

Robustness of topology of digital images and point clouds

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Abstract

Such modern applications of topology as digital image analysis and data analysis have to deal with noise and other uncertainty. In this environment, the data structures often appear "filtered" into a sequence of cell complexes. We introduce the homology group of the filtration as a generalization of the homology group of a single cell complex. It is the group of all possible homology classes of all elements of the filtration with a certain equivalence relation. This relation equates the classes that represent the same homology class of the original data structure. The persistent homology group of the filtration is obtained similarly with an equivalence relation that equates the classes the differences of which falls outside of user's choice of the acceptable level of noise.

1 Introduction

Since Poincaré, homology has been used as the main descriptor of the topology of geometric objects. In the classical context, however, all homology classes receive equal attention. Meanwhile, applications of topology in analysis of images and data have to deal with noise and other uncertainty. This uncertainty appears usually in the form of a real valued function defined on the topological space. Persistence is a measure of robustness of the homology classes of the lower level sets of this function [6], [2], [4], [3].

Since it's unknown beforehand what is or is not noise in the dataset, we need to capture all homology classes including those that may be deemed noise later. In this paper we introduce an algebraic structure that contains, without duplication, all these classes. Each of them is associated with its persistence and can be removed when the threshold for acceptable noise is set. The last step can be carried out repeatedly in order to find the best possible threshold. The construction follows the approach to analysis of digital images presented in [8].

2 Background

The topological spaces subject to such analysis are cell complexes. A *cell complex* is a combinatorial structure

that describes how k -dimensional cells are attached to each other along $(k-1)$ -dimensional cells. Cell complexes come from the following two main sources.

First, a gray scale image is a real-valued function f defined on a rectangle. Given a threshold r , the lower level set $f^{-1}((-\infty, r))$ can be thought of as a binary image. Each black pixel of this image is treated as a square cell in the plane. These 2-dimensional cells have to be combined with their edges (1-cells) and vertices (0-cells) while in the n -dimensional case the image is decomposed into a combination of 0-, 1-, ..., n -cubes. This process is called *thresholding*. The result is a cell complex K for each r , see [7].

Second, a point cloud is a finite set S in some Euclidean space of dimension d . Given a threshold r , we deem any two points that lie within r from each other as "close". In this case, this pair of points is connected by an edge. Further, if three points are "close", pairwise, to each other, we add a face spanned by these points. If there are four, we add a tetrahedron, and, finally, any $d+1$ "close" points create a d -cell. The process is called the *Vietoris-Rips construction*. The result is a cell complex K for each r [6].

Next, we would like to quantify the topology of the cell complex K . It is done via the *Betti numbers* of K : B_0 is the number of connected components in K ; B_1 is the number of holes or tunnels (1 for letter O or the donut; 2 for letter B and the torus); B_2 is the number of voids or cavities (1 for both the sphere and the torus), etc.

The Betti numbers are computed via *homology theory* [1]. One starts by considering the collection $C_k(K)$ of all formal linear combinations (over a ring R) of k -cells in K , called *k -chains*. Combined they form a finitely generated abelian group called the *chain complex* $C_k(K)$, or collectively $C_*(K)$. A k -chain can be recorded as an N_k -vector, where N_k is the total number of k -cells in K . The boundary of a k -chain is the chain comprised of all $(k-1)$ -faces of its cells taken with appropriate signs. Then the *boundary operator* $\partial : C_k(K) \rightarrow C_{k-1}(K)$, $k = 0, 1, \dots$, acts on the chain complex and is represented by a $N_k \times N_{k-1}$ matrix.

From the chain complex $C_*(K)$, the homology group is constructed by means of the standard algebraic tools. To capture the topological features one concentrates on *cycles*, i.e., chains with zero boundary, $\partial A = 0$. Further, one can verify whether two given k -cycles A and B are *homologous*: the difference between them is the

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boundary of a $(k+1)$ -chain $T : A - B = \partial T$ (such as two meridians of the torus). In this case, A and B belong to the same *homology class* $H = [A] = [B]$. The totality of these equivalence classes in each dimension k is called the k -th *homology group* $H_k(K)$ of K , collectively $H_*(K)$. Then, Betti number B_k is the rank of $H_k(K)$.

