Approximating Local Homology from Samples

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Abstract. Recently, multi-scale notions of local homology (a variant of persistent homology) have been used to study the local structure of spaces around a given point from a point cloud sample. Current reconstruction guarantees rely on constructing embedded complexes which become difficult in high dimensions. We show that the persistence diagrams used for estimating local homology, can be approximated using families of Vietoris-Rips complexes, whose simple constructions are robust in any dimension. To the best of our knowledge, our results, for the first time, make applications based on local homology, such as stratification learning, feasible in high dimensions.

1 Introduction

Advances in scientific and computational experiments have improved our ability to gather large collections of data points in high-dimensional spaces. One aspect in topological data analysis is to infer the topological structure of a space given a point cloud sample. We often assume the space has manifold structure, however, more interesting cases arise when we relax our assumptions to include spaces that contain singularities and mixed dimensionality, for example, stratified spaces.

Stratified spaces can be decomposed into manifold pieces that are glued together in some uniform way. An important tool in studying these spaces is the study of the neighborhoods surrounding singularities, where manifolds of different dimensionality intersect. We focus on sampling conditions for such neighborhoods, which allow us to begin examining how difficult certain reconstruction techniques are with respect to the geometric properties of the underlying shape. Our main task is to infer sampling conditions suitable for recovering local structures of stratified spaces, in particular, the local homology groups, from a possibly noisy sampled point set.

Stratification learning. In stratification learning (or mixed manifold learning), a point cloud is assumed to be sampled from a mixture of (possibly intersecting) manifolds. The objective is to recover the different pieces, often treated as clusters, of the data associated with different manifolds of varying dimensions. Stratified spaces has been studied extensively in mathematics, see seminal work in \cite{1,2}. Recently, topological data analysis, relying heavily on ingredients from computational topology \cite{3,4} and intersection homology \cite{5,6,7} has gained momentum in stratification learning. In particular, the work in \cite{8} focuses on studying the local structure of a sampled stratified spaces based on a multi-scale notion of local homology (see Section \textsuperscript{2}). More recent work in \cite{9} studies how
point cloud data could be clustered by strata based on how the local homology of nearby sampled points map into one another.

**Reconstruction and sampling.** Reconstructing shapes from potential noisy point cloud samples has been studied in many fields. Most often the work is heavily tied to a reconstruction criteria (e.g. homotopic, homeomorphic, etc.) and the assumptions on the underlying space (e.g. manifold). Combinatorial algorithms in geometry are generally derived from Delaunay triangulations and alpha shapes, and provide correctness proofs associated with such reconstructions. As the dimension increases, reconstruction efforts have been redirected towards alternative combinatorial structures such as tangential Delaunay complexes, witness complexes, Čech complexes and the closely related Vietoris-Rips complexes.

However, these existing techniques are primarily concerned with global reconstruction. Providing reconstruction guarantees for local structures is more challenging. To guarantee theoretical correctness in computing persistence local homology, both [8] and [9] use Delaunay complexes and their variants. However constructing Delaunay complexes in high dimensions is known to be difficult due to scaling and numerical issues with predicates. On the other hand, methods for fast and efficient constructions of Vietoris-Rips complexes are available, and there have been theoretical advances on their topology-preserving qualities, making it appealing for computations in high dimensions. The goal of this paper is to make persistent local homology computation more practical through approximations.

**Contributions.** Our contributions focus on providing sampling conditions to recover the local structure of a space from a point cloud sample, based on previously introduced multi-scale notions of local homology. Our main results are:

- We extend previously introduced algebraic constructions in the analysis of scalar fields over point cloud data to two multi-scale notions of local homology.
- For both multi-scale notions of local homology, we approximate their persistence diagrams by constructing families of Vietoris-Rips complexes based on a set of sample points, formalized within Theorem 2 and 3. The simplicity and efficiency of building the these complexes in any dimension makes, for the first time, applications based on local homology such as stratification learning feasible in high dimensions.
- We show that relative persistent modules are interleaved if the respective absolute persistent modules are interleaved. We consider such a technical result (Theorem 1) of independent interest.
- Our results imply algorithms for computing the local homology either by a reduction to standard persistence or a known variant.

## 2 Background

The background material focuses on the introduction of persistence modules, local homology and its multi-scale notions. We assume a basic knowledge of...
homology and persistent homology, see [22,23] for a readable background of the former, and [21] for a computational treatment of the latter.

**Persistence Modules.** We use the definition of persistence modules adapted from [21]. A persistence module $\mathcal{F} = \{F_\alpha\}_{\alpha \in \mathbb{R}}$ is a collection of vector spaces $F_\alpha$ (over any fields) together with a family $\{f_\beta^\alpha : F_\alpha \rightarrow F_\beta\}_{\alpha \leq \beta}$ of linear maps such that $\alpha \leq \beta \leq \gamma$ implies $f_\gamma^\alpha = f_\beta^\gamma \circ f_\alpha^\beta$, and $f_\alpha^\alpha = \text{id}_{F_\alpha}$. A persistence module is *tame* if it has finite number of critical values and all $F_\alpha$ are of finite rank. Unless otherwise specified, we suppose all persistence modules we encounter in this paper are tame.

Two persistence modules $\{F\}_\alpha$ and $\{G\}_\alpha$ are *(strongly) $\varepsilon$-interleaved* if there exists two families of homomorphisms, $\mu_\alpha : F_\alpha \rightarrow G_{\alpha+\varepsilon}$ and $\nu_\alpha : G_\alpha \rightarrow F_{\alpha+\varepsilon}$, that make the following diagrams (Fig. 1) commute for all $\alpha \leq \beta \in \mathbb{R}$ [21]. The information contained in a persistence module can be encoded by a multi-set of points in the extended plane $\mathbb{R}^2$ (where $\mathbb{R} = \mathbb{R} \cup \{-\infty, \infty\}$), called a *persistence diagram* [25]. If two tame persistence modules are $\varepsilon$-interleaved, the bottleneck distance between their persistence diagrams are upper bounded by $\varepsilon$ ([25], Theorem 4.4). In this paper, we consider persistence modules of homology groups and relative homology groups over a field. Given a family of topological spaces $\{X_\alpha\}_\alpha$ connected by inclusions $X_\alpha \hookrightarrow X_\beta$, the inclusions induce a sequence of homology groups connected by homomorphisms, $H_k(X_\alpha) \rightarrow H_k(X_\beta)$, where $k$ is the homological dimension. We therefore obtain persistence modules of the form $\{H_k(X_\alpha)\}_\alpha$. Specifically, when the linear maps associated with two persistence modules $\{H_k(X_\alpha)\}_\alpha$ and $\{H_k(Y_\alpha)\}_\alpha$ are induced by inclusions at the space level $X_\alpha \hookrightarrow Y_{\alpha+\varepsilon}$ and $Y_\alpha \hookrightarrow X_{\alpha+\varepsilon}$, their $k$-th persistence modules are $\varepsilon$-interleaved [21]. For the rest of the paper, we sometimes abuse this notation by omitting the $k$-th homology functor unless necessary. We work with singular homology here but our results are applicable in the simplicial setting as well.

**Local Homology.** The *local homology groups* at a point $x \in X$ is defined as the relative homology groups $H(X, X - x)$ ([22], page 126). In this paper, we assume that the topological space $X$ is embedded in some Euclidean space $\mathbb{R}^d$ [3]. Let $d_x : \mathbb{R}^d \rightarrow \mathbb{R}$ be the Euclidean distance function from a fixed $x \in X$, $d_x(y) := d(x, y) = ||y - x||$. Let $B_r = B_r(x) = d_x^{-1}[0, r]$ and $B^r = B^r(x) = d_x^{-1}[r, \infty)$ be the sublevel sets and superlevel sets of $d_x$. Taking a small enough $r$, the local homology groups in questions are in fact the *direct limit* of relative homology groups, $\lim_{r \rightarrow 0} H(X, X \cap B^r)$, or alternatively $\lim_{r \rightarrow 0} H(X \cap B_r, X \cap \partial B_r)$ [6], see Fig. 2. We then adapt two multi-scale notions of this concept based

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3 This assumption can be relaxed in several ways but this setting is most common in our applications.
on persistence (which are first introduced in [8]), referred to as the \( r \)-filtration and the \( \alpha \)-filtration. The goal of this paper is to derive sampling conditions that are appropriate to compute the persistence diagrams with respect to these filtrations, therefore approximating the local homology at \( x \in X \).

For a fixed \( \alpha \geq 0 \), let \( X_\alpha \) be the “thickened” or “offset” version of \( X \), that is, the space of points in \( \mathbb{R}^d \) at Euclidean distance at most \( \alpha \) from \( X \). Suppose \( L \) is a finite set of points sampled from \( X \).\(^4\) where \( L \subset X \) and \( L_\alpha = \bigcup_{x \in L} B_\alpha(x) \). In subsequent sections, we put further restrictions on \( L \) where we suppose \( L \) is an \( \varepsilon \)-sample of \( X \), that is, \( \forall x \in X, d(x, L) := \inf_{y \in L} d(x, y) \leq \varepsilon \).

