

# A Topological Method for Shape Comparison

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## Abstract

We develop a topology-based method which can be used as a measure of the dissimilarity between shapes. For us, a shape is a point cloud dataset in Euclidean space. In the experiments described in this paper a shape comes with a particular choice of triangulation (mesh). However, the method can be easily applied to a more general situation when no particular triangulation is given. We test our method on a database of models achieving only a minor misclassification error.

**Keywords** : topology; filtration; persistent homology; multiple persistence; shape matching.

## 1 Introduction

### Approach

Our method makes use of a recently developed branch of computational topology called persistent homology ([3]). This technique proceeds by constructing a filtered simplicial complex approximating the space in question and then computing the homology groups of the resulting object (see section 2 for a more detailed discussion). In our case, we in fact use a 2-dimensional filtration determined by an intrinsic metric on the shape. We derive our dissimilarity measure between shapes by comparing the persistence homology groups of filtered simplicial complexes associated to them.

### Background and Prior Work

The problem of comparing shapes is well-studied in Computer Science and many algorithms have been developed for this purpose. Perhaps,

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the most widely used approaches include computing medial axis, finding feature correspondences, and fitting model parameters. Different topology-based approaches were taken, for instance, in [5] and [1].

## 2 Computational Algebraic Topology

Algebraic topology aims at distinguishing spaces by, first, giving them a rigid geometric structure (e.g. the structure of a cell space) and, second, building algebraic invariants using these structures. The most convenient such structure for the use in computations is a simplicial complex. Simplicial complexes are a special case of cell complexes with the advantage that their data (simplices and boundary maps) have an easy combinatorial description. In practice, to build a simplicial complex we need a rule specifying when a particular set of  $k + 1$  points of our point cloud data forms a  $k$ -simplex. Assuming that we choose such a rule and build a simplicial complex approximating our space, one natural choice of an invariant which can be computed from this data is a sequence of Betti numbers. The  $n$ th Betti number is the rank of  $n$ th homology group. Roughly speaking, the  $n$ th homology of the space  $X$  measures the number of  $n$ -dimensional subspaces of  $X$  that have no boundary in  $X$  and themselves are not a boundary of any  $n + 1$ -dimensional subspace. For instance, the 0th Betti number counts the number of connected components the space has, the 1st Betti number counts the number of closed curves in the space which cannot be shrunk to a point within the space, etc. We refer the interested reader to [4] for an in-depth introduction to algebraic topology.

### Persistent Homology

The main idea behind persistence is to construct a simplicial complex one simplex at a time rather than to add all simplices at once. In other words, each simplex has one more piece of data - a filtration value  $t$ , which can be thought of as the time the simplex enters a simplicial complex. This turns out to be an extremely powerful idea. Since the complex looks different values of  $t$  we have a whole range of homology groups for each dimension. It might seem, at first, that it brings with it a huge increase in computational complexity, but, in fact, there is a way to compute all these homology groups simultaneously. ([7]). In this new interpretation of homology (called persistent homology) we can talk about the birth and death of generators (cycles) of homology groups. For example, a

new cycle can appear at some time  $t_0$  due to the addition of a simplex to our simplicial complex and disappear (become a boundary) at some later time  $t_1$  when addition of some other simplex turns this cycle into a boundary. To elucidate this discussion let us turn to an example.

Consider a point cloud data set  $X$  in Euclidean space and a number  $\epsilon > 0$ . We let  $R(X, \epsilon)$  denote the simplicial complex whose vertex set is  $X$ . We declare that the set  $\{x_0, x_1, \dots, x_k\}$  spans a  $k$ -simplex if and only if  $d(x_i, x_j) \leq \epsilon$  (the complex built by using this rule is called the Rips complex).

Figure 1 shows two contrasting situations (vertices of the complex are vertices of the polygon). The Rips complex on the left is built with  $\epsilon$  equal to the longest side of the polygon (denote its length by  $A$ ); in the Rips complex on the right  $\epsilon$  is equal to the longest diagonal  $ab$  (denote its length by  $B$ ) which results in all possible simplices being present. The homology groups are different in these two cases and it is not clear a priori which choice of  $\epsilon$  is "correct". Turning to persistence, we can think of  $\epsilon$  as our filtration parameter. Computing the rank  $b_1$  of the 1st persistent homology group yields the following result:  $b_1 = 0$  if  $\epsilon < A$ ,  $b_1 = 1$  when  $A \leq \epsilon < B$  and  $b_1 = 0$  again when  $\epsilon \geq B$ .