3 Prior work and outline

The methods for computing homology groups are well developed. In real-life applications however both digital images and point clouds may be noisy and one needs to evaluate the significance of their homology classes. The approach to this problem has been the following. Instead of using a single threshold and studying a single cell complex, one considers all thresholds and all possible cell complexes. Since increasing threshold r enlarges the corresponding complex, we have a sequence of complexes:

$$K^1 \hookrightarrow K^2 \hookrightarrow K^3 \hookrightarrow K^4 \hookrightarrow \dots \hookrightarrow K^s,$$

where the arrows represent the inclusions: $i^{n,n+1} : K^n \hookrightarrow K^{n+1}$. Let $i^{nm} : K^n \hookrightarrow K^m, n \leq m$, also be the inclusion. This structure $\{K^n, i^{nm}\}$ is called a *filtration*.

Now, each of these inclusions generates a homomorphism $i_*^{nm} : H_*(K^n) \rightarrow H_*(K^m)$ called the *homology map induced by i^{nm}* . As a result, we have a sequence of homology groups connected by these homomorphisms:

$$H_*(K^1) \rightarrow H_*(K^2) \rightarrow \dots \rightarrow H_*(K^s) \rightarrow 0.$$

These homomorphisms record how the homology changes as the complex grows at each step. For example, a component appears, grows, and then merges with another one, or a hole is formed, shrinks, and then is filled. We refer to these events as *birth and death* of the corresponding homology class.

In order to evaluate the robustness of an element of one of these groups the *persistence of a homology class* is defined as the number of steps in the homology sequence it takes for the class to end at 0. In other words,

$$\text{persistence} = \text{death date} - \text{birth date}.$$

The p -*persistent homology group* of K^i is defined as the image of $i_*^{i,i+p}$. It is what's left from $H_*(K^i)$ after p steps in the filtration. Now the robustness of the homology classes of the filtration is evaluated in terms of the set of intervals $[birth, death]$ representing the life-spans, called *barcodes*, of the homology classes [5].

Our approach is similar but more algebraic. It consists of two steps.

First stage: we pool all possible homology classes in all elements of the filtration together in a single algebraic structure (Sections 4 and 5). The presence of noise

at this point is ignored. The homology group $H_*(\{K^n\})$ of filtration $\{K^n\}$ captures all homology classes in the whole filtration – without double counting. The latter is achieved by an equivalence relation that equates the classes that, in a sense, represent the same homology class in the filtration: $y = i_*^{n,n+1}(x)$.

Second stage: for a given positive integer p , the p -noise group $N_*^p(\{K^n\})$ is comprised of the homology classes in $H_*(\{K^n\})$ with the persistence less than p . Next, we "remove" the noise from the homology group of filtration by using the quotient (Sections 6 and 7):

$$H_*^p(\{K^n\}) = H_*(\{K^n\}) / N_*^p(\{K^n\}).$$

In other words: if the difference between two homology classes is deemed noise, they are equivalent. This is the persistent homology group of filtration. The second stage can be repeated as needed.

The (persistent) homology group of filtration is a graded group and is intended to stand for **the homology group of the data set that is behind the filtration**.

The main contribution of the present paper is an algebraic treatment of persistence that is alternative to the persistence module [3]. In the case of image analysis, the homology group of the image, unlike the barcodes, captures only the topology independent from the gray levels. This is why one might say that our approach provides a coarser classification of the homology of filtrations.

We also discuss the computational aspects of this approach (Section 8) and multiparameter filtrations (Section 9).

4 Motivation: the homology of a gray scale image

In this section we will try to understand the meaning of the homology of the gray scale image in Figure 1. For simplicity we assume that there are only 2 levels of gray in addition to black and white. A visual inspection of the image suggests that it has three connected components each with a hole. Therefore, its 0- and 1-homology groups should have three generators each. We now develop an algebraic procedure to arrive at this result.