The \( r \)-filtration (Fig. 3) is a sequence of relative homology groups connected by linear maps induced by inclusion and excision, constructed by fixing a thickening parameter \( \alpha \) and varying parameter \( r \), for \( r' > r \),

\[
\cdots \rightarrow \text{H}(X_\alpha, X_\alpha \cap B^r') \rightarrow \text{H}(X_\alpha, X_\alpha \cap B^r) \rightarrow \cdots.
\]

The same filtration could be built on a set of points \( L \) sampled from \( X \), that is,

\[
\cdots \rightarrow \text{H}(L_\alpha, L_\alpha \cap B^r') \rightarrow \text{H}(L_\alpha, L_\alpha \cap B^r) \rightarrow \cdots.
\]

Here, we fix the space at resolution \( \alpha \), and vary the scale \( r \) at which we analyze the local neighborhood, analog to changing the lens from the front of the camera.

The \( \alpha \)-filtration (Fig. 4) is a sequence of relative homology groups connected by inclusion, constructed by fixing \( r \) and varying \( \alpha \), for \( \alpha < \alpha' \),

\[
\cdots \rightarrow \text{H}(X_\alpha \cap B_r, X_\alpha \cap \partial B_r) \rightarrow \text{H}(X_{\alpha'} \cap B_r, X_{\alpha'} \cap \partial B_r) \rightarrow \cdots.
\]

Its discrete counterpart built on a set of points \( L \) sampled from \( X \) is,

\[
\cdots \rightarrow \text{H}(L_\alpha \cap B_r, L_\alpha \cap \partial B_r) \rightarrow \text{H}(L_{\alpha'} \cap B_r, L_{\alpha'} \cap \partial B_r) \rightarrow \cdots.
\]

Here, we fix the size of the ball which defines the locality, i.e. the size \( r \) of the local neighborhood, and we vary the scale \( \alpha \) at which we analyze the space.

\textbf{Čech and Vietoris-Rips Complexes.} Suppose \( L \) is a finite point set in \( \mathbb{R}^d \) and \( L_\alpha = \bigcup_{x \in L} B_\alpha(x) \). The nerve of \( L_\alpha \) is the \( \check{\text{Čech}} \) complex of \( L \), denoted as \( \mathcal{C}_\alpha(L) \) (omitting \( L \) from the notation unless necessary). The \textit{Vietoris-Rips complex} of \( L \) is denoted as \( \mathcal{R}_\alpha \), whose simplicies correspond to non-empty subsets of \( L \) of diameter less than \( \alpha \). For Euclidean metric space, we have, \( \forall \alpha > 0, \mathcal{C}_{\alpha/2} \subseteq \mathcal{R}_\alpha \subseteq \mathcal{C}_\alpha \subseteq \mathcal{R}_{2\alpha} \). This implies that the persistence modules \( \{ \text{H}(\mathcal{C}_\alpha) \}_\alpha \) and \( \{ \text{H}(\mathcal{R}_\alpha) \}_\alpha \) are \( \alpha \)-interleaved.

\(^4\) Our results would hold with minor modifications in the setting of sampling with noise, where elements of \( L \) lie on or near \( X \).
Fig. 3: The $r$-filtration for space $X$ and its offsets (left), and the same filtration built on a set of points $L$, sampled from $X$.

Fig. 4: The $\alpha$-filtration for space $X$ and its offset (left), and on the right, the same filtration built on a set of points $L$, sampled from $X$.

3 Approximating Local Homology: $\alpha$-Filtration

In the $\alpha$-filtration, since we will be computing relative persistent homology, there are certain requirements on the pairs, such that the maps of the relative filtration are well-defined. Two filtrations, $A = \{A_\alpha\}_{\alpha \in \mathbb{R}}$ and $F = \{F_\alpha\}_{\alpha \in \mathbb{R}}$ are called compatible if for all $\alpha \leq \beta$, the following diagram commutes:

$$
\begin{array}{ccc}
A_\alpha & \longrightarrow & F_\alpha \\
\downarrow & & \downarrow \\
A_\beta & \longrightarrow & F_\beta
\end{array}
$$

This ensures that the relative persistence module is well-defined\(^5\). In our context, all the maps are induced by inclusions hence the above diagram commutes. We highlight steps involved to obtain our approximation results:

- First, we show that under certain conditions, the relative homology of a ball modulo its boundary is isomorphic to that of the entire space modulo the subspace outside the ball.
- Second, we prove that if we have two compatible filtrations $F$ and $A$ which are respectively interleaved with $G$ and $B$, the relative persistent homology $H(F, A)$ is approximated by $H(G, B)$. This result may be of independent interest.
- Last, we prove a series of inter-leavings to show that both filtrations in our case can be interleaved with a Vietoris-Rips construction on the samples.

We first show that the following two filtrations are equivalent (as $\alpha$ increases):

$$
\begin{align*}
0 & \rightarrow H(X_\alpha \cap B_r, X_\alpha \cap \partial B_r) \rightarrow \ldots \rightarrow H(B_r, \partial B_r), \\
0 & \rightarrow H(X_\alpha, X_\alpha - \text{int } B_r) \rightarrow \ldots \rightarrow H(\mathbb{R}^n, \mathbb{R}^n - \text{int } B_r).
\end{align*}
$$

\(^5\) Note that this is equivalent to the condition given on pairs of filtrations under the two function setting \([26]\).
Note that $X_\alpha \cap B_r = X_\alpha \cap \partial B_r$. Unless otherwise specified, $\alpha \in [0, \infty)$. Graphically, these filtrations are shown in Fig. 5. As it turns out, it is easier to argue about the filtration in Fig. 5 (right) than Fig. 5 (left), as shown in the following lemma. Recall a pair of space $(A, B)$ forms a good pair if $B$ is a nonempty closed subspace that is a deformation retract of some neighborhood in $A$ (23, page 114).

**Lemma 1.** Assuming that spaces $X_\alpha \cap B_r$ and $X_\alpha \cap \partial B_r$ form a good pair, then $H(X_\alpha \cap B_r, X_\alpha \cap \partial B_r) \cong H(X_\alpha, X_\alpha \cap \text{int} B_r)$.

**Proof Sketch.** This follows from the Excision Theorem (27, Theorem 15.1, page 82) and the Excision Extension Theorem (27, Theorem 15.2, page 82). We excise the space $X_\alpha - B_r$ from the pair $(X_\alpha, X_\alpha - \text{int} B_r)$, and obtain $H(X_\alpha, X_\alpha - \text{int} B_r) \cong H(X_\alpha - (X_\alpha - B_r), X_\alpha - \text{int} B_r - (X_\alpha - B_r)) \cong H(X_\alpha \cap B_r, X_\alpha \cap \partial B_r)$. Since the closure of $X_\alpha - B_r$ needs not be contained in the interior of $X_\alpha - \text{int} B_r$, there are some technical conditions which require some care. See Appendix A for details.

We now show that we can approximate local homology at multi-scale via the $\alpha$-filtration using sample points. We begin with sequence (2). Specifically, we first consider the filtration corresponding to the whole space $(X_\alpha)$, and then the filtration corresponding to the subspace we quotient by, $(X_\alpha \cap \text{int} B_r)$. The key is a technical result described in Theorem 1 which says that if we can approximate filtrations independently, we can approximate their corresponding quotient filtration. We consider this result to be of independent interest.

**Theorem 1.** If we have two compatible filtrations interleaved with two other compatible filtrations, the relative filtration is also interleaved. Formally, if compatible persistence modules $F = \{F_\alpha\}_{\alpha \in \mathbb{R}}$ and $G = \{G_\alpha\}_{\alpha \in \mathbb{R}}$ are $\varepsilon_1$-interleaved, $\mathcal{A} = \{A_\alpha\}_{\alpha \in \mathbb{R}}$ and $\mathcal{B} = \{B_\alpha\}_{\alpha \in \mathbb{R}}$ are $\varepsilon_2$-interleaved, then the relative modules $\{(F_\alpha, A_\alpha)\}_{\alpha \in \mathbb{R}}$ and $\{(G_\alpha, B_\alpha)\}_{\alpha \in \mathbb{R}}$ are $\varepsilon$-interleaved, where $\varepsilon = \max\{\varepsilon_1, \varepsilon_2\}$.

