f is changed into the concatenation of traces $g = u \star f \star u$ by some extension (u, v), not the values of the trace f.

This is done by looking at natural homology modulo a notion of bisimulation of natural systems, and more generally of Ab-valued functors, defined in [9] and recalled below.

4.4 Bisimulation

Given two small categories X, Y and two functors $F : X \to \mathsf{Ab}$ and $G : Y \to \mathsf{Ab}$, we call *bisimulation* between F and G any set R of triples (x, η, y) with x a 0-cell of X, y a 0-cell of Y and $\eta : Fx \to Gy$ an isomorphism such that:

i) for every 0-cell x of X, R contains some triple of the form (x, η, y), and similarly for every 0-cell y of Y;

ii) for every triple $(x, \eta, y) \in R$ and every 1-cell $i : x \to x'$ in X, there is a triple $(x', \eta', y') \in R$ and a 1-cell $j : y \to y'$ in Y such that $\eta' \circ Fi = Gj \circ \eta$, and symmetrically, for every $(x, \eta, y) \in R$ and every 1-cell $j : y \to y'$ of Y there is a triple $(x', \eta', y') \in R$ and a 1-cell $i : x \to x'$ such that $\eta' \circ Fi = Gj \circ \eta$:

$$\begin{tikzcd}
x \arrow[d, "i"'] & Fx \arrow[r, "\eta"] \arrow[d, "Fi"'] & Gy \arrow[d, "Gj"] & y \arrow[d, "j"] \\
x' & Fx' \arrow[r, "\eta'"'] & Gy' & y'
\end{tikzcd}$$

We say that F and G are *bisimulation equivalent* if and only if there is a bisimulation R between them. This is an equivalence relation. We now prove that indeed, dihomeomorphic directed spaces have bisimilar natural homologies:

Lemma 1. *Suppose $f : \mathcal{X} \to \mathcal{Y}$ is a morphism of directed spaces with inverse $g : \mathcal{Y} \to \mathcal{X}$. Then the functors $\overrightarrow{H}_n(\mathcal{X})$ and $\overrightarrow{H}_n(\mathcal{Y})$ are bisimulation equivalent, for every $n \in \mathbb{N}$.*

Proof. For some n in $\mathbb{N}$, we need to construct R, a set of triples (x, η, y), with x a 0-cell of $F\overrightarrow{\mathbf{P}}(\mathcal{X})$, y a 0-cell of $F\overrightarrow{\mathbf{P}}(\mathcal{Y})$, that is x and y are traces of $\mathcal{X}$ and $\mathcal{Y}$ respectively, and $\eta : \overrightarrow{H}_n(\mathcal{X})_x \to \overrightarrow{H}_n(\mathcal{Y})_y$ is an isomorphism making this set of triples a bisimulation.

We define the R from f and g as follows. It is going to contain all triples $(x, \eta_{x,y}, y)$ with x any trace of $\mathcal{X}$, $y = f^*(x)$ which is a trace of $\mathcal{Y}$, and $\eta_{x,y}$ is the map from $\overrightarrow{H}_n(\mathcal{X})_x$ to $\overrightarrow{H}_n(\mathcal{Y})_y$ which sends class $[p]$ of a directed path p starting from $x(0)$ and ending in $x(1)$ within $\mathcal{X}$, to class $[f^*(p)]$. This is well defined since, first $f^*(p)$ is a directed path from $f^*(p)(0) = f(p(0)) = f(x(0)) = y(0)$ to $y(1)$ and as f is a directed homeomorphism, f^* induces an homeomorphism between trace spaces $F\overrightarrow{\mathbf{P}}(\mathcal{X})$ and $F\overrightarrow{\mathbf{P}}(\mathcal{Y})$, hence induces an isomorphism between their homology groups.

Now we check that the set of triples R is indeed a bisimulation. Consider a morphism $i : x \to x'$ in X, i.e. $i = (\alpha, \beta)$ with α and β, traces in $\mathcal{X}$. We consider now morphism $j : y \to y'$ in $\mathcal{Y}$ defined as $j = (f^*(\alpha), f^*(\beta))$ and $y' = f^*(\alpha) \star y \star f^*(\beta) = f^*(x')$. As before, f^* induces an isomorphism $\eta_{x',y'}$ between $\overrightarrow{H}_n(\mathcal{X})_{x'}$ and $\overrightarrow{H}_n(\mathcal{X})_{y'}$ and $(x', \eta_{x',y'}, y')$ is in R. Furthermore, $\eta_{x',y'} \circ \overrightarrow{H}_n(\mathcal{X})_i = \overrightarrow{H}_n(\mathcal{Y})_j \circ \eta_{x,y}$ since, for p a trace in $\mathcal{X}$ from $x(0)$ to $x(1)$:

$$\begin{aligned}
\eta_{x',y'} \circ \overrightarrow{H}_n(\mathcal{X})_i([p]) &= \eta_{x',y'}([\alpha \circ p \circ \beta]) \\
&= [f^*(\alpha) \circ f^*(p) \circ f^*(\beta)] \\
&= \overrightarrow{H}_n(\mathcal{Y})_j([f^*(p)]) \\
&= \overrightarrow{H}_n(\mathcal{Y})_j \circ \eta_{x,y}([p])
\end{aligned}$$

hence R is a bisimulation. $\square$

5 Persistent homology of directed spaces

In this section we explore the use of persistent homology as an invariant of directed spaces, as well as its relationship to natural homology in the context of partially ordered spaces. First, we show that for these directed spaces, the associated natural homology modules are in fact persistence objects as defined in Section 3. We then define persistent homology along traces in a directed space and show the compatibility of this definition with the interpretation of natural homology as a persistence object. To finish the section, we illustrate our constructions on the matchbox example.

5.1 Natural homology as a persistence object

Consider a directed space $\mathcal{X} = (X, dX)$ and its trace category $\overrightarrow{\mathbf{P}}(\mathcal{X})$. We define a relation on traces in $\mathcal{X}$ by setting

$$f \leq g \qquad \Longleftrightarrow \qquad \exists\, u, v \in dX, \quad g = ufv.$$

We recall that a *pospace* $\mathcal{X} = (X, \leq_X)$ consists of a Hausdorff topological space X and a partial order $\leq_X$ which is closed in the product topology $X \times X$. Pospaces are naturally interpreted as directed spaces by equipping them with the set of increasing paths dX from the unit interval, with its usual ordering, to X.

Lemma 2. *In any directed space, this defines a pre-order. In a pospace, it is a partial order relation.*

Proof. Since constant paths are directed, the relation is reflexive, and we have transitivity by associativity of concatenation of traces. Indeed, if $f \leq g$ and $g \leq h$, there exist extensions (u, v) and (u', v') such that

$$f = ugv \qquad \text{and} \qquad g = u'hv'.$$

Thus, $f = u(u'hv')v = (uu')h(v'v)$, and $f \leq h$. In the case of a loop-free directed space, we also need to prove anti-symmetry of $\leq$. Consider $f, g \in dX$ such that $f \leq g$ and $g \leq f$. By definition there exist extensions such that $f = ugv$ and $g = u'fv'$. Thus $f = uu'fv'v$, so uu' and vv' are loops, and must therefore be constant paths. By Theorem 1 below, this means that the image of both uu' and $v'v$ are the singleton space, meaning that the image of each of the dipaths u, u', v, v' are the singleton space, *i.e.* these are all constant paths, concluding the proof. $\square$