There are many ways to use the persistence idea in practice. For example, when dealing with noisy or poorly sampled data one can interpret the short-lived cycles as coming from noise or inconsistency in sampling. In this paper we actually use 2-dimensional persistence. Multidimensional persistence, introduced in [2], is a natural generalization of the persistence idea. We will briefly describe this concept next.

## Multidimensional Persistence

Multidimensional persistence arises in the situation when there is more than one filtration parameter. Usually the first filtration parameter comes from the metric on the data, but it is often useful to keep track of some auxiliary function defined on the data such as, for example, a density function. If one fixes a threshold  $Th$  for density one can study a one-dimensional filtered simplicial complex built on those vertices whose density is below  $Th$ . Varying  $Th$  one obtains a family of filtered simplicial complexes which can be thought of as a 2-dimensional filtered complex.

Algebraically,  $N$ -dimensional persistence homology groups are considerably harder to compute for  $N > 1$  than for  $N = 1$ . This is a direct consequence of the fact that there exists a nice classification for

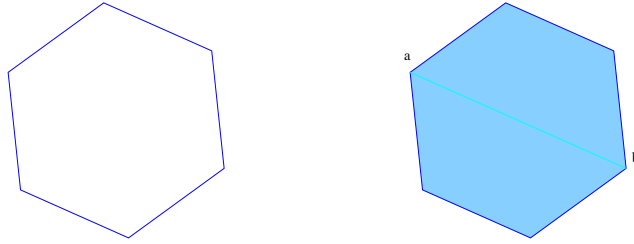


Figure 1: Left. Rips complex with a smaller  $\epsilon$ . Right. larger  $\epsilon$ , no 1-dimensional homology

modules over a polynomial ring  $k[x]$ , but the situation gets much more complex when  $k[x]$  is replaced by  $k[x_1, x_2, \dots, x_n]$ , ( $k$  is a field in both cases). We refer an interested reader to [2] for in-depth discussion of multidimensional persistence. In this paper we only need to compute the 0-dimensional homology groups of filtered simplicial complexes.

### 3 Method

Our shape comparison method can be naturally broken into two parts. The first part is preprocessing which takes a triangulation of a shape as input and outputs the intrinsic distance matrix between the set of vertices of the triangulation. The second part is the main algorithm. Let us start by describing the preprocessing step first.

For a given shape  $S$  and its triangulation  $T_S$  we compute an adjacency matrix  $A$ . Namely, if  $v_i$  and  $v_j$  are two vertices of  $T_S$  and there exists a simplex  $\delta \in T_S$  involving  $v_i$  and  $v_j$  we set  $A_{ij} = d(v_i, v_j)$ , where  $d$  is the Euclidean distance. If no such simplex exists we set  $A_{ij} = 0$ . Next, we compute the intrinsic distance matrix  $D$  between the vertices by applying the Dijkstra algorithm to  $A$ . Let us denote by  $N$  the total number of vertices, and by  $V$  the total collection of vertices representing a shape  $S$  or possibly its subset. As an additional piece of data we compute the eccentricity of each vertex defined as

$$E(v) = \frac{\sum_{i=1}^N D(v, v_i)}{N}.$$

Thus, the function  $E : V \rightarrow \mathbb{R}$  measures the average distance from a given vertex to all of the points of  $V$ .

To the space of points  $V$  we associate the space  $W$  defined

$$W = \frac{V \times V}{(v_i, v_j) \sim (v_j, v_i)} - \text{Diag}$$

In words,  $W$  is a quotient of a product  $V \times V$ , where we identify two points if they are the same in the set-theoretic sense, and then exclude points of the form  $(v, v)$ . It is the space  $W$  on which we define our 2-filtration  $(F_1, F_2)$ . The filtered simplicial complex we are about to construct for  $W$  will be a graph whose number of vertices will increase in  $F_1$ -dimension and whose number of edges will increase in  $F_2$ -dimension. Let  $w = (v_1, v_2)$  be a point of  $W$ . We define

$$F_1(w) = \text{diam}(D) - D(v_1, v_2).$$

With this definition of  $F_1$ , pairs of points of  $V$  enter the growing simplicial complex at the "time" inversely proportional to the distance between them.