**Proof Sketch.** Without loss of generality, assume $\varepsilon_1 = \varepsilon_2 = \varepsilon$. Each pair, $\{(F, A)\}$ and $\{(G, B)\}$, gives rise to a long exact sequence which are related by the interleaving maps. This gives the following commutative diagram:
\[
\begin{align*}
&H_n(A_\alpha) \xrightarrow{\phi_n^\alpha} H_n(F_\alpha) \xrightarrow{\delta_n^\alpha} H_n(F_\alpha, A_\alpha) \xrightarrow{k_n^\alpha} H_{n-1}(A_\alpha) \xrightarrow{\delta_{n-1}^\alpha} H_{n-1}(F_\alpha)
&| \quad | \quad | \quad | \quad |
&H_n(B_{\alpha+\epsilon}) \xrightarrow{\phi_n^{\alpha+\epsilon}} H_n(G_{\alpha+\epsilon}) \xrightarrow{\delta_n^{\alpha+\epsilon}} H_n(G_{\alpha+\epsilon}, B_{\alpha+\epsilon}) \xrightarrow{k_n^{\alpha+\epsilon}} H_{n-1}(B_{\alpha+\epsilon}) \xrightarrow{\delta_{n-1}^{\alpha+\epsilon}} H_{n-1}(G_{\alpha+\epsilon})
&| \quad | \quad | \quad | \quad |
&H_n(A_{\alpha+2\epsilon}) \xrightarrow{\phi_n^{\alpha+2\epsilon}} H_n(F_{\alpha+2\epsilon}) \xrightarrow{\delta_n^{\alpha+2\epsilon}} H_n(F_{\alpha+2\epsilon}, A_{\alpha+2\epsilon}) \xrightarrow{k_n^{\alpha+2\epsilon}} H_{n-1}(A_{\alpha+2\epsilon}) \xrightarrow{\delta_{n-1}^{\alpha+2\epsilon}} H_{n-1}(F_{\alpha+2\epsilon})
\end{align*}
\]

To prove that the inter-leavings between individual modules imply an inter-leaving between \{(F, A)\} and \{(G, B)\}, we would need some careful diagram chasing at the chain level. That is, we need to prove each of the four diagrams (reviewed in Fig. 1) needed for interleaving commutes, i.e. diagrams in Fig. 6 must commute. The key issue is that although each row is exact, maps between persistence modules do not split — therefore we may have one persistent relative class without a persistent class in either component filtrations. The full details of the proof (with diagram chasing arguments) are given in Appendix A.

![Commuting diagrams for \(\varepsilon\)-interleaved persistence modules.](image)

Before we state our main theorem below, we define the set of sample points which lie outside the ball, \(\bar{L} = \{p \in L | p \notin B_\varepsilon\}\), and \(\bar{L}_\alpha = \cup_{x \in L} B_\alpha(x)\). We have:

**Theorem 2.** The persistence module with respect to the Vietoris-Rips filtration of \((L_\alpha, \bar{L}_\alpha)\), that is, \((\mathcal{R}_\alpha(L), \mathcal{R}_\alpha(\bar{L}))\) is \((2\varepsilon + \alpha + \frac{\alpha^2}{r})\)-interleaved with the \(\alpha\)-filtration \((\mathcal{X}_\alpha, \mathcal{X}_\alpha - \text{int} \, B_r)\), for \(\alpha < r\).

**Proof Sketch.** Since we would like to approximate the persistence diagram of the pair \((\mathcal{X}_\alpha, \mathcal{X}_\alpha - \text{int} \, B_r)\), we could approximate each filtration independently. We describe the key ingredients in our proof here and defer the technical details involving each step to Appendix X.

First, we consider the whole space filtration \(\mathcal{X}_\alpha\), and show that \(\mathcal{X}_\alpha\) is \(\varepsilon\)-interleaved with \(\{L_\alpha\}\) (Fig. 7(a)), which is relatively straightforward assuming \(L\) is an \(\varepsilon\)-sample of \(\mathcal{X}\). Since the nerve of \(L_\alpha\) is the Čech complex \(\mathcal{C}_\alpha(L)\), then \(\{X_\alpha\}\) is \(\varepsilon\)-interleaved with \(\{\mathcal{C}_\alpha(L)\}\).

Second, approximating the subspace filtration \(\mathcal{X}_\alpha - \text{int} \, B_r\) is more involved. The straightforward approach is to simply remove \(\text{int} \, B_r\) from \(\{L_\alpha\}\) and consider \(\{L_\alpha - \text{int} \, B_r\}\) (Fig. 7(b)). This is computational expensive, so instead, we consider \(\{\bar{L}_\alpha - \text{int} \, B_r\}\) (Fig. 7(c)), note its subtle difference with Fig. 7(b). We then show that \(\mathcal{X}_\alpha - \text{int} \, B_r\) is \(2\varepsilon\)-interleaved with \(\{\bar{L}_\alpha - \text{int} \, B_r\}\), by showing that \(\bar{L}\) is a \(2\varepsilon\)-sample of \(\mathcal{X} - \text{int} \, B_r\), that is, removing sampled points in the ball gives a good sample of \(\mathcal{X} - \text{int} \, B_r\).
Third, we further prove that \{ \tilde{L}_\alpha - \text{int } B_r \} is \( (\alpha^2 r) \)-interleaved with \{ \tilde{L}_\alpha \}. This is illustrated in Fig. 7(d), where we allow the offset to intersect inside the ball, and show that the error remains controlled. In addition, the nerve of \tilde{L}_\alpha is the \v{C}ech complex \( \mathcal{C}_\alpha(\tilde{L}) \). A combination of these results implies that \{ \chi_\alpha - \text{int } B_r \} is \( (2\varepsilon + \alpha^2 r) \)-interleaved with \{ \mathcal{C}_\alpha(\tilde{L}) \}. Finally, having shown that we can approximate both the filtration on the whole space and on the subspace (which we quotient by), we invoke Theorem 1. Finally, based on that the Vietoris-Rips and \v{C}ech complexes are \( \alpha \)-interleaved, that is, \( \mathcal{R}_\alpha \subseteq \mathcal{C}_\alpha \subseteq \mathcal{R}_{2\alpha} \), we obtain the additional \( \alpha \) factor in the approximation result. However, the limiting factor in this case is the subspace filtration. The results are only meaningful over a range of values for \( \alpha \). For example, if \( \alpha \geq r \), the local homology is isomorphic to a \( (d+1) \)-sphere. This is discussed further in Appendix A.

Computation. Using Theorem 2, we can compute relative persistent homology of the filtrations built on the sample points using the algorithm described in [28].

4 Approximating Local Homology: \( r \)-Filtration

In this section, we describe approximating local homology with respect to a fixed point \( x \) at multi-scale via \( r \)-filtration (Fig. 3). We fix a thickening parameter \( \alpha \) and drop it from the notation, using only \( X \). Consider the following filtration, for \( r \geq s \geq t \),

\[
\ldots \to \mathcal{H}(X, X \cap B^r) \to \mathcal{H}(X, X \cap B^s) \to \mathcal{H}(X, X \cap B^t) \to \ldots ,
\]

Now we endow the space \( X \) with a function \( g : X \to \mathbb{R} \), which is the Euclidean distance to a fixed point \( x \), \( g(x) = d(x, y) = d_x(y) \). \( g \) could be viewed as the restriction onto the space \( X \) of a Euclidean distance function to a point \( x \), \( d_x : \mathbb{R}^d \to \mathbb{R} \), that is, \( g = d_x|_X \). The function \( g \) is 1-Lipschitz and we see that \( X \cap B^r = g^{-1}[r, \infty) \), the superlevel set of \( g \). The above sequence becomes,

\[
\ldots \to \mathcal{H}(X, g^{-1}[r, \infty)) \to \mathcal{H}(X, g^{-1}[s, \infty)) \to \mathcal{H}(X, g^{-1}[t, \infty)) \ldots .
\]

This is the relative persistence module of \( g \). Now let \( f = -g : X \to \mathbb{R} \), \( f \) is also 1-Lipschitz. Sequence (5) holds the same information as sequence (4) assuming tame functions \footnote{It is unclear whether this holds in the case of non-tame functions which could arise as a consequence of a pathological underlying space.} according to Extended Persistence Symmetry Corollary [29].
(that is, the ordinary persistence diagram of a function \( f \) equals the relative persistence diagram of \(-f\) up to a dimension shift and central reflection),

\[
\ldots \rightarrow \text{H}(f^{-1}(-\infty, a]) \rightarrow \text{H}(f^{-1}(-\infty, b]) \rightarrow \text{H}(f^{-1}(-\infty, c]) \ldots ,
\]

where \( a \leq b \leq c \), which corresponds to the persistence module of \( f \) based on its sublevel sets. Since the filtrations in sequence (5) and sequence (4) hold the same information, we can translate the diagram and recover the information for the original \( r \)-filtration (sequence (3)).

The key insight is that in this case, the \( r \)-filtration amounts to studying the persistent homology of a function on the space — the distance function to a point, which is a particularly nice function, i.e. 1-Lipschitz. In this section, we give results under strong assumptions on the space \( X \) with some further discussions deferred to Appendix B.

We introduce a strong assumption on homotopy between a pair of spaces, which requires that points are only moved a bounded amount in the homotopy. Two subsets of Euclidean space, \( X \) and \( Y \) are \( \varepsilon \)-homotopy equivalent, if there exists two functions \( i: X \rightarrow Y \) and \( h: Y \rightarrow X \) such that \( h \circ i \) is homotopic to the identity map \( id_X \), \( i \circ h \) is homotopic to \( id_Y \), \( d(p, h \circ i(p)) \leq \varepsilon \) and \( d(p, i \circ h(p)) \leq \varepsilon \). The consequence of such an assumption is discussed further in Appendix B. In our context, the map \( i \) is typically the canonical inclusion map, therefore if \( d(p, i \circ h(p)) \leq \varepsilon \) then \( d(p, h \circ i(p)) \leq \varepsilon \). Then we refer to \( h: Y \rightarrow X \) as the \( \varepsilon \)-homotopy equivalence between \( Y \) and \( X \), where \( d(p, h(p)) \leq \varepsilon \).

