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Topological tracking of connected components in image sequences

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ABSTRACT

Taking as input a time-varying sequence of 2D binary digital images, we develop an algorithm for encoding, in the so-called spatiotemporal barcode, lifetime of connected components that are moving in the sequence over time. Given a connected component in a specific time in the sequence, we can track it backwards, by what we call a spatiotemporal path. The main contribution of this paper lies in a new algorithm that computes spatiotemporal paths valid for both foreground and background and developed in a general context, setting the ground for tracking higher dimensional topological features in nD.

1. Introduction

Persistent homology [3,15] and zigzag persistence [2] provide information about lifetime of homology classes along a filtration of cell complexes. Such a filtration might be determined by time in a set of spatiotemporal data. Our general aim is to compute the "spatiotemporal" topological information of such filtration, taking into account that it is not possible to move backwards in time. This is not obvious if we use the known algorithms for computing (zigzag) persistent homology using time as filter function.

In the context of mobile sensor networks, [4] is devoted to the problem of finding an *evasion* path that describes a moving intruder avoiding being detected by the sensors. In [4], the region covered by sensors at time t is encoded using a Rips complex $R(t)$. A single cell complex SR is computed by stacking the complexes $R(t)$ for all t. Th. 7 of [4] proves that there is no evasion path under a "homological" criterion. Using zig–zag persistent homology, an equivalent condition is provided in [1]. A necessary and sufficient *positive cohomological criterion* for evasion in a general case is given in [8]. Finally, in [6], the authors analyze time-varying coverage properties in dynamic sensor networks by means of zigzag persistent homology. In all the mentioned papers, vertices represent sensors and edges are provided whenever two sensors can detect each other but their specific locations are unknown.

We are concerned with the treatment of time-varying sequences of nD binary digital images and the tracking of homology classes over time inspired by persistent homology methods. We deal with vertices at exact positions in each nD image and adjacency relations between consecutive images are provided whenever there are cells in homologous positions (that is, the cells are in the same spatial position but at different times). Our general goal is to compute a *spatiotemporal* barcode storing the evolution of homology classes *over time*. In this paper, we concentrate our effort in 2D images and track

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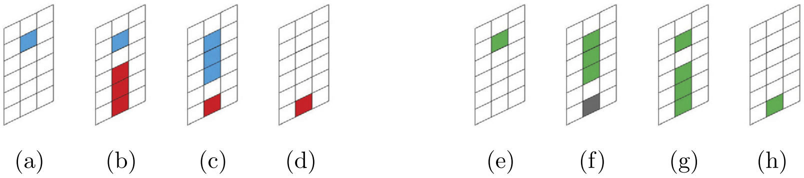

Fig. 1. Two different sequences of 2D images with pixels appearing and disappearing over time. The reader is referred to the online version for color version of this figure.

connected components of both the background and the foreground over time. Roughly speaking, a spatiotemporal path will track a connected component over time and a spatiotemporal barcode will encode the evolution of homology classes over time. For example, the spatiotemporal barcode of the sequence of the four 2D binary digital images given in Fig. 1(a)–(d) reflects the fact that a connected component is born in the first image and dies in the third one, and another connected component is born in the second image and dies in the fourth one. This paper is an extension of our previous work [11] in which we also focused on computing a spatiotemporal barcode for a time-varying sequence of 2D binary digital images. There, we used the construction of an algebraic-topological model (AT-model) [10] to compute spatiotemporal paths. In the present paper, though, we compute the spatiotemporal paths and barcode directly (without computing AT-models).

We also extend the definition of spatiotemporal filtration and spatiotemporal path to any dimension, what facilitates future extensions of our work to compute spatiotemporal d-barcodes in any dimension d.

Basics of persistent homology and AT-models are given in Section 2. We introduce the problem of computing the "correct" topological information of spatiotemporal data through two simple examples in Section 3. Formal definitions to deal with a temporal sequence of cubical complexes are set in Section 4. Our method to solve the problem is then introduced in Section 5. In Section 5.1, we extend the definition of spatiotemporal path to any dimension. We conclude in Section 6 and describe possible directions for future work.

