Strong Collapse for Persistence

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Abstract

We introduce a fast and memory efficient approach to compute the persistent homology (PH) of a sequence of simplicial complexes. The basic idea is to simplify the complexes of the input sequence by using strong collapses, as introduced by J. Barmak and E. Miniam [DCG (2012)], and to compute the PH of an induced sequence of reduced simplicial complexes that has the same PH as the initial one. Our approach has several salient features that distinguishes it from previous work. It is not limited to filtrations (i.e. sequences of nested simplicial subcomplexes) but works for other types of sequences like towers and zigzags. To strong collapse a simplicial complex, we only need to store the maximal simplices of the complex, not the full set of all its simplices, which saves a lot of space and time. Moreover, the complexes in the sequence can be strong collapsed independently and in parallel. As a result and as demonstrated by numerous experiments on publicly available data sets, our approach is extremely fast and memory efficient in practice.

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1 Introduction

In this article, we address the problem of computing the Persistent Homology (PH) of a given sequence of simplicial complexes (defined precisely in Section 4) in an efficient way. It is known that computing persistence can be done in $O(n^\omega)$ time, where n is the total number of simplices and $\omega \leq 2.4$ is the matrix multiplication exponent [20, 15]. In practice, when dealing with massive and high-dimensional datasets, n can be very large (of order of billions) and computing PH is then very slow and memory intensive. Improving the performance

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of PH computation has therefore become an important research topic in Computational Topology and Topological Data Analysis.

Much progress has been accomplished in the recent years in two directions. First, a number of clever implementations and optimizations have led to a new generation of software for PH computation [16, 27, 24, 13]. Secondly, a complementary direction has been explored to reduce the size of the complexes in the sequence while preserving (or approximating in a controlled way) the persistent homology of the sequence. Examples are the work of Mischaikow and Nanda [21] who use Morse theory to reduce the size of a filtration, and the work of Dłotko and Wagner who use simple collapses [14]. Both methods compute the exact PH of the input sequence. Approximations can also be computed with theoretical guarantees. Approaches like interleaving smaller and easily computable simplicial complexes, and sub-sampling of the point sample works well upto certain approximation factor [8, 5, 25, 19, 9, 12].

In this paper, we introduce a new approach to simplify the complexes of the input sequence which uses the notion of strong collapse introduced by J. Barmak and E. Miniam [2]. Specifically, our approach can be summarized as follows. Given a sequence $\mathcal{Z} : \{K_1 \xrightarrow{f_1} K_2 \xleftarrow{g_2} K_3 \xrightarrow{f_3} \cdots \xrightarrow{f_{(n-1)}} K_n\}$ of simplicial complexes K_i connected through simplicial maps $\{\xrightarrow{f_i}$ or $\xleftarrow{g_j}\}$, we independently strong collapse the complexes of the sequence to reach a sequence $\mathcal{Z}^c : \{K_1^c \xrightarrow{f_1^c} K_2^c \xleftarrow{g_2^c} K_3^c \xrightarrow{f_3^c} \cdots \xrightarrow{f_{(n-1)}^c} K_n^c\}$, with *induced simplicial maps* $\{\xrightarrow{f_i^c}$ or $\xleftarrow{g_j^c}\}$ (defined in Section 4). The complex K_i^c is called the **core** of the complex K_i and we call the sequence $\mathcal{Z}^c$ the **core sequence** of $\mathcal{Z}$. We show that one can compute the PH of the sequence $\mathcal{Z}$ by computing the PH of the core sequence $\mathcal{Z}^c$, which is of much smaller size.

Our method has some similarity with the work of Wilkerson et. al. [29] who also use strong collapses to reduce PH computation but it differs in three essential aspects: it is not limited to filtrations (i.e. sequences of nested simplicial subcomplexes) but works for other types of sequences like towers and zigzags. It also differs in the way strong collapses are computed and in the manner PH is computed.

A first central observation is that to strong collapse a simplicial complex K, we only need to store its maximal simplices (i.e. those simplices that have no coface). The number of maximal simplices is smaller than the total number of simplices by a factor that is exponential in the dimension of the complex. It is linear in the number of vertices for a variety of complexes [4]. Working only with maximal simplices dramatically reduces the time and space complexities compared to the algorithm of [30]. We prove that the complexity of our algorithm is $\mathcal{O}(v^2\Gamma_0 d + m^2\Gamma_0 d)$. Here d is the dimension of the complex, v is the number of vertices, m is the number of maximal simplices and Γ_0 is an upper bound on the number of maximal simplices incident to a vertex. As observed in [3, 4], usually m is much smaller than the total number of simplices and Γ_0 is much smaller than m (see Section 3 for a discussion).