The first step in approximating the \( r \)-filtration is relating the sublevel set filtration of a 1-Lipschitz function \( f: X \rightarrow \mathbb{R} \) on the space \( X \), and the sublevel set filtration of a corresponding function \( f_\varepsilon : X_\varepsilon \rightarrow \mathbb{R} \) on \( X_\varepsilon \). These filtrations together with maps induced by space inclusions form the (homology) persistence module of \( f \) and \( f_\varepsilon \), respectively. Recall that \( f \) is the negative of \( d_\varepsilon \) restricted to \( X \), \( f_\varepsilon = -d_\varepsilon|_{X_\varepsilon} \). Likewise, \( f_\varepsilon = -d_\varepsilon|_{X_\varepsilon} \). Since there is an inclusion \( X \hookrightarrow X_\varepsilon \), it follows that \( f = f_\varepsilon|_X \). For the rest of the section we use the following notation for sublevel sets: \( F(a) = f^{-1}(-\infty, a] \), \( F_\varepsilon(a) = f_\varepsilon^{-1}(-\infty, a] \), for every \( a \in \mathbb{R} \). The persistence module of \( f \) and \( f_\varepsilon \) are represented as \( \{\text{H}(F(a))\}_a \) and \( \{\text{H}(F_\varepsilon(a))\}_a \), respectively.

**Lemma 2.** Suppose \( X \) and \( X_\varepsilon \) are \( \varepsilon \)-homotopy equivalent through the canonical inclusion map \( i: X \rightarrow X_\varepsilon \) and the map \( h: X_\varepsilon \rightarrow X \). Then the persistence modules of \( f \) and \( f_\varepsilon \), that is, \( \{\text{H}(F(a))\}_a \) and \( \{\text{H}(F_\varepsilon(a))\}_a \), are \( \varepsilon \)-interleaved.

**Proof.** Consider the following sequence of maps:

\[
F(\alpha) \xrightarrow{i'} F_\varepsilon(\alpha + \varepsilon) \xrightarrow{h'} F(\alpha + 2\varepsilon).
\]

We define the map \( i' = i|_{F(\alpha)} \) and show that \( i' \) is well-defined. \( \forall p \in F(\alpha) \), by definition, we have \( f(p) \leq \alpha \) and \( f = f_\varepsilon|_X \), therefore \( f_\varepsilon(p) \leq \alpha \). This implies that \( p \in F_\varepsilon(\alpha) \subseteq F_\varepsilon(\alpha + \varepsilon) \), therefore, \( i' \) is a well-defined inclusion, which induces inclusion on the homology level, \( i_* : \text{H}(F(\alpha)) \rightarrow \text{H}(F_\varepsilon(\alpha + \varepsilon)) \).
We define \( h' = h|_{F_ε(α+ε)} \), and we need to show that \( h' \) is well-defined, that is, the image of \( h' \) lies in \( F(α+2ε) \). \( \forall p \in F_ε(α+ε) \), by definition, we have \( f_ε(p) \leq α + ε \). Since \( f_ε = -d_ε|_{\mathbb{X}_ε} \), then \( -d(x, p) \leq α + ε \). Combining with \( d(p, h(p)) \leq ε \), we have \( f(h(p)) := -d(x, h(p)) \leq d(p, h(p)) - d(x, p) \leq α + 2ε \). This implies that \( h(p) \in F(α + 2ε) \). Therefore \( h' \) is well-defined. In addition, based on our assumption that \( \mathbb{X} \) and \( \mathbb{X}_ε \) are homotopy equivalent through maps \( i \) and \( h \), this implies that \( h' \) is a homotopy equivalence, which induces an isomorphism \( h_* \) on the homology level, \( h_* : H(F_ε(α+ε)) \to H(F(α+2ε)) \).

In order to show persistence modules \( \{H(F(α))\}_α \) and \( \{H(F_ε(α))\}_α \) are \( ε \)-interleaved, we could easily verify that the four diagrams in Fig. 1 commute.

The next step is to relate the above filtrations to the union of balls on the samples. For notational convenience we define the union of balls centered around points with a function value less than some threshold \( α \). For \( \forall p \in F_ε(α+ε) \), by definition, we have \( f_ε(p) \leq α + ε \). Since \( f_ε = -d_ε|_{\mathbb{X}_ε} \), then \( -d(x, p) \leq α + ε \). Combining with \( d(p, h(p)) \leq ε \), we have \( f(h(p)) := -d(x, h(p)) \leq d(p, h(p)) - d(x, p) \leq α + 2ε \). This implies that \( h(p) \in F(α + 2ε) \). Therefore \( h' \) is well-defined. In addition, based on our assumption that \( \mathbb{X} \) and \( \mathbb{X}_ε \) are homotopy equivalent through maps \( i \) and \( h \), this implies that \( h' \) is a homotopy equivalence, which induces an isomorphism \( h_* \) on the homology level, \( h_* : H(F_ε(α+ε)) \to H(F(α+2ε)) \).

In order to show persistence modules \( \{H(F(α))\}_α \) and \( \{H(F_ε(α))\}_α \) are \( ε \)-interleaved, we could easily verify that the four diagrams in Fig. 1 commute.

Lemma 3. Suppose \( \mathbb{X} \) and \( \mathbb{X}_ε \) are \( ε \)-homotopy equivalent through the canonical inclusion map \( i : \mathbb{X} \to \mathbb{X}_ε \) and the map \( h : \mathbb{X}_ε \to \mathbb{X} \). Suppose \( L \) is an \( ε \)-sample of \( \mathbb{X} \). Then the persistence modules \( \{H(F(α))\}_α \) of \( f \) and \( \{H(\mathbb{C}_ε(α))\}_α \) are \( 2ε \)-interleaved.

Proof. The proof is nearly identical to the proof of Lemma 2. Consider the following sequence:

\[
F(ε) \xrightarrow{i'} U_ε(α + ε) \xrightarrow{h'} F(α + 2ε)
\]

We define the map \( i' = i|_{F(α)} \) and show \( i' \) is well-defined. \( \forall p \in F(α) \), by definition, \( f(p) = -d(x, p) \leq α \). Since \( L \) is an \( ε \)-sample of \( \mathbb{X} \), there exists \( q \in L \) such that \( p \in B_ε(q) \), that is, \( d(p, q) \leq ε \). Combining the above inequalities, we obtain \( f(q) = -d(x, q) \leq -d(x, p) + d(p, q) \leq α + ε \), implying that \( p \in U_ε(α + ε) \).

For map \( h' \), since \( U_ε(α + ε) \subseteq F_ε(α + 2ε) \), based on the results in Lemma 2 that the map \( F_ε(α + 2ε) \to F(α + 3ε) \) is well-defined, we can define \( h' = h|_{U_ε(α + ε)} \).

Following similar argument in Lemma 2 \( \{H(U_ε(α))\}_α \) is \( 2ε \)-interleaved with \( \{H(F(α))\}_α \). By the Nerve Lemma, the union of balls \( \mathbb{C}_ε(α) \) is homotopic to the Čech complex for all \( α \), leading to \( H(\mathbb{C}_ε(α)) \cong H(U_ε(α)) \).

Note the definition of the union of balls filtration – it precisely equals to the lower star filtration of the Čech complex.
Theorem 3. Suppose $h$ is an $2\varepsilon$-homotopy equivalence between $X_{2\varepsilon}$ and $X$, and $L$ is an $\varepsilon$-sample of $X$. Then the Vietoris-Rips filtration $\{H(R_{2\varepsilon}(a))\}_a$ is a $4\varepsilon$-approximation of the $r$-filtration $\{H(F(a))\}_a$.

Proof. Suppose $X_{2\varepsilon}$ and $X$ are $2\varepsilon$-homotopy equivalent through the canonical inclusion map $i : X \rightarrow X_{2\varepsilon}$ and the map $h : X_{2\varepsilon} \rightarrow X$. We can construct the following commutative diagram on the space level:

\[\begin{array}{cccccc}
F(\alpha) & \rightarrow & C_\varepsilon(\alpha + \varepsilon) & \rightarrow & C_{2\varepsilon}(\alpha + \varepsilon) & \rightarrow & U_{2\varepsilon}(\alpha + \varepsilon) \\
U_{\varepsilon}(\alpha + \varepsilon) & \rightarrow & R_{2\varepsilon}(\alpha + \varepsilon) & \rightarrow & C_{2\varepsilon}(\alpha + \varepsilon) & \rightarrow & U_{2\varepsilon}(\alpha + \varepsilon) \\
F'(\alpha + 5\varepsilon) & \rightarrow & C_\varepsilon(\alpha + 6\varepsilon) & \rightarrow & C_{2\varepsilon}(\alpha + 6\varepsilon) & \rightarrow & U_{2\varepsilon}(\alpha + 6\varepsilon) \\
U_{\varepsilon}(\alpha + 6\varepsilon) & \rightarrow & R_{2\varepsilon}(\alpha + 6\varepsilon) & \rightarrow & C_{2\varepsilon}(\alpha + 6\varepsilon) & \rightarrow & U_{2\varepsilon}(\alpha + 6\varepsilon) \\
\end{array}\]

First we consider the top and bottoms rows in the diagram. The 1st map is an inclusion on the space level. The 2nd and 5th maps are homotopy equivalences based on the Nerve Lemma (which induces isomorphisms on the homology level). The 3rd and 4th maps are inclusions based on interleaving between Čech and Vietoris-Rips complexes, i.e. $C_\varepsilon \subseteq R_{2\varepsilon} \subseteq C_{2\varepsilon}$. Second, all the vertical maps between the top and bottom rows are inclusions. Finally, we define the connecting map $U_{2\varepsilon}(\alpha + \varepsilon) \rightarrow F(\alpha + 5\varepsilon)$ as $h' = h|_{U_{2\varepsilon}(\alpha + \varepsilon)}$. To show $h'$ is well-defined, $\forall p \in U_{2\varepsilon}(\alpha + \varepsilon)$, $f(p) \leq \alpha + 3\varepsilon$, since $h'$ is a $2\varepsilon$-homotopy, $h'(p)$ has a function value at most $\alpha + 5\varepsilon$, therefore $h'(p) \in F(\alpha + 5\varepsilon)$.