This poset, denoted by $\mathbb{P}(X)$, will be called the *trace poset* of $(X, \leq_X)$. Consider a pospace $\mathcal{X} = (X, \leq)$. We know from [24] that dipaths in $\mathcal{X}$ are characterized by their image:

Theorem 1 ([24, Thm. 3.15])**.** *The image of a dipath in a pospace is isomorphic to either the directed unit interval or the singleton space.*

The above results essentially state that two dipaths are equal modulo reparametrisation if and only if they have the same image, and that this induces a partial ordering on traces. In particular, we obtain the following result:

Proposition 1. *For a pospace $\mathcal{X}$, $\mathbb{P}(\mathcal{X})$ is isomorphic to $F\overrightarrow{\mathbf{P}}(\mathcal{X})$.*

Proof. By the above theorem, we have

$$ufv = u'fv' \qquad \Longleftrightarrow \qquad u = u' \text{ and } v = v',$$

meaning that there is at most one extension between any two traces. □

This allows us to interpret natural homology as a functor on a poset, *i.e.* as a persistence object. Indeed, in a pospace $\mathcal{X}$, the ith natural homology diagram associated to $\mathcal{X}$ is a $\mathbb{P}(\mathcal{X})$-persistence group. Taking coefficients in a field $\Bbbk$, we obtain $\mathbb{P}(\mathcal{X})$-persistence $\Bbbk$-vector spaces.

5.2 Persistent homology along a trace

Here, we show how unidimensional persistence modules may be obtained from parametrisations of traces. Let $\overline{f}$ be a trace in $\mathcal{X}$ a pospace for which we have fixed some parametrisation f. For a given point α_f in the image of f, denote by $[\alpha_f, f]$ the interval between α_f, identified with the constant trace $f(t_0) = \alpha_f$ for some $t_0 \in [0,1]$, and f, *i.e.* traces p in the poset $\mathbb{P}(\mathcal{X})$, such that $\alpha_f \leq p \leq f$.

Given parametrisations of $[0, t_0]$ and $[t_0, 1]$ within $[0,1]$ via maps $\gamma_- : [0,1] \to [0, t_0]$ and $\gamma_+ : [0,1] \to [t_0, 1]$ respectively, we denote by ${}_sf_s$ the trace of f restricted to $[t_0 - \gamma_-(s), t_0 + \gamma_+(s)]$. We thus obtain a $[0,1]$-persistence simplicial complex $\{K({}_sf_s)\}_s$. This is a filtration of the trace space associated to the trace $\overline{f}$. Notice that we are always considering a chain in the poset of traces from the constant trace $f(0)$, $f(1)$, or $f(t_0)$ to f. We call such filtrations initial (resp. terminal) point filtrations when $\alpha_f = f(0)$ (resp. $\alpha = f(1)$)

Taking some order preserving map $\mathbb{N} \to [0,1]$, we obtain $\mathbb{N}$-persistence simplicial complexes from the above constructions. All of these persistence objects can be considered as $\mathbb{R}$-persistence objects as follows: $[0,1]$-persistence objects are $\mathbb{R}$-persistence objects which are constant on negative parameters and on parameters greater or equal than one. $\mathbb{N}$-persistence objects will be considered as piecewise constant $\mathbb{R}$-persistence objects in what follows. However, for questions of computability, it is useful to consider $\mathbb{N}$-persistence.

In all the above cases, we obtain a chain $c = (f_i)_{i \in \mathbb{R}}$ in the interval $[\alpha_f, f]$ and define the *persistent homology along a trace f with respect to c* as a functor from $\mathbb{R}$, seen as the poset category (with the usual ordering) to the category of abelian groups, associating $i \in \mathbb{R}$ to:

$$\overrightarrow{H}_n(f, c)_i := \overrightarrow{H}_n(\mathcal{X})_{f_i}$$

where we recall that $\overrightarrow{H}_n(\mathcal{X})_{f_i}$ is the natural homology in dimension n of $\mathcal{X}$ at trace f_i. This $\mathbb{R}$-persistence module is constructed as described above, that is by considering the $[0,1]$-persistence module given by a trace as a $\mathbb{N}$-persistence module and completing by constants.

5.3 Maximal traces and maximal chains

In order to make the link between parametrisations and chains more concrete, we present the link between maximal chains in the trace poset and parametrisations of extensions along maximal

traces. In fact, the chain we use does not depend on (re)parametrisations, but rather on the pair of end-points visited along a trace.

Recall from the previous subsection that given a trace $\overline{f}$, we construct a persistence module using the following data:

- A point α in the image of f.
- A parametrisation f of $\overline{f}$.
- Reparametrisations $\gamma_- :\ [0,1] \to [0,t_0]$ and $\gamma_+ :\ [0,1] \to [t_0,1]$, where $f(t_0) = \alpha$.

A *maximal trace* is a trace which cannot be extended on either side. Hence, these are the maximal elements in $\mathbb{P}(\mathcal{X})$. Maximal chains in $\mathbb{P}(\mathcal{X})$ link minimal elements, *i.e.* constant dipaths, to maximal traces along a sequence of extensions. Clearly, for a trace $\overline{f}$, the above data encodes a maximal chain in the trace poset. Indeed, we obtain a chain ${}_sf_s$ from α, seen as a constant trace, to $\overline{f}$, which is maximal since it is derived from the continuous maps γ_+ and γ_-.

Consider $t \in \mathbb{P}(\mathcal{X})$ a maximal trace. Let $\alpha_0 \in \mathcal{X}$ be the beginning-point of t, and consider the interval $[\alpha_0, t]$ in $\mathbb{P}(\mathcal{X})$. For any $g, h \in [\alpha_0, t]$, we have either $g \leq h$ or $h \leq g$, since all elements of this interval are traces starting at α_0 and which are sub-traces of t. Thus the interval $[\alpha_0, t]$ is itself a chain.

From this we deduce that there is a unique maximal chain from α_0 to t, which we denote by C_t^0, namely the interval between them. A symmetric argument shows that this is also the case when we consider chains from α_1, the terminal point of t, in which case the unique chain, denoted by C_t^1 is the interval $[\alpha_1, t]$.

Now let us consider a point α in the trace t which is neither the beginning nor end-point of t. Let $t_1 \leq t$ the trace from α_0 to α, and $t_2 \leq t$ the trace from α to α_1. We claim that the interval $[\alpha, t]$ is the cartesian product, as posets, of the chains $C_{t_1}^1$ and $C_{t_2}^0$. Indeed, given any trace $f \in [\alpha, t]$, we know that f is a subtrace of t which passes through α. Thus there exist a unique pair of traces $(f_1, f_2) \in [\alpha, t_1] \times [\alpha, t_2]$ such that $f = f_1 \star f_2$. Conversely, any pair $(f_1, f_2) \in [\alpha, t_1] \times [\alpha, t_2]$ of traces can be concatenated to obtain a trace in the interval $[\alpha, t]$. So any chain from α to t is a chain in the product $[\alpha, t_1] \times [\alpha, t_2]$, ordered coordinate-wise.

More generally, given *any* maximal chain C in $\mathbb{P}(\mathcal{X})$, we know that it has a maximal element, namely the union of all traces in C, which we denote by t. Furthermore, since every trace is a compact subspace of X, it has a minimal element, α, which must be a constant trace by maximality of C. Thus every maximal chain in $\mathbb{P}(\mathcal{X})$ is of the type described in the previous paragraphs.

