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## **HOMOLOGICAL METHODS FOR SENSOR NETWORK INTEGRITY**

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UNIVERSITY OF CONNECTICUT

*FEBRUARY 2020*

FINAL TECHNICAL REPORT

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# 1 Summary

We have investigated applications of homological methods to coordinate free sensor networks. Specifically, we considered ways to compute global signatures for behaviors observed by a sensor network over time without specific coordinate information. This report gives a high level description of the homological methods we employed, previous experiments on sensor network integrity and topological signatures, and a summary of our most recent work. We found that work on the analysis of scalar fields can be applied directly to the setting of homological sensor networks. This provides a pipeline which first verifies coverage of a domain by a network, then computes a topological signature for some phenomenon observed by the network. Both stages use the same structures computed from the information provided by the sensors. First, a geometric representation of the network is constructed from pairwise proximity information alone in order to verify coverage. Function values which are measured by the sensors can then be superimposed onto this structure in order to compute the signature. Moreover, we investigate situations in which the function changes over time, considering the case in which the network changes between measurements.

## 2 Introduction

In many settings, large networks of sensors collect data. We are studying methods to measure, analyze, visualize, summarize, and compare global behaviors of the network over time. Major challenges include sensor errors, gaps in coverage, and a changing network.

**Homological Sensor Networks** Our work has focused on the **homological sensor network (HSN)** setting. Also known as coordinate-free sensor networks, this model attempts to impose minimal local assumptions on the underlying network. It is well-suited to address the following challenging settings.

- The sensor do not have GPS or other coordinates. They do not know where they are, only which other sensors are nearby (their neighborhood).
- The underlying domain the sensors are intended to cover is unknown. The sensors can detect if they are near the boundary of the domain, but that is all.
- Everything about the network can change from one time to the next including the positions and identities of the sensors. Only the underlying domain and the phenomenon they are measuring is assumed to be constant or changing continuously.

A naive approach to computing signatures or summaries of data collected from such a network, would be to compute statistics from the sensors, say the mean or variance of the collected data. This approach throws out the fundamental information about local neighborhoods that is inherent in the network and reflects the underlying domain. Surprisingly, it's possible to have methods that both reflect shape information (from the local neighborhoods to the global network) and operate without coordinates or geometry.

HSNs address these challenges by integrating data collected locally using the neighborhood information into a single global signature called a *persistence diagram*. These signature are defined in terms of an algebraic topological invariant called (persistent) homology, from whence they derive the name. The homology characterizes the shape in a way that does not depend on how it is situated in space. The persistence diagram then captures aspects of the data that do not depend on positions of the sensors. The only requirement is that the sensors have sufficeint coverage.

Persistence diagrams are a natural choice for data analysis on sensor networks due to several desirable properties.

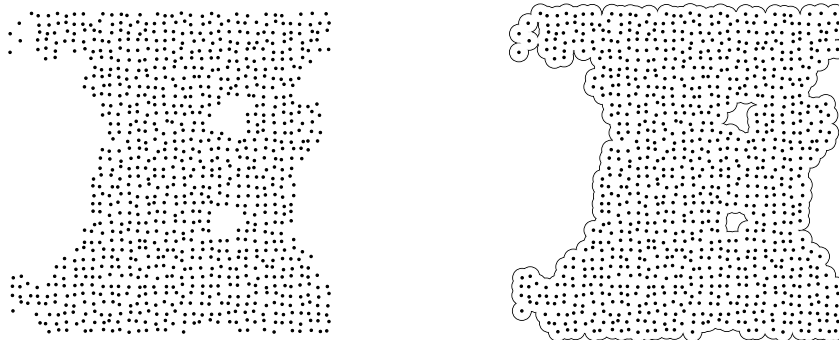
- The persistence diagram uses global shape features rather than coordinates or landmarks to summarize the data.
- The persistence diagram is naturally stable to perturbations in the data.
- The persistence diagram is invariant to continuous (invertible) changes in the underlying domain.
- The persistence diagram from a network with good coverage can be related directly to the ground truth on the domain, and so the specific choice of the sensor locations and the underlying network have a negligible impact on the persistence diagram.
- Persistent homology can even be used to verify coverage in the network. The *Topological Coverage Criterion (TCC)* of de Silva and Ghrist [SG07a] uses persistent homology to verify coverage of an unknown domain by a coordinate-free sensor network, and was extended to weighted  $k$ -coverage in a more general setting in [CGS17].

These advantages bring with them some new challenges that we addressed in this research. Because the signature is using both the measurements and the local neighborhoods defined by the network, there are very distinct reasons why two signatures might differ:

1. The data could be different.
2. The domain could be different.
3. The network could be different.

As a result, the major thrust of our research looked at the relative magnitude of these differences. For example, can we tell if the persistence diagram changed because of a significant change in data or because of a significant change in the underlying network? These issues make it difficult to distinguish network anomalies from meaningful changes in the data.

Another major challenge we address is how to analyze networks that change over time. That is, we want to characterize the behavior of a network in a way that allows us to compare the behavior of a network from one day to the next or to compare one network's measurements over time to that of another network. Constructing a summary of such an event that is both descriptive and discriminative is increasingly difficult when the network is allowed to change over time. Persistent homology is particularly well-suited to this setting as it provides a reliable summary of global behavior from local information alone. This summary is robust to missing data and stable under reasonable changes to the network.



**Figure 1:** A collection of points representing sensors in some domain and the region they cover.

Our initial experiments focused on evaluating the robustness of persistent homology to missing

data and how it could be used to compare data sets. Persistent homology can be computed from a similarity matrix, such as a matrix of pairwise distances between points. In theory, unreliable data should be omitted, because it may appear as a significant feature in the persistence diagram. To this end, we conducted an experiment in which pairwise distances were removed from a sample of a 2-torus, a surface for which the persistent homology is known. We found that even when over 50% of the edges were removed the most significant features remained, with additional features resulting from the missing data presenting as additional noise.

**Stability and its Consequences** A fundamental feature of persistent homology is its stability to small changes in the network. As a result, we can compare diagrams of networks exhibiting similar behavior when they would otherwise be incomparable using traditional methods. We demonstrated one way to express the usefulness of this property using collections of parametric surfaces. The persistence diagrams of random samples of surfaces with different parameters, namely 2-tori with varying radii, were compared and embedded in low dimensional space. We found that the embedding reflected the parameter space from which the tori themselves were constructed, indicating that the persistent homology could be used to expose global structural differences. Moreover, because the metric on persistence diagrams focuses on the most prominent features our experiments on the robustness of persistence diagrams indicates that these these structural differences are still exposed in the presence of missing data.

**Extending the HSN setting** Current work has been focused on applying the observations made in these experiments to sensor network data. This differs from the traditional setting of coverage in homological sensor networks in a fundamental way. Previous work on coverage verification used a pair of neighborhood graphs constructed from sensor proximity data at two scales. Coverage is verified by the homology of the inclusion from one scale into another, which may be seen as a small subset of the persistent homology of the distance to the network. It has been shown that function values (i.e. measurements) on a collection of points which cover some unknown domain can be used to approximate the persistent homology of the function on the entire domain [Cha+09]. Once we have verified coverage, sensor measurements give a reliable signature of the measured event. Persistence stability allows us to aggregate signatures of events occurring over time even when the network is changing, provided coverage is maintained.

Lastly, verifying coverage requires that sensors can detect the boundary of the domain. We are currently investigating how this additional information can be used to compare networks covering distinct domains that observe a common event.

## 2.1 Related Work

Stability results indicate that, under mild sampling conditions, the persistent homology of a sequence of spaces formed from the  $\alpha$ -offsets of a point cloud correspond with the homology of the underlying space [CEH07]. The persistent homology of this sequence can be computed efficiently using the persistence algorithm, first proposed in [ELZ02] for simplicial complexes in  $\mathbb{R}^3$ , and extended to discrete functions over arbitrary finite simplicial complexes in [ZC05]. In [ZC05] it is also shown that the persistent homology of a sequence of spaces can be encoded in a finite set of intervals known as the *persistent barcode* or *diagram*.