From the above commutative diagram, we consider the following maps between spaces: $F(\alpha) \rightarrow R_{2\varepsilon}(\alpha + \varepsilon) \rightarrow F(\alpha + 5\varepsilon)$. This leads to a factor of $4\varepsilon$ in the interleaving between persistence modules $\{H(R_{2\varepsilon}(a))\}_a$ and $\{H(F(a))\}_a$.

Computation. Here we have reduced the computation of persistent local homology to standard persistence on the sample points [3,4].

5 Discussion

Local homology and relative homology are common tools in algebraic topology. In this paper, we recounted two different multi-scale notions of local homology: the $\alpha$- and $r$-filtrations. We show that both can be well-approximated using Vietoris-Rips complexes based on a finite sample of the space and therefore efficiently computed. We also prove a novel technical result involving interleaving between relative persistence modules derived from interleaving between absolute persistence modules. Several open questions remain: Are there better geometric measures to describe the sampling conditions in approximating local homology? Could a similar sampling theory be developed for witness complexes? Under what conditions on the space are the underlying filtrations we study tame?

Our work was motivated by stratification learning. However the results in this paper could be applied to any applications where local or relative homology computations are relevant, i.e. for future directions, the approximation of Conley index or well groups [30].
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A Detailed Proofs for Approximating Local Homology at Multi-scale via $\alpha$-filtration

A.1 Lemma

Lemma. Assuming that spaces $X_\alpha$ and $X_\alpha - \text{int } B_r$ form a good pair, then $H(X_\alpha \cap B_r, X_\alpha \cap \partial B_r) \cong H(X_\alpha, X_\alpha - \text{int } B_r)$.

Proof. First we recall several theorems related to excisions. Let $Y, U, A$ be topological spaces. The inclusion map of pairs $(Y - U, A - U) \to (Y, A)$ is called an excision if it induces a homology isomorphism. In this case, one says that $U$ can be excised. We will make use of the following two results about excision ([27]).

Theorem 4 (Excision Theorem). ([27], Theorem 15.1, page 82) If the closure of $U$ is contained in the interior of $A$, that is, $\text{cl } U \subseteq \text{int } A$, then $U$ can be excised.

Theorem 5 (Excision Extension). ([27], Theorem 15.2, page 82) Suppose $V \subset U \subset A$ and (i) $V$ can be excised; (ii) $(Y - U, A - U)$ is a deformation retract of $(Y - V, A - V)$. Then $U$ can be excised.

In our context, let $Y = X_\alpha$, $A = X_\alpha - \text{int } B_r$, $U = X_\alpha - B_r$. Therefore $Y - U = X_\alpha \cap B_r$ and $A - U = X_\alpha \cap \partial B_r$. However, since $\text{cl } U$ needs not be contained in $\text{int } A$, we need to define a suitable $V \subset U$. One direct way is to choose some small enough positive $\delta$ and a neighborhood $I$, such that we define, $I = X_\alpha \cap \partial B_r \cap \text{cl } U$, $I_\delta = \{ x \in \text{cl } U | d_I(x) \leq \delta \}$, and $V = U - I_\delta$, where $d_I(x)$ is the Euclidean distance from $x$ to the set $I$.

The existence of this $\delta$ follows from the assumption that the pair $(X_\alpha, X_\alpha - \text{int } B_r) := (Y, A)$ form a good pair. This is a technical condition which implies the existence of a neighborhood of $Y - U$ (i.e. $Y - V$) that deformation retracts to $Y - U$. It is then straightforward to verify that $V \subset U \subset A$ satisfies the hypotheses of Theorem 5.

Therefore the chain map $k : C(Y, A) \to C(Y - U, A - U)$ is an excision. It is defined as $k = r_\# \circ s$, where $r_\#$ is the chain map induced by the retraction $r : (Y - V, A - V) \to (Y - U, A - U)$, and $s$ is the chain-homotopy inverse of the chain map included by the inclusion of pairs $(Y - V, A - V) \to (Y, A)$.

A.2 Theorem

We describe our long and technical proof of Theorem 1 based on diagram chasing. We first need the following lemma that comes from the short exact sequences of a pair ([22], page 140).

Lemma 4. The quotient map on the chain level commutes. That is, for compatible maps $A \to B$ and $X \to Y$ there is a map $(X, A) \to (Y, B)$ such that the diagram in Fig. 8 is commutative.
Proof. The assumption of compatibility ensures the left square commutes. Note that $i, j$ must be injective maps and in all the cases we consider $f$ and $g$ are also injective, which is sufficient for compatibility. To define $h$ we note that $\text{im } h = \text{im } g / (\text{im } (g \circ i) \oplus \text{im } j)$. To show that the right square commutes $(h \circ q = r \circ g)$, we note that any class in $\text{im } (r \circ g)$ must be in $\text{im } g$ by exactness and the assumption that the left square commutes $(g \circ i = j \circ f)$. Since it is not in $\text{im } i$ or map to $\text{im } j$, it is in $\text{im } h$. Alternatively, any class in $\text{im } (h \circ q)$ must have a lift to $C(Y)$ since $r$ is a surjection. This must be in $\text{im } g$ by the definition of $h$, which concludes the proof.

Theorem 1. If we have two compatible filtrations interleaved with two other compatible filtrations, the relative filtration is also interleaved. Formally, if compatible persistence modules $F = \{F_{\alpha}\}_{\alpha \in \mathbb{R}}$ and $G = \{G_{\alpha}\}_{\alpha \in \mathbb{R}}$ are $\varepsilon_1$-interleaved, $A = \{A_{\alpha}\}_{\alpha \in \mathbb{R}}$ and $B = \{B_{\alpha}\}_{\alpha \in \mathbb{R}}$ are $\varepsilon_2$-interleaved, then the relative modules $\{(F_{\alpha}, A_{\alpha})\}_{\alpha \in \mathbb{R}}$ and $\{(G_{\alpha}, B_{\alpha})\}_{\alpha \in \mathbb{R}}$ are $\varepsilon$-interleaved, where $\varepsilon = \max\{\varepsilon_1, \varepsilon_2\}$.

Proof. We begin with a list of notations. Suppose $\{F\}$ and $\{G\}$ are compatible and are $\varepsilon$-interleaved with homomorphisms $\{f_{\alpha} : H(F_{\alpha}) \to H(G_{\alpha+\varepsilon})\}$ and $\{g_{\alpha} : H(G_{\alpha}) \to H(F_{\alpha+\varepsilon})\}$. Suppose $\{A\}$ and $\{B\}$ are also compatible and $\varepsilon$-interleaved, with homomorphisms $\{\phi_{\alpha} : H(A_{\alpha}) \to H(B_{\alpha+\varepsilon})\}$ and $\{\psi_{\alpha} : H(B_{\alpha}) \to H(A_{\alpha+\varepsilon})\}$. For relative homology to be well-defined, we have injective maps at chain level, for simplicity, we further require $A_{\alpha} \hookrightarrow F_{\alpha}$ and $B_{\alpha} \hookrightarrow G_{\alpha}$.

We would like to prove that $\{(F, A)\}$ and $\{(G, B)\}$ are also interleaved, and we could construct their corresponding homomorphisms, $\{\mu_{\alpha} : H(F_{\alpha}, A_{\alpha}) \to H(F_{\alpha+\varepsilon}, A_{\alpha+\varepsilon})\}$ and $\{\nu_{\alpha} : H(G_{\alpha}, B_{\alpha}) \to H(G_{\alpha+\varepsilon}, B_{\alpha+\varepsilon})\}$.

To prove the result, we pass to the stack of long exact sequences in Fig. [9]. First, we explain the notation. A map, i.e. $\phi_{\alpha}^n$, represents a map that maps $n$-dimensional homology groups of $A_{\alpha}$ to some other homology groups. We note that all the squares in this diagram (Fig. [9]) commute based on Lemma 4 and by assumption the two component filtrations are interleaved, so the first, second, fourth and fifth columns commute with the maps induced by inclusion. For example, the map induced by inclusion $\text{im } (H_n(F_n) \to H_n(F_{n+2\varepsilon}))$ equals $\text{im } (g_{n+2\varepsilon}^n \circ f_n^n)$. Commutativity implies interleaving in some of the cases. We prove the following triangle commutes (Fig. [6]) through four claims.

