Computational Topology in Image Context

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I. Introduction

It is well known that visual perception and topology are closely related to each other. In his book "The child's conception of space" Jean Piaget and Bärbel Inhelder wrote "the child starts by building up and using certain primitive relationships ... [which] correspond to those termed 'topological' by geometricians." Even if further research in cognitive science has moderated this position, the importance of topology in visual perception is no longer questionable.

The topological approach can be seen both as a method to reduce the usually big amount of information that is associated with visual data, and as a particularly convenient and meaningful pass key to human perception [1], [2].

Recent progress in applied topology allows for its use beyond low level image processing, extending the application of topological techniques to image interpretation and analysis. However, this often requires advanced and not trivial theoretical frameworks that are still not well known in the computer vision community.

The goal of the Vision Mathematics Group is to develop new topological ideas useful for shape analysis.

The research problems presently tackled by members of the Vision Mathematics Group cover several subjects that are relevant to shape analysis: topological analysis of shape similarity, the use of persistent homology and Reeb graphs to reveal the global structure of similarities between the data, the application of persistent homology to study stability and topological correctness in images, a methodology for classifying melanomas using multidimensional persistent homology, a new framework to estimate the matching distance between persistent diagrams of 3D-models.

II. TOPOLOGICAL ANALYSIS OF SHAPE SIMILARITY

In shape comparison, a widely used scheme is to measure the dissimilarity between signatures associated with each shape rather than match shapes directly.

Persistence diagrams and Reeb graphs are signatures describing shapes from topological and geometrical perspectives. In this framework, shapes are modeled as spaces X endowed with real functions f. The role of f is to explore geometrical properties of the space X. The Reeb graph of f is obtained by shrinking each connected component of a level set of f to

a single point. The persistence diagram is obtained by pairing births and death of topological feature along a filtration of X by sublevel sets of f.

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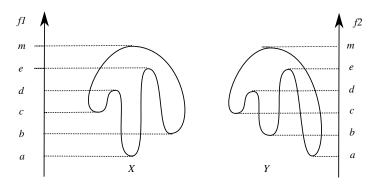


Fig. 1. Two curves which are not distinguishable by persistence modules, but with nonvanishing natural pseudodistance.

Metrics measuring the dissimilarity of Reeb graphs and persistence spaces are thus a proxy to direct shape comparison. One such metric is the *natural pseudodistance* between two *size pairs* (X,f), (Y,g), with X,Y homeomorphic; given a homeomorphism $\varphi: X \to Y$, we consider the sup of the values $|f(P) - g(\varphi(P))|$; the natural pseudodistance is the inf of such values over all possible homeomorphisms from X to Y (Fig. 1). Persistent homology provides lower bounds to this metric [3].

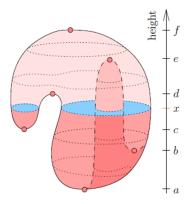


Fig. 2. The inclusion maps of sublevel sets induce homomorphisms between the respective homology modules.

III. PERSISTENT HOMOLOGY

In classical persistence [4], a topological space X is explored through the evolution of the sublevel sets of a real-valued continuous function f defined on X (see Fig. 2). The role of

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X is to represent the data set, while f is a descriptor of some property which is considered relevant for the analysis. These sublevel sets, being nested by inclusion, produce a filtration of X. Focusing on the occurrence of important topological events along this filtration — such as the birth and death of connected components, tunnels and voids — it is possible to obtain a global description of data, which can be formalized via an algebraic structure called a persistence module [5]-[7]. Such information can be encoded in a parameterized version of the Betti numbers, known in the literature as persistent Betti numbers, a rank invariant and — for the 0th homology a size function. The key point is that these descriptors can be represented in a very simple and concise way, by means of multi-sets of points called *persistence diagrams*. Moreover, they are stable with respect to the bottleneck and Hausdorff distances, thus implying resistance to noise. Thanks to this property, persistence is a viable option for analyzing data from the topological perspective, as shown, for example, in a number of concrete problems concerning shape comparison and retrieval [8]-[11].

A. Multidimensional persistent homology

A common scenario in applications is to deal with multiparameter information. The use of vector-valued functions enables the study of multi-parameter filtrations, whereas a scalar-valued function only gives a one-parameter filtration. Therefore, Frosini and Mulazzani [12], as well as Carlsson and Zomorodian [13] proposed multidimensional persistence to analyze richer and more complex data. Research is in fast progress on the development and application of this new tool [14]–[19].

A major issue in multidimensional persistence is that, when filtrations depend on multiple parameters, it is not possible to provide a complete and discrete representation for multidimensional persistence modules analogous to that provided by persistence diagrams for one-dimensional persistence modules.