We now consider PH computation. All PH algorithms take as input a full representation of the complexes. We thus have to convert the representation by maximal simplices used for strong collapses into a full representation of the complexes, which takes exponential time in the dimension (of the collapsed complexes). This exponential burden is to be expected since it is known that computing PH is NP-hard when the complexes are represented by their maximal faces [1]. Nevertheless, we demonstrate in this paper that strong collapses combined with known persistence algorithms lead to major improvements over previous methods to compute the PH of a sequence. This is due in part to the fact that strong collapses reduce the size of the complexes on which persistence is computed. Two other factors also play a role:

- The collapses of the complexes in the sequence can be performed independently and in parallel. This is due to the fact that strong collapses can be expressed as simplicial maps unlike simple collapses [28].
- The size of the complexes in a sequence does not grow by much in terms of maximal simplices, as observed in many practical cases. As a consequence, the time to collapse the i-th simplicial complex K_i in the sequence is almost independent of i. For filtrations, this is a clear advantage over methods that use a full representation of the complexes and suffer an increasing cost as i increases.

As a result, our approach is extremely fast and memory efficient in practice as demonstrated by numerous experiments on publicly available data sets.

An outline of this paper is as follows. Section 2 recalls the basic ideas and constructions related to simplicial complexes and strong collapses. We describe our core algorithm in Section 3. In Section 4, we prove that zigzag modules are preserved under strong collapse. In Section 5, we provide experimental results.

2 Preliminaries

In this section, we provide a brief review of the notions of simplicial complex and strong collapse as introduced in [2]. We assume some familiarity with basic concepts like homotopic maps, homotopy type, homology groups and other algebraic topological notions. Readers can refer to [17] for a comprehensive introduction of these topics.

Simplex, simplicial complex and simplicial map. An **abstract simplicial complex** K is a collection of subsets of a non-empty finite set X, such that for every subset A in K, all the subsets of A are in K. From now on we will call an *abstract simplicial complex* simply a *simplicial complex* or just a *complex*. An element of K is called a **simplex**. An element of cardinality $k+1$ is called a k-simplex and k is called its **dimension**. A simplex is called **maximal** if it is not a proper subset of any other simplex in K. A sub-collection L of K is called a **subcomplex**, if it is a simplicial complex itself. L is a **full subcomplex** if it contains all the simplices of K that are spanned by the vertices (0-simplices) of the subcomplex L.

A vertex to vertex map $\psi : K \rightarrow L$ between two simplicial complexes is called a **simplicial map**, if the images of the vertices of a simplex always span a simplex. Simplicial maps are thus determined by the images of the vertices. In particular, there is a finite number of simplicial maps between two given finite simplicial complexes. Simplicial maps induce continuous maps between the underlying *geometric realisations* of the simplicial complexes. Two simplicial maps $\phi : K \rightarrow L$ and $\psi : K \rightarrow L$ are contiguous if, for all $\sigma \in K$, $\phi(\sigma) \cup \psi(\sigma) \in L$. Two contiguous maps are known to be homotopic [22, Theorem 12.5].

Dominated vertex. Let σ be a simplex of a simplicial complex K, the **closed star** of σ in K, $st_K(\sigma)$ is a subcomplex of K which is defined as follows, $st_K(\sigma) := \{\tau \in K | \ \tau \cup \sigma \in K\}$. The **link** of σ in K, $lk_K(\sigma)$ is defined as the set of simplices in $st_K(\sigma)$ which do not intersect with σ, $lk_K(\sigma) := \{\tau \in st_K(\sigma) | \tau \cap \sigma = \emptyset\}$.

Taking a join with a vertex transforms a simplicial complex into a simplicial cone. Formally if L is a simplicial complex and a is a vertex not in L then the **simplicial cone** aL is defined as $aL := \{a, \tau \, | \ \tau \in L \ \ or \ \ \tau = \sigma \cup a; \ \ where \ \ \sigma \in L\}$. A vertex v in K is called a **dominated vertex** if the link of v in K, $lk_K(v)$ is a simplicial cone, that is, there exists a vertex $v' \neq v$ and a subcomplex L in K, such that $lk_K(v) = v'L$. We say that the vertex v'

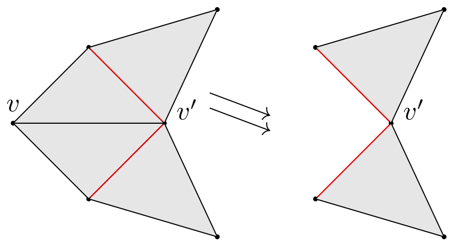


Figure 1 Illustration of an *elementary strong collapse*. In the complex on the left, v is dominated by v'. The link of v is highlighted in red. Removing v leads to the complex on the right.

is *dominating* v and v is *dominated* by v'. The symbol $\boldsymbol{K \setminus v}$(deletion of v from K) refers to the subcomplex of K which has all simplices of K except the ones containing v. Below is an important remark from [2, Remark 2.2], which proposes an alternative definition of dominated vertices.

▶ Remark (1). A vertex $v \in K$ is dominated by another vertex $v' \in K$, *if and only if* all the maximal simplices of K that contain v also contain v' [2].

Strong collapse. An **elementary strong collapse** is the deletion of a dominated vertex v from K, which we denote with $K \searrow\searrow^{e} K \setminus v$. Figure 1 illustrates an easy case of an elementary strong collapse. There is a **strong collapse** from a simplicial complex K to its subcomplex L, if there exists a series of elementary strong collapses from K to L, denoted as $K \searrow\searrow L$. The inverse of a strong collapse is called a **strong expansion**. If there exists a combination of strong collapses and/or strong expansion from K to L then K and L are said to have the same **strong homotopy type**.