Claim 1: if a relative class is in $\text{im } (H_n(F_{\alpha}, A_{\alpha}) \to H_n(F_{\alpha+2\varepsilon}, A_{\alpha+2\varepsilon}))$, and it is in $\text{im } j_{\alpha}^n$ and $\text{im } j_{\alpha+2\varepsilon}^n$, then it is in $\text{im } q_{n+2\varepsilon}^n$. 

\[
\begin{array}{cccccc}
0 & \longrightarrow & C_n(A) & \xrightarrow{i} & C_n(X) & \xrightarrow{q} & C_n(X, A) & \longrightarrow & 0 \\
\text{Fig. 8: Commuting diagrams on the chain level.} & & \text{f} & & \text{g} & & \text{h} & & \text{0} \\
0 & \longrightarrow & C_n(B) & \xrightarrow{j} & C_n(Y) & \xrightarrow{r} & C_n(Y, B) & \longrightarrow & 0
\end{array}
\]

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If a relative class $\gamma$ in $\text{im}(H_n(F_\alpha, A_\alpha) \to H_n(F_{\alpha+2}, A_{\alpha+2}))$ is in $\text{im} \, j_n^{\alpha+2\epsilon}$ and $\text{im} \, j_n^{\alpha+2\epsilon}$, then by the interleaving, it must be in $H_n(G_{\alpha+\epsilon})$. Therefore suppose $\gamma$ is not in $\text{im} \, q_n^{\alpha+\epsilon}$, it must have a preimage in $H_n(B_{\alpha+\epsilon})$. Since $\gamma$ is in $\text{im} \, j_n^{\alpha+2\epsilon}$, it does not have a preimage in $H_n(A_{\alpha+2\epsilon})$. This would imply that the lower left square does not commute ($g_n^{\alpha+\epsilon} \circ p_n^{\alpha+\epsilon} \neq \mu_n^{\alpha+2\epsilon} \circ \psi_n^{\alpha+\epsilon}$). That is a contradiction, therefore it must be in $\text{im} \, q_n^{\alpha+\epsilon}$.

**Claim 2:** If a relative class is in $\text{im}(H_n(F_\alpha, A_\alpha) \to H_n(F_{\alpha+2\epsilon}, A_{\alpha+2\epsilon}))$, then it is in $\text{im} \, j_n^{\alpha+2\epsilon}$ and $\text{im} \, j_n^{\alpha+2\epsilon}$, it must be in $\text{im} \, k_n^{\alpha+2\epsilon}$ and $\text{im} \, k_n^{\alpha+2\epsilon}$. If the relative class $\gamma$ in $\text{im}(H_n(F_\alpha, A_\alpha) \to H_n(F_{\alpha+2\epsilon}, A_{\alpha+2\epsilon}))$ is in $\text{im} \, j_n^{\alpha}$ and $\text{im} \, j_n^{\alpha+2\epsilon}$, then by exactness $\gamma$ maps into $\text{im} \, k_n^{\alpha}$ and $\text{im} \, k_n^{\alpha+2\epsilon}$, that is, it maps to a non-trivial element in $H_{n-1}(A_\alpha)$ and $H_{n-1}(A_{\alpha+2\epsilon})$. By the interleaving between $A$ and $B$, it must also map to an element of $H_{n-1}(B_{\alpha+\epsilon})$. Furthermore, it must be in ker $i_n^{\alpha+\epsilon}$. Therefore suppose $\gamma$ is not in $\text{im} \, q_n^{\alpha+\epsilon}$ (or equivalently, $\text{im} \, r_n^{\alpha+\epsilon}$ or ker $p_n^{\alpha+\epsilon}$), it must map to $G_{\alpha+\epsilon}$, which implies that the top right square does not commute ($f_n^{\alpha} \circ i_n^{\alpha+\epsilon} \neq \mu_n^{\alpha+2\epsilon} \circ \psi_n^{\alpha+\epsilon}$) leading to a contradiction.

We now show that commutativity is not a sufficient argument. Consider a persistent relative class in $H_n(F_\alpha, A_\alpha) \to H_n(F_{\alpha+2\epsilon}, A_{\alpha+2\epsilon})$ such that it is in $\text{im} \, j_n^{\alpha}$ and $\text{im} \, j_n^{\alpha+2\epsilon}$. Alternatively, it may be in $\text{im} \, j_n^{\alpha}$ and $\text{im} \, j_n^{\alpha+2\epsilon}$ in these cases, we may map this class to zero the middle row and still maintain the commutativity of the diagram (although this implies the relative filtrations are not interleaved). This problem stems from the fact that the maps between persistent modules do not split (The relative persistence module does not split into direct sum of the image and cokernel in the long exact sequence).

**Claim 3:** If the relative class is in $\text{im}(H_n(F_\alpha, A_\alpha) \to H_n(F_{\alpha+2\epsilon}, A_{\alpha+2\epsilon}))$, then it is not possible that it is in $\text{im} \, j_n^{\alpha}$ and $\text{im} \, j_n^{\alpha+2\epsilon}$ at the same time.

First we handle the case where the relative class is in $\text{im} \, j_n^{\alpha}$ and $\text{im} \, j_n^{\alpha+2\epsilon}$ by showing this cannot occur. Since it is in $\text{im} \, j_n^{\alpha}$ at the chain level, there is a cycle representative in $Z_n(F_\alpha)$. Since this maps to a cycle representative in $Z_n(K_{\alpha+2\epsilon})$, this implies that the cycle is in the boundary. However, looking at the relevant part of the short exact sequence shown in Fig. 10.

The cycle representative in $C_n(F_{\alpha+2\epsilon})$ lifts to some element in $C_{n+1}(F_{\alpha+2\epsilon})$. Now by assumption, there is still some cycle representative in $C_n(F_{\alpha+2\epsilon}, A_{\alpha+2\epsilon})$. 

Fig. 9: Commuting diagrams for the long exact sequence involving two pairs of filtrations.
Fig. 10: Short exact sequence on chain level.

By commutativity, the bounding element in $C_{n+1}(F_{n+2})$ must also map to a bounding element of the cycle representative in $C_n(F_{n+2}, A_{n+2})$, meaning it cannot be a relative homology class. If on the other hand, the cycle representative in $C_n(F_{n+2})$ is in the kernel of the quotient map, a relative homology class would appear one dimension up. This is the case we deal with next.

**Claim 4:** If the relative class is in $\text{im} \{ H_n(F_{n'}, A_{n'}) \to H_n(F_{n+2}, F_{n+2}) \}$, and it is in $\text{cok} j_n^o$ and $\text{im} j_n^{o+2}$, then it must be in $\text{im} q_n^{o+\varepsilon}$ or $\text{cok} q_n^{o+\varepsilon}$ (i.e. it must be $H_n(G_{\alpha+\varepsilon}, B_{\alpha+\varepsilon})$).

For a relative class in $\text{cok} j_n^o$, there is a cycle representative in $C_{n-1}(A_n)$ of the corresponding class $H_{n-1}(A_{n'})$ which by the injectivity of the interleaving, maps to a cycle in $C_{n-1}(B_{n'+\varepsilon})$ and $C_{n-1}(A_{n'+2\varepsilon})$. Further, since it is in $\text{cok} j_n^o$, it follows that it maps to a bounded cycle in $C_{n-1}(F_n)$ (and by injectivity) the corresponding cycle representatives in $C_{n-1}(G_{\alpha+\varepsilon})$ and $C_{n-1}(F_{n+2})$ are also bounded. Since this relative class is assumed to be in $\text{im} j_n^o$, it follows that the cycle representative in $C_{n-1}(A_{n'+2\varepsilon})$ is now bounded, with the pre-boundary mapping to a cycle in $C_n(F_{n+2})$. This follows from a chain level understanding of the exactness of the bottom row. Take the representative $(n-1)$-cycle in $C_{n-1}(A_{n'})$ denoted by $a$ and map it into $C_{n-1}(F_{n'})$. $i_n^{o-1}(a)$ has a pre-boundary in $C_{n-1}(F_{n'})$ which maps to the cycle representative of the relative class in $C_n(F_{n'}, A_{n'})$. This is just the connecting homomorphism construction. If we map this relative cycle representative to $C_{n-1}(A_{n'+2\varepsilon})$, since the class is in $j_n^{o+2\varepsilon}$, it lifts to a non-trivial cycle in $C_n(F_{n+2})$. This cycle is precisely the image of the pre-boundary of $a$ in $C_{n-1}(A_{n'+2\varepsilon})$ mapped to $C_n(F_{n+2})$ plus the pre-boundary of the image of $i_n^{o-1}(a)$ in $C_{n-1}(F_{n+2})$.

There are two case to consider. If $\phi_{n-1}^o(a)$ is a non-trivial cycle, then there is a homology class in $\ker j_n^{\alpha+\varepsilon}$ and by exactness, a corresponding class in the $\text{cok} q_n^{\alpha+\varepsilon}$.