Persistent homology was first applied to sensor networks by de Silva & Ghrist over a series of papers [GM05; SG06; SG07b; SG07a]. This work introduces a computable, sufficient condition for coverage of a domain with a smooth boundary by a coordinate-free sensor network network [SG07a].

The theory of so-called homological sensor networks has since been extended to consider robustness of coverage by probabilistic models and  $k$ -coverage [MSH12; CGS17], distributed computation [Dlo+12], and coverage in dynamic settings [JK11; GCK14]. Developments of this theory outside of coverage is limited to work by Adams and Carlsson which considered ways to evade a collection of moving sensors [AC13].

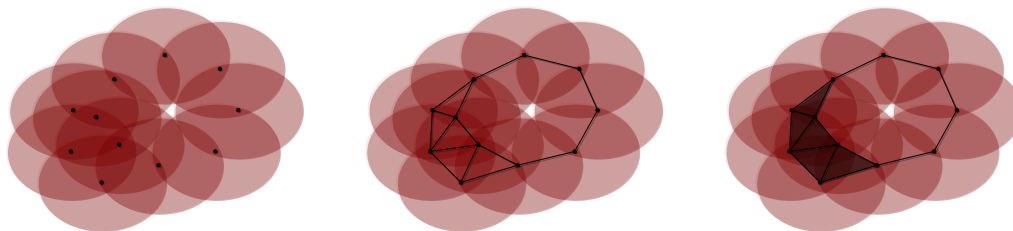
The Topological Coverage Criterion (TCC) applies persistent homology to sensor networks in a limited sense through what may be considered a short filtration, which are generally used as a tool for de-noising data. These short filtrations, which arise from the inclusion of a complex into another at a larger scale, are required in order to eliminate any spurious components that could lead to false positives.

In [CO08] these short filtrations are shown to capture the homology of the underlying space, and applied to the analysis of scalar fields in [Cha+09]. This work considers a setting similar to that of homological sensor networks in which the persistent homology of a function is approximated from its values on a finite sample and the pairwise distances between these points.

In the intersection of coverage in homological sensor networks and the analysis of scalar fields our goal is to compare a collection of unknown domains by the signature of a common function with values given only at a finite sample of points in the domain. We consider a specific class of functions which evolve over time, which arise naturally in the setting of sensor networks. Moreover, we consider classes of known functions in which this same procedure may be used to extract structural information about the domain itself.

### 3 Methods, Assumptions, and Procedures

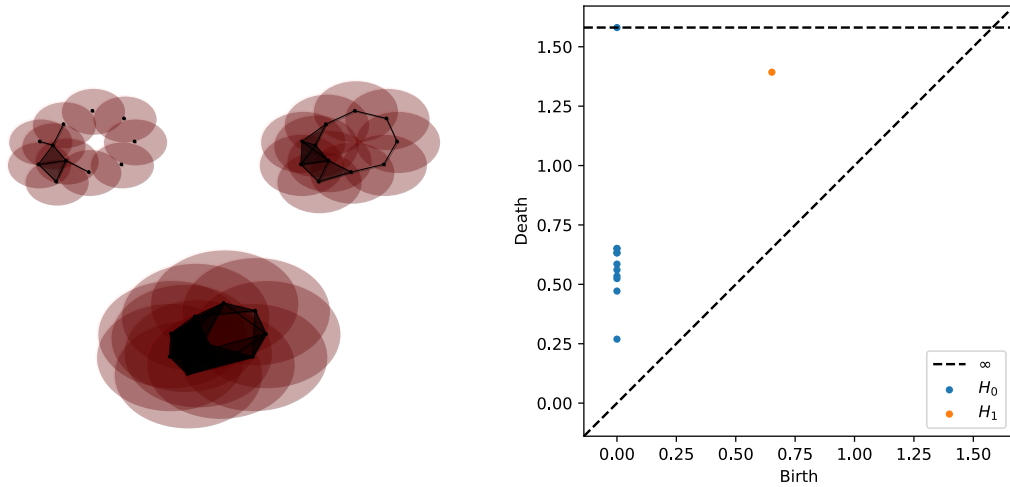
#### 3.1 Topological Data Analysis



**Figure 2:** (Left) The coverage regions of a collection of points  $P$  at some scale  $\alpha$ . (Middle) The neighborhood graph with edges for each pair of points within pairwise distance  $\alpha$ . (Right) If we attempt to fill cycles in the graph with triangles we identify a cycle that cannot be filled which reflects 1-dimensional homological feature, a loop.

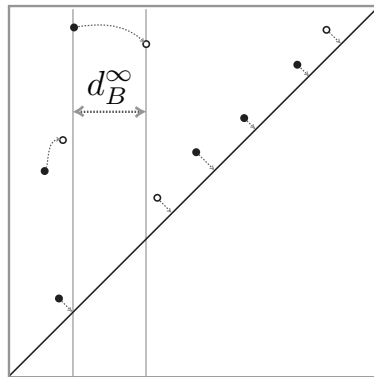
Topological Data Analysis (TDA) is an approach to studying potentially high-dimensional, incomplete, or noisy data by studying its “shape.” The primary assumption is that this data carries relevant geometric and topological information about the “system” from which it has been generated. Homology is a powerful tool from algebraic topology which can be generally understood as a way to measure the components, loops, and voids in a space. Persistent homology is a popular tool in TDA which tracks the evolution of the homology of a space over a range of scales. For example, the homology of a sensor network can be used to detect holes in coverage at a given scale, where scale can be understood as the sensor’s coverage radius.

The key observation motivating the use of homology in coverage verification is that it can be



**Figure 3:** (Left) A filtration of Rips complexes at scales 0.5, 0.7, and 1.4 illustrating a point (0.7, 1.4) in the corresponding 1-dimensional persistence diagram (right, orange). The 1-dimensional feature that is born at scale 0.7 persists until it dies at scale 1.4.

computed without coordinate information. If a network’s sensors can simply detect the presence within some radius a representative structure known as the *(Vietoris-)Rips Complex* can be computed from the resulting neighborhood graph, as shown in Figure 2. As this radius increases, holes in coverage may appear or disappear, giving a topological signature for the network as the sensor’s coverage radius increases. The changes in the homology of the corresponding complex, as shown in Figure 3 (left), can be readily computed and reflect the changes in the coverage region itself. The resulting signature is known as a *persistence diagram*, depicted in Figure 3 (right).



**Figure 4:** The bottleneck distance is given by a matching of points in two diagrams. Points that are considered noise may be matched with the diagonal.

The space of persistence diagrams comes equipped with a metric known as the *bottleneck distance*, depicted in Figure 4. We use the bottleneck distance extensively as a way to compare collections of closely related spaces, such as networks covering the same domain or phenomenon measured by different networks.

### 3.2 Technical Background

**Simplicial Complexes.** A **simplicial complex**  $K$  with vertex set  $V$  is a collection of **simplices**  $\sigma \subset V$  that is closed under taking subsets. We define a **pair of complexes** to be a pair  $(K, L)$  where  $K$  is a simplicial complex and  $L$  is a subcomplex of  $K$ .

Given a metric space  $(X, d)$  we define the  $\varepsilon$ -offsets of a point  $p \in X$  as

$$\text{ball}(p, \varepsilon) = \{x \in X \mid d(x, p) \leq \varepsilon\}.$$

For a subset  $P \subseteq X$  the *nerve* of a family  $\{\text{ball}(p, \varepsilon)\}_{p \in P}$  is the abstract simplicial complex with vertex set  $P$  with simplices corresponding to subsets of elements with nonempty intersections, and is known as the *Čech complex*

$$\check{C}_\varepsilon(P) := \left\{ \sigma \subseteq P \mid \bigcap_{p \in \sigma} \text{ball}(p, \varepsilon) \neq \emptyset \right\}.$$

The **(Vietoris-)Rips complex** of  $P$  at scale  $\varepsilon$  is defined as

$$\text{Rips}_\varepsilon(P) := \{ \sigma \subseteq P \mid \{p, q\} \in \check{C}_\varepsilon(P) \text{ for all } p, q \in \sigma \}.$$

For any metric space  $(X, d)$  the Čech and Rips complexes of a subset  $P \subset X$  are related by the following interleaving for all  $\varepsilon > 0$

$$\check{C}_{\varepsilon/2}(P) \subseteq \text{Rips}_\varepsilon(P) \subseteq \check{C}_\varepsilon(P).$$

**Homology and Persistent Homology.** Homology is a tool from algebraic topology that provides a topological signature for a shape that may be readily computed from a matrix representation of a finite simplicial complex through matrix reduction. The resulting signature is invariant under homeomorphisms and homotopy equivalences, and may be thought of as quantifying the components, loops, and voids in a topological space.