The notion of strong homotopy type is stronger than the notion of simple homotopy type in the sense that if K and L have the same strong homotopy type, then they have the same simple homotopy type, and therefore the same homotopy type [2]. There are examples of contractible or simply collapsible simplicial complexes that are not strong collapsible.

A complex without any dominated vertex will be called a **minimal complex**. A **core** of a complex K is a minimal subcomplex $K^c \subseteq K$, such that $K \searrow\searrow K^c$. *Every simplicial complex has a* ***unique core*** *up to isomorphism. The core decides the strong homotopy type of the complex*, and two simplicial complexes have the same strong homotopy type *if and only if* they have isomorphic cores [2, Theorem 2.11].

Retraction map. If a vertex $v \in K$ is dominated by another vertex $v' \in K$, the vertex map $r : K \to K \setminus v$ defined as: $r(w) = w$ if $w \neq v$ and $r(v) = v'$, induces a simplical map that is a *retraction* map. The homotopy between r and the identity $i_{K \setminus v}$ over $K \setminus v$ is in fact a strong deformation retract. Furthermore, the composition $(i_{K \setminus v})r$ is contiguous to the identity i_K over K [2, Proposition 2.9].

Nerve of a simplicial complex. A closed **cover** $\mathcal{U}$ of a topological space $\mathcal{X}$ is a set of closed sets of $\mathcal{X}$ such that $\mathcal{X}$ is a subset of their union. The **nerve** of a cover $\mathcal{U}$ is an abstract simplicial complex, defined as the set of all non-empty intersections of the elements of $\mathcal{U}$. The nerve is a well known construction that transforms a continuous space to a combinatorial space preserving its homotopy type. The *nerve* $\mathcal{N}(K)$ of a simplicial complex K is defined as the nerve of the set of maximal simplices of the complex K (considered as a cover of the complex). Hence all the maximal simplices of K will be the vertices of $\mathcal{N}(K)$ and their

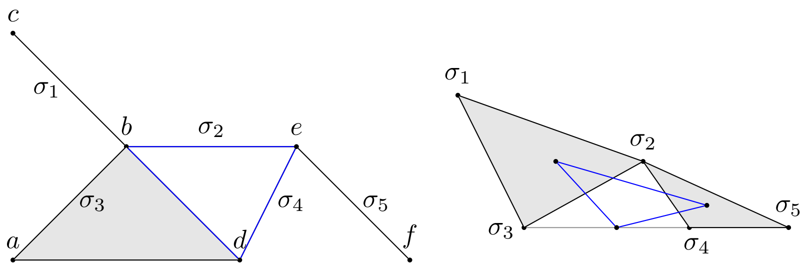


Figure 2 Left: K (in grey), Right: $\mathcal{N}(K)$ (in grey) and $\mathcal{N}^2(K)$ (in blue). $\mathcal{N}^2(K)$ is isomorphic to a full-subcomplex of K highlighted in blue on the left.

non-empty intersection will form the simplices of $\mathcal{N}(K)$. For $j \geq 2$ the iterative construction is defined as $\mathcal{N}^j(K) = \mathcal{N}(\mathcal{N}^{j-1}(K))$. This definition of nerve preserves the homotopy type, $K \simeq \mathcal{N}(K)$[2]. A remarkable property of this nerve construction is its connection with strong collapses.

Taking the nerve of any simplicial complex K twice corresponds to a strong collapse.

▶ **Theorem 1.** *[2, Proposition 3.4] For a simplicial complex K, there exists a subcomplex L isomorphic to $\mathcal{N}^2(K)$, such that $K \searrow\searrow L$.*

An easy consequence of this theorem is that a complex K is *minimal* if and only if it is isomorphic to $\mathcal{N}^2(K)$ [2, Lemma 3.6]. This means that we can keep collapsing our complex K by applying $\mathcal{N}^2(.)$ iteratively until we reach the core of the complex K. The sequence $K, \mathcal{N}^2(K), ..., \mathcal{N}^{2p}(K)$ is a decreasing sequence in terms of number of simplices.

3 Algorithm

In this section, we describe an algorithm to strong collapse a simplicial complex K, provide the details of the implementation and analyze its complexity. We construct $\mathcal{N}^2(K)$ as defined in Section 2.

Data structure. Basically, we represent K as the adjacency matrix M between the vertices and the maximal simplices of K. We will simply call M the adjacency matrix of K. The rows of M represent the vertices and the columns represent the maximal simplices of K. For convenience, we will identify a row (resp. column) and the vertex (resp. maximal simplex) it represents. An entry $M[v_i][\sigma_j]$ associated with a vertex v_i and a maximal simplex σ_j is set to 1 if $v_i \in \sigma_j$, and to 0 otherwise. For example, the matrix M in the left of the Table 1 corresponds to the leftmost simplicial complex K in Figure 2. Usually, M is very sparse. Indeed, each column contains at most $d+1$ non-zero elements since the simplices of a d-dimensional complex have at most $d+1$ vertices, and each line contains at most Γ_0 non-zero elements where Γ_0 is an upper bound on the number of maximal simplices incident to a given vertex. As already mentionned, in many practical situations, Γ_0 is a small fraction of the number of maximal simplices. It is therefore beneficial to store M as a list of vertices and a list of maximal simplices. Each vertex v in the list of vertices points to the maximal simplices that contain v, and each simplex in the list of maximal simplices points to its vertices. This data structure is similar to the SAL data structure of [3].