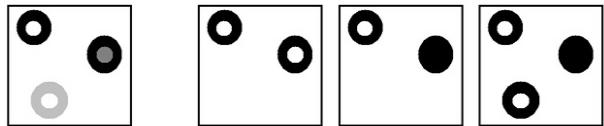


Figure 1: A gray scale image and the corresponding filtration

First the image is "thresholded". The lower level sets of the gray scale function of the image form a filtration:

a sequence of three binary images, i.e., cell complexes: $K^1 \hookrightarrow K^2 \hookrightarrow K^3$, where the arrows represent the inclusions. Suppose A_i, B_i, C_i are the homology classes that represent the components of K^i and a_i, b_i, c_i are the holes, clockwise starting at the upper left corner. The homology groups of these images also form sequences – one for each dimension 0 and 1.

Suppose F_1, F_2 are the two homology maps, i.e., homomorphisms of the homology groups generated by the inclusions of the complexes, with $F_3 = 0$ included for convenience. These homomorphisms act on the generators, as follows:

$$\begin{aligned} A_1 &\rightarrow A_2 \rightarrow A_3 \rightarrow 0, B_1 \rightarrow B_2 \rightarrow B_3 \rightarrow 0, \\ C_2 &\rightarrow C_3 \rightarrow 0, a_1 \rightarrow a_2 \rightarrow a_3 \rightarrow 0, \\ b_1 &\rightarrow 0, c_3 \rightarrow 0. \end{aligned}$$

To avoid double counting, we want to count only the homology classes that don't reappear in the next homology group. As it turns out, a more algebraically convenient way to accomplish this is to count only the homology classes that go to 0 under these homomorphisms. These classes form the kernels of F_1, F_2, F_3 . Now, we choose the homology group of the original, gray scale image to be the direct sum of these kernels:

$$H_0(\{K^i\}) = \langle A_3, B_3, C_3 \rangle, \quad H_1(\{K^i\}) = \langle b_1, a_3, c_3 \rangle.$$

Thus the image has three components and three holes, as expected.

5 Homology groups of filtrations

In the following sections we provide formal definitions. All cell complexes are finite.

Suppose we have a one-parameter filtration:

$$K^1 \hookrightarrow K^2 \hookrightarrow K^3 \hookrightarrow \dots \hookrightarrow K^s.$$

Here K^1, K^2, \dots, K^s are cell complexes, the arrows represent the inclusions $i^{n,n+1} : K^n \hookrightarrow K^{n+1}$, and so do $i^{nm} : K^n \hookrightarrow K^m, n \leq m$. We will denote the filtration by $\{K^n, i^{nm} : n, m = 1, 2, \dots, s, n \leq m\}$, or simply $\{K^n\}$. Next, homology generates a "direct system" of groups and homomorphisms:

$$H_*(K^1) \rightarrow H_*(K^2) \rightarrow \dots \rightarrow H_*(K^s) \longrightarrow 0.$$

We denote this direct system by $\{H_*(K^n), i_*^{nm} : n, m = 1, 2, \dots, s, n \leq m\}$, or simply $\{H_*(K^n)\}$. The zero is added in the end for convenience.

Our goal is to define a single structure that captures all homology classes in the whole filtration without double counting. The rationale is that if $x \in H_*(K^n), y \in H_*(K^m)$, $y = i_*^{nm}(x)$, and there is no other x satisfying this condition, then x and y may be thought of as

representing the same homology class of the geometric object behind the filtration.

The *homology group of filtration* $\{K^n\}$ is defined as the product of the kernels of the inclusions:

$$H_*(\{K^n\}) = \ker i_*^{1,2} \oplus \ker i_*^{2,3} \oplus \dots \oplus \ker i_*^{s,s+1}.$$

Here, from each group we take only the elements that are about to die. Since each dies only once, there is no double-counting. Since the sequence ends with 0, we know that everyone will die eventually. Hence every homology class appears once and only once.

These are a few simple facts about this group.

Proposition 1 If $i_*^{n,n+1}$ is an isomorphism for each $n = 1, 2, \dots, s - 1$, then $H_*(\{K^n\}) = H_*(K^1)$.

Proposition 2 If $i_*^{n,n+1}$ is a monomorphism for each $n = 1, 2, \dots, s - 1$, then $H_*(\{K^n\}) = H_*(K^s)$.

Proposition 3 Suppose $\{K^n, i^{nm}, n, m = 1, 2, \dots, s\}$ and $\{L^n, j^{nm}, n, m = 1, 2, \dots, s\}$ are filtrations. Then $H_*(\{K^n \sqcup L^n\}) = H_*(\{K^n\}) \oplus H_*(\{L^n\})$.