This theoretical obstruction discouraged so far the introduction of a multidimensional analogue of the persistence diagram. One can immediately see that the lack of such an analogue is a severe drawback for the actual application of multidimensional persistence to the analysis of data. Therefore a natural question we may ask ourselves is the following one: In which other sense may we hope to construct a generalization of a persistence diagram for the multidimensional setting?

A. Cerri and C. Landi recently proposed *persistence spaces* as a generalization of persistence diagrams (see Fig. 3), proving their stability in a (weak, but still non-trivial) Hausdorff sense [20]. The larger point is that stability (already faced in [16]) is the most crucial property of persistence, and so it makes sense to understand when we can preserve it in the multi-dimensional setting.

B. G-invariant persistent homology

In several applications of pattern recognition we are required to compare two real-valued continuous functions f', f'' defined on a topological space X, under the assumption that f', f'' are considered equivalent to each other if a homeomorphism

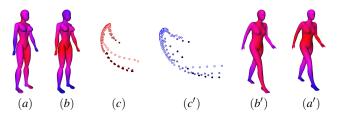


Fig. 3. (a), (b): An example of a 3D-model endowed with two different functions; (c) a visualization of the associated persistence space. (a'), (b'), (c'): same for a different model.

 φ exists in a given group G of self-homeomorphisms of X, such that f'' is equal to the composition of f' with φ . As an example, let us consider the case of a series of photos taken by a camera rotating around an object. This corresponds to considering the function f that associates each point v of the circle S^1 with a matrix describing the picture of the object taken from the oriented direction defined by the unit vector v. If there is no fixed start point for the series of pictures, comparing the functions f', f'' obtained for two different objects is equivalent to trying to minimize the sup-norm distance between the functions f'' and f' o φ , where φ varies in the group G of the rotations of S^1 . This approach - mainly led by P. Frosini - produces the already mentioned natural pseudodistance associated with the group G. Unfortunately, this pseudometric is difficult to compute and to be used in real applications, if the group G is not small. However, lower bounds for this pseudodistance can be easily obtained by using G-invariant persistent homology, an adaptation of persistent homology that is invariant under the action of the group G [21].

IV. REEB GRAPHS

Reeb graphs are combinatorial signatures that capture shape properties from the perspective of a chosen function [22]. One of the most important questions is whether Reeb graphs are robust against function perturbations that may occur because of noise and approximation errors in the data acquisition process.

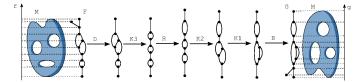


Fig. 4. An example of two Reeb graphs Γ_f and Γ_g associated with simple Morse functions $f,g:S\to\mathbb{R}$. The leftmost is transformed into the rightmost one by applying a finite sequence of editing deformations (all the admissible ones are displayed). A cost is associated with each deformation. The editing distance between Γ_f and Γ_g is equal to the infimum cost over all the deformations taking Γ_f to Γ_g .

Currently B. Di Fabio and C. Landi are tackling the problem of stability providing an editing distance between Reeb graphs of orientable surfaces in terms of the cost necessary to transform one graph into another by edit operations (see Fig. 4). The editing distance turns out to have all the properties of a pseudometric [23]. The main result is that changes in the functions, measured by the maximum norm, imply not greater changes in this distance, yielding the stability property under function perturbations.

Further efforts are needed to show that this editing distance coincides with the natural pseudodistance, and hence results to be more discriminative than the bottleneck distance of persistent homology.

V. APPLICATIONS TO DERMATOLOGY

With the experience of a EU project of some years ago, we have weaved a common language with dermatologists on a terribly serious problem: the early diagnosis of melanoma [24]. We presently profit of this experience for two research programs - mainly manged by M. Ferri - in collaboration with IRST (Romagna Institute for study and cure of tumors). One program is with the University of Graz on the evolution from naevus to melanoma. It is based both on persistent homology, mediated by a graph representation of the lesion coming from the watershed transform (Fig. 5).

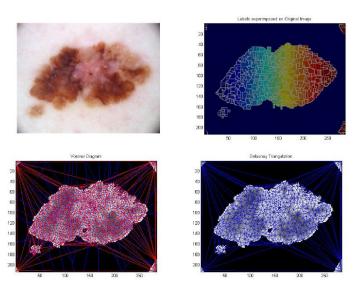


Fig. 5. A segmentation and graph representation of a melanocytic lesion.

A second program is with an Italian industry for a system supporting the physician with a smart retrieval of dermatological images. This will strongly depend on the new techniques of multidimensional persistent homology.

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