Table 1 From left to right M, $\mathcal{N}(M)$ and $\mathcal{N}^2(M)$.

	σ_1	σ_2	σ_3	σ_4	σ_5
a	0	0	1	0	0
b	1	1	1	0	0
c	1	0	0	0	0
d	0	0	1	1	0
e	0	1	0	1	1
f	0	0	0	0	1

	b	d	e
σ_1	1	0	0
σ_2	1	0	1
σ_3	1	1	0
σ_4	0	1	1
σ_5	0	0	1

	σ_2	σ_3	σ_4
b	1	1	0
d	0	1	1
e	1	0	1

Core algorithm. Given the adjacency matrix M of K, we compute the adjacency matrix C of the *core* K^c. It turns out that using basic row and column removal operations, we can easily compute C from M. Loosely speaking our algorithm recursively computes $\mathcal{N}^2(K)$ until it reaches K^c.

The columns of M (which represent the maximal simplices of K) correspond to the vertices of $\mathcal{N}(K)$. Also, the columns of M that have a non-zero value in a particular row v correspond to the maximal simplices of K that share the vertex associated with row v. Therefore, each row of M represents a simplex of the nerve $\mathcal{N}(K)$. Not all simplices of $\mathcal{N}(K)$ are associated with rows of M but all maximal simplices are since they correspond to subsets of maximal simplices with a common vertex. To remedy this situation, we *remove* all the rows of M that correspond to non-maximal simplices of $\mathcal{N}(K)$. This results in a new smaller matrix M whose transpose, noted $\mathcal{N}(M)$, is the adjacency matrix of the nerve $\mathcal{N}(K)$. We then exchange the roles of rows and columns (which is the same as taking the transpose) and run the very same procedure as before so as to obtain the adjacency matrix $\mathcal{N}^2(M)$ of $\mathcal{N}^2(K)$.

The process is iterated as long as the matrix can be reduced. Upon termination, we output the reduced matrix $C := \mathcal{N}^{2p}(M)$, for some $p \geq 1$, which is the adjacency matrix of the core K^c of K. Removing a row or column is the most basic operation of our algorithm. We will discuss it in more detail later in the paragraph *Domination test.*

Example. As mentioned before, the matrix M in the left of the Table 1 represents the simplicial complex K in the left of Figure 2. We go through the rows first, rows a and c are subsets of row b and row f is a subset of e. Removing rows a, c and f and transposing M yields the adjacency matrix $\mathcal{N}(M)$ of $\mathcal{N}(K)$ in the middle. Now, row σ_1 is a subset of σ_2 and of σ_3, and σ_5 is a subset of σ_2 and of σ_4. We remove these two rows of $\mathcal{N}(M)$ and transpose $\mathcal{N}(M)$ so as to get $\mathcal{N}^2(M)$ (the rightmost matrix of Figure 2), which corresponds to the core drawn in blue in Figure 2.

Domination test. Now we explain in more detail how to detect the rows that need to be removed. Let v be a row of M and σ_v be the associated simplex in $\mathcal{N}(K)$. If σ_v is not a maximal simplex of $\mathcal{N}(K)$, it is a proper face of some maximal simplex $\sigma_{v'}$ of $\mathcal{N}(K)$. Equivalently, the row v' of M that is associated with $\sigma_{v'}$ contains row v in the sense that the non zero elements of v appear in the same columns as the non zero elements of v'. We will say that row v is dominated by row v' and determining if a row is dominated by another one will be called the row domination test. Notice that when a row v is dominated by a row v', the same is true for the associated vertices since all the maximal simplices that contain vertex v also contain vertex v', which is the criterion to determine if v is dominated by v' (See Remark 1 in Section 2). The algorithm removes all dominated rows and therefore all dominated vertices of K.

After removing rows, the algorithm removes the columns that are no longer maximal in K, which might happen since we removed some rows. Removing a column may lead in turn to new dominated vertices and therefore new rows to be removed. When the algorithm stops, there are no rows to be removed and we have obtained the core K^c of the complex K. Note that the algorithm provides a constructive proof of Theorem 1.

Removing columns is done in very much the same way: we just exchange the roles of rows and columns.

Computing the retraction map r. The algorithm also provides a direct way to compute the retraction map r defined in Section 2. The retraction map corresponding to the strong collapses executed by the algorithm can be constructed as follows. A row r being removed in M corresponds to a dominated vertex in K and the row which *contains* r corresponds to a dominating vertex. Therefore we map the dominated vertex to the dominating vertex and compose all such maps to get the final retraction map from K to its core K^c. The final map is simplicial as well, as it is a composition of simplicial maps.