Summing this up, we obtain the following result:

Theorem 2. *Let $\mathcal{X}$ be a pospace, consider its trace poset $\mathbb{P}(\mathcal{X})$, and let C be a maximal chain therein. Then C has a maximal element which is a maximal trace t_C, and has a minimal element which is a constant trace α_C. Furthermore,*

- *If α_C is the beginning-point α_0 or end-point α_1 of t, then C is unique and is equal to the interval $[\alpha_C, t_C]$.*
- *If not, then C is a chain in the product of chains $C_{t_1}^1$ and $C_{t_2}^0$, where t_1 (resp. t_2) is the unique subtrace of t going from α_0 to α (resp. from α to α_1).*

This shows that maximal chains in the trace poset are independent of the parametrisation we choose for our maximal traces. Indeed, given a maximal trace $\overline{f}$ the first item above states that there is only one chain from the initial or terminal point, which can be obtained from *any* parametrisation f of $\overline{f}$. The second item states that if we are considering extensions from an interior point α, the maximal chains from α to $\overline{f}$ correspond to directed paths in the cartesian square $[0,1]\times[0,1]$. These directed paths correspond to equivalence classes of pairs γ_+, γ_- under the equivalence relation which identifies pairs which visit the same pairs of extremal points.

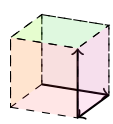
To make the construction above more clear, we will show explicitly how to find the homology along a trace by restriction of the natural homology diagram. Recall that in a pospace $\mathcal{X}$, the trace poset $\mathbb{P}(\mathcal{X})$ and the factorisation category of the trace category $F\overrightarrow{\mathbf{P}}(X)$ are isomorphic, so we may view natural homology $\overrightarrow{H}_n(\mathcal{X})$ as a functor on $\mathbb{P}(\mathcal{X})$ with values in the category Ab. In practice, persistent homology is defined with coefficients in $\mathbb{R}$ or in a field $\Bbbk$, whereas natural homology generally considers more general abelian group coefficients. We will restrict in all practical cases to homology with coefficients in $\Bbbk$ so that to make comparisons possible.

Proposition 2. *Let $\mathcal{X} = (X, dX)$ be a pospace and f a trace in $\mathcal{X}$. Let C be a chain in the interval $[\alpha_f, f]$ in the poset of traces. Let $(f_i)_{i\in\Bbbk}$ be a parametrisation of C obtained as described in Section 5.2. Restricting the natural homology functor $\overrightarrow{H}_n(\mathcal{X})$ to C, we obtain a persistence $\Bbbk$-vector space $\overrightarrow{H}_n(\mathcal{X})_{f_i}$.*

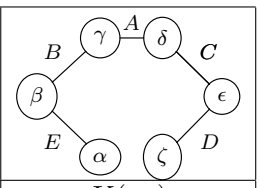
5.4 Example: persistent homology of the matchbox

Consider the case of matchbox example presented in Section 2. Let us calculate the persistent homology along each of its maximal traces, starting at the initial point and extending into the future. We fix some field $\Bbbk$ and will proceed via the method developed in [36]. To each of the maximal traces $\zeta, \epsilon, \alpha, \beta, \delta, \gamma$ pictured in (2), we associate a sequence of subtraces corresponding to a decomposition of the trace along each 1-simplex in the matchbox. For example, the trace α is decomposed into the chain

$$\alpha_0 \leq \alpha_1 \leq \alpha_2 \leq \alpha_3 = \alpha,$$



where α_0 is the constant path equal to $(0,0,0)$, which α_1 extends to $(0,1,0)$. This trace is further extended to $(0,1,1)$ obtaining α_2, and then finally extended to $(1,1,1)$ giving the total trace α. A similar decomposition, which we will denote with the same indices, can be found for each of the maximal traces. This sequence of traces gives a filtration of the simplicial complex pictured above. In the case of α, we obtain the following filtration:

α_0	α_1	α_2 ζ_2	
$K(\alpha_0)$	$K(\alpha_1)$	$K(\alpha_2)$	$K(\alpha_3)$

We extend this filtration into a $\mathbb{N}$-persistence simplicial complex by considering copies of $K(\alpha_3)$ for all $i \geq 4$. We denote by $C_*(K(\alpha_i))$ the chain complex over $\Bbbk$ obtained from the simplicial complex $K(\alpha_i)$, obtaining a $\mathbb{N}$-persistence chain complex

$$C_*(K(\alpha_0)) \xrightarrow{f_{0,1}} C_*(K(\alpha_1)) \xrightarrow{f_{1,2}} C_*(K(\alpha_2)) \xrightarrow{f_{2,3}} C_*(K(\alpha_3)) \xrightarrow{f_{3,4}} \cdots$$

where $f_{n,n+1}$ are induced by the inclusions of simplicial sets given by the filtration. For each natural number p, we denote by H_p^i the pth homology group of $C_*(K(\alpha_i))$, thus obtaining a sequence of homology groups

$$H_p^0 \xrightarrow{\phi_{0,1}} H_p^1 \xrightarrow{\phi_{1,2}} H_p^2 \xrightarrow{\phi_{2,3}} H_p^3 \xrightarrow{\phi_{3,4}} H_p^3 \xrightarrow{\phi_{4,5}} \cdots \xrightarrow{\phi_{n-1,n}} H_p^3 \xrightarrow{\phi_{n,n+1}} \cdots ,$$

where the $\phi_{n,n+1}$ are identities for $n \geq 3$. This is in fact an $\mathbb{N}$-persistence $\Bbbk$-vector space. We define a non-negatively graded module over $\Bbbk[t]$ by setting

$$H_p := \left(\bigoplus_{i=0}^{2} H_p^i \right) \oplus \left(\bigoplus_{i=3}^{\infty} H_p^3 \right),$$

and defining the action of t by $t \cdot (h_i)_i = (\phi_{i,i+1}(h_i))_i$, where the h_i belongs to H_p^i.

We will calculate the graded module of persistent homology via matrix representations of the boundary maps ∂_k associated to the persistence chain complex $C_*(K(\alpha_i))$ as described in [36]. We calculate $H_0(\alpha)$, the 0th persistent homology along α. For this, we fix homogeneous bases for Z_0 and $\mathcal{C}_1$. Since $Z_0 = \mathcal{C}_0$, we may take the standard basis in both cases. Thus, for $\mathcal{C}_0$ we obtain the basis $\{\alpha_0, \zeta_2, \beta, \gamma, \delta, \epsilon\}$, and for $\mathcal{C}_1$ we obtain the basis $\{A, B, C, D, E\}$. We now calculate the matrix of ∂_1 with respect to these bases, taking care to order the basis of $\mathcal{C}_0$ in reverse degree order:

	B	A	C	D	E
β	-1	0	0	0	1
γ	1	-1	0	0	0
δ	0	1	-1	0	0
ϵ	0	0	1	-1	0
ζ_2	0	0	0	t	0
α_0	0	0	0	0	$-t^3$

We now calculate the column-echelon form of the above matrix, obtaining

	B	A	C	D	E'
β	$\boxed{-1}$	0	0	0	0
γ	1	$\boxed{-1}$	0	0	0
δ	0	1	$\boxed{-1}$	0	0
ϵ	0	0	1	$\boxed{-1}$	0
ζ_2	0	0	0	t	$\boxed{t}$
α_0	0	0	0	0	$-t^3$

where $E' = A + B + C + D + E$. In the case of the persistent homology along α, we see that the first four rows contribute nothing to the description of $H_0(\alpha)$, and that the last two contribute $\Sigma^2\Bbbk[t]/t$ and $\mathbb{K}[t]$ respectively, *i.e.*

$$H_0(\alpha) \cong \Bbbk \oplus \Bbbk \oplus \Bbbk^2 \oplus \Bbbk \oplus \cdots \oplus \Bbbk \oplus \cdots$$