2. Persistent homology through AT-models

Consider $\mathbb{Z}/2$ as the ground ring throughout the paper (i.e. $1+1=0$). Roughly speaking, a cell complex K is a general topological structure by which a space is decomposed into basic elements (cells) of different dimensions that are glued together by their boundaries (see the definition of CW-complex in [12]). The dimension of a cell $\sigma \in K$ is denoted by $dim(\sigma)$. A cell $\mu \in K$ is a *d-face* of a cell $\sigma \in K$ if μ lies in the boundary of σ and $d = dim(\mu) < dim(\sigma)$. The cell complex ∂K is built as follows: add a d-cell σ of K to ∂K together with all its faces if σ is face of exactly one $(d+1)$-cell in K.

If the cells in K are d-dimensional *cubes* then K is a *cubical complex*. A d-dimensional cube (d-cube) is a product of d elementary intervals $\prod_{i=1}^{d} I_i$. An elementary interval is defined as a unit interval $I = [k, k+1]$, with $k \in \mathbb{Z}$ or a degenerate interval $[k, k]$. The number of non-degenerate intervals in such product is the dimension of the cube. 0-cubes, 1-cubes, 2-cubes and 3-cubes are vertices, edges, squares and 3D cubes (voxels) respectively. A cube c_1 is a face of a given cube c_2 if $c_1 \subset c_2$. Given two cubes, all the faces of a cube must also be a cube, as well as the intersection of any two cubes. A cubical complex has dimension D if the cubes are all of dimension at most D. The barycentric coordinates of a cube c will be denoted by r_c.

A *d-chain* is a formal sum of d-cells in K. Since coefficients are either 0 or 1, we can think of a d-chain as a set of d-cells, namely those with coefficients equal to 1. In set notation, the sum of two d-chains is their symmetric difference. The d-chains together with the addition operation form a group denoted as $C_d(K)$. Besides, the set $\{C_d(K)\}_{0 \le d \le D}$, is denoted by $C(K)$. A set of homomorphisms $\{f_d : C_d(K) \to C_d(K')\}_{0 \le d \le D}$, is called a *chain map* and denoted by $f : C(K) \to C(K')$. Given two d-cells $\sigma \in K$ and $\sigma' \in K'$, we say that $\sigma' \in f(\sigma)$ if σ' belongs to the d-chain $f_d(\sigma)$ (in set notation). The *boundary map* $\partial : C(K) \to C(K)$ is defined on a d-cell σ as the sum of its $(d-1)$-faces. The d-chains with zero boundary form a subspace $Z_d(K)$ of $C_d(K)$. The d-chains that are the boundary of $(d+1)$-chains form a subspace $B_d(K)$ of $Z_d(K)$. The quotient group $H_d(K) = Z_d(K)/B_d(K)$ is the d-th homology group of K (with $\mathbb{Z}/2$ coefficients). The rank of $H_d(K)$, denoted by $\beta_d(K)$, is the d-th Betti number of K. For a deeper introduction of these concepts, see [14,13,12].

A *filtration* of K is an increasing sequence of cell complexes: $\emptyset = K_0 \subset K_1 \subset \cdots \subset K_\ell = K$. The partial ordering given by such a filtration can be extended to a *total ordering* of the cells of K: $\{\sigma_1, \dots, \sigma_m\}$, satisfying that for each i, $1 \le i \le m$, the faces of σ_i lie on the set $\{\sigma_1, \dots, \sigma_i\}$. The map $index : K \to \mathbb{Z}$ is defined by $index(\sigma_i) := i$. Informally, the d-th persistent homology group [3,15,5] can be seen as a collection of d-homology classes (representing connected components when $d = 0$, tunnels when $d = 1$, cavities when $d = 2$, ...) that are born at or before we go from K_{i-1} to K_i and die after we go from K_i to K_{i+1}. A persistence *d-barcode* [7] is a graphical representation of the d-th persistent homology groups as a collection of horizontal line segments (*bars*) in a plane. Axis correspond to the indices of the cells in K. For example, if a d-homology class is born at time i (i.e. when σ_i is added) and dies at time j $(1 \le i < j \le m)$, then a bar $b = ((i,i),(j,i))$ with endpoints (i,i) and (j,i) is added to the d-barcode.

In [9] the authors establish a correspondence between the incremental algorithm for computing AT-models [10] and the one for computing persistent homology [3]. More precisely, an *AT-model* for a cell complex K is a quintuple (f, g, ϕ, K, H), where:

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