Reducing the number of domination tests. We first observe that, when one wants to determine if a row v is dominated by some other row, we don't need to test v with all other rows but with at most d of them. Indeed, at most $d+1$ rows can intersect a given column since a simplex can have at most $d+1$ vertices. For example, in Table 1 (Left), to check if row e (highlighted in brown) is dominated by another row, we pick the first non-zero column σ_2 (highlighted in Gray) and compare e with the non-zero entries $\{\mathrm{b}\}$ of σ_2.

A second observation is that we don't need to test all rows and columns for domination, but only the so-called candidate rows and columns. We define a row r to be a **candidate row** for the next iteration if at least one column containing one of the non-zero elements of r has been removed in the previous column removal iteration. Similarly, by exchanging the roles of rows and columns, we define the **candidate columns**. Candidate rows and columns are the only rows or columns that need to be considered in the *domination* tests of the algorithm. Indeed, a column τ of M whose non-zero elements all belong to rows that are present from the previous *iteration* cannot be dominated by another column τ' of M, since τ was not dominated at the previous iteration and no new non-zero elements have ever been added by the algorithm. The same argument follows for the candidate rows.

We maintain two *queues*, one for the candidate columns (colQueue) and one for the candidate rows (rowQueue). These queues are implemented as First in First out (FIFO) queues. At each iteration, we *pop out* a candidate row or column from its respective queue and test whether it is dominated or not. After each successful domination test, we *push* the candidate columns or rows in their appropriate queue in preparation for the subsequent iteration. In the first iteration, we *push* all the rows in rowQueue and then alternatively use colQueue and rowQueue. Algorithm 1 gives the pseudo code of our algorithm.

Time Complexity. The most basic operation in our algorithm is to determine if a row is dominated by another given row, and similarly for columns. In our implementation, the rows (columns) of the matrix that are considered by the algorithm are stored as sorted lists. Checking if one sorted list is a subset of another sorted list can be done in time $\mathcal{O}(l)$, where l is the size of the longer list. Note that the length of a row list is at most Γ_0 where Γ_0 denotes

Algorithm 1 Core algorithm.

```
 1: procedure CORE($M$)          ▷ Returns the matrix corresponding to the core of $K$
 2:     $rowQueue \leftarrow$ push all rows of M (all vertices of K)
 3:     $colQueue \leftarrow$ empty
 4:     while rowQueue is not empty do
 5:         $v \leftarrow pop(rowQueue)$
 6:         $\sigma \leftarrow$ the first non-zero column of $v$
 7:         for non-zero rows $w$ in $\sigma$ do
 8:             if $v$ is a subset of $w$ then
 9:                 Remove $v$ from $M$
10:                 push all non-zero columns $\tau$ of $v$ to colQueue if not pushed before
11:                 break
12:             end if
13:         end for
14:     end while
15:     while colQueue is not empty do
16:         $\tau \leftarrow pop(colQueue)$
17:         $v \leftarrow$ the first non-zero row of $\tau$
18:         for non-zero columns $\sigma$ in $v$ do
19:             if $\tau$ is subset of $\sigma$ then
20:                 Remove $\tau$ from $M$
21:                 push all non-zero rows $w$ of $\tau$ to rowQueue if not pushed before
22:                 break
23:             end if
24:         end for
25:     end while
26:     if rowQueue is not empty then
27:         GOTO 4
28:     end if
29:     return $M$          ▷ The core consists of the remaining rows and columns
30: end procedure
```

an upper bound on the number of maximal simplices incident to a vertex. The length of a column list is at most $d+1$ where d is the dimension of the complex. Hence checking if a row is dominated by another row takes $\mathcal{O}(\Gamma_0)$ time and checking if a column is dominated by another column takes $\mathcal{O}(d)$ time.

At each iteration on the rows (Lines 7-13 of Algorithm 1), each row is checked against at most d other rows (since a maximal simplex has at most $d+1$ vertices), and at each iteration of the columns (Lines 18-24 of Algorithm 1), each column is checked against at most Γ_0 other columns (since a vertex can belong to at most Γ_0 maximal simplices). Since, at each iteration on the rows, we remove at least one row, the total number of iterations on the rows is at most $O(v^2)$, where v is the total number of vertices of the complex K. Similarly, at each iteration on the columns, we remove at least one column and the total number of iterations on columns is $O(m^2)$, where m is the total number of maximal simplices of the complex K. The worst-case time complexity of our algorithm is therefore $\mathcal{O}(v^2\Gamma_0 d + m^2\Gamma_0 d)$. In practice, m is much smaller than n, the total number of simplices, and Γ_0 is much smaller than Γ, the maximum number of simplices incident on a vertex. Typically Γ grows exponentially with d while Γ_0 remains almost constant as d increases. See Table 5 in [3] and related results in [4], and also the plots in Section 5.

4 Strong collapse of zigzag sequences

To be able to present our main result, we need to begin with some brief background on zigzag persistence. Readers interested in more details can refer to [6, 7, 11].