Throughout, we assume singular homology over a field, where the *kth homology group* of a space  $X$  is a vector space denoted  $H_k(X)$ . We will write  $H_*(X)$  to denote the homology of all dimensions. For a pair of spaces  $(X, Y)$  with  $Y \subseteq X$  the *relative homology groups* gives the homology of  $X$  relative to  $Y$ , and are denoted  $H_*(X, Y)$ .

A *filtration* is a sequence of topological spaces  $\mathcal{F} = \{F_\alpha\}_{\alpha \in \mathbb{R}}$  that are nested by inclusions  $F_\alpha \hookrightarrow F_\beta$  for  $\alpha \leq \beta$ . Each inclusion  $F_\alpha \hookrightarrow F_\beta$  induces homeomorphisms between homology groups  $h_*^{\alpha, \beta} : H_*(F_\alpha) \rightarrow H_*(F_\beta)$ . The *persistent homology modules* of  $\mathcal{F}$  are the pairs

$$\mathcal{H}_*(\mathcal{F}) = (\{H_*(F_\alpha)\}_{\alpha \in \mathbb{R}}, \{h_*^{\alpha, \beta}\}_{\alpha \leq \beta \in \mathbb{R}}).$$

The persistent homology modules of a filtration  $\mathcal{F}$  are each given by a signature known as a *persistence diagram*, denoted  $\mathcal{P}_*(\mathcal{F})$ , where  $\mathcal{P}(\mathcal{F})$  is used to refer to the collection of persistence diagrams of all dimensions. Unless otherwise noted we will refer  $\mathcal{P}(\mathcal{F})$  as the persistence diagram of  $\mathcal{F}$ .

The space of persistence diagrams is a metric space  $(\mathbb{P}, \mathbf{d}_B)$  under the *bottleneck distance* which is defined for diagrams  $A, B$ , taken as multisets in  $\mathbb{R}^2$  equipped with the  $l^\infty$ -norm, as

$$\mathbf{d}_B(A, B) = \min_{\gamma: A \rightarrow B} \max_{p \in A} \|p - \gamma(p)\|_\infty$$

where  $\gamma$  ranges over all bijections from  $A$  to  $B$ .

**Stability of Persistent Homology.** Given a topological space  $X$  and a real-valued function  $f : X \rightarrow \mathbb{R}$  the *sublevel-set filtration* of  $f$  is the sequence  $\{X_\alpha^f\}_{\alpha \in \mathbb{R}}$  of sublevel-sets  $X_\alpha^f = f^{-1}(-\infty, \alpha]$ . We define a metric  $\mathbf{d}_{\max}$  between two real-valued functions  $f, g : X \rightarrow \mathbb{R}$  by taking the maximum difference of the functions on any point, i.e.

$$\mathbf{d}_{\max}(f, g) := \max_{x \in X} |f(x) - g(x)|.$$

**Lemma 3.1.** *Let  $X$  be a topological space and  $f, g : X \rightarrow \mathbb{R}$  are tame functions such that  $\mathbf{d}_{\max}(f, g) \leq \varepsilon$ . Then the sublevel-set filtrations  $\{X_\alpha^f\}_{\alpha \in \mathbb{R}}$  of  $f$  and  $\{X_\alpha^g\}_{\alpha \in \mathbb{R}}$  of  $g$  are  $\varepsilon$ -interleaved.*

The following is a standard result in the stability of persistence diagrams.

**Lemma 3.2.** *If two filtrations  $\mathcal{F}$  and  $\mathcal{F}'$  are  $\varepsilon$ -interleaved then*

$$\mathbf{d}_B(\mathcal{P}(\mathcal{F}), \mathcal{P}(\mathcal{F}')) \leq \varepsilon.$$

The persistent homology modules of the sublevel-set filtration  $\{X_\alpha^f\}_{\alpha \in \mathbb{R}}$  are referred to as the persistent homology modules  $\mathcal{H}_*(f)$  of  $f$  with its diagram denoted  $\mathcal{P}(f)$ .

**Corollary 1.** *If  $X$  is a topological space and  $f, g : X \rightarrow \mathbb{R}$  are tame functions then*

$$\mathbf{d}_B(\mathcal{P}(f), \mathcal{P}(g)) \leq \mathbf{d}_{\max}(f, g).$$

**Stability of Relative Persistent Homology.** Let  $(X, Y)$  be a pair of spaces with  $Y \subseteq X$ . For  $f : X \rightarrow \mathbb{R}$  we define a function  $\tilde{f}$  on the pair  $(X, Y)$  as the pair  $(f, f|_Y)$  where  $f|_Y : Y \rightarrow \mathbb{R}$  is the restriction of  $f$  to  $Y$ . The *sublevel-set filtration of  $\tilde{f}$  on the pair  $(X, Y)$*  is the sequence of pairs of sublevel-sets  $\{(X_\alpha^f, Y_\alpha^f)\}_{\alpha \in \mathbb{R}}$  where  $X_\alpha^f = f^{-1}(-\infty, \alpha]$  and  $Y_\alpha^f = f|_Y^{-1}(-\infty, \alpha] = X_\alpha^f \cap Y$  are the sublevel-sets of  $f$  and  $f|_Y$ , respectively.

**Lemma 3.3.** *Let  $X$  be a topological space and  $Y \subseteq X$ . Let  $f, g : X \rightarrow \mathbb{R}$  be tame functions such that  $\mathbf{d}_{\max}(f, g) \leq \varepsilon$ . Then the sublevel-set filtrations  $\{(X_\alpha^f, Y_\alpha^f)\}_{\alpha \in \mathbb{R}}$  of  $\tilde{f}$  and  $\{(X_\alpha^g, Y_\alpha^g)\}_{\alpha \in \mathbb{R}}$  of  $\tilde{g}$  on the pair  $(X, Y)$  are  $\varepsilon$ -interleaved.*

*Proof.* By Lemma 3.1 we have that the sublevel-set filtrations of  $f$  and  $g$  are  $\varepsilon$ -interleaved. Note that, because  $Y \subseteq X$ , we have that  $Y_\alpha^f \subseteq X_\alpha^f$  and  $Y_\alpha^g \subseteq X_\alpha^g$  for all  $\alpha \in \mathbb{R}$ , so the sublevel-set filtrations  $\{Y_\alpha^f\}_{\alpha \in \mathbb{R}}$  of  $g|_Y$  and  $\{Y_\alpha^g\}_{\alpha \in \mathbb{R}}$  of  $f|_Y$  are  $\varepsilon$ -interleaved. It follows that the sublevel-set filtrations  $\{(X_\alpha^f, Y_\alpha^f)\}_{\alpha \in \mathbb{R}}$  of  $\tilde{f}$  and  $\{(X_\alpha^g, Y_\alpha^g)\}_{\alpha \in \mathbb{R}}$  of  $\tilde{g}$  are  $\varepsilon$ -interleaved.  $\square$

The *persistent relative homology modules* of a real-valued function  $\tilde{f}$  on the pair  $(X, Y)$  is a pair consisting of the family of relative homology groups of  $\{(X_\alpha^f, Y_\alpha^f)\}_{\alpha \in \mathbb{R}}$  and the connecting homeomorphisms on relative homology groups induced by inclusions of pairs  $(X_\alpha^f, Y_\alpha^f) \hookrightarrow (X_\beta^f, Y_\beta^f)$ :

$$\mathcal{H}_*(\tilde{f}) = (\{H_*(X_\alpha^f, Y_\alpha^f)\}_{\alpha \in \mathbb{R}}, \{H_*(X_\alpha^f, Y_\alpha^f) \rightarrow H_*(X_\beta^f, Y_\beta^f)\}_{\alpha \leq \beta \in \mathbb{R}}).$$

The corresponding *relative persistence diagram* is denoted  $\mathcal{P}(\tilde{f})$ .