The second filtration function  $F_2$  is one of the natural choices for the distance function on  $W$ . Namely, let  $w_1 = (v_{11}, v_{12})$  and  $w_2 = (v_{21}, v_{22})$ , and let  $e = (w_1, w_2)$  denote an edge between  $w_1$  and  $w_2$ . Define

$$F_2(e) = \min\left(\frac{D(v_{11}, v_{21}) + D(v_{12}, v_{22})}{2}, \frac{D(v_{11}, v_{22}) + D(v_{12}, v_{21})}{2}\right).$$

Hence the filtration for an edge is the minimum of the two distinct possible average distances when vertices of one edge are put into one-to-one correspondence with vertices of the other edge.

A triple  $K = (W, F_1, F_2)$  is an essential tool we use to obtain our dissimilarity measure between a pair of shapes. Other ingredients of our construction are as follows. A threshold for the eccentricity function  $E$  - once the threshold  $Th$  is chosen we draw the vertices to form  $V$  only from the set of points  $v$  for which  $E(v) \leq Th$ . A size  $|V|$  of subset of vertices  $V$  from which we build the associated space  $W$ . Finally, we specify a grid in the filtration plane  $(F_1, F_2)$ ; note that once a particular choice of values for  $F_1$  and  $F_2$  is specified, we can determine the rank of the persistence homology group at that point, and once the particular rectangular grid  $G = G_{ij}$  is specified we obtain a matrix whose  $ij$ th entry is the rank of the homology group at the pair of filtration values  $(F_1(i), F_2(j))$ . We write these ingredients compactly as a triple  $P = (|V|, G, Th)$ . The construction  $K$  and a choice of values for  $P$  give rise to a homology grid (matrix) consisting of the ranks of 0-dimensional homology groups at

the grid points. Let us denote such a grid by  $HG = HG(P)$  and, when necessary, emphasize dependence on a shape by writing  $HG(P, S)$ .

Instead of selecting a particular choice of values for  $P$ , we obtain a set of them by letting  $|V|$ ,  $Th$  and  $G$  vary independently. This, in turn, gives us a set of homology grids  $\{HG(P)\}$ .

Finally we are ready to define the dissimilarity measure between shapes  $S_1$  and  $S_2$ . Choose a number  $n > 0$ . Compute a set of  $n$  homology grids  $\{HG(P_k, S_1)\}$  for  $S_1$  and  $\{HG(P_k, S_2)\}$  for  $S_2$ ,  $k = 1, \dots, n$ . For each pair of corresponding grids, i.e. the ones obtained with the same choices of  $|V|$ ,  $G$  and  $Th$ , compute the distance

$$GD_k(HG(P_k, S_1), HG(P_k, S_2)) = \frac{\sum_i \sum_j |HG(P_k, S_1)(i, j) - HG(P_k, S_2)(i, j)|}{m_1 \cdot m_2}$$

between them. Here  $m_1$  and  $m_2$  are the number of rows and columns in the grid.

We define dissimilarity measure

$$M(S_1, S_2) = \frac{\sum_{k=1}^n GD_k}{n}.$$

Therefore,  $M$  is an average value of the homology grid distance across  $n$  choices of parameters. One might hope that the performance of this shape recognition algorithm improves as  $n$  increases. This is, indeed, the case for the experiments which we describe in the next section.

## 4 Experimental Results

We applied the method presented in the previous section to a publicly available database of objects [6]. These objects correspond to 6 classes of shapes (horse, cat, lion, camel, elephant and head). Each class in our experiment consists of 6 nearly isometric models. We would like to estimate how well our algorithm can distinguish distinct shape classes. See figure 2 which shows one model out of each class as well as the coloring of it by the eccentricity function. Figure 3 shows a pairwise dissimilarity measure matrix, i.e. the  $ij$ th entry in the color matrix is the value of  $M$  on the pair  $(S_i, S_j)$  of shapes with  $n = 100$ .