Given a **zigzag sequence** of simplicial complexes $\mathcal{Z} : \{K_1 \xrightarrow{f_1} K_2 \xleftarrow{g_2} K_3 \xrightarrow{f_3} \cdots \xrightarrow{f_{(n-1)}} K_n\}$, if we compute the homology classes of all K_is, we get the sequence $\mathcal{P}(\mathcal{Z}) : \{H_p(K_1) \xrightarrow{f_1^*} H_p(K_2) \xleftarrow{g_2^*} H_p(K_3) \xrightarrow{f_3^*} \cdots \xrightarrow{f_{(n-1)}^*} H_p(K_n)\}$. Here $H_p(-)$ denotes the homology class of dimension p with coefficients from a field $\mathbb{F}$ and $*$ denotes an induced homomorphism. $\mathcal{P}(\mathcal{Z})$ is a sequence of vector spaces connected through homomorphisms, called a **Zigzag module**. More formally, a *zigzag module* $\mathbb{V}$ is a sequence of vector spaces $\{V_1 \rightarrow V_2 \leftarrow V_3 \rightarrow \cdots \leftrightarrow V_n\}$ connected with homomorphisms $\{\rightarrow, \leftarrow\}$ between them. A zigzag module arising from a sequence of simplicial complexes captures the evolution of the topology of the sequence.

For two integers b and d, $1 \leq b \leq d \leq n$; we can define an **interval module** $\mathbb{I}[b, d]$ by assigning V_i to $\mathbb{F}$ when $i \in [b, d]$, and null spaces otherwise, the maps between any two $\mathbb{F}$ vector spaces is identity and is zero otherwise. For example $\mathbb{I}[2, 4] : \{0 \xrightarrow{0} \mathbb{F} \xleftarrow{I} \mathbb{F} \xrightarrow{I} \mathbb{F} \xleftarrow{0} 0 \xrightarrow{0} 0\}$, here $n = 6$. Any zigzag module can be *decomposed* as the direct sum of *finitely* many interval modules, which is unique upto the permutations of the interval modules [6]. The multiset of all the intervals $[b_j, d_j]$ corresponding to the interval module decomposition of any zigzag module is called a **zigzag (persistence) diagram**. The zigzag diagram completely characterizes the zigzag module, that is, there is bijective correspondence between them [6, 31].

Two different zigzag modules $\mathbb{V} : \{V_1 \rightarrow V_2 \leftarrow V_3 \rightarrow \cdots \leftrightarrow V_n\}$ and $\mathbb{W} : \{W_1 \rightarrow W_2 \leftarrow W_3 \rightarrow \cdots \leftrightarrow W_n\}$, connected through a set of homomorphisms $\phi_i : V_i \rightarrow W_i$ are **equivalent** if the ϕ_is are isomorphisms and the following diagram commutes [6, 11].

$$\begin{tikzcd}
V_1 \arrow[r] \arrow[d, "\phi_1"] & V_2 \arrow[d, "\phi_2"] & V_3 \arrow[l] \arrow[d, "\phi_3"] & \cdots & {} \arrow[r] & V_{n-1} \arrow[r] \arrow[d, "\phi_{n-1}"] & V_n \arrow[d, "\phi_n"] \\
W_1 \arrow[r] & W_2 & W_3 \arrow[l] & \cdots & {} \arrow[r] & W_{n-1} \arrow[r] & W_n
\end{tikzcd}$$

Note that the *length* of the modules and the directions of the arrows in them should be consistent. Two equivalent zigzag modules will have the same interval decomposition, therefore the same zigzag diagram.

A zigzag sequence is called a simplicial **tower** if all maps are forward. i.e. only f_is. A tower is called a **filtration** if the maps are only inclusions.

Strong collapse of the zigzag module. Given a zigzag sequence $\mathcal{Z} : \{K_1 \xrightarrow{f_1} K_2 \xleftarrow{g_2} K_3 \xrightarrow{f_3} \cdots \xrightarrow{f_{(n-1)}} K_n\}$. We define the **core sequence** $\mathcal{Z}^c$ of $\mathcal{Z}$ as $\mathcal{Z}^c : \{K_1^c \xrightarrow{f_1^c} K_2^c \xleftarrow{g_2^c} K_3^c \xrightarrow{f_3^c} \cdots \xrightarrow{f_{(n-1)}^c} K_n^c\}$. Where K_i^c is the core of K_i. The forward maps are defined as, $f_j^c := r_{j+1} f_j i_j$; and the backward maps are defined as $g_j^c := r_j g_j i_{j+1}$. The maps $i_j : K_j^c \hookrightarrow K_j$ and $r_j : K_j \rightarrow K_j^c$ are the composed inclusions and the retractions maps defined in Section 2 respectively.