We obtain a similar result for the persistent homology along ζ. Below are the standard and column-echelon forms of ∂_1 in this case:

	B	A	C	D	E
β	-1	0	0	0	1
γ	1	-1	0	0	0
δ	0	1	-1	0	0
ϵ	0	0	1	-1	0
ζ_2	0	0	0	0	$-t$
α_0	0	0	0	t^3	0

	B	A	C	D	E'
β	$\boxed{-1}$	0	0	0	0
γ	1	$\boxed{-1}$	0	0	0
δ	0	1	$\boxed{-1}$	0	0
ϵ	0	0	1	$\boxed{-1}$	0
ζ_2	0	0	0	0	$\boxed{-t}$
α_0	0	0	0	t^3	t^3

We therefore obtain the same isomorphism class for $H_0(\zeta)$ as we did in the case of α:

$$H_0(\zeta) \cong \Bbbk \oplus \Bbbk \oplus \Bbbk^2 \oplus \Bbbk \oplus \cdots \oplus \Bbbk \oplus \cdots$$

The other four dipaths yield a simple persistent homology. Indeed, there is only one class which persists throughout the sequence. Indeed, along β for example, a homogeneous basis of C_0 is $\{\beta_0, \gamma_2, \epsilon, \zeta, \delta, \alpha\}$. The basis for C_1 is the same, but now B has degree two rather than three. We obtain the following matrix representation of ∂_1:

	E	A	C	D	B
α	-1	0	0	0	0
δ	0	1	-1	0	0
ζ	0	0	0	1	0
ϵ	0	0	1	-1	0
γ_2	0	$-t$	0	0	1
β_0	t^3	0	0	0	$-t^2$

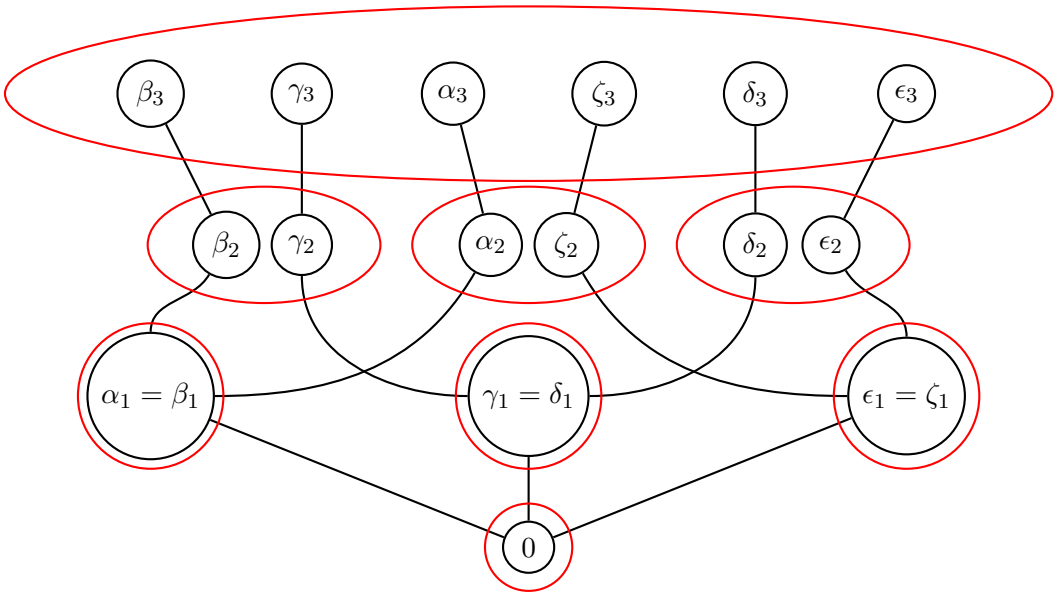
	E	A	D	$A+C$	B
α	$\boxed{-1}$	0	0	0	0
δ	0	$\boxed{1}$	0	0	0
ζ	0	0	$\boxed{1}$	0	0
ϵ	0	0	-1	$\boxed{1}$	0
γ_2	0	$-t$	0	$-t$	$\boxed{1}$
β_0	t^3	0	0	0	$-t^2$

We indeed see that the graded module $H_0(\beta)$ is simply $\Bbbk[t]$, since all pivots are of degree zero and there is one non-pivot row.

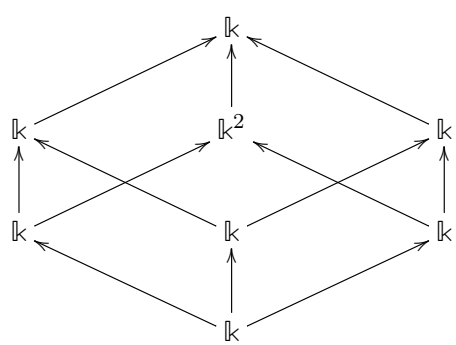
5.5 Natural homology of the matchbox

Now we describe the natural homology diagram of the matchbox. First we will describe its restriction to the principal upset in $\mathbb{P}(\mathcal{X})$ given by the constant path at the initial point $(0, 0, 0)$.

The following diagram depicts the Hasse diagram of this upset:



Traces in the same red circle yield the same trace space, *i.e.* have the same beginning and end points. Each line corresponds to an extension. The natural homology diagram is depicted below, the arrows being induced by extensions:



Each path of length 3 in the above diagram corresponds to the persistence vector space obtained by taking the persistent homology along one of the maximal traces. Note that since none of the maps depicted in the diagram are identically zero, the only maps which are not uniquely defined are those with codomain $\Bbbk^2$.

Comparing the above with the Hasse diagram of the trace poset of the matchbox, it is clear that "glueing" the persistence modules along chains while taking end-points into account relates the uni-dimensional persistence complexes to natural homology. This will be made explicit in the next section.

6 Simultaneous persistence of directed spaces

In this section, we give methods for amalgamating information from persistent homology along traces. We recall constructions in the category of posets which will be useful when using persistent homology along traces to recover natural homology. We will denote by **Pos** the category of posets and order preserving maps, and by $\mathbf{Pos}_{in}$ the wide subcategory with order preserving inclusions.

6.1 Colimits of chains in posets

In order to reconstruct natural homology from persistent homology along traces, we must amalgamate information from each chain in the trace poset. For this reason, we discuss here how to construct a poset from its (maximal) chains.

Firstly, notice that in general, using exclusively maximal chains is not enough to reconstruct a poset. Indeed, consider the poset whose Hasse diagram is depicted below:

$$\begin{tikzcd}
 & z & \\
y_1 \arrow[ur] & & y_2 \arrow[ul] \\
 & x \arrow[ul] \arrow[ur] &
\end{tikzcd}$$

Its maximal chains are (x, y_1, z) and (x, y_2, z). In order to obtain the whole poset as a colimit, we additionally need the inclusions of x and z into these chains.