Proposition 4 Suppose $\{K^n, i^{nm}, n, m = 1, 2, \dots, s\}$ and $\{L^n, j^{nm}, n, m = 1, 2, \dots, s\}$ are filtrations and $f : K^s \rightarrow L^s$ is a cell map. Then the homology map of the homology groups of these filtrations $f_* : H_*(\{K^n\}) \rightarrow H_*(\{L^n\})$ is well defined as

$$f_*(x_1, x_2, \dots, x_s) = (f_1^1(x_1), f_2^2(x_2), \dots, f_s^s(x_s)),$$

where f^n is the restriction of f to K^n .

The stability of the homology group of a filtration follows from the stability of its persistence diagram, i.e., the set of points $\{(birth, death)\} \subset \mathbf{R}^2$ for the generators of the homology groups of the filtration, plus the diagonal. It is proven in [5] that $d_B(D(f), D(g)) \leq \|f - g\|_\infty$, where d_B is the "bottle-neck distance" between the persistence diagrams $D(f), D(g)$ of two filtrations generated by tame functions f, g . Function $F(x, y) = y - x$ creates an analogue bottle-neck distance for the set of points $\{persistence\} \subset \mathbf{R}$ and its stability follows from the continuity of F .

6 Motivation: the high contrast homology of a gray scale image

To justify our approach to persistence, we observe that some of the features in the gray scale image in Figure 1 are more prominent than others. Specifically, some of the features have lower contrast. These are the holes in the second and the third rings as well as the third ring itself. By *contrast* of a lower level set of the gray level function we understand the difference between the highest gray level adjacent to the set and the lowest gray level within the set.

An easy computation shows that the homology generators with persistence of 3 or higher among the generators are: A_1, B_1, a_1 . However, the set of the classes of high persistence isn't a subgroup of the homology group of the respective complex. Instead, we look at the classes with *low* persistence, i.e., classes that represent the noise. In particular, the classes in $H_*(K^1)$ of persistence 2 or lower form the kernel of F_2F_1 . We now "remove" this noise from the homology groups of the filtration by considering their quotients over these kernels. In particular, the 3-persistent homology groups of the image are:

$$\begin{aligned} H_0^3(\{K^i\}) &= \langle A_1, B_1 \rangle / 0 = \langle A_1, B_1 \rangle, \\ H_1^3(\{K^i\}) &= \langle a_1, b_1 \rangle / \langle b_1 \rangle = \langle a_1 \rangle. \end{aligned}$$

It is important that the output is identical to the homology of a single complex, i.e., a binary image, with two components and one hole. The way persistence is defined ensures that we can never remove a component as noise but keep a hole in it.

This approach to image analysis was tested with real-life images in [8].

Observe now that the holes in the second and third rings have the same persistence (contrast) and, therefore, occupy the same position in the homology group regardless of their birth dates (gray level). Second, if we shrunk one of these rings, its persistence and, therefore, its place in the homology group wouldn't change. These observations confirm the fact that the homology group of the gray scale image, unlike the barcodes, captures only its topology.

In the case of a Vietoris-Rips complex, not only the barcode, the interval [birth, death], but also the persistence, the number death - birth, of a homology class contains information about the size of representatives of these classes. For example, a set of points arranged in a circle will produce a 1-cycle with twice as large birth, death, and persistence than the same set shrunk by a factor of 2. However, persistence defined as death/birth will have the desired property of scale independence. The same result can be achieved by an appropriate reparametrizing of the filtration.

7 Persistent homology groups of filtrations

In the general context of filtrations the measure of importance of a homology class is its persistence which is the length of its lifespan within the direct system of homology of the filtration.

Given filtration $\{K^n\}$, we say that *the persistence $P(x)$ of $x \in H_*(K^n)$ is equal to p* if $i_*^{n,n+p}(x) = 0$ and $i_*^{n,n+p-1}(x) \neq 0$. Our interest is in the "robust" homology classes, i.e., the ones with high persistence. However, the collection of these classes is not a group as it doesn't even contain 0. So we deal with "noise"

first. Given a positive integer p , the *p-noise (homology) group* $N_*^p(K^n)$ of $\{K^n\}$ is the group of all elements of K^n with persistence less than p .