**Lemma 3.4.** *Let  $X$  be a topological space and  $Y \subseteq X$ . If  $f, g : X \rightarrow \mathbb{R}$  are tame functions such that  $\mathbf{d}_{\max}(f, g) \leq \varepsilon$  then*

$$\mathbf{d}_B(\mathcal{P}(\tilde{f}), \mathcal{P}(\tilde{g})) \leq \varepsilon.$$

*Proof.* Because  $\mathbf{d}_{\max}(f, g) \leq \varepsilon$  the sublevel-set filtrations of  $\tilde{f}$  and  $\tilde{g}$  on the pair  $(X, Y)$  are  $\varepsilon$ -interleaved by Lemma 3.3. So, by Lemma 3.2, we have that  $\mathbf{d}_B(\mathcal{P}(\tilde{f}), \mathcal{P}(\tilde{g})) \leq \varepsilon$ .  $\square$

**Corollary 2.** *If  $X$  is a topological space,  $Y \subseteq X$ , and  $f, g : X \rightarrow \mathbb{R}$  are tame functions then*

$$\mathbf{d}_B(\mathcal{P}(\tilde{f}), \mathcal{P}(\tilde{g})) \leq \mathbf{d}_{\max}(f, g).$$

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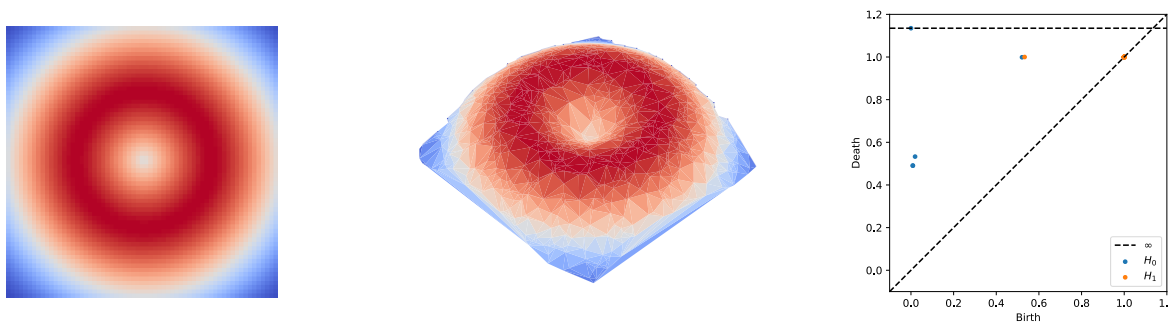
### 3.3 Software Testbed



**Figure 5:** Multiple samples of the same domain with samples close to the boundary in red.

Our implementation of the TCC, which is detailed in our preliminary report, has been extended to the analysis of scalar fields over coordinate-free sensor networks. In particular, we have modified our software to generate domains can be sampled with varying resolution to simulate networks which cover the domain over a range of scales, as seen in Figure 5. Assume we are given such a sequence of networks in addition to a corresponding sequence of sensor measurements taken as a subset of the values of some function over time defined on the domain. We demonstrate a novel signature these time-varying functions that extends the tools used in the TCC to the analysis of scalar fields over time.

Our initial experiments, detailed in the following section, focused on the persistent homology of Rips filtrations constructed from point clouds in euclidean space. This filtration is closely related to the sequence of metric balls growing around the point cloud as the persistent homology of both gives a signature for distance to the point cloud. In particular, the persistent homology of the Rips complex of a point cloud approximates that of the distance to the point cloud as a function on the underlying metric space.



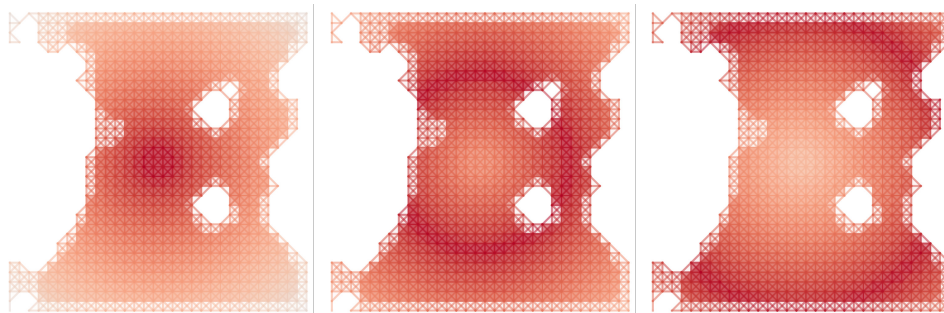
**Figure 6:** (Left) Continuous function on the plane. (Middle) Function values (as  $z$ -axis) on a random sample extended to a simplicial complex. (Right) Persistence diagram of an induced filtration.

More generally, the persistent homology of a real-valued function captures the changes in the homology groups of its *sublevel-sets*—the set of points with function values below a given scale. The

distance to a point cloud is a real-valued function with sublevel-sets equal to the union of metric balls at a given scale. Under certain conditions we can approximate the persistent homology of a real-valued function given only its values on a finite subset of its domain. Figure 6 depicts a function on a subset of the plane and its function values on the simplices of a simplicial complex defined on a subset of the plane. The filtration given by ordering the simplices of this complex by their function values is known as an *induced filtration*. Chazal et. al. detail how to construct a filtration (in fact, the inclusion of two filtrations) that approximates the persistence diagram of the function itself [Cha+09] that has a natural application to measurements by coordinate-free sensor networks. Extending our testbed to explore this result was a natural next step as it assumes coverage and the structures required are a subset of those used in the computation of the TCC. This extension has led to promising results on applications to functions on coordinate-free networks over time as well as interesting theoretical questions on the role of the boundary in these experiments.

A coordinate-free sensor network defined on an unknown, bounded domain consists of a nested pair of neighborhood graphs as well as a nested pair of subgraphs. The vertices of the neighborhood graphs correspond to sensors in the network with edges representing the presence of nearby sensors at two scales. The subgraphs are the restriction of the two neighborhood graphs to sensors close to the boundary of the domain. Moreover, we assume that sensors can measure the value of a real-valued Lipschitz function defined the domain. A measurement made by a sensor corresponds to the function value at the location of that sensor, which remains unknown. Similarly, a sensor network is said to cover a domain at a given scale if the union of metric balls centered at the locations of the sensors includes the domain at that scale.

The proposed setting is a dynamic collection of sensors. Sensors can be moved, added, or deleted but always maintain coverage of the underlying domain at some scale. An event that occurs on the domain is captured by the sensors over time in a sequence of measurements by distinct networks.



**Figure 7:** Function values on a single network over time (top row) and their corresponding persistence diagrams.

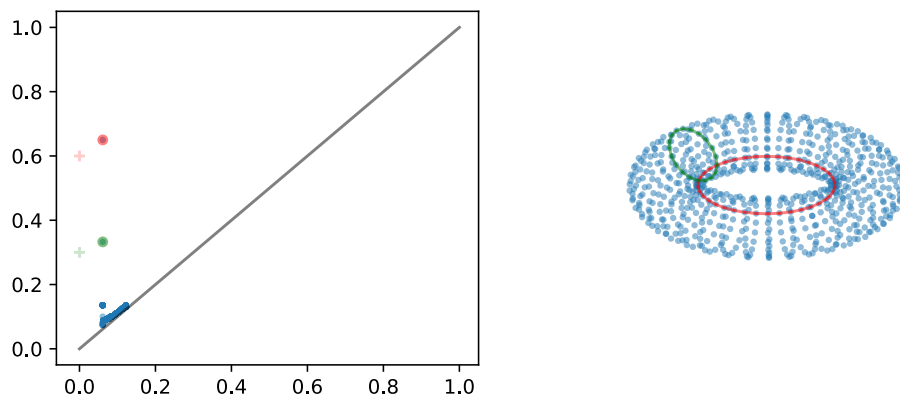
That is, we are given a sequence of coordinate-free sensor networks which all cover some unknown, bounded domain. Each network in the sequence corresponds to a step in time and measures a real-valued Lipschitz function defined on the domain. Rips complexes are constructed from the provided neighborhood graphs and their simplices are reordered to form a sequence of nested pairs of Rips complexes. As in [Cha+09] the persistent homology of this sequence of nested pairs approximates that of the function within a factor proportional to the coverage radius. The resulting sequence of persistence diagrams therefore approximates that of the function over time and traces a curve in persistence space, referred to as a *trajectory signature*, as seen in Figure 12.