While a poset is in general, not the colimit of its maximal chains, it is the colimit of all of its chains. Given a poset P, we consider the full subcategory Ch_P of $\mathbf{Pos}_{in}$ consisting of the chains of P, called the *poset of chains*. The *diagram of chains* associated to P is the inclusion functor $\mathcal{F}_P : \mathsf{Ch}_P \to \mathbf{Pos}$. We have:

Proposition 3. *For any poset P,*

$$\operatorname{colim} \mathcal{F}_P = P.$$

Proof. The colimit of $\mathcal{F}_P$ is computed as follows, in **Pos**: first we take the coproduct of all chains of P, which is the union of all sub-linear orders $(x_i^j)_{i \in I}$ of P where j ranges over all chains of P, for some indexing family I and $x_i^j \in P$ for all $i \in I$. Then we identify all common subchains within the $(x_i^j)_{i \in I}$, in particular the elements themselves. Therefore we identify all x_i^j within these linear orders that have to be identified, and take the transitive closure of the corresponding orders. This is indeed the poset P. □

When considering exclusively maximal chains, we may obtain P by adding their intersections to the diagram of inclusions. This can be done in two ways: either taking full intersections or restricting to chains. In the latter approach, the colimit is of a functor whose domain is a subcategory of Ch_P, whereas in the former, the posets used in the colimit are not necessarily chains.

Consider a (finite) poset P and two maximal chains C_1, C_2 of P. The pullback of C_1, C_2 in **Pos** corresponds to the full sub-poset of P given by the intersection $C_1 \cap C_2$. Denote by pmCh_P the subcategory of $\mathbf{Pos}_{in}$ consisting of maximal chains in P and their pullbacks. By maximality of the considered chains, this category looks like a zig-zag.

Recall that a *chain quasi-pullback* of two chains C_1 and C_2 in P is a chain C_{12} such that $C_{12} \to C_1, C_2$ in $\mathbf{Pos}_{in}$ and such that for any chain $C' \to C_1, C_2$, there exists $C' \to C_{12}$ in $\mathbf{Pos}_{in}$. This is summed up in the diagram below:

$$\begin{tikzcd}
 & & C_1 \arrow[dr] & \\
C' \arrow[urr, dashed] \arrow[r, dotted, "\exists"] \arrow[drr, dashed] & C_{12} \arrow[ur] \arrow[dr] & & P \\
 & & C_2 \arrow[ur] &
\end{tikzcd}$$

The category Ch_P of chains in P is closed under quasi-pullback. Indeed, the poset induced by the intersection C_1 and C_2 is a collection of chains. The maximal chains of this intersection are precisely the quasi-pullbacks of C_1 and C_2. Consider the (discrete) subcategory of $\mathbf{Pos}_{in}$ consisting of the maximal chains in P. The completion of this category by chain quasi-pullbacks is denoted by mCh_P. It is a subcategory of Ch_P.

Compiling all of this, we obtain the following result:

Proposition 4. *A poset P is the colimit of the following inclusion functors:*

i) *The minimal (completed) diagram of maximal chains* $\mathsf{pmCh} \to \mathbf{Pos}$.

ii) *The (completed) diagram of maximal chains* $\mathsf{mCh} \to \mathbf{Pos}$.

Proof. These follow the same schema as the proof of Proposition 3. □

6.2 Application to diagrams

Now that we have assembled information on colimits of chains, we will see how these constructions carry over to diagrams over chains. We fix a category $\mathcal{C}$.

First, we introduce a category representing persistence objects of a certain type $\mathcal{C}$, without fixing the indexing poset. Specifically, this category, denoted by $Pers(\mathcal{C})$, has for objects pairs $(P, F : P \to \mathcal{C})$ where P is a poset (*i.e.* F is a P-persistence object in $\mathcal{C}$). A morphism from $(P, F : P \to \mathcal{C})$ to $(Q, G : Q \to \mathcal{C})$ is a pair (ϕ, σ) where ϕ is a morphism $P \to Q$ of **Pos** and σ is a natural transformation $F \Rightarrow G \circ \phi$:

$$\begin{tikzcd}
P \arrow[rr, "\phi"] \arrow[dr, "F"'] & \arrow[d, phantom, "\overset{\sigma}{\Longrightarrow}"] & P' \arrow[dl, "G"] \\
 & \mathcal{C} &
\end{tikzcd}$$

Composition of morphisms is given by $(\psi, \tau) \circ (\phi, \sigma) = (\psi \circ \phi, \tau_\phi \circ \sigma)$, and the identity on (P, F) is the pair $(1_P, 1_F)$. We denote by $IsoPers(\mathcal{C})$ the subcategory of $Pers(\mathcal{C})$ in which we only take morphisms (ϕ, σ) such that σ is a natural isomorphism.

Note the following: consider the wide sub-category of $\mathsf{opNat}(\mathcal{C})$, as defined in Section 4.2, consisting of natural systems with values in $\mathcal{C}$, with base category being a poset. This category naturally embeds in the category of diagrams $Pers(\mathcal{C})$.

Let P be a poset and an inclusion $G : \Phi \to \mathbf{Pos}_{in}$, where Φ is a category of sub-posets of P and inclusions such that $\operatorname{colim}_{\Phi} G = P$. Suppose that we are given a functor $D : P \to \mathcal{C}$, *i.e.* an object of $Pers(\mathcal{C})$. Since the colimit of G is P, for each p in Φ, we have an inclusion $i_p : P_p \to P$. Using these inclusions, we define a functor $F : \Phi \to Pers(\mathcal{C})$, sending each p to the restriction of D to P_p, denoted by $F_p := (i_p)^* D$. We denote by F_p the functor associated to $p \in \Phi$, and by $(P_p, \leq_p)$ its domain. When $p \leq_\Phi p'$, we obtain a morphism $(F^1_{p,p'}, F^2_{p,p'})$ of $Pers(\mathcal{C})$. Note that F is a functor $F : \Phi \to IsoPers(\mathcal{C})$, since $F_{p'}$ is the restriction of D to $P_{p'}$, hence agree with F_p which is the restriction of D to $P_p \subseteq P_{p'}$.

Proposition 5. *Let P, G, D and F be as defined in the above paragraph. We have*

$$\operatorname*{colim}_{Pers(\mathcal{C})} F = D.$$

Proof. The functor F determines a functor G_F from Φ to $\mathbf{Pos}$:

$$\begin{tikzcd} G_F : \Phi \arrow[r] & \mathbf{Pos} \\ p \arrow[r, mapsto] \arrow[d, "\leq_\Phi"'] & P_p \arrow[d, "F^1_{p,p'}"] \\ p' \arrow[r, mapsto] & P_{p'} \end{tikzcd}$$

By hypothesis, we have $G_F = G$, so the colimit of G_F is equal to P. In this optic elements of P are equivalence classes $[x]$ of elements $x_p \in P_p$ under the equivalence relation generated by $x_p \sim x_{p'}$ if, and only if, $p \leq_\Phi p'$ and $F^1_{p,p'}(x_p) = x_{p'}$. Notice that if $[x_p] = [x_{p'}]$, there exists a zig-zag of $F^1_{q,q'}$'s between them. Therefore, since the components $F^2_{q,q'}$'s are all natural isomorphisms, we have $F_p(x_p) \simeq F_{p'}(x_{p'})$, hence

$$[x_p] = [x_{p'}] \Rightarrow F_p(x_p) \simeq F_{p'}(x_{p'}) \tag{4}$$

Furthermore, we know that $[x] \leq_P [y]$ if, and only if, there exists a finite sequence $p = p_0, \ldots, p_n = p'$ and elements v_i, w_i of P_{p_i} such that

$$x_p = v_{p_0} \leq_{p_0} w_{p_0} \simeq v_{p_1} \leq_{p_1} w_{p_1} \simeq \cdots \simeq v_{p_{n-1}} \leq_{p_{n-1}} w_{p_{n-1}} \simeq v_{p_n} \leq_{p_n} w_{p_n} = y_{p'}, \tag{5}$$

and $[x_p] = [x]$, $[y_{p'}] = [y]$.