▶ **Theorem 2.** *Zigzag modules $\mathcal{P}(\mathcal{Z})$ and $\mathcal{P}(\mathcal{Z}^c)$ are equivalent.*

Proof. Consider the following diagram

$$\begin{tikzcd}
K_1 \arrow[r, "f_1"] \arrow[d, "r_1"] & K_2 \arrow[d, "r_2"] & K_3 \arrow[l, "g_2"] \arrow[d, "r_3"] & \cdots & {} \arrow[r] & K_{n-1} \arrow[r, "f_{n-1}"] \arrow[d, "r_{n-1}"] & K_n \arrow[d, "r_n"] \\
K_1^c \arrow[r, "f_1^c"] & K_2^c & K_3^c \arrow[l, "g_2^c"] & \cdots & {} \arrow[r] & K_{n-1}^c \arrow[r, "f_{n-1}^c"] & K_n^c
\end{tikzcd}$$

and the associated diagram after computing the p-th homology groups

$$\begin{tikzcd}
H_p(K_1) \arrow[r, "f_1^*"] \arrow[d, "r_1^*"] & H_p(K_2) \arrow[d, "r_2^*"] & H_p(K_3) \arrow[l, "g_2^*"] \arrow[d, "r_3^*"] & \cdots & {} \arrow[r] & H_p(K_{n-1}) \arrow[r, "f_{n-1}^*"] \arrow[d, "r_{n-1}^*"] & H_p(K_n) \arrow[d, "r_n^*"] \\
H_p(K_1^c) \arrow[r, "(f_1^c)^*"] & H_p(K_2^c) & H_p(K_3^c) \arrow[l, "(g_2^c)^*"] & \cdots & {} \arrow[r] & H_p(K_{n-1}^c) \arrow[r, "(f_{n-1}^c)^*"] & H_p(K_n^c)
\end{tikzcd}$$

Since there exists a strong deformation retract between r_j and i_j, the induced homomorphisms r_j^* and i_j^* are isomorphisms [17, Corollary 2.11]. Also, $f_j^c r_j = r_{j+1} f_j i_j r_j$ is contiguous to $r_{j+1} f_j$, since $i_j r_j$ is contiguous to the identity on K_j and contiguity is preserved under composition, see [2, Proposition 2.9] and similarly $g_j^c r_{j+1}$ is contiguous to $r_j g_j$. Now, since contiguous maps are homotopic at the level of geometric realization and homotopic maps induce the same homomorphism, we have $(f_j^c r_j)^* = (r_{j+1} f_j)^*$ and thus $(f_j^c)^* r_j^* = r_{j+1}^* f_j^*$ and similarly $(g_j^c)^* r_{j+1}^* = r_j^* g_j^*$, see [17, Proposition (1) page 111]. Therefore all the squares in the lower diagram commute and the set of maps r_j^*s are isomorphisms, therefore $\mathcal{P}(\mathcal{Z})$ and $\mathcal{P}(\mathcal{Z}^c)$ are *equivalent* and hence their zigzag diagrams are identical. ◀

In fact, using the more general notion of quiver representation [11], this result follows for the multidimensional persistence as well.

5 Computational experiments

For each data set, we consider as the input sequence a nested sequence (filtration) of Vietoris-Rips (VR) complexes associated with a set of increasing values of the scale parameter (called snapshots). The snapshots are specific values of the scale parameter at which we choose to strong collapse the complex. The choice of snapshots strongly dictates the performance and the quality of computed PD. Sparse snapshots will lead to faster computation but to coarser PD where the points of persistence less than the interval between two snapshots have been removed. On the other hand, choosing denser snapshots will lead to a comparatively slower algorithm but will provide more refined PD. We first *independently* strong collapse all these complexes, then assemble the resulting individual *cores* using the induced simplicial maps introduced in Section 4. The resulting new sequence with induced simplicial maps between the collapsed complexes is usually a simplicial tower we call the *core tower.* We then convert the core tower into an equivalent filtration using the Sophia software [26], which implements the algorithm described by Kerber and Schreiber in [18]. Finally, we run the persistence algorithm of the Gudhi library [16] to obtain the persistence diagram (PD) of the equivalent filtration. By the results of Section 4, the obtained PD is the same as the PD of the initial sequence.

The total time to compute the PD of the core sequence is the sum of three terms: 1. the *maximum* time taken to collapse all the individual complexes (assuming they are computed in parallel), 2. the time taken to assemble the individual *cores* to form the core tower, 3. the time to compute the persistent diagram of the core tower. Table 2 summarises the results of the experiments. In both cases, the original filtration and the core tower, we use Gudhi through Sophia using the command <./sophia -cgudhi inputTowerFile outputPDFile>. When we use the -cgudhi option, Sophia reports two computation times. The first one is the total time

Table 2 The rows are, from top to down: dataset $\mathcal{X}$, number of snapshots (snp), total number of simplices in the original filtration (Flt) in millions, number of simplices in the collapsed tower (Twr), total number of simplices in the equivalent filtration (EqF), ratio of Flt and EqF (Flt/EqF) in thousands, PD computation time for the original filration (PDF), maximum collapse time (MCT), assembly time (AT), PD computation time of the tower (PDT), sum MCT+AT+PDT (Total), ratio of PDF and Total (PDF/Total). All times are noted in seconds. For the first three datasets, we sampled points randomly from the initial datasets and averaged the results over five trials.