If $\phi_{n-1}^o(a)$ maps to a bounded cycle, then by the same reasoning as above, the pre-boundary of this cycle in $C_n B_{n+\varepsilon}$ must map to a non-trivial cycle in $C_n G_{n+\varepsilon}$. Hence there is a corresponding class in $\text{im} q_n^{\alpha+\varepsilon}$. Proving the claim.

Following the above four claims, we’ve shown the triangle in Fig. [6] commutes. 

Fig. [6] equals the trapezoid in Fig. [11] (a) by setting $\alpha' = \alpha$. It follows that the trapezoid in Fig. [11] (a) commutes based on similar diagram chasing argument.
The other diagrams in Fig. 11 follow similar proofs. For example, to show that the diagram in Fig. 11(d) commutes, the argument goes through in precisely the same way, on diagrams shown in Fig. 12 and Fig. 13.

\[ H(F_\alpha, A_\alpha) \rightarrow H(F_{\alpha'+2\epsilon}, A_{\alpha'+2\epsilon}) \]
\[ H(G_\alpha, B_\alpha) \rightarrow H(G_{\alpha'+2\epsilon}, B_{\alpha'+2\epsilon}) \]

(a)

\[ H(F_{\alpha+\epsilon}, A_{\alpha+\epsilon}) \rightarrow H(F_{\alpha'+\epsilon}, A_{\alpha'+\epsilon}) \]
\[ H(G_\alpha, B_\alpha) \rightarrow H(G_{\alpha'+\epsilon}, B_{\alpha'+\epsilon}) \]

(b)

\[ H(F_{\alpha+\epsilon}, A_{\alpha'+\epsilon}) \rightarrow H_{\alpha}(F_{\alpha'+\epsilon}, A_{\alpha'+\epsilon}) \]
\[ H(G_\alpha, B_\alpha) \rightarrow H(G_{\alpha'}, B_{\alpha'}) \]

(c)

\[ H(F_\alpha, A_\alpha) \rightarrow H(F_{\alpha'}, A_{\alpha'}) \]
\[ H(G_{\alpha+\epsilon}, B_{\alpha+\epsilon}) \rightarrow H(G_{\alpha'+\epsilon}, B_{\alpha'+\epsilon}) \]

(d)

Fig. 11: Commuting diagrams for $\varepsilon$-leaving of the pairs.

This shows that the two commute and hence we conclude that the relative filtrations are interleaved.

A.3 Theorem 2

First we prove a collection of lemmas (5, 6, 7, 8, 9, 10) that are relevant in proving Theorem 2.
Lemma 5. If $L$ is an $\epsilon$-sample of $X$ then $\{X_\alpha\}$ is $\epsilon$-interleaved with $\{L_\alpha\}$.

Proof. Given that $L$ is an $\epsilon$-sample of $X$, by definition, $L \subseteq X$, this implies that (a) $L_\alpha \subseteq X_\alpha$ and (b) $L_{\alpha+\epsilon} \subseteq X_{\alpha+\epsilon}$. Subsequently, we would prove by the triangle inequality that, (c) $X_\alpha \subseteq L_{\alpha+\epsilon}$. Combining (a), (b) and (c), we have,

$$L_\alpha \subseteq X_\alpha \subseteq L_{\alpha+\epsilon} \subseteq X_{\alpha+\epsilon}.$$  

By the special case of $\epsilon$-interleaving, we have $L_\alpha \subseteq X_{\alpha+\epsilon}$ and $X_\alpha \subseteq L_{\alpha+\epsilon}$, therefore the persistent homology modules of $\{X_\alpha\}$ and $\{L_\alpha\}$ is $\epsilon$-interleaved.

Now we prove that the inclusion in (c) holds. For any point $p \in X_\alpha$, let $q = \arg \min_{x \in X} d(p, x)$, therefore by definition of $X_\alpha$, $d(p, q) \leq \alpha$. Since $q \in X$ and $L$ is an $\epsilon$-sample, let $s = \arg \min_{z \in L} d(p, z)$, by definition of $L$, $d(q, s) \leq \epsilon$. By triangle inequality, $d(p, s) \leq d(p, q) + d(q, s) \leq \alpha + \epsilon$. Therefore $p \in L_{\alpha+\epsilon}$.

Lemma 6. The nerve of $L_\alpha$, $\mathcal{N}(L_\alpha)$, is homotopic to $L_\alpha$.

Proof. This is an application of the Nerve Theorem. Since these are Euclidean balls in Euclidean space, they are all convex as are all their intersections. They are hence contractible and the Nerve Theorem applies.
Lemma 7. If \( L \) is an \( \epsilon \)-sample of \( X \), then \( \tilde{L} \) is a \( 2\epsilon \) sample of \( X - \text{int} B_r \).

Proof. Consider a point outside in \( X \) but not in \( \text{int} B_r \). If it is covered by a sample lying outside of \( \text{int} B_r \), then it is still with \( \epsilon \) of a sample point. If it is covered by a point within \( \text{int} B_r \), then the closest sample point outside of \( \text{int} B_r \) can be no further than \( 2\epsilon \). This follows since all points \( \epsilon \) away from the \( \text{int} B_r \) cannot be covered by a sample point which lies within \( \text{int} B_r \), and therefore any point outside \( \text{int} B_r \) but covered by a sample point within \( \text{int} B_r \), lies at most \( 2\epsilon \) from a sample point with lies outside \( \text{int} B_r \) and so is in \( \tilde{L} \).

Formally, consider a point \( p \in X - \text{int} B_r \). Let \( s = \arg \min_{z \in L} d(p, z) \), that is, \( p \) is covered by \( s \). If \( s \) is outside of \( \text{int} B_r \), that is, \( s \in \tilde{L} \), then \( d(p, s) \leq \epsilon \). If \( s \in \text{int} B_r \), let \( t = \arg \min_{z \in \tilde{L}} d(p, z) \), we claim that \( d(p, t) \leq 2\epsilon \). Therefore \( \tilde{L} \) is a \( 2\epsilon \) sample of \( X - \text{int} B_r \). Now we prove the claim that \( d(p, t) \leq 2\epsilon \). We could prove by contradiction. Suppose \( d(p, t) > 2\epsilon \) and \( p \) is just on the boundary of \( X \cap B_r \). Then there exists at least a point \( z \) that is \( \epsilon \) away from \( p \) that is not covered by any sample point in \( L \). This contradicts with \( L \) being an \( \epsilon \)-sample.

Lemma 8. \( \{\tilde{L}_\alpha - \text{int} B_r \} \) is \( 2\epsilon \)-interleaved with \( \{X_\alpha - \text{int} B_r \} \).

Proof. The proof follows from the Lemma 7 and precisely the same argument as in Lemma 5.

Lemma 9. For \( \alpha < r \), the nerve of \( \tilde{L}_\alpha - \text{int} B_r \) is homotopic to the union of balls \( \tilde{L}_\alpha \) with \( \text{int} B_r \) removed.

Proof. Since we are removing the ball the intersections are no longer convex. However the condition \( \alpha < r \) ensures that they are still contractible. This is only an outline of the proof. The goal is to prove that from any intersection there is a homotopy to a convex body and hence all the intersections are contractible. Take an arbitrary intersection. If it does not intersect \( \text{int} B_r \), it is convex. If it does, then take the tangent plane to \( B_r \) at a point on the boundary within the intersection. Clear the half-plane which does not contain the \( B_r \) intersected with the intersection is convex and hence contractible.

The rest of the intersection can by retracted to the tangent plane, which we prove by giving an explicit deformation retract. The tangent plane will be referred to as \( T(s) \) (the tangent plane at point \( s \)).

First, we define a deformation retract before we remove \( B_r(x) \). We consider a straight-line homotopy to the \( T(s) \) by projection. We project each point \( p \) to \( T(s) \) within the intersection. We call this point \( q \). By convexity of the intersection, this path is a geodesic which lies completely in the intersection. It is also continuous. With \( B_r(x) \) removed this will remain a valid deformation retract if all geodesics remain in the space (i.e. pass through \( B_r(x) \)). The points \( p, q, s \) as above shown in Fig. 14(a).
We prove that the geodesic does not leave the space by contradiction. Without loss of generality assume the point $p$ is on the boundary. To leave the space, it must cross the boundary of $B_r(x)$, and the shortest path from that point must also go through the ball. In particular, we see that to pass through $B_r(x)$, the geodesic must form a negative angle with the tangent plane, shown by $\alpha$ (Compare Fig. 14(b) and (c)). Since the line $(p,q)$ is a shortest path to $T(s)$, it must be perpendicular to $T(s)$. This implies that the angle between $T(p)$ and $T(s)$, denoted by $\beta$, must be acute.

This, however implies that the point of contact of the two hyperplanes is at least $\sqrt{2}r$ far apart as shown in Fig. 14(d). Since we can choose the point of contact such that no point on the ball in the intersection is more that $\alpha$ from the point of contact and $\alpha < r$ (this is obvious if we take $2\alpha < r$), this implies that such a point cannot be in the intersection.