We also point out that each equivalence class $[x]$ of P is endowed with an order which is inherited from Φ: $x_p \leq_{[x]} x_{p'}$ if, and only if, $p \leq_\Phi p'$. For each of these equivalence classes, we

consider a functor

$$\begin{tikzcd}
F_{[x]} : [x] \arrow[r] & \mathcal{C} \\
x_p \arrow[r, mapsto] \arrow[d, "\leq_{[x]}"'] & F_p(x_p) \arrow[d, "F^2_{p,p'}(x_p)"] \\
x_{p'} \arrow[r, mapsto] & F_{p'}(x_{p'})
\end{tikzcd}$$

By hypothesis, $\mathcal{C}$ is co-complete, so we obtain the colimit $c_{[x]}$ in $\mathcal{C}$ of the diagram given by $F_{[x]}$. For every $x_p, x_{p'}$, $F_p(x_p) \cong F_{p'}(x_{p'})$ since the natural transformations induced by F are isomorphisms. Thus

$$F_p(x_p) \cong c_{[x]} \text{ for any } x_p \in [x] \tag{6}$$

Now suppose that $[x] \leq [y]$. We want to prove that $c_{[y]}$ is a co-cone for $F_{[x]}$. We reason by induction on the length n of the sequence given in Equation (5). If $n = 0$, Equation (5) amounts to the existence of $p_0 \in \Phi$ and representatives $v_{p_0}, w_{p_0} \in P_{p_0}$ with $v_{p_0} \leq_{p_0} w_{p_0}$, $p = p_0 = p'$, $x_p = v_{p_0}$, $w_{p_n} = y_{p'}$ and $[x_p] = [x]$, $[y_{p'}] = [y]$. We must show that for all $x_p \leq_{[x]} x_{p'}$, we have a commutative diagram of the following shape:

$$\begin{tikzcd}
F_p(x_p) \arrow[rr, "F^2_{p,p'}(x_p)"] \arrow[dr] & & F_{p'}(x_{p'}) \arrow[dl] \\
& c_{[y]} &
\end{tikzcd} \tag{7}$$

Since $v_{p_0} \leq_{p_0} w_{p_0}$, functoriality of F_{p_0} gives an arrow

$$F_{p_0}(v_{p_0} \leq_{p_0} w_{p_0}) : F_{p_0}(v_{p_0}) \to F_{p_0}(w_{p_0}).$$

This means that we have the following diagram, where all of the morphisms in the top triangle are isomorphisms induced by the natural transformations F^2 (by Equation (4) in particular):

$$\begin{tikzcd}
F_p(x_p) \arrow[r, dash, "\simeq"] \arrow[rr, bend left, "\simeq"] & F_{p_0}(v_{p_0}) \arrow[r, dash, "\simeq"] \arrow[d] & F_{p'}(x_{p'}) \\
& F_{p_0}(w_{p_0}) \arrow[d] & \\
& c_{[y]} &
\end{tikzcd}$$

Therefore $c_{[y]}$ is a co-cone for $F_{[x]}$ and we obtain a unique arrow $\Gamma_{[x],[y]} : c_{[x]} \to c_{[y]}$ in $\mathcal{C}$.

Suppose now that we have the property that $c_{[y]}$ is a co-cone for $F_{[x]}$ when the length of the sequence in Equation (5) is strictly below n. We want to prove the property still holds when

the sequence has length n. In the latter case, we have a finite sequence $p = p_0, \ldots, p_n = p'$ and elements v_i, w_i of P_{p_i} such that

$$x_p = v_{p_0} \leq_{p_0} w_{p_0} \simeq v_{p_1} \leq_{p_1} w_{p_1} \simeq \cdots \simeq v_{p_{n-1}} \leq_{p_{n-1}} w_{p_{n-1}} \simeq v_{p_n} \leq_{p_n} w_{p_n} = y_{p'},$$

and $[x_p] = [x]$, $[y_{p'}] = [y]$, and we suppose that $c_{[w_{p_{n-1}}]}$ is a co-cone for $F_{[x]}$.

By Equation (6), we have $c_{[w_{p_{n-1}}]} \cong F_{p_{n-1}}(w_{p_{n-1}})$, and since $w_{p_{n-1}} \simeq v_{p_n}$, we also have $F_{p_{n-1}}(w_{p_{n-1}}) \cong F_{p_n}(v_{p_n})$ by Equation (4). Finally, since $v_{p_n} \leq_{p_n} w_{p_n} = y_{p'}$, we have a morphism $F_{p_n}(v_{p_n}) \to F_{p'}(y_{p'})$ in $\mathcal{C}$ induced by $F_{p'}$. So we have the following:

$$\begin{tikzcd}
F_p(x_p) \arrow[r, dash, "\simeq"] \arrow[rr, bend left, "\simeq"] & F_{p_0}(x_{p_0}) \arrow[r, dash, "\simeq"] \arrow[d] & F_{p'}(x_{p'}) \\
& F_{p_n}(v_{p_n}) \arrow[d] & \\
& F_{p'}(y_{p'}) \arrow[d] & \\
& c_{[y]} &
\end{tikzcd}$$

Therefore $c_{[y]}$ is again a co-cone for $F_{[x]}$, giving the unique arrow $\Gamma_{[x],[y]} : c_{[x]} \to c_{[y]}$ in $\mathcal{C}$.

We define a functor $\Gamma : P \to \mathcal{C}$ which sends $[x]$ to $c_{[x]}$ and $[x] \leq [y]$ to the arrow $\Gamma_{[x],[y]}$ given by the argument above. It is clear that $\Gamma = D$; it remains to show that Γ is indeed the colimit of F.

Let $D' : p' \to \mathcal{C}$ another co-cone for F. For every $p \in \Phi$, we have morphisms (j_p^1, j_p^2) such that the following diagram commutes in $Pers(\mathcal{C})$ for all $p \leq p'$:

$$\begin{tikzcd}
F_p \arrow[rr, "(F^1_{p,p'}, F^2_{p,p'})"] \arrow[dr, "(j_p^1, j_p^2)"'] & & F_{p'} \arrow[dl, "(j_{p'}^1, j_{p'}^2)"] \\
& D &
\end{tikzcd}$$

In particular, this means we have the following commutative diagram in **Pos**:

$$\begin{tikzcd}
P_p \arrow[rr, "F^1_{p,p'}"] \arrow[dr, "j_p^1"'] & & P_{p'} \arrow[dl, "j_{p'}^1"] \\
& P' &
\end{tikzcd}$$

This in turn means that P' is a co-cone over G, so we obtain a unique morphism $\phi : P \to P'$. Furthermore, D' being a co-cone over F implies that for all $x_p, x_{p'} \in [x]$, we have the following commutative diagram in $\mathcal{C}$:

$$\begin{tikzcd}
F_p(x_p) \arrow[rr, "F^2_{p,p'}(x_p)"] \arrow[dr, "j^2_p(x_p)"'] & & F_{p'}(x_{p'}) \arrow[dl, "j^2_{p'}(x_{p'})"] \\
& D'(j^1_p(x_p)) = D'(j^1_{p'} \circ F^1_{(p,p')(x_p)}) &
\end{tikzcd}$$