## 4 Results and Discussion

### 4.1 Robustness to Incomplete Data

Interpreting sensor network data requires integrating information from multiple sources that may be prone to error. Although most sources may be functioning properly missing data has the potential to corrupt an entire dataset when analyzed with traditional methods. Topological methods, on the other hand, integrate local information in a way that is robust to missing data. This property was one of the original motivations for the use of persistent homology in the study of data. In particular, the stability theorem states that the persistent homology of the filtered Vietoris-Rips complex built from a point cloud is robust to slight perturbation of the points.

In order to test the extent of this stability we investigated the effect of gaps in the pairwise similarity matrix used to construct the complex. Such a situation may arise as the result of a missing, corrupted, or untrustworthy measurement, or as a result of intentional sparsification or subsampling of the similarity matrix.

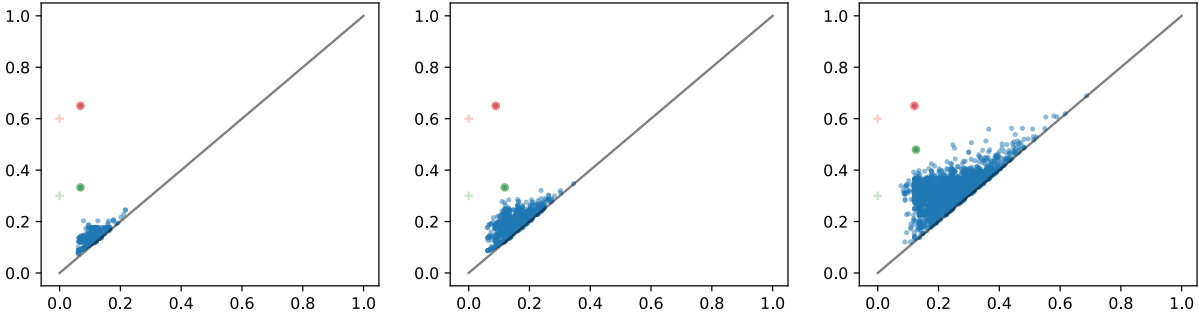


**Figure 8:** Persistent features of 722 uniformly spaced points sampled from  $T$ . The green and red + markers represent expected features at  $r = 0.3$  and  $R - r = 0.6$  respectively.

The goal was to assess the impact of missing data by identifying subsets of the complete graph that provide a good approximation to the persistence diagram of the complete graph. Our initial tests investigated the effects of removing edges from the complete graph of a 2-Torus both at random, as well as from a uniform distribution. Figure 8 shows the persistence diagram of Vietoris-Rips complex on the complete neighborhood graph of a 2-torus, as well as the representative cycles corresponding to the two most prominent features. Figure 9 shows the persistence diagrams of the same torus with 25%, 50%, and 75% of edges removed at random.

### 4.2 Embeddings of Persistence Diagrams

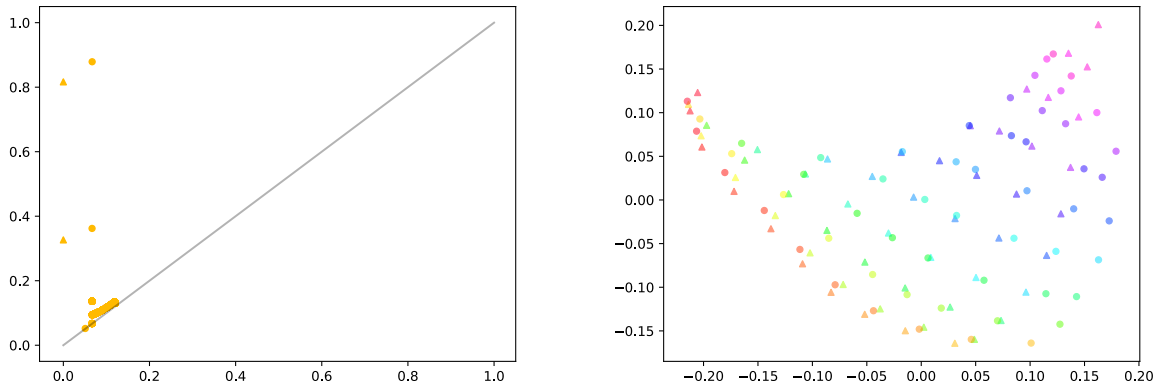
Often data that is collected in some high dimensional space has a far lower intrinsic dimension. Moreover, the same event may be measured in different ways that renders two measurements incomparable, despite similar fundamental structure. Persistent homology has been shown to be a useful tool for studying point clouds that are sampled from a single unknown space in order to learn something about this structure. We instead considered collections of point clouds sampled from a family of related spaces defined by a so-called parameter space. Our hypothesis was that



**Figure 9:** Persistence diagrams of 722 uniformly spaced points sampled from a 2-torus with 25%, 50%, and 75% of the edges removed at random.

we could use the bottleneck distance to embed the diagrams of this family of spaces in order to learn something about the structure of the underlying parameter space. Specifically, we used Multidimensional Scaling (MDS) to embed collections of persistence diagrams in low-dimensional space.

We also formalized the notion of parametric families of spaces and attempted to characterize those with common topological structure. Namely, Tori, Spheres, and Klein bottles. Our goal was to relate this structure to that of the parameter space by first developing a theory on the spaces themselves.



**Figure 10:** (Left) Ideal barcode (triangles) and sampled barcode (circles) of a 2-torus parameterized by  $(0.2, 0.7)$ . (Right) 2D MDS embedding of the pairwise bottleneck distances between 110 ideal (triangles) and sampled (circles) barcodes.

Figure [10](#) shows an ideal (triangle markers) and sampled (circle markers) persistence diagram, and the 2D MDS embeddings of a collection 110 diagrams with varying major and minor radii. This suggests that diagrams of sampled tori may be used to recover their corresponding radii by comparison with their expected diagrams in the embedding.

This initial experiment on parametric families of shapes is closely related to our current research in a fundamental way. Instead of collections of closely related shapes, we use this same embedding technique to study collections of measurements by one or many networks. The resulting collection of persistence diagrams traces a collection of curves in persistence space in the same way a parametric

family of tori traces out its parameter space. Our hope is that this technique can be used to quantify changes in a network, or a some phenomenon observed by the network in the same way it can be used to recover the parameters in this experiment.

### 4.3 Stability of Trajectories

The existing work on the stability of persistence diagrams can be used to show that a continuous function  $f : X \times [0, 1] \rightarrow \mathbb{R}$  traces out a continuous path through persistence space. For such a function  $f$  and  $f_t = f(\cdot, t)$  we define this trajectory as  $\mathbb{T}_f : [0, 1] \rightarrow \mathbb{P}$ , where

$$\mathbb{T}_f(t) := \mathcal{P}(f_t).$$

We define a metric on trajectories though  $\mathbb{P}$  as the maximum distance between diagrams for  $t \in [0, 1]$ . That is, for  $f, g : X \times [0, 1] \rightarrow \mathbb{R}$  the distance between trajectories  $\mathbb{T}_f, \mathbb{T}_g : [0, 1] \rightarrow \mathbb{P}$  is

$$\mathbf{d}_{\max}(\mathbb{T}_f, \mathbb{T}_g) = \max_{t \in [0, 1]} \mathbf{d}_B(\mathbb{T}_f(t), \mathbb{T}_g(t)).$$

**Theorem 4.1.** *Let  $X$  be a topological space. If  $f, g : X \times [0, 1] \rightarrow \mathbb{R}$  are tame for all  $t \in [0, 1]$  then*

$$\mathbf{d}_{\max}(\mathbb{T}_f, \mathbb{T}_g) \leq \mathbf{d}_{\max}(f, g).$$

*Proof.* It suffices to employ Corollary [1](#) and the definitions as follows.