Note that the original projection was to $T(s)$ within the intersection. This means that $(p,q)$ may not be perpendicular to $T(s)$. However in this case, $(p,q)$ will not go through the $B_r(x)$. Since $(p,q)$ must form a chord of a ball of radius $\alpha$, passing through $B_r(x)$ would generate a chord in $B_r(x)$. This implies that either the center of the ball of radius $\alpha$ lies within $B_r(x)$ or that $\alpha > r$. 

Fig. 14: (a) The layout of the points $p, q, s$ along with the deformation retract. (b) The situation when $\alpha$ is positive. (c) The situation when $\alpha$ is negative (cannot occur). (d) A bound on the distance between $p$ and $s$. Note that although this is in high dimensions, these figures are general since we can restrict ourselves to the plane defined by $p, q, s$. 

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Hence, the projection to $T(s)$ is a deformation retract and the non-convex part is contractible as well.

**Lemma 10.** $\{\bar{L}_\alpha - \text{int } B_r\}$ is $\left(\frac{\alpha^2}{r}\right)$-interleaved with $\{\bar{L}_\alpha\}$.

**Proof.** This proof works at the nerve level. We show that if an intersection between balls exists in $L_\alpha$ it will exist in $\bar{L}_\alpha + \alpha^2/r - \text{int } B_r$. Clearly any intersection $\bar{L}_\alpha - \text{int } B_r$ is also in $L_\alpha$. If an intersection is in $L_\alpha$ but not in $\bar{L}_\alpha - \text{int } B_r$, this implies it lies in $\text{int } B_r$. Assuming that there is an intersection contained within $\text{int } B_r$. Note that the furthest this intersection can be from the edge of $\text{int } B_r$ is bounded by $\alpha^2/r$. The derivation can be found blow. Hence the two filtrations are $(\alpha^2/r)$-interleaved.

Now we focus on the derivation of $(\alpha^2/r)$-bound.

![Fig. 15: The geometric situation illustrating how deep in the interior of $B_r$ two offsets from the exterior of the ball can intersect in terms of the radius of the ball $r$ and the offset filtration parameter $\alpha$.](image)

To prove that the we still get a good approximation we need to show that if offsets intersect in the ball, they will intersect soon after outside the ball. The situation is illustrated in Fig. [15](#). Normalizing by $r$, it is a basic geometric fact that

$$\frac{s}{r} = 1 - \sqrt{1 - \frac{\alpha^2}{r^2}}$$

The distance we must bound, by the Pythagorean theorem is

$$\frac{d}{r} = \sqrt{\left(1 - \sqrt{1 - \frac{\alpha^2}{r^2}}\right)^2 + \frac{\alpha^2}{r^2}}$$
Since $\sqrt{1 - \frac{\alpha^2}{r^2}} \geq 1 - \frac{\alpha^2}{r^2}$ for $0 \leq \frac{\alpha^2}{r^2} \leq 1$

\[
\frac{d}{r} \leq \sqrt{(1 - 1 + \frac{\alpha^2}{r^2})^2 + \frac{\alpha^2}{r^2}} \leq \sqrt{(\frac{\alpha^2}{r^2})^2 + \frac{\alpha^2}{r^2}} \leq \frac{\alpha^4}{r^4} + \frac{\alpha^2}{r^2} \leq \frac{\alpha^2}{r^2} + \frac{\alpha}{r}
\]

Multiplying by $r$, we see that for $\alpha < r$, we see that any simplex (intersection of balls) in $\{\tilde{L}_\alpha\}_{\alpha \in [0,\alpha]}$ will be in $\{\tilde{L}_\alpha - \text{int } B_r\}_{\alpha' \in [0,\alpha]}$ for $\alpha + \frac{\alpha^2}{r} \leq \alpha' \leq r$. We obtained our desired bound.

Finally we prove our main theorem for $\alpha$-filtration.

**Theorem 2.** The persistence module with respect to the Vietoris-Rips filtration of $\{(L_\alpha, L_\alpha)\}$, that is, $\{(\mathcal{R}_\alpha(L), \mathcal{R}_\alpha(\tilde{L}))\}$ is $(2e + \alpha + \frac{\alpha^2}{r})$-interleaved with the $\alpha$-filtration, $\{(\mathcal{X}_\alpha, \mathcal{X}_\alpha - \text{int } B_r)\}$, for $\alpha < r$.

**Proof.** Lemma 5 tells us $\{X_\alpha\}$ and $\{L_\alpha\}$ are $\varepsilon$-interleaved. Lemma 6 shows $N(L_\alpha) \simeq L_\alpha$. Lemma 8 states $\mathcal{X}_\alpha - \text{int } B_r$ and $\mathcal{L}_\alpha - \text{int } B_r$ are 2-$\varepsilon$-interleaved. Lemma 9 shows $N(\tilde{L}_\alpha - \text{int } B_r) \simeq \tilde{L}_\alpha - \text{int } B_r$. Lemma 10 indicates $\{\tilde{L}_\alpha - \text{int } B_r\}$ and $\{\tilde{L}_\alpha\}$ are $\frac{\alpha^2}{r}$-interleaved.

Lemma 8 and 10 implies that $\mathcal{X}_\alpha - \text{int } B_r$ and $\tilde{L}_\alpha$ are $(2\varepsilon + \frac{\alpha^2}{r})$-interleaved. Combined with Lemma 5 we have the relative modules, $\{\mathcal{X}_\alpha, \mathcal{X}_\alpha - \text{int } B_r\}$ and $\{(L_\alpha, \tilde{L}_\alpha)\}$ are $(2e + \frac{\alpha^2}{r})$-interleaved. This means, the persistence diagram of the Čech filtration of $\{(L_\alpha, \tilde{L}_\alpha)\}$ is $(2e + \frac{\alpha^2}{r})$ approximation of the persistence diagram of $\alpha$-filtration.

Now we consider Čech filtrations for both $\{L_\alpha\}$ and $\{\tilde{L}_\alpha\}$, that is, $\{C_\alpha(L)\}$ and $\{C_\alpha(\tilde{L})\}$. Since both are $\alpha$-interleaved with their Vietoris-Rips counterparts, that is, $\{C_\alpha(L)\}$ is $\alpha$-interleaved with $\{\mathcal{R}_\alpha(L)\}$, and $\{C_\alpha(\tilde{L})\}$ is $\alpha$-interleaved with $\{\mathcal{R}_\alpha(\tilde{L})\}$. We lose a factor $\alpha$ in the approximation by switching to Vietoris-Rips filtration of $\{(L_\alpha, \tilde{L}_\alpha)\}$.

**B Discussion on the $r$-filtration**

Here we give a short discussion on the assumptions made in the Section 4 and relate it to existing work. Our primary assumption is an $\varepsilon$-homotopy equivalence between a pair of spaces. This is a strong assumption since it requires that points are only moved a bounded amount in the homotopy, essentially excluding situations illustrated in Fig. 16. Here we define the Euclidean distance function to the point $p$ as $d_p(x) := d(p, x) = ||x - p||$. Now consider $d_p$ restricted to $X$ and
\( X_\alpha \). Although \( X \) could be approximated via a retract from \( X_\alpha \), it is insufficient to guarantee that we could well-approximate the persistence module of \( d_p|_X \) through that of \( d_p|_{X_\alpha} \). In other words, in Fig. 16, the persistence diagram of these persistence modules could differ by at least \( \delta \).

Fig. 16: The space \( X \), its \( \alpha \)-offset \( X_\alpha \) and a point \( p \). Consider the distance function \( d_p \) to \( p \). This is an example where the offset \( X_\alpha \) and space \( X \) are homotopy equivalent but the persistence diagrams of the functions \( d_p|_X \) and \( d_p|_{X_\alpha} \) are potentially far apart.

The problem of approximating a sublevel set filtration of a function on a space has been studied before. The setting is closely related to the results of [20]. In [20], there is an approximation guarantee between a sublevel set filtration of a \( c \)-Lipschitz function on a space and an image persistence filtration on two nested Vietoris-Rips complexes with an appropriately chosen parameter. There are numerous requirements to apply such results, which we outline here.

The first requirement is that we have access to geodesic distances or some provable approximation of it. While the geodesic distance can be inferred from the Euclidean distance in certain cases, this can be a difficult problem depending on how our space is embedded. The second requirement is that the space has positive convexity radius. While this is generally a safe assumption for manifolds; for spaces where local homology yields interesting information, such as stratified spaces, this measure can often be zero (i.e. a cone has zero convexity radius). If, however such requirement is satisfied, we can apply the results in [20] directly. The resulting algorithm is to build the underlying simplicial complex using geodesic distances, which given a sufficiently dense sampling relative to the convexity radius, gives an approximation for any \( c \)-Lipschitz function. Since distance functions are 1-Lipschitz, the approximation results follow.

This highlights a key obstacle in stating sampling results for function filtrations as well as an open problem we discuss below: in terms of which measures should we state sampling results? Is there a global geometric measure which is meaningful for stratified spaces? Are there weaker conditions than \( \varepsilon \)-homotopy for approximating sublevel set behavior? As pointed out above, geometric measures, such as reach or convexity radius can be zero even for nice spaces. It would be preferable to use quantifiers such as homological feature size [25]. Research in these directions is left for future work.