Since $c_{[x]}$ is the colimit of $F_{[x]}$, we therefore obtain a unique arrow $\sigma_{[x]} : c_{[x]} \to D'(j^1_p(x_p))$ for any representative $x_p \in [x]$. Denoting by $i_p : P_p \to P$ the morphisms in **Pos** induced by the colimit of G, we have that $\phi([x]) = \phi(i_p(x_p)) = j^1_p(x_p)$ for any $p \in \Phi$ such that P_p contains a representative of $[x]$. With some diagram chasing, we find that (ϕ, σ) is a morphism of $Pers(\mathcal{C})$ from Γ to D', and by construction is the unique map making the colimit triangles commute. Thus D is the colimit of F in $Pers(\mathcal{C})$. □

6.3 Natural homology as a colimit

Using the above proposition, and constructions similar to that explained above, we obtain the following results:

Theorem 3. *Let $\mathcal{X} = (X, dX)$ be a pospace and α a point in X and* Vect *the category of $\Bbbk$-vector spaces.*

1. *The natural homology of $\mathcal{X}$ is the colimit in $Pers(\mathsf{Vect})$ of the persistent homology along each of its traces.*

2. *The natural homology of $\mathcal{X}$ is the colimit in $Pers(\mathsf{Vect})$ of the persistent homology of its maximal traces, seen as maximal chains in $\mathbb{P}(\mathcal{X})$, completed with pullbacks (resp. quasi-pullbacks).*

3. *The natural homology of the up-set of α, seen as a constant trace, in $\mathbb{P}(\mathcal{X})$ is the colimit in $Pers(\mathsf{Vect})$ of the persistent homologies along the maximal chains passing through α, completed with pullbacks or quasi-pulbacks.*

Proof. These are direct consequences of Propositions 5 and 3. □

7 Further remarks

In this section we discuss two lines of research concerning the persistence homology of trace spaces and its potential application.

7.1 Metric structure on natural homology

An important feature of persistent homology is that it gives information about a space in terms of its metric and not just its topology. We show that the construction of persistence homology bears similarities with the one of natural homology construction, with particular functors from a factorization category to Top. One may ask whether, when the directed space X we consider has a metric space structure, if there is a metric structure that can be exploited in the corresponding persistence modules.

In the case of the geometric realization of finite geometric precubical sets without loops, as we saw in Section 4.1, we can define the l_1-arc length $l_1(p)$ of a directed path p. From this, we can define a distance between elements of the trace poset, or more precisely, we can see the trace poset as a weighted poset as in [3, 4] as follows: $w(p,q) = 0$ if $p \not\leq q$, otherwise $q = upv$ and $w(p,q) = max\{l_1(u), l_1(v)\}$. Interleaving distances in such contexts are expressed in terms of translations on posets, that vastly generalize the translations $t \in \mathbb{R} \to t + \epsilon$ that defines that usual interleaving distance in unidimensional persistence. Here, we will only briefly discuss the classical interleaving distance in unidimensional persistence homology, extracted along a trace of a directed spaces, that will be induced by translations on the trace poset. The construction of interleaving distances for the full persistence object derived from natural homology is left for future work.

Take two directed spaces $\mathcal{X}$ and $\mathcal{Y}$, geometric realizations of finite geometric precubical sets without loops, p a trace of $\mathcal{X}$ and q a trace of $\mathcal{Y}$. We also suppose we are given a chain $(p_i)_{i\in\mathbb{R}}$ in the interval $[p(0), p]$, and a chain $(q_i)_{i\in\mathbb{R}}$ in the interval $[q(0), q]$. In what follows, we write p_i to be the trace going from x_i^p to y_i^p (resp. q_i the trace going from x_i^q to y_i^q) and $(\alpha_{i,j}^p, \beta_{i,j}^p)$ the morphism from p_i to p_j (resp. $(\alpha_{i,j}^q, \beta_{i,j}^q)$ the morphism from q_i to q_j).

We construct by Proposition 2 a persistence $\Bbbk$-vector space $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ indexed by the chain $(p_i)_{i\in\mathbb{R}}$ and a persistence $\Bbbk$-vector space $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$ indexed by the chain $(q_i)_{i\in\mathbb{R}}$. In particular we have linear maps $\overrightarrow{H}_n(\mathcal{X})_{(\alpha_{i,j}^p, \beta_{i,j}^p)}$ from $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ to $\overrightarrow{H}_n(\mathcal{X})_{p_j}$ (resp. $\overrightarrow{H}_n(\mathcal{Y})_{(\alpha_{i,j}^q, \beta_{i,j}^q)}$ from $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$ to $\overrightarrow{H}_n(\mathcal{X})_{q_j}$).

The *interleaving distance* between $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ and $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$ is defined as follows. We say that $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ and $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$ are *ϵ-interleaved*, for some $\epsilon \geq 0$ if we have families of linear maps $(\phi_i : \overrightarrow{H}_n(\mathcal{X})_{p_i} \to \overrightarrow{H}_n(\mathcal{Y})_{q_{i+\epsilon}})_{i\in\mathbb{R}}$ and $(\psi_i : \overrightarrow{H}_n(\mathcal{Y})_{q_i} \to \overrightarrow{H}_n(\mathcal{X})_{p_{i+\epsilon}})_{i\in\mathbb{R}}$ such that for all $i \leq j \in \mathbb{R}$:

$$\phi_j \circ \overrightarrow{H}_n(\mathcal{X})_{(\alpha_{i,j}^p, \beta_{i,j}^p)} = \overrightarrow{H}_n(\mathcal{Y})_{(\alpha_{i+\epsilon,j+\epsilon}^q, \beta_{i+\epsilon,j+\epsilon}^q)} \circ \phi_i \tag{8}$$

$$\psi_j \circ \overrightarrow{H}_n(\mathcal{Y})_{(\alpha_{i,j}^q, \beta_{i,j}^q)} = \overrightarrow{H}_n(\mathcal{X})_{(\alpha_{i+\epsilon,j+\epsilon}^p, \beta_{i+\epsilon,j+\epsilon}^p)} \circ \psi_i \tag{9}$$

$$\psi_{i+\epsilon} \circ \phi_i = \overrightarrow{H}_n(\mathcal{X})_{(\alpha_{i,i+2\epsilon}^p, \beta_{i,i+2\epsilon}^p)} \tag{10}$$

$$\phi_{i+\epsilon} \circ \psi_i = \overrightarrow{H}_n(\mathcal{Y})_{(\alpha_{i,i+2\epsilon}^q, \beta_{i,i+2\epsilon}^q)} \tag{11}$$

Then the interleaving distance between $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ and $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$ is the infimum of all $\epsilon \geq 0$ such that $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ and $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$ are ϵ-interleaved, ∞ if there is no such ϵ.

There are similarities and essential differences between bisimulation equivalent natural homologies, and having non-infinite interleaving distance, as we show below.

When there exists a dihomeomorphism $f : \mathcal{X} \to \mathcal{Y}$, we know from Lemma 1 that their corresponding natural homologies are bisimulation equivalent, and we now show that there are particular relations between the persistent objects $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ and $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$. Then, for any chain $(p_i)_{i\in\mathbb{R}}$ in the interval $[p(0), p]$, for any dipath p in $\mathcal{X}$, $\overrightarrow{H}_n(\mathcal{X})_{p_i}$ and $\overrightarrow{H}_n(\mathcal{Y})_{f^*(p_i)}$ have interleaving distance 0.