$$\mathbf{d}_{\max}(\mathbb{T}_f, \mathbb{T}_g) = \max_{t \in [0, 1]} \mathbf{d}_B(\mathcal{P}(f_t), \mathcal{P}(g_t)) \leq \max_{t \in [0, 1]} \mathbf{d}_{\max}(f_t, g_t) = \mathbf{d}_{\max}(f, g)$$

□

This result is easily extended to the relative setting. For a topological space  $X$  and a subset  $Y \subseteq X$  and  $f : X \times [0, 1] \rightarrow \mathbb{R}$  and a function  $\tilde{f} = (f, f|_Y)$  on the pair  $(X, Y)$  let  $\tilde{f}_t = \tilde{f}(\cdot, t)$  be the pair  $(f_t, f_t|_Y)$  where, for all  $t \in [0, 1]$ ,  $f_t|_Y : Y \rightarrow \mathbb{R}$  is the restriction of  $f_t$  to  $Y$ . We define the trajectory of  $\tilde{f}$  on the pair  $(X, Y)$  as  $\mathbb{T}_{\tilde{f}} : [0, 1] \rightarrow \mathbb{P}$ , where

$$\mathbb{T}_{\tilde{f}}(t) := \mathcal{P}(\tilde{f}_t).$$

**Theorem 4.2.** *Let  $X$  be a topological space and  $Y \subseteq X$ . If  $f, g : X \times [0, 1] \rightarrow \mathbb{R}$  are tame for all  $t \in [0, 1]$  then*

$$\mathbf{d}_{\max}(\mathbb{T}_{\tilde{f}}, \mathbb{T}_{\tilde{g}}) \leq \mathbf{d}_{\max}(f, g).$$

*Proof.* The proof is the same as Theorem [4.1](#) with Lemma [3.4](#)

$$\mathbf{d}_{\max}(\mathbb{T}_{\tilde{f}}, \mathbb{T}_{\tilde{g}}) = \max_{t \in [0, 1]} \mathbf{d}_B(\mathcal{P}(\tilde{f}_t), \mathcal{P}(\tilde{g}_t)) \leq \max_{t \in [0, 1]} \mathbf{d}_{\max}(f_t, g_t) = \mathbf{d}_{\max}(f, g)$$

□

### 4.4 Working with Samples

The stability of trajectories (Theorem [4.1](#)) gives a theoretical guarantee under the assumption that one can really compute the persistence diagram of the given function. However, our knowledge of the function  $f_t$  is limited. We only know the value at some finite set of points. These points can be thought of as the sensors in a network or simply as a sample of the domain of the function. In this section, we will show how to build a discrete approximation to  $f_t$  so that one can compute the

persistence diagram. An important feature of this approximation is that it comes with a guarantee with respect to the approximation error. This will be leveraged into an approximation guarantee for the discrete trajectory signatures.

We will make the following relatively standard sampling assumptions.

1. The set  $P \subset D$  of points is an  $\varepsilon$ -sample of the domain  $D$  in the sense that for all  $x \in D$ , there is a sample  $p \in P$  such that  $\mathbf{d}(x, p) \leq \varepsilon$ .
2. The function  $f$  is  $c$ -Lipschitz for some constant  $c$ .

Recall that real-valued a function on a metric space is  $c$ -Lipschitz if for all  $x, y$ , we have

$$f(x) \leq f(y) + c\mathbf{d}(x, y).$$

These assumptions give a natural way to guarantee that the sample is sufficiently dense to capture the main features of the function. They may be understood as a generalization of the Nyquist sampling rate in signal processing.

The first step is to approximate the function  $f$  using another function that is only defined with respect to the sample  $P$  and the metric. Under the sampling and Lipschitz assumptions above, there is an easy way to define an upper bound on  $f$ , the maximum  $c$ -Lipschitz extension:

$$\hat{f}(x) = \min_{p \in P} f(p) + c\mathbf{d}(p, x).$$

We use the known values of  $f$  at the points of  $P$  to define  $\hat{f}(x)$ . Despite the min in the definition, this is the “maximum extension”, because it is pointwise greater than or equal to any other  $c$ -Lipschitz function that agrees with  $f$  on the points of  $P$ . The following standard fact gives the approximation guarantee in terms of  $\mathbf{d}_{\max}$  as is used in the persistence stability theorem.

**Lemma 4.1.** *If  $P \subset D$  is an  $\varepsilon$ -sample and  $f : D \rightarrow \mathbb{R}$  is  $c$ -Lipschitz, then,*

$$\mathbf{d}_{\max}(\hat{f}, f) \leq 2c\varepsilon.$$

*Proof.* For any  $x \in D$ , by definition, there is a point  $p \in P$  such that

$$\hat{f}(x) = f(p) + c\mathbf{d}(x, p).$$

The function  $f$  is  $c$ -Lipschitz, so

$$f(p) \leq f(x) + c\mathbf{d}(p, x),$$

and thus,

$$\hat{f}(x) \leq 2c\mathbf{d}(x, p).$$

By the  $\varepsilon$ -sampling assumption  $\mathbf{d}(x, p) \leq \varepsilon$ , so

$$\hat{f}(x) \leq f(p) + c\varepsilon.$$

It follows that  $\hat{f}(x) - f(x) \geq 2c\varepsilon$ .

On the other hand, using the same facts as above, we get the following bound.

$$f(x) - \hat{f}(x) \leq f(p) + c\mathbf{d}(x, p) - \hat{f}(x) \tag{1}$$

$$\leq (f(p) + c\mathbf{d}(x, p)) - \hat{f}(p) + c\mathbf{d}(x, p) \tag{2}$$

$$\leq f(p) - \hat{f}(p) \tag{3}$$

$$\leq 0. \tag{4}$$

□

An immediate corollary is that the maximum  $c$ -Lipschitz extension has a persistence diagram that is close to that of the original function.

**Corollary 3.** *If  $P \subset D$  is an  $\varepsilon$ -sample and  $f : D \rightarrow \mathbb{R}$  is  $c$ -Lipschitz, then,*

$$\mathbf{d}_{\max}(\mathbb{T}_f, \mathbb{T}_g) \leq 2c\varepsilon.$$

The role of the constants in this result should be clear. As you sample more densely, the approximation gets correspondingly tighter.

The approximation now needs to be discretized to allow for computation. This can be done by observing that the sublevels of  $\hat{f}$  are unions of metric balls. Let  $\text{ball}(c, r)$  denote the metric ball with center  $c$  and radius  $r$ . If  $r < 0$ , we define  $\text{ball}(c, r)$  to be the empty set.

**Lemma 4.2.** *Let  $\hat{f}$  be the  $c$ -Lipschitz extension of a function  $f : D \rightarrow \mathbb{R}$  on a points set  $P$ . Then, for all  $\alpha \in \mathbb{R}$ ,*

$$X_{\alpha}^{\hat{f}} = \bigcup_{p \in P} \text{ball}\left(p, \frac{\alpha - f(p)}{c}\right)$$

*Proof.* For any  $x \in X_{\alpha}^{\hat{f}}$ , we know that for some  $p \in P$ ,

$$f(p) + c\mathbf{d}(x, p) = \hat{f}(x) \leq \alpha.$$

It follows that

$$\mathbf{d}(x, p) \leq \frac{\alpha - f(p)}{c},$$

and thus

$$x \in \text{ball}\left(p, \frac{\alpha - f(p)}{c}\right) \subseteq \bigcup_{p \in P} \text{ball}\left(p, \frac{\alpha - f(p)}{c}\right).$$

To prove the other inclusion, let  $x$  be a point in the union of balls. Let  $q \in P$  be the center of any one of these balls containing  $x$ . We can now see that

$$\hat{f}(x) = \min_{p \in P} f(p) + c\mathbf{d}(x, p) \leq f(q) + c\mathbf{d}(x, q) \leq f(q) + c\left(\frac{\alpha - f(q)}{c}\right) = \alpha. \quad (5)$$