Let us now describe the error estimation procedure. First, we construct a basis set by randomly choosing one model out of each class. This yields the set  $B$  of 6 basis shapes. Next, for each shape  $S$  which is not in  $B$ , we compute the closest basis shape to  $S$  using our dissimilarity

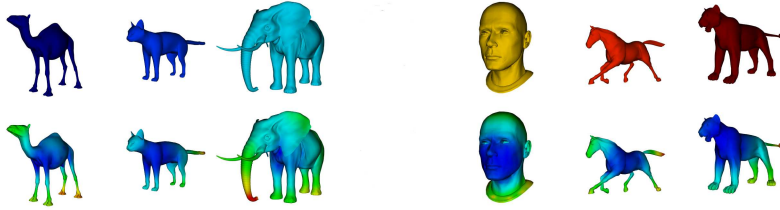


Figure 2: Top row. Rendering of one model out of each of 6 classes. Bottom row. Coloring of the same model by the eccentricity function  $E$ . See section 3 for details.

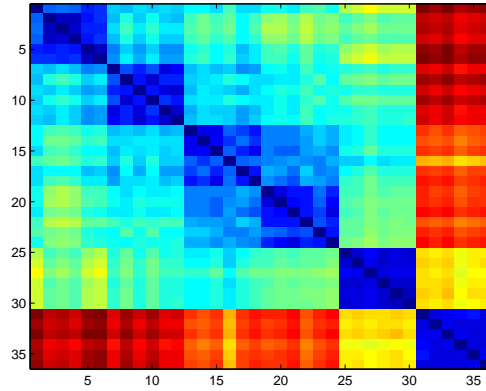


Figure 3: Dissimilarity Measure matrix

measure  $M$ . Let us denote by  $B_S$  the basis element from the same class as  $S$  and by  $B_{\tilde{S}}$  the basis element whose dissimilarity measure with  $S$  is the smallest among all basis shapes. We obtain the number

$$Err(B) = \frac{\#(B_{\tilde{S}} \neq B_S)}{\#S},$$

where  $\#S$  is the total number of models minus the size of the basis set  $B$ . This number is 30 ( $36 - 6$ ) in our case.

$Err(B)$  is the probability that a given shape will be misclassified in the given basis  $B$ . Now, since the choice of  $B$  is random we repeat this procedure  $K$  times each time selecting a new basis at random to obtain the probability of shape misclassification

$$Err = \frac{\sum_{i=1}^K Err(B_i)}{K}.$$

$n$	Error
50	1.63%
75	1.48%
100	0.27%

Table 1: Misclassification error with different choices of  $n$ .

Table 1 summarizes the misclassification errors we achieved using different values of  $n$  (with  $K = 50,000$ ).

## 5 Summary and concluding remarks

In this paper we presented a topological method for shape recognition based on multidimensional persistence. Our approach can easily be extended beyond considering only the 0th persistent homology group. This would probably significantly increase its power.

We applied the method to a dataset of models achieving only a minor classification error of 0.27%.

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## References

- [1] Bisciotti S., Falcidieno B., Spagnuolo M. *Extended Reeb graph for surface understanding and description*. In DGCI '00: Proceedings of the 9th International Conference on Discrete Geometry for Computer Imagery, London, 2000, Springer-Verlag, pp. 185-197.
- [2] Carlsson G. and Zomorodian A. *The theory of multidimensional persistence* 23rd ACM Symposium on Computational Geometry, Gyeongju, South Korea, June 67, 2007.

- [3] Edelsbrunner H., Letscher D., Zomorodian A. *Topological persistence and simplification*. IEEE Symposium on Foundations of Computer Science (2000).
- [4] Hatcher A. *Algebraic topology*. Cambridge University Press (2001).
- [5] Singh G., Memoli F., Carlsson G. *Topological Methods for the Analysis of High Dimensional Data Sets and 3D Object Recognition*. Symposium on Point-Based Graphics (2007).
- [6] Sumner R.W., Popovic J. *Mesh data from deformation transfer for triangle meshes*.  
<http://people.csail.mit.edu/sumner/research/deftransfer/data.html>.
- [7] Zomorodian A., Carlsson G. *Computing persistent homology*. 20th ACM Symposium on Computational Geometry (2004).