Indeed, we take $\phi_t : \overrightarrow{H}_n(\mathcal{X})_{p_t} \to \overrightarrow{H}_n(\mathcal{Y})_{f^*(p_t)}$ to be $[f^*(x)]$, for each $[x] \in \overrightarrow{H}_n(\mathcal{X})_{p_t}$, the homology class of path $f^*(x)$, for $[x]$ the homology class of any dipath x from $p_t(0)$ to $p_t(1)$. Similarly, The equations (10) and (11) are trivially verified since $(f^{-1})^* \circ f^* = f^* \circ (f^{-1})^*$ and $\overrightarrow{H}_n(\mathcal{X})_{(\alpha^p_{i,i},\beta^p_{i,i})}$, $\overrightarrow{H}_n(\mathcal{Y})_{(\alpha^{f^*(p)}_{i,i},\beta^{f^*(p)}_{i,i})}$ are identities (since $\alpha^p_{i,i}$, $\beta^p_{i,i}$), $\alpha^{f^*(p)}_{i,i}$ and $\beta^{f^*(p)}_{i,i}$) are constant dipaths. Simarly, Equations (8) and (9) are trivially satisfied since $\overrightarrow{H}_n(\mathcal{X})_{(\alpha^p_{i,i},\beta^p_{i,i})}$, $\overrightarrow{H}_n(\mathcal{Y})_{(\alpha^{f^*(p)}_{i,i},\beta^{f^*(p)}_{i,i})}$ are identities

In a smilar manner, we prove that for any chain $(q_i)_{i\in\mathbb{R}}$ in the interval $[q(0), q]$, for any dipath q in $\mathcal{Y}$, $\overrightarrow{H}_n(\mathcal{X})_{(f^{-1})^*(q_i)}$ and $\overrightarrow{H}_n(\mathcal{Y})_{q_i}$ have interleaving distance 0.

Of course, we miss an important point about persistence if we do not insist on considering only representative p of $\overline{p}$ that are parameterized by the arc-length. In that case, the interleaving distance is zero only when f is an isometry.

For geometric realizations $\mathcal{X}$ of finite geometric precubical sets S, there are natural $\mathbb{N}$-persistence objects, given by, for the geometric realization p in $\mathcal{X}$ of any combinatorial directed edge-path p_S in of S the filtration of $[p(0), p]$ in the trace poset of $\mathcal{X}$ given by C_i being the geometric realization of the prefix with i steps of p_S. Considering this $\mathbb{N}$-persistence object as a $\mathbb{R}$-persistence object $\overrightarrow{h}_n(\mathcal{X})_p$, which is constant between two integers, we get that the interleaving distance between $\overrightarrow{H}_n(\mathcal{X})_p$ and $\overrightarrow{h}_n(\mathcal{X})_p$ is at most 1. Whereas for such geometric realizations it is known (see [9]) that the "combinatorial" natural homology of S is bisimulation equivalent to the natural homology of $\mathcal{X}$ only in some particular cases, e.g. when S is a cubical complex.

7.2 Algorithmical considerations

In this section, we sketch practical calculations of the persistence module that corresponds, by Theorem 3, to natural homology, in the case of directed spaces arising in concurrency theory, which was the original motivation of this work. It has been shown in e.g. [16] that concurrent languages, such as the shared memory PV language, can be given semantics in pre-cubical sets, hence of a directed space. This has been been implemented in such software as ALCOOL [2] and oplate [25]. It has been shown that under some hypotheses, validated for such concurrent languages as the PV language, the natural homology computed on pre-cubical sets K, which is the homology of the diagram of traces spaces $\mathfrak{T}(K)(f)$, for all a, b vertex in K_0, and f dipath from a to b in K_1, is bisimulation equivalent to the natural homology of the dspace, geometric realization of K, [9].

For finite pre-cubical sets, Raussen [32] and Ziemianski [35] showed that singular homology groups of trace spaces such as $\mathfrak{T}(K)(a, b)$ (which is isomorphic to all $\mathfrak{T}(K)(f)$, f dipath from a to b) are computable, by calculating a finite presentation of the trace spaces (prod-simplicial, simplicial or CW-complex) from which we can compute homology using Smith normal form of

matrices. This has also been implemented in e.g. [15].

For "nice" precubical sets X such as the ones given by the PV language (without loops), and for any vertices a and b in X, there is a way to get a finite combinatorial model $T(X)(a,b)$ (a finite CW-complex, or a finite simplicial set) that is homotopy equivalent to the trace space of X from a to b, $\mathfrak{T}(X)(a,b)$, which is both functorial in X, a, b and also minimal among such functors [35]. Algorithmically, this relies on the cells of the CW-complex being identified with certain combinatorial paths in X, as was exemplified in Section 2. This algorithm allows to construct the (poset) filtration of CW-complexes (or homotopy equivalent simplicial sets) $T(X)(a,b)$ and therefore compute their homology, for each a and b in X. Thus this would algorithmically build the persistence module, or natural homology, of the precubical set X. Of course this is a rather naive algorithm, in that we compute homology separately for each pair of points. We postpone the discussion of non naive algorithms similar to rank invariant computations for a future article.

8 Conclusion and future work

In [5], we related natural homotopy, a natural system of homotopy groups associated to a dispace, to group objects in a certain category. This was achieved via the notion of composition pairing, introduced by Porter and largely inspired by lax functors. This extra structure of composition pairing is also present in natural homology, and we believe such "homological" operations may have some interesting counterparts in persistence homology, which we are planning on studying in future work.

In hybrid systems theory, there is a natural sheaf theoretic formulation of dynamical systems, starting from [29], put in action (in particular, concerning temporal logic formulas and verification) and extended in [34] [33]. The formalization bears similarities with natural homology for directed spaces, except that it takes a sheaf-theoretic view, leading to contravariant, instead of covariant, functors.

Consider the monoid $(\mathbb{R}_+,+)$, seen as a one 0-cell category $\mathbb{R}$. Its factorization category $\mathcal{F}\mathbb{R}$ has as 0-cells, intervals $[0,l]$ for $l \in \mathbb{R}$, and as 1-cells, inclusions of such intervals into larger intervals $[0,l']$, translated by some value $k \leq l'-l$. Presheaves on $\mathcal{F}\mathbb{R}$ can be endowed with a Grothendieck topology, Johnstone topology [28], so that sheaves correspond to dynamical systems (in some ways, "continuous graphs" described locally by gluings of paths of various lengths, that agree on subpaths).

Therefore, dynamical systems on some metric space X are considered as being particular presheaves, *i.e.* functors $D:\ \mathcal{F}\mathbb{R} \to Set$, describing, for each length l, the set of paths of length l, and for each inclusion Tr_k of $[0,l]$ into $[0,l']$ as $[k,k+l]$ (with $k \leq l'-l$), a restriction map from the length l' paths to length $l \leq l'$ paths.

Of course, for real continuous dynamical systems, we have an extra structure, which is that the set of paths on X is a topological space, with the compact-open topology (equivalently, uniform convergence). Hence what we really have is a presheaf $D:\ \mathcal{F}\mathbb{R} \to \mathsf{Top}$, where Top is a convenient category of topological spaces.

This means that D belongs to a certain ∞-topos [31], but the point for now is to notice that D gives in particular a filtration of topological spaces from $\mathbb{R}_-$ to Top, by setting $X_{-l} = D([0,l])$ and maps $X_{-l'} \to X_{-l}$ when $-l' \leq -l$, that we can choose to be $D(Tr_0:\ X_{-l'} \to X_{-l})$. Hence

this filtration looks at a dynamical system on X through, successively, its set of smaller initial paths.

Similarly, taking the additive monoid $\mathbb{N}$, the same sheaf construction gives the ordinary category of graphs, and the filtration we have been giving starts with the topological space of maximal length in X, and carries on with paths of smaller length.

The persistent homology for these filtrations is an interesting invariant of dynamical systems, and has a metric information induced by the metric on X that we are planning on examining in future work.

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