So,  $x \in X_{\alpha}^{\hat{f}}$  as desired.  $\square$

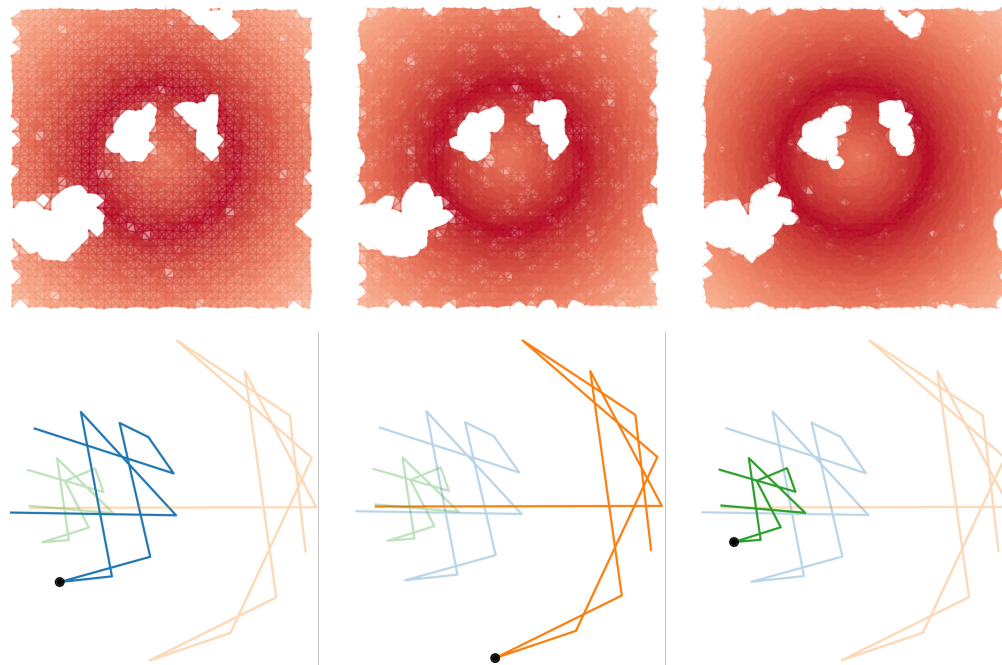
We will add one more assumption, namely that intersections of metric balls are contractible or empty. This is easily satisfied in Euclidean space and in many other natural spaces to consider. This topological condition is required to use the so-called Persistent Nerve Lemma to relate unions of metric balls to a discrete simplicial complex. For the most common case where the balls all have equal radii, the Nerve construction is the Čech complex. We can define a generalized Čech for any set  $B$  of balls as follows.

$$\check{C}(B) := \left\{ \sigma \subseteq B \mid \bigcap_{b \in \sigma} b \neq \emptyset \right\}.$$

There is also a generalized Vietoris-Rips complex defined to include all the cliques in the graph whose edges are in  $\check{C}(B)$ . The advantage of using a filtration based on the Vietoris-Rips complex is that there is no need to do any computations on the underlying domain. Only pairwise distances are needed. Moreover, there is substantial optimized code to compute the persistence diagrams of such filtrations. This is the complex we used to do produce the following experiments.

## 4.5 Trajectory Signatures

Throughout, the time-varying function used is the distance to a ring in the plane with increasing radius. The function values on simplices of a network are depicted by color in Figure 7. Reordering these simplices by function value gives a filtration for each time step.

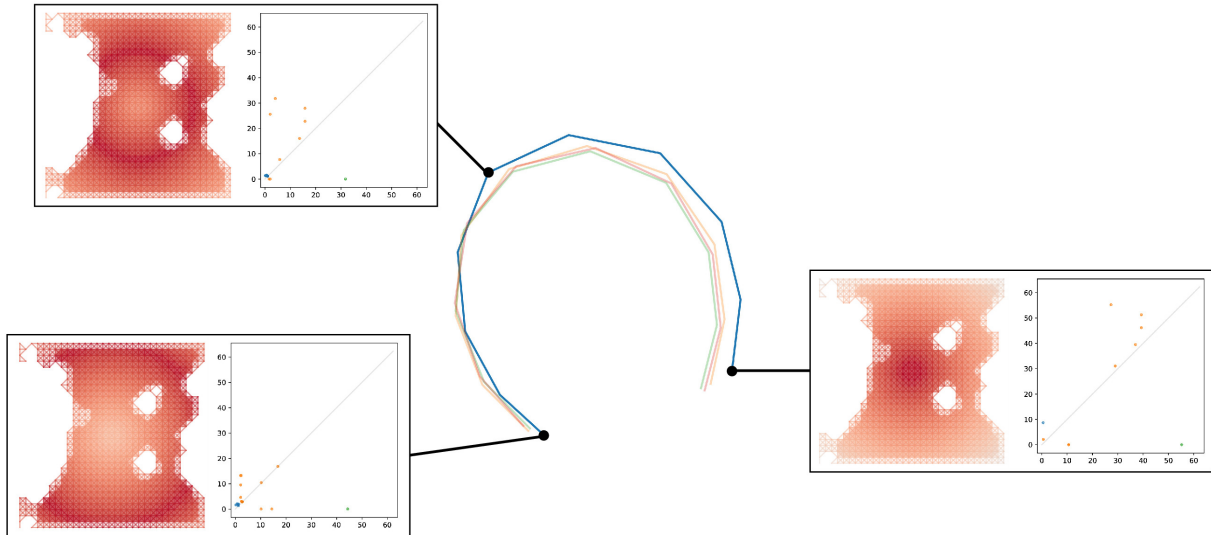


**Figure 11:** (Top) Function values on three different networks that cover the same domain with at a single time step. (Bottom) Trajectories of the function on the networks computed without boundary information. The black the point corresponds to the point on the curve corresponding to the time step shown.

**When is information about the boundary needed?** Our software was first applied to time-varying functions on domains without any information about the boundary of the domain. Although the resulting signatures were sensitive to changes in the function we found that they were too sensitive to features of the network. Moreover, the trajectories did not appear to reflect the simple structure of the function as demonstrated in previous experiments. This can be seen in Figure 11 which depicts three curves of the same function on three different networks covering the same domain. The curves represent three very different signatures as a result of noise in the individual networks and a general lack of persistent features due to obstruction by features of the domain. Because information about the boundary is required in order to verify coverage using the TCC we then considered how this additional information could be used to account for known features of the domain.

**What do we learn when the boundary is needed?** Our algorithm was modified to use information about the boundary of the domain instead computing the persistent homology of the function relative to the restriction to the boundary. Our hope was that, by accounting for known features of the domain captured by the boundary we could direct the focus of the signature to the features of the function. The results, as depicted in Figure 12, show that this modification

yields signatures that are stable to changes in the domain while also reflecting the behavior of the observed function. The curves seem to follow a common path, unlike those in Figure 11, indicating that information about a common boundary yields a signature stable to changes in the network. However, it is possible that these signatures are a result of too much dependence on the function and tell us nothing about the domain.