Alternatively, we can define these groups via kernels of the homomorphisms of the inclusions: $N_*^p(K^n) = \ker i_*^{n,n+p}$.

Proposition 5 $N_*^{p+1}(K^n) \subset N_*^p(K^n)$.

Next, we "remove" the noise from the homology group. The *p-persistent (homology) group* of K^n with respect to the filtration $\{K^n\}$ is defined as

$$H_*^p(K^n) = H_*(K^n)/N_*^p(K^n).$$

The point of this definition is that, given a threshold for noise, if the difference between two homology classes is noise, they should be equivalent.

Next, just as in the case of noise-less analysis, we define a single structure to capture all (robust) homology classes. Let p be a positive integer. Suppose $x \in \ker i_*^{k,k+p}$ and let $y = i_*^{k,k+1}(x)$. Then

$$\begin{aligned} i_*^{k+1,k+1+p}(y) &= i_*^{k+1,k+1+p}(i_*^{k,k+1}(x)) \\ &= i_*^{k,k+1+p}(x) = i_*^{k+p,k+p+1}(i_*^{k,k+p}(x)) \\ &= i_*^{k+p,k+p+1}(0) = 0. \end{aligned}$$

Hence $y \in \ker i_*^{k+1,k+1+p}$. We have proved that

$$i_*^{k,k+1}(\ker i_*^{k,k+p}) \subset \ker i_*^{k+1,k+1+p}.$$

It follows that the homomorphism $i_*^{k,k+1} : \ker i_*^{k,k+p} \rightarrow \ker i_*^{k+1,k+1+p}$ generated by the inclusion is well-defined.

Next, we use these homomorphisms to define the *p-noise (homology) group* $N_*^p(\{K^n\})$ of filtration $\{K^n\}$ as

$$N_*^p(\{K^n\}) = \ker i_*^{1,2} \oplus \dots \oplus \ker i_*^{s,s+1}.$$

Observe that the formula is the same as the one in the definition of $H_*^p(\{K^n\})$. Since $i_*^{k,k+1} : \ker i_*^{k,k+p} \rightarrow \ker i_*^{k+1,k+1+p}$ is a restriction of $i_*^{k,k+1} : H_*^p(K^k) \rightarrow H_*^p(K^{k+1})$, each term in the above definition is a subgroup of the corresponding term in the definition of $H_*(\{K^n\})$. The proposition below follows.

Proposition 6 $N_*^p(\{K^n\}) \subset H_*(\{K^n\})$.

Finally, the *p-persistent (homology) group* of filtration $\{K^n\}$ is

$$H_*^p(\{K^n\}) = H_*(\{K^n\})/N_*^p(\{K^n\}).$$

The results about $H_*^p(\{K^n\})$ analogous to the ones about $H_*(\{K^n\})$ in Section 5 hold.

8 Computational aspects

For 2-dimensional gray scale images, this approach to homology and persistence has been used in an image analysis program. The algorithm described in [8] has complexity of $O(n^2)$, where n is the number of pixels in the image, in the worst case. As a result, the processing time for images of common sizes is several seconds on a typical PC.

For the general case, the analysis algorithm may be outlined as follows:

1. The input is a filtration.
2. The homology groups of its members and the homomorphisms induced by inclusions are computed.
3. The homology group of the filtration is computed.
4. The persistence of all elements of the homology groups is computed.
5. The user sets a threshold p for persistence and the p -noise group of the filtration is computed.
6. The p -persistent homology group of the filtration is computed and given as output.

If the user changes the threshold, the last two steps are repeated as necessary without repeating the rest.

The algorithm above computes the homology group of filtration, as defined, incrementally. This may be both a disadvantage and an advantage. In comparison, the *persistence complex* [3] also contains information about all homology classes of the filtration but its computation does not require computing the homology of each complex of the filtration. Meanwhile, the above algorithm may have to compute the same homology over and over if consecutive complexes are identical. Hence, the algorithm has a disadvantage in terms of processing time. On the other hand, the incremental nature of the algorithm makes its use of memory independent from the length of the filtration. Another advantage is that multi-parameter filtrations are dealt with in the exact same manner (see next section).