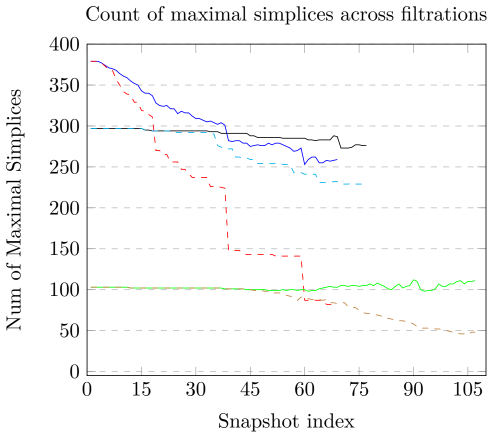
$\mathcal{X}$	1-sphere	2-Annulus	dragon	netw-sc	senate	eleg
Snp	80	80	46	69	107	77
Flt(10^6)	0.12	13.91	7.96	22.35	2.56	1.18
Twr	54	252	1,641	380	104	298
EqF	573	1,954	8,437	957	270	431
Flt/EqF(10^3)	0.21	7.12	0.94	23.35	9.48	2.74
PDF	0.65	174.18	69.92	243.86	24.92	10.87
MCT	0.005	0.022	0.065	0.009	0.003	0.002
AT	0.045	0.136	0.408	0.078	0.06	0.157
PDT	0.01	0.02	0.08	0.01	0.005	0.006
Total	0.060	0.178	0.553	0.097	0.068	0.165
PDF/Total	10.8	978.5	126.4	2514.0	366.5	65.9

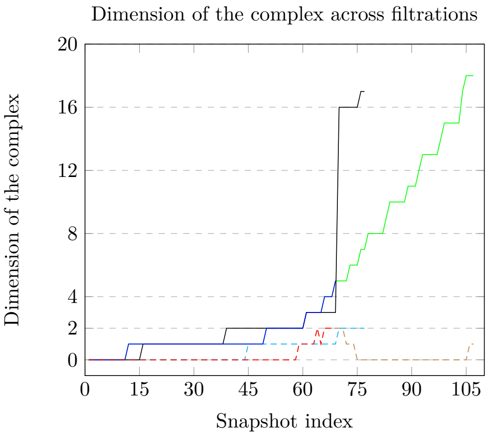
taken by Sophia which includes (1) reading the tower, (2) transforming it to a filtration and (3) computing PD using Gudhi. The second reported time is just the time taken by Gudhi to compute PD. In our comparisons, we just report the time taken by Gudhi for the original filtration, while, for the core tower, we report the total time taken by Sophia.

The dataset of the first column (1-sphere) of Table 2 consists of 100 random points sampled from a unit circle in dimension 2. The dataset of the second column (2-Annulus) consists of 150 random points sampled from a two dimension annulus of radii $\{0.6, 1\}$. For all the other experiments, we use datasets from a publicly available repository [10]. These datasets have been previously used to benchmark different publicly available software computing PH [23]. For the third experiment (*dragon*), we randomly picked 150 points from the 2000 points of the dataset **drag 2** of [10]. The fourth and fifth column respectively correspond to the dataset **netw-sc** and **senate** of [10], here we used the distance matrix. The sixth column corresponds to the dataset **eleg** of [10], and here again we used the distance matrix. The first three datasets are point sets in Euclidean space. For the other three, the distance matrices of the datasets were available at [10]. The [initial value, increment, final value] of the scale parameter are $[0.1, 0.005, 0.5]$, $[0.1, 0.005, 0.5]$, $[0, 0.001, 0.046]$, $[0.1, 0.05, 3.5]$, $[0, 0.001, 0.107]$ and $[0, 0.001, 0.077]$ for the examples in Table 2 (from left to right). The filtration value of a simplex is the value of the snapshot at which it first appeared. For more detail about the datasets and the computation of the distance matrices of the last three datasets please refer to [23].

The plots below count the maximal simplices and the dimensions of the complexes across the filtration (in solid) and the collapsed tower (as dashed). Blue and red correspond respectively to the filtration and the collapsed tower of the data **netw-sc**. Similarly green and brown correspond respectively to the filtration and the collapsed tower of the data **senate**. Finally, **black** and cyan correspond to the filtration and the collapsed tower of the data

eleg respectively. We can observe that in all cases the number of maximal simplices never increases. Also they are far fewer in number compared to the total number of simplices. Observe that for the uncollapsed filtrations blue, green and **black**, the dimension of the complexes increases quite rapidly with the snapshot index. Another key fact to observe is that the dimension of the complexes in the corresponding core tower are much smaller than their counterparts in the filtration. This has a huge effect on the performances since the total number of simplices depends exponentially on the dimension.





Noticeably, in our experiments, the computing time of our approach is reduced by 1 to 3 orders of magnitude, and the gain increases with the size of the filtration. A similar reduction of 2 to 4 orders of magnitude is achieved for the number of simplices. Observations from the plots combined with the experimental results of Table 2 clearly indicate that our method is extremely fast and memory efficient.

The implementation of the Core algorithm 1 bench-marked here is coded in C++ and will be available as an open-source package of the next release of the Gudhi library [16]. The code was compiled using the compiler <clang-900.0.38> and all computations were performed on <2.8 GHz Intel Core i5> machine with 16 GB of available RAM.

The experiments above are limited to filtrations of VR-complexes, by far the most commonly used type of sequences in Topological Data Analysis. We intend to experiment on Zigzag sequences in future work.

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