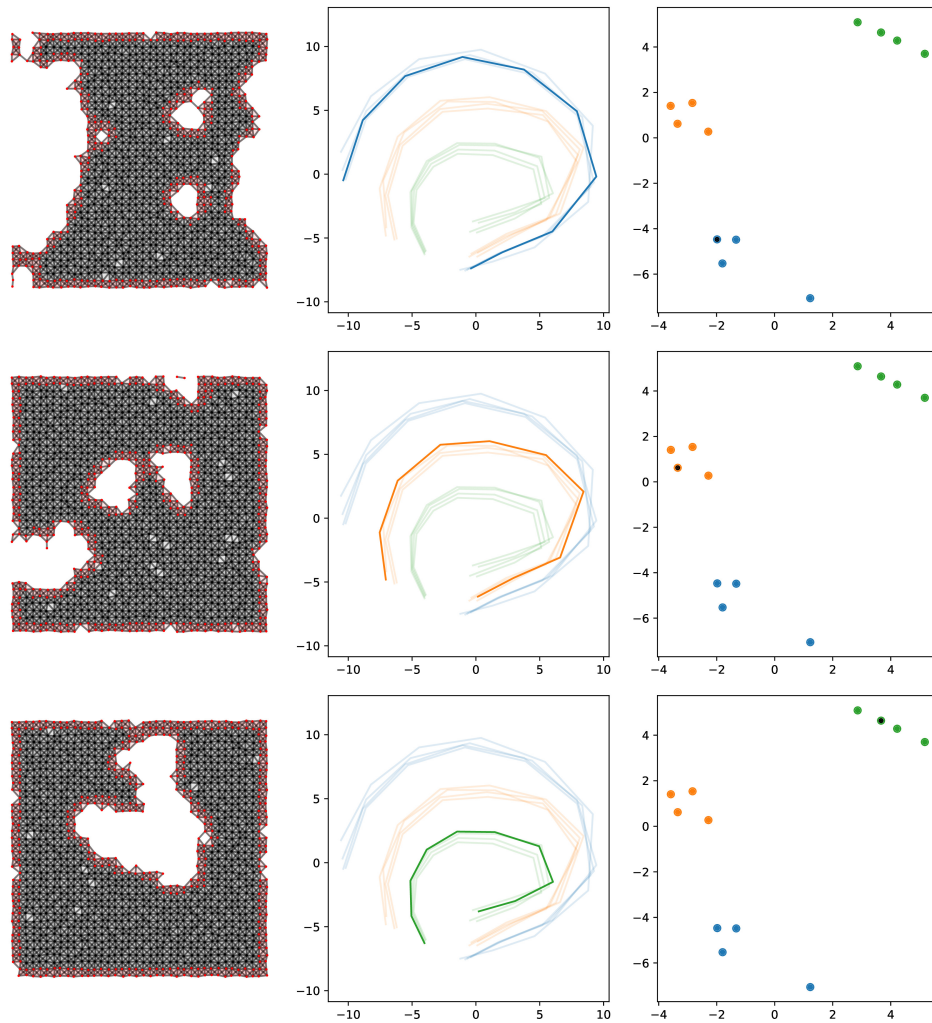
**Figure 12:** A collection of overlaid trajectories from different networks. For three time steps of one of these trajectories the function values on the corresponding networks and resulting persistence diagrams are shown.

**What can we learn about the domain?** To eliminate the possibility that this signature is dominated by the topology of the function we applied the same process to the same function applied to multiple domains. We found that the resulting trajectories clustered into distinct groups, indicating that changes in the domain are clearly reflected, as seen in Figure 13. This suggests that the signature is sufficiently discriminative, and may therefore be useful for detecting changes in the domain.

## 5 Conclusions

Through our preliminary experiments we discovered a natural application of persistent homology in the intersection of homological sensor networks and the analysis of time-varying functions. In particular, we considered an event observed by a network that covers some unknown domain that is changing over time. Each measurement of the event by the network, formalized as a sample of some function on the domain, is integrated and summarized by the persistence diagram of the function as “seen” by the network. This allows us to compare global behaviors of the network over time in a way that is robust to missing data as well as changes in the network.

We found that applying the machinery used to confirm coverage by a coordinate-free network can be applied to the analysis of scalar fields on these networks. In particular, we propose a signature for time-varying functions on coordinate-free networks that is stable to changes in the network.



**Figure 13:** (Left column) networks constructed from samples of 3 distinct domains corresponding to blue (top), orange (middle), and green curves/points in the following. (Middle column) A low-dimensional embedding of curves drawn by the same function on each domain. (Right column) An embedding of the maximum distance between curves for each network.

The extension of scalar field analysis to bounded domains alone is an interesting direction for future theoretical work. Preliminary work indicates that this requires formalizing fundamental results in algebraic topology to the persistent homology of functions on pairs of spaces. This work may lead to useful theoretical guarantees assuming the conditions in [CGS17].

Another future direction is to look at more interesting time-varying functions such as heat flow and real-world sensor data. Lastly, Figure 13 indicates potential for these signatures as a way to identify changes in the domain or as tool for the “fuzzy” classification of spaces parameterized by a function.

## References

- [ELZ02] Edelsbrunner, Letscher, and Zomorodian. “Topological Persistence and Simplification”. In: *Discrete & Computational Geometry* 28.4 (Nov. 2002), pp. 511–533. ISSN: 1432-0444. DOI: [10.1007/s00454-002-2885-2](https://doi.org/10.1007/s00454-002-2885-2). URL: <https://doi.org/10.1007/s00454-002-2885-2>.
- [GM05] Robert Ghrist and Abubakr Muhammad. “Coverage and Hole-detection in Sensor Networks via Homology”. In: *Fourth International Conference on Information Processing in Sensor Networks (IPSN’05), UCLA*. 2005, pp. 254–260.
- [ZC05] Afra Zomorodian and Gunnar Carlsson. “Computing Persistent Homology”. In: *Discrete & Computational Geometry* 33.2 (Feb. 2005), pp. 249–274. ISSN: 1432-0444. DOI: [10.1007/s00454-004-1146-y](https://doi.org/10.1007/s00454-004-1146-y). URL: <https://doi.org/10.1007/s00454-004-1146-y>.
- [SG06] Vin De Silva and Robert Ghrist. “Coordinate-free Coverage in Sensor Networks with Controlled Boundaries via Homology”. In: *International Journal of Robotics Research* 25 (2006), pp. 1205–1222.
- [CEH07] David Cohen-Steiner, Herbert Edelsbrunner, and John Harer. “Stability of Persistence Diagrams”. In: *Discrete & Computational Geometry* 37.1 (Jan. 2007), pp. 103–120. ISSN: 1432-0444. DOI: [10.1007/s00454-006-1276-5](https://doi.org/10.1007/s00454-006-1276-5). URL: <https://doi.org/10.1007/s00454-006-1276-5>.
- [SG07a] Vin de Silva and Robert Ghrist. “Coverage in Sensor Networks via Persistent Homology”. In: *Algebraic & Geometric Topology* 7 (2007), pp. 339–358.
- [SG07b] Vin de Silva and Robert Ghrist. “Homological Sensor Networks”. In: *Notices Amer. Math. Soc.* 54.1 (2007), pp. 10–17.
- [CO08] Frédéric Chazal and Steve Yann Oudot. “Towards Persistence-based Reconstruction in Euclidean Spaces”. In: *Proceedings of the Twenty-fourth Annual Symposium on Computational Geometry*. SCG ’08. College Park, MD, USA: ACM, 2008, pp. 232–241. ISBN: 978-1-60558-071-5. DOI: [10.1145/1377676.1377719](http://doi.acm.org/10.1145/1377676.1377719). URL: <http://doi.acm.org/10.1145/1377676.1377719>.
- [Cha+09] F. Chazal et al. “Analysis of Scalar Fields over Point Cloud Data”. In: *Proc. 19th ACM-SIAM Sympos. on Discrete Algorithms*. 2009, pp. 1021–1030.
- [JK11] Harish Chintakunta Jennifer Gamble and Hamid Krim. “Applied Topology in Static and Dynamic Sensor Networks”. In: *Signal Processing and Communications (SPCOM), 2012 International Conference* (2011), pp. 1–5.
- [Dło+12] Paweł Dłotko et al. “Distributed computation of coverage in sensor networks by homological methods”. In: *Applicable Algebra in Engineering, Communication and Computing* 23 (2012), pp. 29–58. DOI: [10.1007/s00200-012-0167-7](https://doi.org/10.1007/s00200-012-0167-7).

- [MSH12] Elizabeth Munch, Michael Shapiro, and John Harer. “Failure Filtrations for Fenced Sensor Networks”. In: *International Journal of Robotics Research* (2012).
- [AC13] Henry Adams and Gunnar Carlsson. “Evasion Paths in Mobile Sensor Networks”. In: *International Journal of Robotics Research* 34 (2014) (2013), pp. 90–104.
- [GCK14] Jennifer Gamble, Harish Chintakunta, and Hamid Krim. “Coordinate-Free Quantification of Coverage in Dynamic Sensor Networks”. In: *CoRR* abs/1411.7337 (2014). URL: <http://arxiv.org/abs/1411.7337>.
- [CGS17] Nicholas J. Cavanna, Kirk P. Gardner, and Don Sheehy. “When and Why the Topological Coverage Criterion Works”. In: *SODA*. 2017.

## List of Acronyms

**HSN** Homological Sensor Network.

**MDS** Multidimensional Scaling.

**TCC** Topological Coverage Criterion.

**TDA** Topological Data Analysis.