The inefficiency of the above algorithm can be addressed with a proper algebraic tool. This tool is the mapping cone [9]. Suppose, for simplicity, that our filtration has only two elements: $i : K^1 \hookrightarrow K^2$. The mapping cone is, in a sense, a combination of the kernel and the cokernel of i_* . It captures the difference between K^1 and K^2 on the chain level: everything in $C_*(K^1)$ is killed unless it also appears in $C_*(K^2)$ under i_* . Then the algorithm is to construct the homology group from the chain complexes $C_*(K^1), C_*(K^2)$ of the elements of the filtration and the chain map $i_* : C_*(K^1) \rightarrow C_*(K^2)$.

9 Multiparameter filtrations

Multiparameter filtrations come from the same main sources as one-parameter filtrations. First, color images are thresholded according to their three color channels. Second, point clouds are thresholded by the closeness of their points and, for example, the density of the points.

Let's limit our attention to the two-parameter case. A (finite) two-parameter filtration $\{K^{nm}\}$ is a table of complexes connected by inclusions

$$i(n, m, n+p, m+q) : K^{nm} \rightarrow K^{n+p, m+q}, p, q \geq 0,$$

These inclusions generate homomorphisms

$$i_*(n, m, n+q, m+p) : H_*(K^{nm}) \rightarrow H_*(K^{n+q, m+p}),$$

with 0s added in the end of each row and each column. Define the *homology group of the filtration* $\{K^{nm}\}$ as

$$\begin{aligned} H_*(\{K^{nm}\}) \\ = \bigoplus_{nm} \ker i_*(n, m, n+1, m) \cap \ker i_*(n, m, n, m+1). \end{aligned}$$

The analogues of the results in Section 5 hold.

There are many ways to define persistence in the multiparameter setting. For example, we can evaluate the robustness of a homology class $x \in H_*(K^{nm})$ in terms of the pairs (p, q) of positive integers satisfying

$$i_*(n, m, n+p, m)(x) = 0 \text{ and } i_*(n, m, n, m+q)(x) = 0.$$

Next, just as in Section 7, we restrict the homomorphisms generated by the inclusions to the homology classes of low persistence:

$$\begin{aligned} i_*(n, m, n+1, m) : \\ \ker i_*(n, m, n+p, m) \rightarrow \ker i_*(n+1, m, n+1+p, m), \\ i_*(n, m, n, m+1) : \\ \ker i_*(n, m, n, m+q) \rightarrow \ker i_*(n+1, m, n, m+1+q). \end{aligned}$$

Then the (p, q) -noise group of K^{nm} is defined via these homomorphisms:

$$\begin{aligned} N_*^{pq}(\{K^{nm}\}) \\ = \bigoplus_{nm} \ker i_*(n, m, n+1, m) \cap \ker i_*(n, m, n, m+1). \end{aligned}$$

Finally, the (p, q) -persistent (homology) group of filtration $\{K^{nm}\}$ is defined as

$$H_*^{pq}(\{K^n\}) = H_*(\{K^{nm}\}) / N_*^{pq}(\{K^{nm}\}).$$

The results about $H_*^{pq}(\{K^{nm}\})$ analogous to the ones about $H_*^p(\{K^n\})$ in Section 7 hold.

10 Summary and further research

The main contributions of the present paper are the following.

- Homology group of filtration is defined to serve as a substitute for the homology group of the dataset that produced the filtration.
- This group is an algebraic treatment of persistence alternative to the persistence module. It is arguably easier to compute as it is simply the sum of kernels.
- The algorithm has been tested with real-life images and proven practical in terms of both output and processing time.
- For analysis of point clouds, the approach provides the output that is scale independent.
- For image analysis, the approach provides the output that is both scale independent and gray-level independent.
- Unlike the persistence module, our approach yields a natural generalization to multiparameter filtrations.

The following issues will be addressed in a forthcoming paper:

- the stability of the homology group of filtration;
- the functoriality properties of the homology group of filtration;
- the relation between the homology group of filtration and the persistence complex;
- the mapping cone construction for the homology group of filtration;
- the homology group of multiparameter and poset filtrations.

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